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Biodiversity Loss by Interspecific Hybridization and Invasive Species

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Résumé

Les conséquences diverses de la rupture des barrières reproductives entre espèces, menant à l’hybridation interspécifique, sont d’un intérêt croissant en écologie et en évolution. Le rôle de l’hybridation dans l’histoire évolutive des organismes a été mis en évidence grâce aux développements des outils moléculaires. Cela a alerté les biologistes de la conservation sur la menace que ce phénomène peut représenter sur la biodiversité lorsqu’elle est provoquée par des facteurs anthropiques, comme l’introduction des espèces invasives et la modification de l’habitat. Dans ma thèse, j’explore l’ampleur des conséquences que l’hybridation peut produire autant dans la perspective de la biologie de la conservation que de l’évolution. Mon principal objectif est d’explorer l’impact de l’hybridation interspécifique sur la diversité des organismes grâce au développement des nouvelles approches de modélisation qui intègrent des facteurs naturels et anthropiques.

Pendant ma recherche, j’ai donc créé des modèles qui permettent de mieux évaluer les risques d’extinction et les opportunités évolutives induites par l’hybridation. Pour cela, j’ai d’abord identifié trois types d’hybridation définis par les propriétés reproductives des hybrides de la première génération (F_1 , chapitre 1). Ensuite, je les ai utilisés comme base guidant les développements des approches par modélisation pour déterminer les effets démographiques et génétiques de l’hybridation. Le premier type d’hybridation est défini par une progéniture F_1 non-viable ou infertile, laquelle est souvent observée dans les cas d’hybridation entre espèces évolutivement éloignées. Dans le chapitre 2, je démontre que ce type d’hybridation représente une menace démographique dû à une extrême dépression hybride, provoquant de sérieux risques d’extinction pour les espèces rares qui se reproduisent avec des espèces plus abondantes, tout comme pour les espèces déjà menacées. Le deuxième type d’hybridation, aussi fréquemment observé entre les espèces évolutivement éloignées, est caractérisé par la production d’hybrides F_1 fertiles, qui excluent le génome d’une espèce parentale pendant la gamétogénèse, produisant des gamètes clonales. Dans les chapitres 3 et 4, je démontre que ce type d’hybridation peut faciliter l’invasion d’espèces par la production de gamètes clonaux qui contiennent le génome invasif (chapitre 3). Le risque d’extinction n’est pas conduit génétiquement mais il est déterminé par le « flux démographique » entre espèces parentales, géré par la progéniture hybride. Dans le chapitre 4, je démontre en outre que ce type d’hybridation demeure un risque sous-estimé pouvant amener à l’extinction d’une espèce très rapidement. Par conséquent, il est urgent de considérer ce type d’hybridation dans les stratégies de conservation. Finalement, le

troisième type d'hybridation est défini par la production d'hybrides F_1 fertiles menant à l'introgression génétique entre les espèces parentales. Dans le chapitre 5, je montre que ce type d'hybridation peut être à la fois une menace génétique et démographique pour les organismes natifs qui se trouvent face à une espèce invasive plus compétitive, mais il peut aussi augmenter la diversité génétique de ces organismes et offrir de nouvelles opportunités évolutives. J'ai également fait des simulations spatialement explicites avec le troisième type d'hybridation, afin de considérer la dynamique spatiale des populations (i.e. localisation géographique et migration). Cela est important pour déterminer les conséquences écologiques et génétiques des espèces invasives qui étendent leur aire de distribution géographique et se reproduisent avec des espèces locales. Dans le chapitre 6, j'ai amélioré les modèles d'hybridation incorporés dans SPLATCHE 2, un programme permettant de simuler la diversité génétique dans un contexte spatialement explicite. J'ai contribué à la validation d'une observation préliminaire où l'on attend une introgression plus élevée chez les espèces invasives que chez les espèces locales avec lesquelles elles se reproduisent. Ces résultats montrent que ce phénomène est dû au déséquilibre démographique initial, et aux gènes surfant sur la vague d'expansion spatiale. Dans le chapitre 7, je présente deux nouveaux modèles de dispersion spatiale que j'ai développés pour incorporer les comportements cognitifs et l'histoire de colonisation des espèces plus territoriales ou au contraire plus sociales. Je confirme que la conclusion préliminaire d'une plus grande introgression chez les espèces invasives représente un attendu générale pour les gènes neutres, quel que soit son mode de dispersion spatiale. J'ai également montré que ces modèles ont le potentiel de mieux expliquer l'histoire de l'hybridation et d'améliorer la projection des scénarios futurs.

Le développement des différentes approches de modélisation que j'ai appliquées à plusieurs sujets d'études (poissons, amphibiens, oiseaux, mammifères et humains) m'a permis de distinguer les divers effets de l'hybridation sur la biodiversité. A la fin de ma recherche doctorale, j'ai été capable d'établir les conditions sous lesquelles les trois types d'hybridation peuvent représenter soit des priorités pour les programmes de conservation, soit des nouvelles opportunités évolutives (chapitre 8). Je souligne que l'hybridation peut certainement produire la perte de biodiversité quand elle est liée à des facteurs humains, notamment à travers la dépression hybride où l'introgression de gènes délétères, mais elle peut aussi conduire à l'émergence de nouvelles biodiversités et à des opportunités d'adaptation aux changements climatiques.

Abstract

The various consequences of the breakdown of reproductive barriers between distinct species, leading to interspecific hybridization, are of growing concern in ecology and evolution. The role of hybridization in the evolutionary history of organisms has been recognized in the light of newly developed molecular tools. This has also alerted biologists about the threat that this phenomenon may represent on biodiversity when it is enhanced by anthropogenic factors, such as the introduction of invasive species or habitat modifications. In my PhD research project I explore the large range of outputs that hybridization may produce from both conservation and evolutionary biology perspectives. My main aim is to investigate the impact of interspecific hybridization on the diversity of organisms through the development of novel modelling approaches that integrate natural and anthropogenic factors. During my PhD research, I thus developed original models that allow to better evaluate the extinction risk or the evolutionary opportunities brought by hybridization.

To reach this objective, I first identified three types of hybridization defined by the reproductive properties of the first generation (F_1) hybrids (Chapter 1). I used them as a framework to investigate the demographic and genetic effects of hybridization, thus guiding the development of my modelling approaches. The first type of hybridization is defined by the production of inviable or infertile F_1 offspring, which is often observed for hybridization between distantly-related species. In the Chapter 2 of this thesis, I show that this type of hybridization represents a demographic threat due to an extreme outbreeding depression, driving serious extinction risk for species either with small population sizes and interbreeding with more abundant species, or those species that are already threatened. The second type of hybridization, also frequently found among distantly-related species, is characterized by the production of fertile F_1 hybrids but which are undergoing genome exclusion during their gametogenesis, producing clonal or hemiclonal offspring. In Chapters 3 and 4, I demonstrate that this type of hybridization might facilitate biological invasion by the production of clonal gametes containing the invasive genome (Chapter 3). The extinction risk is not genetically driven but is determined by the "*demographic flow*" between parental species and mediated by hybrid offspring. In Chapter 4, I further

Abstract

demonstrate that this type of hybridization is an underappreciated fast way to extinction, which may be more frequent than currently thought. I thus urge conservation biologists to consider it in the development of conservation plans. Finally, the third type of hybridization is defined by the production of fertile F_1 hybrids that mediate genetic introgression between parental species. In Chapter 5, I show that this type of hybridization can be a genetic and demographic threat for native organisms that are facing a competitive invading species, but it can also represent a new evolutionary opportunity by increasing genetic diversity.

I also performed spatially explicit simulations with the third type of hybridization in order to take the spatial dynamics of populations into account (i.e. geographic locations and migration). This is important to assess the effects of invasive species that are expanding their home range and interbreeding with local native species. In Chapter 6, by improving the admixture model incorporated in the programme SPLATCHE 2, I contributed to the validation of the previous conclusion that an invasive species is expected to carry a higher proportion of introgressed genes than the local species with which it interbreeds. These results show that this phenomenon is due to the initial population imbalance and the surfing of genes during the wave of range expansion. Finally, in Chapter 7, I present two new models of spatial dispersal that I developed to better incorporate the cognitive behaviour and history of colonization of territorial or social species during their spatial expansion. I show that the previous conclusion of larger introgression in the invasive species represents a general expectation for neutral genes, whatever the mode of dispersal. I also demonstrate that these models have the potential to better explain the processes and history of hybridization and to improve the projection of future scenarios.

The development of several modelling approaches that I have applied to very different subjects (fishes, amphibians, birds, mammals and humans) allowed me to draw a large picture of the effects of hybridization on biodiversity. At the end of my PhD research, I was finally able to state the conditions under which our three types of hybridization may represent priorities for conservation programmes or, alternatively, new evolutionary opportunities (Chapter 8). I highlight that hybridization may certainly lead to biodiversity loss when enhanced by human factors, leading for instance to outbreeding depression or the introgression of maladaptive genes, but it may also drive the emergence of new biodiversity and opportunities to adapt to changing environmental conditions.

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CHAPTER 1

Introduction

1.1 General introduction

Hybridization can be defined as the reproduction between genetically distinctive organisms (Taylor et al., 2015). It arises from the mating between different populations, subspecies, species or even genera (e.g. Matondo et al., 2011; Crossman et al., 2014). The independent evolution of each of the involved organisms may therefore be disrupted by the effect of hybridization, either emerging naturally in the early phases of the speciation process (Mallet, 2007; Arnold and Martin, 2010) or, more recently, due to anthropogenic factors (Rhymer and Simberloff, 1996; Allendorf et al., 2001; Todesco et al., 2016).

The increasing rate of human activities breaking the reproductive barriers between organisms, such as translocation of invasive species, modifications of habitats and particularly climate change, altering the times and places of reproduction for many species, leads to the projection that this phenomenon may be more extensive in the near future (Allendorf et al., 2001; Taylor et al., 2015). However, the ecological and evolutionary consequences of hybridization remain poorly understood (Gilman and Behm, 2011). My main research objective is to model the hybridization process by integrating natural and

anthropogenic factors in order to assess its impact on the diversity of organisms. I started by defining hybridization categories based on the reproductive properties of the first generation hybrids, in order to understand the various genetic and demographic consequences impacting on biodiversity (Chapter 1.4). I then developed and gradually improved a series of modelling approaches in order to explore the evolutionary and conservation issues of hybridization (Chapters 2, 3, 4, 5, 6, 7). Finally, the examination of the different categories of hybridization through the models and the analysis of their applications allowed me to draw a general picture of the effects of hybridization on the evolution of biodiversity, either precipitating species loss or driving the emergence of novel biodiversity (Chapter 8).

1.2 Paradoxes around hybridization

The notion of hybridization between different species, or interspecific hybridization, seems to have a double paradox. On the one hand, it disrupts the biological species concept, which does not allow for interbreeding between species (Mayr, 1942), and on the other hand, it is considered either as an evolutionary process leading to the emergence of new biodiversity (e.g. Mallet, 2007) or as a cause of biodiversity loss, with conservation implications (e.g. Todesco et al., 2016).

1.2.1 Species concept and interspecific hybridization

The widely accepted biological species concept formulated by Mayr (1942) states that species are "*groups of actually or potentially interbreeding natural populations which are reproductively isolated from other such groups*". The key idea under this vision is the reproductive isolation that delimits the species unit. This was already proposed by Georges-Louis Leclerc, Comte de Buffon, more than 260 years ago (Buffon, 1753). Buffon realized that a horse and a donkey are morphologically more similar than some differ-

ent races of dogs. However, the reproduction in the first case leads to an infertile offspring (a mule) while in the second case, the offspring is fertile, highlighting that a line can be drawn between organisms that cannot reproduce in order to differentiate species.

Charles Darwin was opposed to this view and dedicated an entire chapter of "*On the Origin of Species*" to the hybridization concept (Darwin, 1859). The observation of interbreeding between distinct morphological species, with different degrees of offspring fertility, from completely sterile to even more fertile than parental species in determined conditions, was an argument against sterility or fecundity as a species delineation factor (Fig. 1.1). Darwin agreed with the notion that species may hardly remain different when free sympatric mating occurs, but supported a more continuous conception of species, influenced by the gradual effect of natural selection. However, the idea of species with various degrees of fertility was abandoned during the modern evolutionary synthesis (Dobzhansky, 1937; Huxley, 1942; Mayr, 1942).

Much of the understanding about reproductive isolation and interspecific hybridization has been revealed by experimental studies in *Drosophila* (Tubaro and Lijtmaer, 2002). Those works revealed that: i) reproductive isolation is positively correlated with the phylogenetic distance between hybridizing species; ii) at the same level of genetic divergence, reproductive isolation is higher between sympatric than allopatric species; and iii) hybrid offspring follow Haldane's rule, meaning that if one sex is less viable or sterile, it is more likely to be the heterogametic sex (Coyne and Orr, 1989, 1997). During most of the 20th century, interspecific hybridization was considered to be rare in nature, mainly arising by human translocation of species and with a small effect in evolution, with hybrids supposedly having lower fertility in most cases (Arnold and Martin, 2010). Despite the large acceptance of reproductive isolation as a key element to define species (Dobzhansky, 1937; Mayr, 1942), a large controversy persisted around the biological species concept. This was mainly motivated by the semipermeable breeding barriers between some species and the difficulty to test this notion in organisms with non-overlapping distribution range (Frankham et al., 2012; Behie and Oxenham, 2015).

Three of the most popular alternative definitions of species are the ecological, phy-

logenetic and evolutionary concepts. Ecological species are of closely related lineage using minimally differentiated adaptive zones, also denominated as ecological niches (Van Valen, 1976). Evolutionary species are defined as ancestral-descendant lineages with their own identity, evolutionary tendency and historical fate (Wiley, 1978). Phylogenetic species are in turn considered to be the minimal cluster of organisms with a pattern of ancestry and descentance (Cracraft, 1983). These three definitions have also been criticised. The ecological and evolutionary species concept has been judged to be too vague to determine a cut-off point between species (Frankham et al., 2012; Behie and Oxenham, 2015). The phylogenetic species concept has been defended by various authors, who considered it as a compressible view of unique primitive and derivate features for separate species (e.g. Papadopoulou et al., 2008; Groves, 2012; Behie and Oxenham, 2015), but this definition has also been the focus of criticisms, mainly due to an inflated number of species. This is because different regions of the genome may express very different evolutionary histories and because hybridization may also perturb phylogenetic classifications by altering monophyletic regions (Mallet, 2008; Frankham et al., 2012). Mallet (2007) recognized various cases of speciation that are influenced by fertile hybridization in nature and tried to rescue and adapt the more continuous view of species proposed by Charles Darwin. He understood species as groups of genotypes that remain distinct in the face of actual or potential hybridization (Mallet, 2007, 2008). He highlighted the fact that genotypes may remain distinct with reproductive isolation, but this would be a way to maintain species or to reach speciation rather than being a means of species discrimination (Mallet, 2007). To date, there are around 30 definitions of species and a large debate about the species concept and its relation with hybridization (e.g. Rundle et al., 2001; Mallet, 2007; Wang, 2007; Mallet, 2008; Frankham et al., 2012; Behie and Oxenham, 2015; Fitzpatrick et al., 2015; Franco-Trecu et al., 2016).

1.2.2 Evolution of new biodiversity

Botanists first highlighted the important role of natural hybridization on the speciation process of several species, i.e. in generating new biodiversity (e.g. Abbott, 1992; Riese-

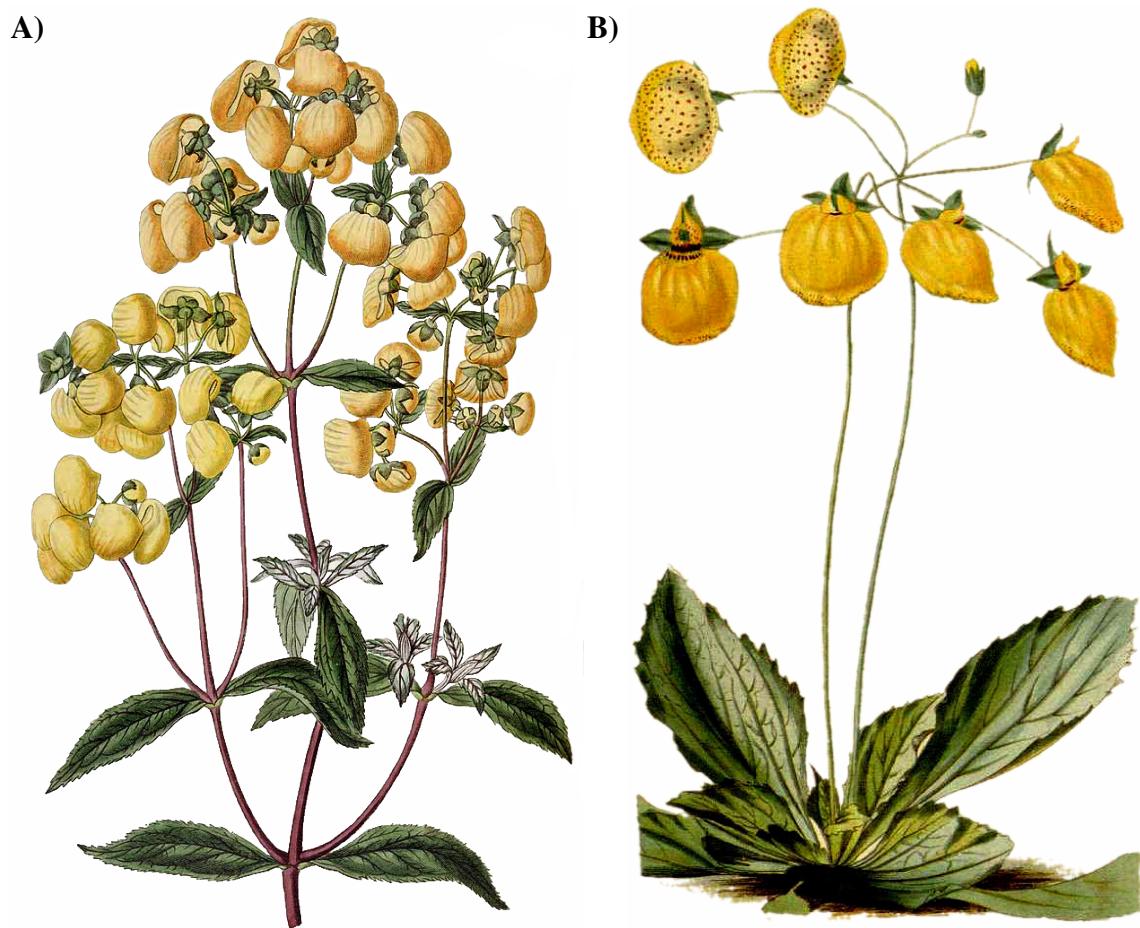


Figure 1.1. Two Chilean *Calceolaria* species used by Charles Darwin to exemplify interspecific hybridization with fertile offspring in "On the Origin of Species" (1859). A) *Calceolaria integrifolia* (Illustration from: Lindley (1835)); B) *Calceolaria plantaginea* (Illustration from: Loddiges (1828)). Pictures courtesy of Peter H. Raven Library/Missouri Botanical Garden

berg, 1995; Ellstrand and Schierenbeck, 2000; Soltis and Soltis, 2009; Brumfield, 2010). Later, zoologists recognized the major evolutionary effects of genetic introgression, the gene flow between different taxa due to hybridization, on numerous insects (e.g. Capblancq et al., 2015), fishes (e.g. Schumer et al., 2016), amphibians (e.g. Streicher et al., 2014), reptiles (e.g. Haines et al., 2014), birds (e.g. Veen et al., 2001), mammals (e.g. Li et al., 2016) and other organisms (e.g. Leducq et al., 2016). There are around 25% of plants and 10% of animals that are currently known to hybridize with another species and the effect of this phenomenon in evolution is considered to be much more important than previously thought (Mallet, 2007).

Species can naturally change their historical home range in response to changing environmental conditions and meet closely-related taxa (Hewitt, 2011). Several species carry signatures of hybrid ancestry from the last Ice Age period (e.g. Maixner et al., 2016; Schumer et al., 2016). For this reason we can find mitochondrial DNA of brown bears in Polar bears, because ancient hybridization events occurred during the Pleistocene (Hailer et al., 2012). The Bering Land Bridge recurrently emerged during this time, allowing organisms to migrate between Eurasia and North America, leading to opportunities of hybridization, such as those observed between Canada lynx (*Lynx canadensis*) and Eurasian lynx (*Lynx lynx*) (Li et al., 2016). Organisms can have introgressed genes from locally extinct species even if they have never been in contact, because a third species, acting as a temporal bridge to gene flow, has hybridized with both of them (e.g. Melo-Ferreira et al., 2007).

Natural selection may fix beneficial alleles obtained by hybridization or, to the contrary, remove detrimental introgressed alleles (see Chapter 5). Adaptive introgression has been important for several speciation processes (Mendelson and Shaw, 2012). For instance, the antipredatory mimicry of three *Heliconius* butterflies in South America has been acquired by interspecific hybridization, for which the parts of the genome related to colour patterns have more introgressed alleles than other regions of the genome (Dasma-hapatra et al., 2012). Introgressed alleles can rapidly spread among individuals when they are related to adaptive traits. For example, "warfarin" is a rodenticide that was developed in 1948 to control house mice (*Mus musculus*). Mice started to be resistant during the 1960s by acquiring a single gene from the Algerian mice (*M. spretus*) through hybridization (Song et al., 2011). These species were isolated until the development of human agricultural lands. They rarely interbreed and hybrids have limited survival with half of them being sterile, but the resistance gene rapidly spread across Europe. In Germany, where both species do not mingle, one third of house mice have the introgressed resistance gene coming from Algerian mice (Song et al., 2011). A similar case was recently documented between two species of mosquitos that are vectors of malaria and have different levels of resistance to an insecticide (Norris et al., 2015). The insecticide acted as

a selective pressure driving the spread of resistant alleles obtained by hybridization, even when hybrids had reduced fertility (Lee et al., 2013). The reduced fertility of the offspring is therefore not necessarily selected against and can also represent adaptive mate choice (Veen et al., 2001).

Opportunities of speciation that are brought by hybridization can be generated when hybrids exploit unique ecological niches (see Chapter 3). For instance, an ancient hybridization event during the last Ice Age between two Western European waterfrogs, *Pelophylax ridibundus* and *P. lessonae*, both using different types of ponds with singular levels of oxygen, generated a hybrid using an intermediate habitat (Holenweg Peter et al., 2002). *P. ridibundus* retracted from the area at the end of the glaciation period, but the hybrid persisted in the unoccupied spaces and was considered as a different species *P. esculentus* (Vorburger and Reyer, 2003). A rapid incipient speciation was recently observed in the offspring between two species of yeast, *Saccharomyces paradoxus* and *S. cerevisiae*, whose hybrids have the potential to exploit a unique ecology that is intermediate to the one of parental species (Leducq et al., 2016). The new genetic architecture generated by hybridization can thus also facilitate ecological divergence, promoting a speciation process by exploiting a specific niche (e.g. Rieseberg et al., 2003).

Positive selection can fix adaptive alleles and purifying selection can remove the detrimental alleles (e.g. Schumer et al., 2016), but introgressed genes can remain even without the effect of natural selection (see Chapters 6 and 7). Neutral introgressed alleles can persist in high proportion, even when the original species is extinct (see Chapters 6 and 7). Currat et al. (2008b) demonstrated, through computer simulations and by a review of the literature, that invasive species may carry a large quantity of neutral alleles that are introgressed from a native species. This is influenced by the demographic effects of population imbalance and the hybridization level at the wave front of the invasion (see Chapter 6), in which introgressed alleles surf and reach a higher frequency than expected under the auspices of a spatially stationary context (Klopfstein et al., 2006). There are several cases of asymmetrical introgression between demographically imbalanced species that have been proposed to follow this neutral expectation (e.g. Colliard et al., 2010; Neiva et al., 2010).

Hybridization has probably also played a role in our own evolution when modern humans spread out of Africa and met other closely related hominids (see Chapter 6 and Annex). Analysis of ancient DNA revealed that around one to four per cent of Neanderthal ancestry is found in the genome of non-African modern humans (Green et al., 2010; Sankararaman et al., 2014; Vernot and Akey, 2014). The introgressed genes can have persisted through neutral processes (Currat and Excoffier, 2011) or by the effect of positive selection (e.g. Ding et al., 2013). Recently, it has been demonstrated that some introgressed alleles, adaptive in the past, may currently be associated to some diseases (Simonti et al., 2016). Modern humans are likely to have met and potentially interbred with other hominids in addition to Neanderthals. Huerta-Sánchez et al. (2014) recognized positive selection in haplotypes related with survival at high altitudes in current Tibetans, which seem to have been introgressed from Denisovans. Other haplotypes coming from Denisovan ancestry seem to be frequent in the current genome of Melanesians (Reich et al., 2010; Meyer et al., 2012). Our own genome may thus carry the influence of various ancient hybridization events during human evolution (Kuhlwilm et al., 2016).

1.2.3 Biodiversity loss

Interspecific hybridization is considered as a major conservation concern when it is motivated by anthropogenic factors, such as translocation of invasive species or by modification of natural habitats (Rhymer and Simberloff, 1996; Allendorf et al., 2001; Todesco et al., 2016). The breakdown of the reproductive barriers between species may disrupt their independent evolution and has already increased the risk of extinction of several plant and animal organisms (e.g. Beaumont et al., 2001; Wolf et al., 2001; Leonard et al., 2013; Guay et al., 2014; Quilodrán et al., 2014a, 2015; Pinto et al., 2016).

Hybridization may lead to different but potentially interacting mechanisms that threaten species persistence. First, outbreeding depression may represent a significant loss of reproductive value and detonate a rapid extinction when it interacts with a demographic decline (see Chapter 2). This may be stronger between genetically distant species (e.g. Konishi and Takata, 2004), but organisms do not need to be distantly related to be af-

fected by outbreeding depression. For instance, the human domestication of Atlantic salmon (*Salmo salar*) has led to a lower fertility when mating conspecifics in the wild, representing a serious threat for wild salmon in Norway (Hindar et al., 2006). Second, native genotypes can disappear by genetic swamping and be replaced by the numerical or competitive advantaged of invasive genotypes (see Chapter 5). Third, the introgression of non-native genes can disrupt local adaptations by introducing maladaptive gene complexes (Kidd et al., 2009). Fourth, the behaviour of wild animals may be perturbed in a way that is difficult to predict, more particularly when it concerns domesticated animals (Driscoll et al., 2009), which have been artificially selected according to human lifestyle and, when spreading their genes in nature, may influence a whole network of ecological interactions (e.g. Ellington and Murray, 2015). Fifth, hybridization may affect the effective population size of the interacting species with major consequences for rare or threatened species, which already have a reduced number of breeders (Macdonald and Sillero-Zubiri, 2004). Finally, a less evident effect of hybridization, but important for conservation, is the change of legal status of threatened species when they are introgressed and for which hybrids are not necessarily considered as protected organisms (Leonard et al., 2013). This may be a serious problem when the few remaining individuals of a critically endangered species are hybrids, with an uncertain status of legal protection (Haig et al., 2011).

The loss of species distinctiveness due to introgressive hybridization has also been called "*speciation reversal*" (Wolfe, 2003; Seehausen et al., 2008; Halas and Simons, 2014). This may seriously affect key ecological adaptations that appeared during species radiation. Vonlanthen et al. (2012) documented the rapid extinction of whitefish (*Coregonus spp.*) in Swiss lakes, which evolved according to ecological opportunities, but human eutrophication and homogenization of the environment is driving extinction by hybridization and demographic decline. A similar case was documented for cichlid fishes of Lake Victoria (East Africa), for which the colouration pattern is a key character that determines mate choice and reproductive isolation, but the turbidity of the water induced by eutrophication relaxed sexual selection, destroying the diversification mechanism (See-

hausen et al., 1997). Speciation reversal is a conservation concern because it erodes the ecological and genetic distinctiveness between closely related, but ecologically divergent, species (Taylor et al., 2006). The various cases of hybridization leading to speciation reversal (e.g. Grant and Grant, 2008; Seehausen et al., 2008) suggest that the extinction risk may be more extensive than previously thought (Vonlanthen et al., 2012).

Hybridization between wild and domesticated organisms is a worldwide problem of conservation (see Chapter 6). For instance, the main current threat for the persistence of European wildcats (*Felis silvestris silvestris*) is the hybridization with domestic cats (*Felis s. catus*) (Yamaguchi et al., 2015). Domestic cats were originally domesticated from a subspecies inhabiting the Near East (*Felis s. lybica*), but they are genetically distinct from all current cat subspecies (Driscoll et al., 2007). There are still some wildcat populations remaining in Europe (e.g. Oliveira et al., 2008b; Nussberger et al., 2014), but the complete admixture and the loss of genetic distinctiveness have already been achieved in some countries (e.g. Beaumont et al., 2001; Lecis et al., 2006). Domestic dogs (*Canis familiaris*) can hybridize with any kind of wolf-like canids and have already led to conservation issues in various cases (Leonard et al., 2013), such as for the grey wolf (*Canis lupus*) in Europe (e.g. Lescureux and Linnell, 2014), the coyote (*Canis latrans*) in North America (e.g. Ellington and Murray, 2015) or the Ethiopian wolf (*Canis simensis*) in Africa (e.g. Gottelli et al., 1994). Ellington and Murray (2015) found that hybridization with domestic dogs was driving changes in the space occupied by coyotes, suggesting consequences at the ecosystem level. A particular threat is the hybridization of domestic dogs with the Ethiopian wolf, which is the world's most endangered canid, persisting with around 500 individuals in six isolated populations (Gottelli et al., 1994, 2013; Marino and Sillero-Zubiri, 2013). The detrimental effects of hybridization with domesticated organisms is reinforced by their outnumbering compared to the abundance of their wild counterparts (e.g. Hughes and Macdonald, 2013), in which the extinction risk can be particularly accelerated when rare species hybridize with more abundant species (see Chapters 2 and 5).

Genetically modified organisms and genetic engineering have generated a large de-

bate on how to regulate the spread of modified genes in nature through hybridization (e.g. Raybould and Gray, 1993; Ellstrand et al., 2010; Myhr, 2010; Devos et al., 2012; Ellstrand et al., 2013). Genomic alteration for economic purposes may induce higher fertility and resistance to pathogens that make crops or hybrids highly invasive (Hails, 2000). The reduced fertility of the first generation hybrids F_1 is not a barrier for the spread of advantageous alleles (Arriaga et al., 2006), which are frequently observed in the wild (e.g. Linder et al., 1998), with hybrids becoming invasive in various cases (e.g. Simberloff, 2008; Laikre et al., 2010). The ecological release from their natural predators or pathogens conferred by the resistant alleles has been proposed as a factor that is initiating this invasion (Hails, 2000). A serious risk has been recently detected in the single wild population of rice in Costa Rica (*Oryza glumaepatula*) that hybridizes with invasive commercial rice (*O. sativa*) (Fuchs et al., 2016). The concerns are not only related to modified plant crops, but also to animals of economic interest, usually with unpredictable ecological effects (e.g. Oke et al., 2013), or to non-target insects, as has been documented for the monarch butterfly of North America (e.g. Losey et al., 1999).

1.3 Invasive species

The colonization of exotic species that are introduced accidentally or deliberately by humans is a serious threat when feral populations are established and become invasive (e.g. Luquet et al., 2011). This is one of the major current threats to biodiversity, worldwide (Mack et al., 2000; Bellard et al., 2016). The risks are usually associated with predation, competition, parasitism and the transmission of disease to native organisms, but hybridization is of growing attention in conservation biology (Hall and Ayres, 2009).

Species with reduced population sizes that are rare or even threatened in their native home range may become invasive in an exotic environment (e.g. Lizarralde et al., 2008). The "enemy release" hypothesis states that introduced species are successful because they are not regulated by their co-evolved enemies (Liu and Stiling, 2006). They can find closely related taxa and hybridize in this new colonized area. The transmission of non-native genes is frequently recognized as a cryptic biological invasion (e.g. Currat et al.,

2008b; Gómez et al., 2015). Native genotypes may progressively be replaced by exotic alleles, influencing morphological and behavioural changes, with ecological effects that are difficult to determine (e.g. Velema et al., 2012). There are various cases of plants and animals introduced by humans that have become invasive and a conservation concern due to hybridization with indigenous species (e.g. Dyer and Williams, 2010; Holsbeek and Jooris, 2010; Larcombe et al., 2014). One of the most documented cases is the mallard (*Anas platyrhynchos*), which has been widely translocated for hunting and ornamental purposes, cohabiting with other closely related taxa and threatening them by interspecific hybridization (e.g. Guay and Tracey, 2009; Van Rensburg et al., 2011; Seyoum et al., 2012). For instance, the Hawaiian duck (*Anas wyvilliana*) was once abundant, but is currently listed as an endangered species and the hybridization with the mallard duck is the main threat for its recovery (Fowler et al., 2009). Mank et al. (2004) documented a historical decrease of genetic differentiation between the mallard duck and the American black duck (*Anas rubripes*). They were previously genetically different, but currently it is difficult to distinguish the two taxa due to introgressive hybridization. A similar case occurred in New Zealand, where grey duck (*Anas superciliosa*) was also abundant before the settlement of the mallard duck, but today grey duck is extremely rare and many of the remaining individuals have hybrid ancestry (Guay et al., 2014). The complete extinction of some populations has already been achieved (e.g. Tracey et al., 2008). Mallards are highly competitive for available resources and their aggressive behaviour to succeed in heterospecific mating has also been observed (Kirby et al., 2004; Williams et al., 2005). They frequently have a demographic advantage by exploiting new human-perturbed habitats, in addition to the habitat that are overlapping with local species (Williams and Basse, 2006). The competitiveness of hybrids may also facilitate the invasion of this exotic species (see Chapter 5).

1.4 Types of hybridization

Interspecific hybridization is therefore an important evolutionary process that may create new biodiversity and possibilities of adaptations, but is also a conservation concern that

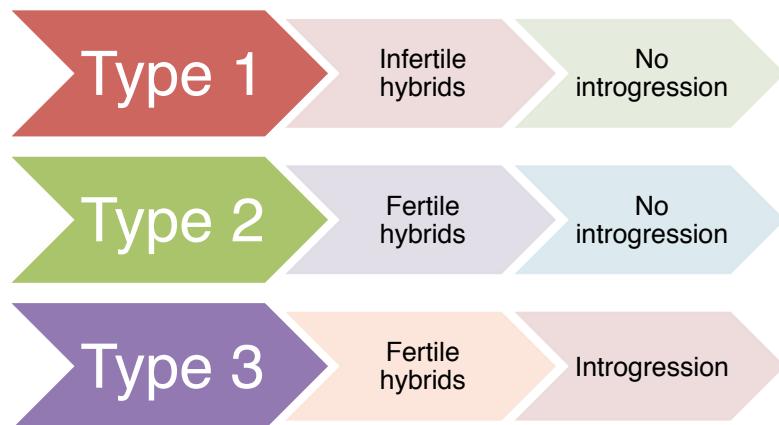


Figure 1.2. Three hybridization types can be defined depending on the resulting F_1 hybrids: inviable or sterile offspring, fertile but without introgression (no recombination during gametogenesis), and fertile with introgression. The first two types are frequently observed between distant species hybridization and the third type in the hybridization between more closely related taxa.

may lead to species loss. However, the long-term effects of hybridization are poorly known (Gilman and Behm, 2011). An extensive review of reported cases of hybridization helped me to distinguish different categories in order to guide the understanding of its effects on biodiversity. I then contributed to defined three main types of hybridization regarding the characteristics of the first generation hybrids F_1 (Fig. 1.2) (Quilodrán et al., 2014a, 2015).

1.4.1 Type I: Infertile hybrids, no introgression

The first type represents species that mate but yield inviable or infertile offspring (see Chapter 2). The underlying causes are post-zygotic reproductive barriers (Dobzhansky, 1970), such as different chromosome numbers and homology. This kind of hybridization is usually regarded as an evolutionary dead-end because genes are not transmitted to further generations by hybrids (Allendorf et al., 2001). However, it represents a strong outbreeding depression and the wasted reproductive effort by parental species may thus precipitate an extinction process, even more when rare populations hybridize with more abundant ones or when one taxon is already threatened (e.g. Konishi and Takata, 2004). In this case, the main risks are driven by demographic swamping, in which the growth

rate of the less abundant species may decline to a lower level than that required for replacement (Wolf et al., 2001). For instance, the European mink (*Mustela lutreola*) has a reduced population size and hybridizes with the American mink (*Mustela vison*), which was introduced and is currently much more abundant than the native European species. In this case, the loss of reproductive value due to sterile mating is seen as a main risk for the persistence of the native mink (Rozhnov, 1993). The karyotype of Atlantic salmon (*Salmo salar*) and brown trout (*Salmo trutta*) is highly differentiated and they rarely hybridize in nature, suggesting strong reproductive barriers (Gray et al., 1993), but the release of farm individuals with relaxed mate choice has increased the hybridization rate (Urke et al., 2010). The offspring are almost completely infertile (Garcia-Vazquez et al., 2004), but hybrids are frequently observed in nature and have already threatened some wild populations of salmon (Jonsson and Jonsson, 2011).

1.4.2 Type II: Fertile hybrids, no introgression

The second type of hybridization produces viable and fertile offspring, but there is no introgression of nuclear genes between parental species through generations via hybrids (see Chapters 3 and 4). The flow of genes is prevented by the absence of recombination between homologous chromosomes during meiosis. The entire genome of one parental species is excluded during gametogenesis by a process termed "*genome exclusion*", leading to clonal or hemiclonal offspring (Lampert, 2009). The real frequency of such type of hybridization is poorly known, but there are around 80 taxa that have been observed to produce hybrids undergoing genome exclusion (Neaves and Baumann, 2011). Hybrids may yield two types of gametes, they may alternate between the exclusion of one or the other parental species (i.e. alternative genome exclusion) (e.g. Yakovlev et al., 2000), or produce a single type of gamete, systematically excluding one of the parental genomes (i.e. non-alternative genome exclusion) (e.g. Crespo-Lopez et al., 2006). One of the most documented cases is found in the *Pelophylax* complex of waterfrogs in Western Europe (e.g. Holsbeek and Jooris, 2010; Luquet et al., 2011; Quilodrán et al., 2015). *P. esculentus* is a hybridogenetic form containing the genome of *P. lessonae* and *P. ridibundus*, but is

clonally transmitting the single genome of the latter species. Deleterious mutations render the crosses between two *P. esculentus* inviable, but this hybrid is regenerated when crossing with *P. lessonae* (Vorburger, 2001a). During a period of 10,000 years, *P. lessonae* and *P. esculentus* were living in equilibrium (the so-called *L/E* system), in the absence of *P. ridibundus* (Vorburger and Reyer, 2003). However, the recent introduction of *P. ridibundus* in France and Switzerland is seriously threatening the persistence of the two native forms, with complete extinction already being reached in some areas (see Chapter 3). This kind of hybridization may represent an underappreciated pathway to very fast extinction (see Chapter 4).

1.4.3 Type III: Fertile hybrids, introgression

In the third type of hybridization, the offspring is viable, fertile and there is introgression of nuclear genes between parental species in the course of successive generations (see Chapters 5, 6 and 7). There is recombination during meiosis between homologous chromosomes and subsequent flow of genes between the interacting taxa. This type of hybridization may create a more- or less-extended hybrid zone (see Chapter 7) and either induce the introgression of some neutral, adaptive or even maladaptive alleles in one of the species, potentially affecting its evolution (see Chapter 6), or drive the replacement of one or both parental taxa by a hybrid swarm (see Chapter 5). This type of hybridization is largely the most documented one, with various cases threatening native forms or influencing the evolution of some new species (e.g. Seyoum et al., 2012; Nussberger et al., 2013; Excoffier et al., 2014; Pinto et al., 2016). In cases where a species is at risk of extinction, increasing its genetic diversity by promoting hybridization with a close relative has been proposed, in order to rescue populations affected by inbreeding depression or perturbed by the effects of global climate change. However, the balance between increasing the genetic diversity and the introduction of non-native, sometimes maladaptive alleles represents an on-going discussion (e.g. Amos and Balmford, 2001; Aitken and Whitlock, 2013; Taylor et al., 2015; Hamilton and Miller, 2016; Kovach et al., 2016).

The three types of hybridization may be related to the phylogenetic distance between

the interacting species pairs, with the first and second types being frequently observed between distant species, sometimes belonging to different genera (e.g. Yakovlev et al., 2000; Quilodrán et al., 2014a), and the third type being more often associated with closely-related taxa (e.g. species or subspecies) (e.g. Vonlanthen et al., 2012; Nussberger et al., 2014).

1.5 Our models of hybridization

By considering the three types of hybridization previously defined, I progressively improved a series of modelling approaches that are described in the following chapters (2 to 7). The modelling of interspecific hybridization is an important tool to investigate the effects of this phenomenon in the evolutionary history of given organisms, but it is also extremely useful in projecting the demographic and evolutionary effects in the near future. I worked with two different kinds of approaches, a model developed from scratch to study complex genetic and demographic interactions (Chapters 2, 3, 4 and 5), and one based in the improvement of a program that includes spatially explicit simulations (Chapters 6 and 7). The set of models presented below aims at proposing a general toolbox that is useful for examining a large variety of issues in the fields of ecology, conservation biology and evolution.

1.5.1 Model for distant species hybridization

Previous modelling approaches have been proposed for the first type of hybridization, when hybrids are inviable or infertile, and for the second type of hybridization, for hybrids performing genome exclusion, but they are case-specific and describe particular systems (Graf, 1986; Rodriguez, 1996; Hellriegel and Reyer, 2000; Som et al., 2000; Som and Reyer, 2006). Hence, I decided to develop a more general model of hybridization between distant species, which is presented in Chapters 2, 3 and 4. This model incorporates three important processes that were not fully taken into account previously: i) dominance/recessivity inheritance of traits in hybrids; ii) assortative mating through various

levels of mate choice relaxation; and iii) density-dependent competition.

In the second chapter, the model is applied to a case study of hybridization type I, between Atlantic salmon and brown trout. I examined the combined effects of various values of assortative mating (i.e. interbreeding success rate), with interspecific competition and resistance to a pathogenic disease; all three processes currently affecting a wild population of salmons (Jonsson and Jonsson, 2011).

The third chapter presents an adaptation and application of the model to a case study involving hybridization type II, among one invasive and two native European waterfrogs undergoing genome exclusion (Quilodrn et al., 2015). The fourth chapter improves the model of distant hybridization to include environmental stochasticity and highlights that this type of hybridization is an underappreciated highway to extinction. These investigations illustrate the potential threats induced by this type of hybridization and assess the magnitude of the extinction risk, identifying the conservation actions that may be important to preserve the native waterfrogs.

1.5.2 General model of hybridization

In the fifth chapter, I present a major improvement of the previous models that incorporates all types of hybridization, including hybridization of type 3. Models have already been proposed for this third type of hybridization (e.g. Huxel, 1999; Ferdy and Austerlitz, 2002; Baskett and Gomulkiewicz, 2011; Satake and Araki, 2012), but they either describe a single gene or do not fully address all the important processes that are included in our own approach. Indeed, in this general model of hybridization, additionally to the three processes previously incorporated in Chapters 2, 3 and 4 (assortative mating, dominance/recessivity inheritance and competition), I added the possibility to simulate multiple genes, to integrate the effect of quantitative and qualitative gene expression and to incorporate the effects of neutral and selective mechanisms. The goal was to propose a more general tool to the scientific community than what was previously available. I applied this model to investigate introgressive hybridization involving the mallard (*Anas platyrhynchos*), as a case study. This species has been widely translocated by humans and

the hybridization with closely-related taxa is a conservation concern in almost all of their geographic distribution (Tubaro and Lijtmaer, 2002). This investigation allowed me to explore the phenotypic landscape that is susceptible to be observed when genetically distinct organisms hybridize, illustrating the interaction between genetic and demographic factors in the fixation of certain phenotypes and highlighting the threat that a genetic swarm may represent for native taxa.

1.5.3 Modelling spatially explicit hybridization

In chapter sixth, I participated in improving the hybridization model implemented in the programme SPLATCHE 2 (Ray et al., 2010), which is a spatially explicit tool that allows the joint simulation of ecological information and molecular diversity (Currat et al., 2004). Zhang (2014) recently criticized the hybridization model that was originally implemented in this programme. He particularly focused on the observation made by Currat et al. (2008b), which observed a general pattern of asymmetrical neutral introgression during species range expansion, stating that invasive species are much more introgressed than local organisms, even with a very low hybridization rate. Zhang (2014) argued that the density-dependent nature of the implemented hybridization model biased this conclusion, suggesting that asymmetry is not a default property of neutral genes and supporting the view that introgression between local and invasive species is symmetrical. However, Zhang (2014) did not present his results in a context of spatial range expansion. In Chapter 6, the new hybridization model implemented in SPLATCHE 2 is a more realistic approach, which solves the issues raised by Zhang (2014). Using this model, I showed that the conclusion of Currat et al. (2008b) is still valid and that asymmetrical introgression during range expansion was consequently not due to the model but to demographic processes. The application of Chapter 6 is based on the potential Neanderthal introgression detected in modern humans (Green et al., 2010; Sankararaman et al., 2014; Vernot and Akey, 2014).

In Chapter 7, I present an additional improvement on what was implemented in the modified version of SPLATCHE 2, by incorporating density-dependent dispersal during

the range expansion. Recent studies highlighted the importance of incorporating density-dependent dispersal when exploring the properties of species range expansion (Altwegg et al., 2013; Bocedi et al., 2014; Ponchon et al., 2015). However, these works are purely ecological and the few studies assessing the molecular effects of range expansion are density-independent (e.g. Currat and Excoffier, 2004; Klopfstein et al., 2006; Currat et al., 2008b; Currat and Excoffier, 2011; Excoffier et al., 2014). Species dispersal may be influenced by social information in surrounding areas, with territorial or social organisms moving, avoiding or being attracted by conspecifics (Quilodrán et al., 2014b). I illustrated the importance of incorporating these features by simulating the hybridization between the European wildcat (*Felis silvestris silvestris*) and the domestic cat (*Felis s. catus*). Autosomal, mitochondrial and Y-chromosome markers are used as references (Nussberger et al., 2013, 2014). The model that best explains the observed introgression is used to project the potential risk of extinction of wildcat in the Jura Mountains for the near future.

The developed modelling approaches are applied to a variety of case studies in order to illustrate the extent of evolutionary and ecological consequences of hybridization (Fig. 1.3). I highlight that interspecific hybridization may precipitate the loss of native biodiversity when interacting with demographic decline and invasive species introduced by humans, but it may also represent a source of new genetic diversity, with opportunities of adaptation and evolution. The different chapters reveal various effects of hybridization on biodiversity by modelling important genetic and demographic features. These models are, therefore, an important toolbox with which to assess the influence of hybridization on species extinction and on the emergence and evolution of biodiversity.

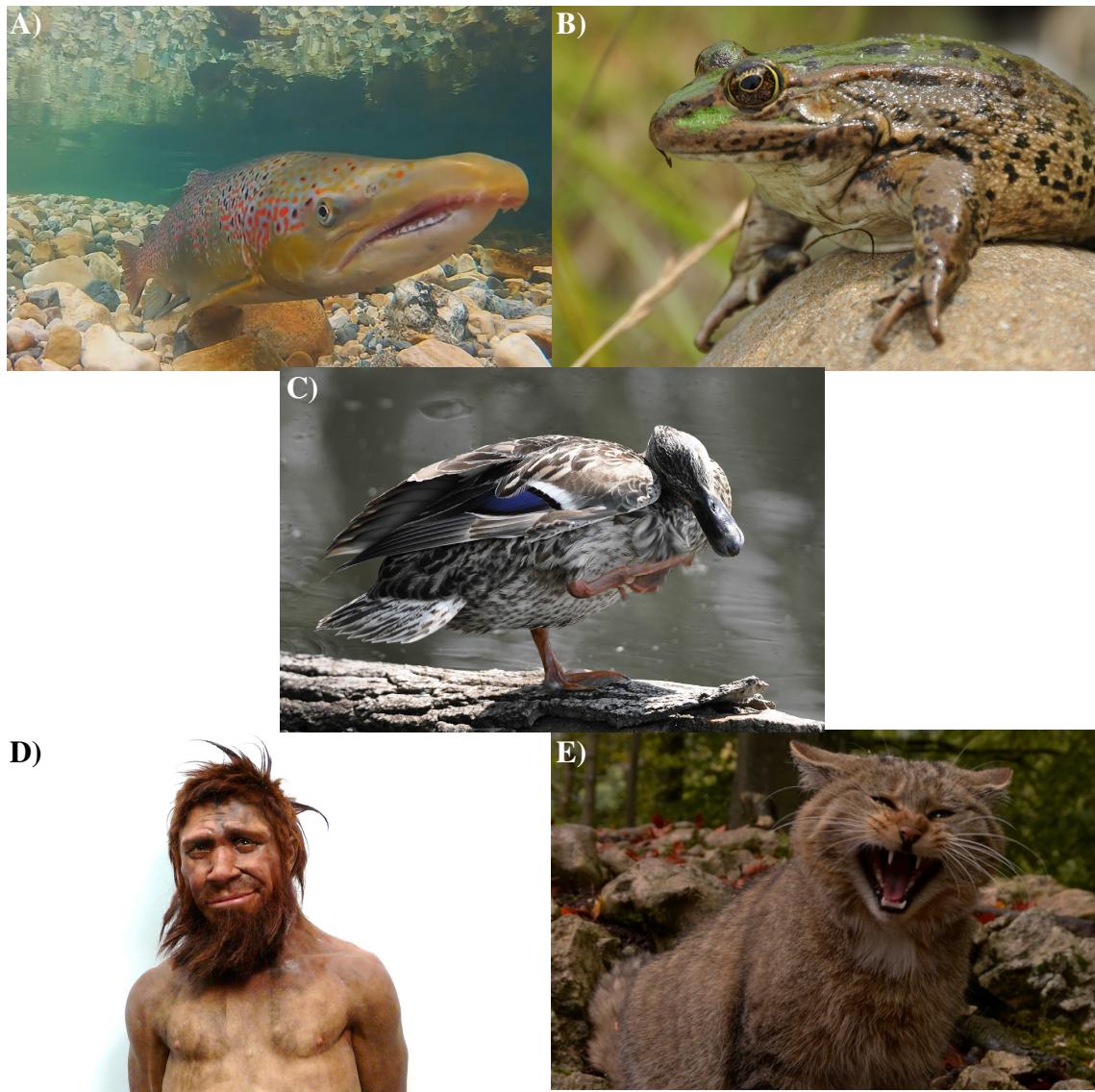


Figure 1.3. Case studies of hybridization explored in the different chapters. These illustrate hybridization involving: A) Atlantic salmon (*Salmo salar*) (Picture: David Alvaréz); B) *Pelophilax* waterfrogs (Picture: Claudio Quilodrán); C) mallards (*Anas platyrhynchos*) (Picture: Claudio Quilodrán); D) Neanderthals (Picture: Kennis&Kennis); and E) European wildcat (*Felis silvestris silvestris*) (Picture: Patricia Huguenin).

CHAPTER 2

A general model of distant hybridization reveals the conditions for extinction in Atlantic salmon and brown trout

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2.1 Project description

This project represents the first attempts in the development of a general model of hybridization. It is focused on the mating between distant species and on hybridization types 1 and 2, for which hybrids are inviable or infertile, or fertile but without genetic introgression as they undergo genome exclusion during their gametogenesis, thus producing clonal or hemiclonal progeny. Previous modelling of these situations focused on particular cases. We aimed here at proposing a more general model in order to explore the consequences of interspecific hybridization on biodiversity. This model is explored analytically and by simulations through the case study of Atlantic salmon and brown trout.

This hybridization is considered to be of type 1 and has recently increased in rate, due to the release of farm individuals displaying a relaxed mate choice in the wild. We showed that this kind of hybridization is not a major threat for the persistence of these species, but it may represent a major threat in local populations by enhancing the effects of additional threats. This is illustrated by the example of a parasitic disease affecting salmon, for which trout is resistant. Our results are in accordance with the extinction risk that is already observed in some salmon populations of Norway, which are affected by the combined effect of hybridization and a parasitic disease. This application illustrates the range of possibilities for which this model is a key toolbox.

Author contributions CSQ collected and analysed the data and drafted the first version of the manuscript. He also participated in the conception and design of the study as well as the interpretation of the results and the final writing of the manuscript.

2.2 Abstract

Interspecific hybridization is common in nature but can be increased in frequency or even originated by human actions, such as species introduction or habitat modification, which may threaten species persistence. When hybridization occurs between distantly related species, referred to as "*distant hybridization*", the resulting hybrids are generally infertile or fertile but do not undergo chromosomal recombination during gametogenesis. Here, we present a model describing this frequent but poorly studied interspecific hybridization to assess its consequences on parental species and to anticipate the conditions under which they can reach extinction. Our general model fully incorporates three important processes: density-dependent competition, dominance/recessivity inheritance of traits and assortative mating. We demonstrate its use and flexibility by assessing population extinction risk between Atlantic salmon and brown trout in Norway, whose interbreeding has recently increased due to farmed fish releases into the wild. We identified the set of conditions under which hybridization may threaten salmonid species. Thanks to the flexibility of our model, we evaluated the effect of an additional risk factor, a parasitic disease, and

showed that the cumulative effects increase dramatically the extinction risk. The consequences of distant hybridization are not genetically, but demographically mediated. Our general model is useful to better comprehend the evolution of such hybrid systems and we demonstrated its importance in the field of conservation biology to set up management recommendations when this increasingly frequent type of hybridization is in action.

2.3 Introduction

The evolution of many plant and animal taxa has been influenced by natural interspecific hybridization (Arnold and Martin, 2010). However, when hybridization originates from or is intensified by anthropogenic factors, it may lead to critical consequences for species' persistence, particularly for native rare or threatened species (Allendorf et al., 2001). Among other risks, interspecific hybridization can impact demography, which is of primary importance for the viability of wild populations (Lande, 1988).

Three types of interspecific hybridization can be defined, depending on the evolutionary closeness of parental species and the reproductive characteristics of the F_1 hybrids. The first type concerns species that hybridize but yield inviable or infertile offspring due to post-zygotic barriers, such as high difference in chromosomes homology and number. In this case, the waste of reproductive effort may threaten parental species (Rhymer and Simberloff, 1996). For example, the replacement of the endangered freshwater fish *Pseudorasbora pumila* by the exotic *P. parva* in Japan is accelerated by their hybridization that produces sterile F_1 hybrids (Konishi and Takata, 2004). In the second type, hybrids are viable and fertile, but no recombination between homologous chromosomes occurs during their meiosis, leading to the formation of clonal or hemiclonal gametes. For example, hybrids from two European freshwater fish, the roach (*Rutilus rutilus*) and the bream (*Abramis brama*), produce non-recombinant gametes of both species (Yakovlev et al., 2000). Other hybrids may yield gametes containing the haploid genome of only one of the species, excluding the genome of the other parent during or before meiosis, resulting in the hemiclonal transmission of the genome of one parental species. Examples are found in many taxa, such as the Bacillus stick insects (Mantovani and Scali, 1992),

in the teleost fish *Squalius* (Crespo-Lopez et al., 2006), or in frogs of the genus *Pelophylax* (Kierzkowski et al., 2011). Finally, the third type of interspecific hybridization is characterised by F_1 hybrids undergoing recombination between homologous chromosomes during meiosis, resulting in reciprocal genetic introgression from one species into the other. This type of interspecific hybridization may lead to various outcomes, such as: i) the replacement of one or both species by a hybrid-swarm (McDevitt et al., 2009); ii) the formation of an hybrid zone more or less extended depending on the intensity of the hybrid depression (Barton and Hewitt, 1985); or iii) the introgression of neutral or beneficial alleles from one species to the other, impacting the evolution of the introgressed species (Currat et al., 2008b; Dasmahapatra et al., 2012).

The first two types are mainly the result of distant hybridization, that is, hybridization between distantly related taxa, which can belong to different species, to different genera, subfamilies or even to different orders (Lampert, 2009; Liu, 2010). In such cases, reproductive behaviour permits interspecific mating to some extent, but genetic barriers of varying intensity constraining offspring fecundity or genetic introgression between parental species exist (Yakovlev et al., 2000). Because types 1 and 2 have been under-studied and no general model exists to predict non-trivial outcomes, our aim is to develop a simple and more general model to study those cases. We did not, however, include hybridization type 3 in the present work.

Attempts have already been made at modelling hybridization of type 1, in which hybrids are viable but infertile (Rodriguez, 1996), or hybridization of type 2, in which hybrids are fertile but with gametes containing a non-recombined genome (Som and Reyer, 2006). However, these models describe particular hybridization systems and are thus taxon-specific. Moreover, they do not fully address a process that is essential to investigate the demography of parental species, namely: density-dependent competition of hybrids with one or both species. Satake and Araki (2012) proposed a one-gene two-alleles model that accounts for density-dependent recruitment from one to the next generation, but this model was intended to study intraspecific population interactions. These authors incorporated only panmictic mating between interacting populations, as they belong to a

single species. In addition, the degree of dominance/recessivity of the alleles coding for the inherited traits in hybrids, such as resistance to diseases or to environmental disturbance, is an important parameter that can substantially modify the outcome of the system. Therefore, no current method allows modelling distant hybridization systems in which assortative mating exists between the interbreeding species and which integrates the degree of dominance/recessivity inheritance and density-dependent competition.

Here we present a general model that describes the interspecific hybridization of type 1 and 2, that is, distant hybridization or the non-introgressive types. Our model considers a community composed of diploid parental species, with or without overlapping generations, and incorporates: 1) intra- and inter-specific density-dependent competition; 2) the degree of dominance/recessivity of the alleles in hybrids; and 3) assortative mating through mate choice relaxation between the interacting species. The model also considers the possibility that post- F_1 individuals can be of different polyploidy forms. Our new general model may be applied in a large range of real situations and we will illustrate its usefulness by assessing extinction risk through the study of a real case of interspecific hybridization of type 1 for which abundant literature exists.

We applied our model to assess the impact of distant hybridization on Atlantic salmon (*Salmo salar*) and brown trout (*Salmo trutta*) in Norwegian rivers, whose hybridization has been increasing due to the release of farmed fishes into the wild. Despite the high difference in chromosome number between Atlantic salmon ($2n = 58$) and brown trout ($2n = 80$), F_1 hybrids are viable and fertile (Gray et al., 1993). However, they show differential mortality depending on the female parent (Fig. 2.1), with high offspring survival when the female is an Atlantic salmon and the opposite when the female is a brown trout (Alvarez and Garcia-Vazquez, 2011). Although F_1 hybrid females produce viable offspring when they mate with an Atlantic salmon, the F_2 hybrids produce essentially inviable offspring when mating with any kind of hybrids or parental species (Garcia-Vazquez et al., 2004; Castillo et al., 2007) (Fig. 2.1). For this reason, we consider interspecific hybridization as being of type 1, with viable but infertile hybrids.

Hybridization rates between Atlantic salmon and brown trout is increased by human

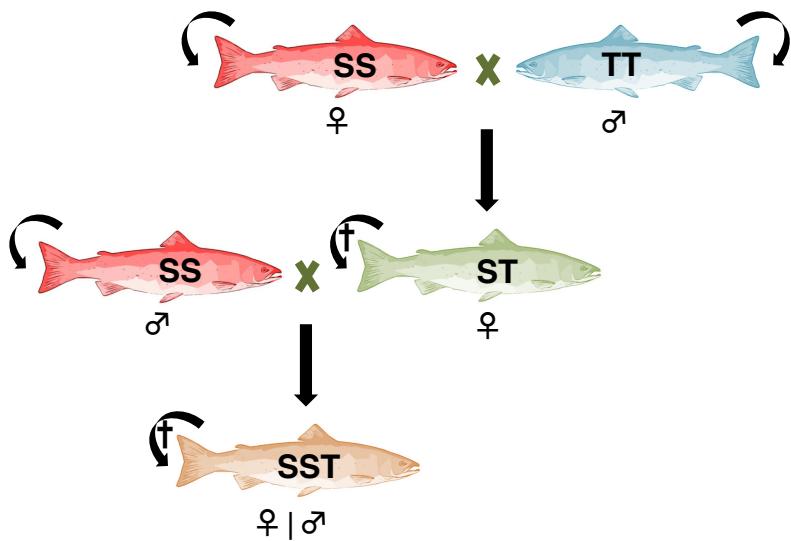


Figure 2.1. Fertile mating pairs of the case study. Straight and curve arrows represent heterotypic and homotypic mating, respectively. SS = Atlantic salmon; TT = brown trout; ST = first-generation hybrid; SST = second-generation hybrid (triploids). The cross symbol (\dagger) means that mating leads to inviable offspring. Other crosses that produce high level of mortality at hatching (>95%) and malformations in the remaining offspring are not shown (see text).

accidental and deliberate releases of farmed fishes. Once in the wild, these fishes show a relaxed mate choice with frequent interspecific crosses, leading to hybrid frequency exceeding 10% (Jansson and Ost, 1997). Levels of up to 29% or even 60% were reported in some Norwegian rivers (Urke et al., 2010), where the hybridization rate seems to be higher in rivers hosting small and threatened populations of Atlantic salmon than in rivers with large populations (Hindar and Balstad, 1994). This human increased hybridization rate between Atlantic salmon and brown trout may threaten local populations of parental species. Using our model, we investigated the potential consequences of this interspecific hybridization on populations of the two salmonids and identified the conditions that lead to local extinction.

2.4 Materials and Methods

2.4.1 Description of the model

Our model considers interspecific hybridization of diploid organisms, without chromosomal recombination in F_1 hybrids. The genotype class of parental species 0 is codified as 00 and that of parental species 1 as 11. The abundance of parental species is noted as N_0 and N_1 , respectively. The number of F_1 hybrids is noted as $N_{\frac{1}{2}}$ and their genotype class is codified as 01. If crosses between F_1 hybrids and the parental species 0 and 1 generate triploid forms, these forms are codified as 001 with abundance $N_{\frac{1}{3}}$, and as 011 with abundance $N_{\frac{2}{3}}$, respectively. Additional polyploidy forms may be easily incorporated into the model following the same reasoning.

The contribution of each genotype class to the next generation is computed as the frequency of mating between individuals of a given genotype class i with individuals of genotype class j (where j can be equal or different from i), compared to all possible mating combinations. Thus, the probability M_{ij} for individuals of class i to mate with one of class j , for all $i,j \in [0,\dots,1]$ is:

$$M_{ij} = \frac{\gamma_{ij} N_{j(t)}}{\phi_{i(t)}} \quad (2.1)$$

Where $\phi_{i(t)}$ is a normalization factor such that $\sum_i M_{ij} = 1$. In our model, the parameter γ_{ij} is a general measure of the mating success between individuals of class i and j and is called hereafter "*interbreeding success rate*". The success rate can be reduced by (1) prezygotic barriers, in which case the resulting value of $1 - \gamma_{ij}$ could represent a measure of assortative mating; by (2) postzygotic barriers, where γ_{ij} may be seen as a measure of hybrid viability and fertility; or by (3) a combination of both types of barriers. In any case, when $\gamma_{ij} = \gamma_{ji}$, mating success is symmetrical between both species while it is asymmetrical when $\gamma_{ij} \neq \gamma_{ji}$. When $\gamma_{ij} = \gamma_{ji} = 0$, there is no interbreeding between the two species, whereas when $\gamma_{ij} = \gamma_{ji} = 1$, the reproduction is panmictic between both

species. Any other value of γ_{ij} between 0 and 1 indicates that mating is locally non-random and reproduction occurs more often between members of the same genotype class i than between individuals of genotype class i and j (see Ferdy and Austerlitz, 2002; Currat et al., 2008b).

To calculate the population renewal of class k , we first calculate the number of breeding pairs composed of individuals of class i and j yielding offspring of class k , weighted by the fraction of the gametes that can lead to an offspring of class k and by the relative fitness of class k , expressed as:

$$b_{ij,k(t)} = N_{i(t)} M_{ij(t)} C_{ij,k} \omega_k \quad (2.2)$$

where $C_{ij,k}$ is the fraction of offspring of class k resulting from a reproduction event between individuals of class i and j . Because in some cases genome exclusion before meiosis leads to the absence of particular gamete types or, alternatively, imperfect meiosis can lead to diploid gametes, the parameter $C_{ij,k}$ is used to determine the proportion of each offspring class resulting from each kind of crosses.

We introduce the parameter ω_k , which represents the fitness of a character in the offspring of class k to which parents of class i and j may contribute. For example, this can be a variable level of resistance to a disease or to environmental disturbances. For the parental species with the highest fitness has $\omega_i = 1$, while for the other parental species ω_j is a fraction of 1. In hybrids, the value of ω_k depends on the dominance degree of the character in one parental species relative to the other (ε). For hybrids of class k , it is calculated as $\omega_k = \varepsilon_{ik} \omega_i + \varepsilon_{jk} \omega_j$, with $\varepsilon_{ik} + \varepsilon_{jk} = 1$. For instance, if $\varepsilon_{ik} = 1$ and $\varepsilon_{jk} = 0$, a character with ω_i is dominant while a character with ω_j is recessive. If $\varepsilon_{ik} = \varepsilon_{jk} = 0.5$, both characters are codominant.

The final weighted number of breeding pairs yielding offspring of class k is obtained by the sum of all weighted breeding pairs generating progeny of class k

$$n_{k(t)} = \sum_i \sum_j b_{ij,k(t)} \quad (2.3)$$

To calculate the population renewal of wild adult populations, we extend a version of the Ricker model (Wilbur, 1976) in which we also take into account the "*lattice effects*" (dynamic outcomes due to the discrete nature of the numbers of individuals in a population) by rounding off its results, with the following recursion equation (Henson et al., 2001).

$$N_{k(t+1)} = \text{round} \left[N_{k(t)} S_k + R_k n_{k(t-\theta)} e^{-\frac{n_{k(t-\theta)} \sum_{k \neq i} \alpha_{ki} n_{i(t-\theta)}}{V_k}} \right] \quad (2.4)$$

The first term on the left side of equation (2.4) represents the fraction of adults that survive from one to the next reproductive season, in which the parameter S_k is the adult survival probability for the genotype class k . The second term of equation (2.4) denotes the expected number of offspring that survive until sexual maturity after intra- and inter-specific density-dependent competition effects, where θ indicates the time to reach maturity in $t + 1$. If S_k and θ are equal to zero, it corresponds to a non-overlapping generation model. The parameter R_k represents the population growth rate, that is, the number of progeny per breeding pair that survive until sexual maturity. The parameter α_{ki} represents the interspecific competition coefficient, with $\alpha_{ki} = 1$ indicating that individuals of class l have as much influence on individuals of class k than those of their own class k . When $\alpha_{ki} = 0$ there is no competition between individuals of class k and l , while values of α_{ki} between 0 and 1 indicate that an individual of class l exerts on an individual of class k only a fraction of the competition exerted by an individual of the same class k . Finally, V_k denotes the habitat size as introduced by Henson et al. (2001), where $\sum_{k \neq i} \frac{\alpha_{ki}}{V_k}$ determines the interspecific density-dependent mortality before sexual maturity.

For clarity, the model described above considers gonochoric organisms (the two sexes are carried by different individuals) with equal sex ratio or hermaphroditic organisms. But

a simple extension of the model can account for gonochoric organisms with unequal sex ratio (see discussion).

2.4.2 Case study

To demonstrate the usefulness of our model we implemented it by studying a case of hybridization type 1, with viable but infertile hybrids. We assess the impact of interbreeding with asymmetrical reproductive success on populations of Atlantic salmon (*Salmo salar*) and brown trout (*Salmo trutta*) in Norwegian rivers. We considered anadromous and iteroparous populations of Atlantic salmon (noted species S with genotype SS) and brown trout (noted species T with genotype TT). According to direct estimates of parameters' values taken from populations of both species in Norwegian rivers (Jonsson and Jonsson, 2011), sexual maturity was set at four years ($\theta = 3$) and adult survival rate was 30% ($S = 0.3$). The parameters of growth rate (R) and habitat size (V) were estimated by a non-linear least square method (see Appendix S1, Supporting Information).

As there is some evidence of species habitat overlap (Armstrong et al., 2003), we compared population dynamics with and without interspecific competition to differentiate the effects of interspecific competition from those of hybridization. However, as habitat requirement and behaviour of F_1 and F_2 hybrids have not been studied yet, we opted not to fix but to use a density-dependent form of competition between genotype classes i and j , calculated as:

$$\alpha_{ij(t)} = \frac{N_{j(t)}}{N_{j(t)} + N_{i(t)}} \quad (2.5)$$

This kind of competition depends on the number of individuals in a given habitat at a given time t (Currat and Excoffier, 2004).

We modelled the mate choice of females assuming an equal sex ratio during the mating phase. The parameter γ_{ST} is the interbreeding success rate between Atlantic salmon females (N_S) and brown trout males (N_T), whereas γ_{TS} is between brown trout females

and Atlantic salmon males (see Table 2.2, Supporting Information, for a list of crosses in this case study). F_1 hybrids ($N_{\frac{1}{2}}$) and F_2 allotriploids ($N_{\frac{2}{3}}$) were considered to have a panmictic reproduction ($\gamma_{\frac{1}{2}S} = \gamma_{\frac{1}{2}T} = \gamma_{\frac{2}{3}S} = \gamma_{\frac{2}{3}T} = \gamma_{\frac{1}{2}\frac{2}{3}} = \gamma_{\frac{2}{3}\frac{1}{2}} = 1$). In accordance with Galbreath and Thorgaard (1995), offspring resulting from crosses between females N_S and males N_T (offspring of type $N_{\frac{1}{2}}$), and from crosses between females $N_{\frac{1}{2}}$ and males N_S (offspring of type $N_{\frac{2}{3}}$) were considered to be as fertile as offspring resulting from homotypic parental species crosses ($C_{ij,k} = 1$). All other mating combinations involving different genotype classes were considered unsuccessful ($C_{ij,k} = 0$) due to the high level of mortality at hatching (>95%) and malformations in the surviving offspring (Galbreath and Thorgaard, 1995; Garcia-Vazquez et al., 2004; Castillo et al., 2007).

Although allotriploid individuals ($N_{\frac{2}{3}}$) have never been detected in the wild, we considered them here because: 1) fecundation success is high between hybrid females and Atlantic salmon males ($N_{\frac{1}{2}} \times N_S$) (Galbreath and Thorgaard, 1995); 2) allotriploid progeny was produced and grown successfully in a semi-natural stream (Garcia-Vazquez et al., 2003); and 3) the ploidy of hybrids and their post- F_1 status have been rarely assessed in the field (Castillo et al., 2007).

Many Norwegian Atlantic salmon populations are affected by a disease caused by the monogenean ectoparasite *Gyrodactylus salaris*, which was introduced in Norway in the 1970's by Atlantic salmon transported from the Baltic sea (Johnsen and Jensen, 1991). Atlantic salmon are severely affected in most of the infected rivers, while brown trout are known to be resistant. Hybrids have an intermediate susceptibility (Bakke et al., 1999). We incorporated the effects of this disease by decreasing the relative fitness of Atlantic salmon; we tested a 20% and a 40% reduction of fitness as compared to brown trout ($\omega_S = 0.8$ and $\omega_S = 0.6$). F_1 and F_2 hybrids were considered to have an intermediate susceptibility between both species ($\epsilon_{S\frac{1}{2}} = \epsilon_{T\frac{1}{2}} = \epsilon_{S\frac{2}{3}} = \epsilon_{S\frac{1}{2}\frac{2}{3}} = 0.5$).

2.5 Results

2.5.1 Analytical exploration of the model

We performed a theoretical description of the dynamics of the populations, first without considering the effect of interspecific hybridization. Considering equation (2.4), the population N_i reaches a non-trivial equilibrium (different from zero) at:

$$\dot{N} = \frac{V_i \ln \frac{R_i \omega_i}{1-S_i} - \alpha_{ij} V_j \ln \frac{R_j \omega_j}{1-S_j}}{\omega_i (1 - \alpha_{ij} \alpha_{ji})} \quad (2.6)$$

The population size increases with higher values of growth rate (R_i) and habitat size (V_i) and decreases with the interspecific competition coefficient (α_{ij}). In cases involving fitness reduction, the density of class i increases with higher values of ω_i and decreases with ω_j , which produces an increase of competitiveness of class j . If both species do not compete, N_i is positive only if $\frac{R_i \omega_i}{1-S_i} > 0$; in this case the output is undefined when the adult survival (S_i) is equal to 1. The Ricker model produces oscillatory population sizes due to the instability of the equilibrium point. Values of growth rate $R_i = \frac{(1-S_i)e^{\frac{2}{1-S_i}}}{\omega_i}$ yield an unstable equilibrium and the population dynamic becomes chaotic, the output being thus strongly affected by the initial conditions of the system.

We further explored the dynamics of our model by including the effects of hybridization. Due to the additional term γ_{ij} in equation (2.1) and the density dependent competition effect included in equation (2.4), the coupled dynamics of parental and hybrid abundances are not analytically solvable. We thus analysed only a special case of interspecific hybridization ($M_{ij} = \frac{\gamma_{ij} N_{j(t)}}{N_{i(t)} + \gamma_{ij} N_{j(t)}}$), with maximum competition ($\frac{\alpha_{ij}}{V_i} = \frac{\alpha_{ji}}{V_j} = 1$) and with symmetric interbreeding success rate and equal demographic parameters for both parental classes ($\gamma_{ij} = \gamma_{ji}$; $R_i = R_j$; $V_i = V_j$). Here, the density-dependent effect among populations is cancelled and the dynamic depends only on the interbreeding rate and the hybrid survival probability. The proportion of parental species N_1 in a community composed of parental species N_0 , F_1 hybrids ($N_{\frac{1}{2}}$) and F_2 hybrids ($N_{\frac{2}{3}}$) reaches non-zero equilibrium at:

$$\frac{\dot{N}_1}{\dot{N}_0 + \dot{N}_1 + \dot{N}_{\frac{1}{2}} + \dot{N}_{\frac{2}{3}}} = \frac{2R_1^2 \left(1 - S_{\frac{2}{3}}\right) \left(1 - S_{\frac{1}{2}}\right)}{\gamma_{10} R_{\frac{1}{2}} \left(1 - S_1\right) \left(2R_1 \left(1 - S_{\frac{2}{3}}\right) + R_{\frac{2}{3}} \left(1 - S_1\right) \left(1 + \gamma_{10}\right) + 4R_1^2 \left(1 - S_{\frac{2}{3}}\right) \left(1 - S_{\frac{1}{2}}\right)\right)} \quad (2.7)$$

The proportion of N_1 increases with higher values of growth rate; it decreases with increasing interbreeding rate (with N_0) and with the survival of F_1 and F_2 hybrids. This analytical exploration of our model showed that, despite its apparent simplicity, the model is nonlinear and the outputs are not trivial, strongly depending on the input parameters. Consequently, no general conclusion can be drawn that would be valid for a wide range of situations; each case should be cautiously investigated. More complex situations, involving competition and interbreeding success rates of varying intensities are difficult to explore analytically, but may be solved numerically as illustrated by our case study.

2.5.2 Assessing extinction risk in salmon and trout

Using our model we analysed a case of hybridization type 1, assessing the potential effects of hybridization between Atlantic salmon and brown trout in Norwegian rivers. This interspecific cross is characterized by a sex-biased reproductive success due to high offspring mortality in crosses where the female is a brown trout. To understand the dynamics of this particular hybridization system and to identify the conditions that can lead to extinction risk, we simulated a wide range of situations by varying the values of key parameters of the model, such as interbreeding success rate, interspecific competition, habitat size and growth rate. We also evaluated the effects of a disease that reduces the fitness of salmons and hybrids.

The parameters R (growth rate) and V (habitat size) were estimated through a non-linear least square method (see Table 2.3, Supporting Information). The best estimated values were $R = 3$ (SE = 0.7) and $V = 51$ (SE = 10) for both species. The same parameter values were used for F_1 and F_2 hybrids (Table 2.1). In the scenario where the popula-

Table 2.1. List of functions and parameters with their case study values (in parenthesis)****List of functions***

N_i	Number of adult individuals of genotypic class i^{\dagger}
M_{ij}	Mating probability between individuals of genotypic class i and j
$b_{ij,k}$	Weighted number of breeding pairs i and j resulting in offspring of class k
n_k	Final weighted number of breeding pairs yielding offspring of class k

Demographic parameter

θ	Time delay from hatching to age of maturity (3)
S	Adult survival probability (0.3)
R	Growth rate per capita (3)
α	Interspecific competition coefficient
V	Habitat size (51)

Interbreeding parameters

γ	Interbreeding success rate (1 ^a)
C	Relative fraction of offspring of various types produced by breeding pairs [‡]
ω	Fitness of an inherited character (1 ^b)
ε	Dominance degree of parental traits on hybrid groups (0.5 ^c)

*Fixed value for: ^a $\gamma_{\frac{1}{2}S}$, $\gamma_{\frac{1}{2}T}$, $\gamma_{\frac{2}{3}S}$, $\gamma_{\frac{2}{3}T}$, $\gamma_{\frac{1}{2}\frac{2}{3}}$, $\gamma_{\frac{2}{3}\frac{1}{2}}$; ^b ω_T ; ^c $\varepsilon_{S\frac{1}{2}}$, $\varepsilon_{T\frac{1}{2}}$, $\varepsilon_{S\frac{2}{3}}$, $\varepsilon_{T\frac{2}{3}}$.

[†] Initial size: $N_T = N_S = 50$; $N_{\frac{1}{2}} = N_{\frac{2}{3}} = 0$.

[‡] see Table S2.2.

tion of Atlantic salmon is not affected by the parasitic disease ($\omega_S = 1$), we simulated the outcomes of a gradual increase of a symmetrical interbreeding success rate ($\gamma_{ST} = \gamma_{TS}$) up to a completely panmictic reproduction between both species; no changes in the proportion of salmon and trout in the community was observed. In simulations with competition we used a density-dependent form of competition between genotype classes (see methods). When interspecific competition is considered only among hybrids and parental classes ($\alpha_{ST} = \alpha_{TS} = 0$), or when competition also occurs between Atlantic salmon and brown trout ($0 < \alpha_{ST} \neq \alpha_{TS} > 0$), no extinctions were observed when the interbreeding success rate is symmetrical (Fig. 2.2a and 2.2b, respectively). In simulations where the interbreeding success rate is asymmetrical ($\gamma_{ST} \neq \gamma_{TS}$), due for instance to unequal mate choice relaxation in the parental species, and when there is no interspecific competition between salmon and trout, then extinction is observed only in extreme situations with high

values of interbreeding success rate (Fig. 2.2a). Overall, these simulation results indicate that, without interspecific competition, hybridization alone is not sufficient to drive one species population to extinction. Interestingly, due to competition with hybrids (which are more abundant when interbreeding success rate is larger in salmon), the critical area of salmon extinction ($N_S = 0$) is three times larger (6%) than the area of brown trout extinction (2%, $N_S = 100$; Fig. 2.2a). Yet, if interspecific competition is considered, these areas are equal and larger for both species (about 36%; Fig. 2.2b). Here, a difference of interbreeding success rates larger than 12% ($\Delta(\gamma_{ST}, \gamma_{TS}) > 0.12$) generates either salmon or trout population extinction, depending on the orientation of the deficit. This indicates that if both species are in competition for resources, the one with the highest mate choice relaxation has the lowest survival probability, due to wasted reproductive effort.

When we simulate the additional effect of the parasitic disease by reducing salmon fitness by 20% ($\omega_S = 0.8$) as compared to brown trout, and in the case of no interspecific competition, the results indicate that both species survive in the fish community at any level of symmetric interbreeding success rate ($\gamma_{ST} = \gamma_{TS}$). However, when this rate is highly asymmetric ($\gamma_{ST} \neq \gamma_{TS}$) with values of $\gamma_{TS} > 0.78$ and $\gamma_{ST} = 0$, then the salmon population become extinct. The critical area of Atlantic salmon extinction ($N_S = 0$) represents 30% of all possible combinations of asymmetric interbreeding (Fig. 2.2c). When we consider interspecific competition (Fig. 2.2d), salmon is completely displaced by brown trout in all simulated conditions of symmetrical interbreeding success rates ($\gamma_{ST} = \gamma_{TS}$) or when interbreeding success rates are skewed towards salmon ($\gamma_{ST} > \gamma_{TS}$). However, when interbreeding success rates are skewed towards trout ($\gamma_{ST} < \gamma_{TS}$), it allows coexistence if $\Delta(\gamma_{ST}, \gamma_{TS}) > 0.11$, or a complete displacement of brown trout if $\Delta(\gamma_{ST}, \gamma_{TS}) > 0.35$.

When we simulate a salmon fitness reduction of 40% ($\omega_S = 0.6$) with no interspecific competition, salmon population become extinct if $\gamma_{ST} > 0.55$ and $\gamma_{TS} = 0$. With other values of γ_{ST} and γ_{TS} , it cannot subsist at a proportion higher than 50% (Fig. 2.2e). The critical area of extinction for the Atlantic salmon represents 51.2% of all combinations of asymmetrical interbreeding success rate. Regarding brown trout, it persists at any level of symmetric or asymmetric interbreeding success rate (Fig. 2.2e). When we consider inter-

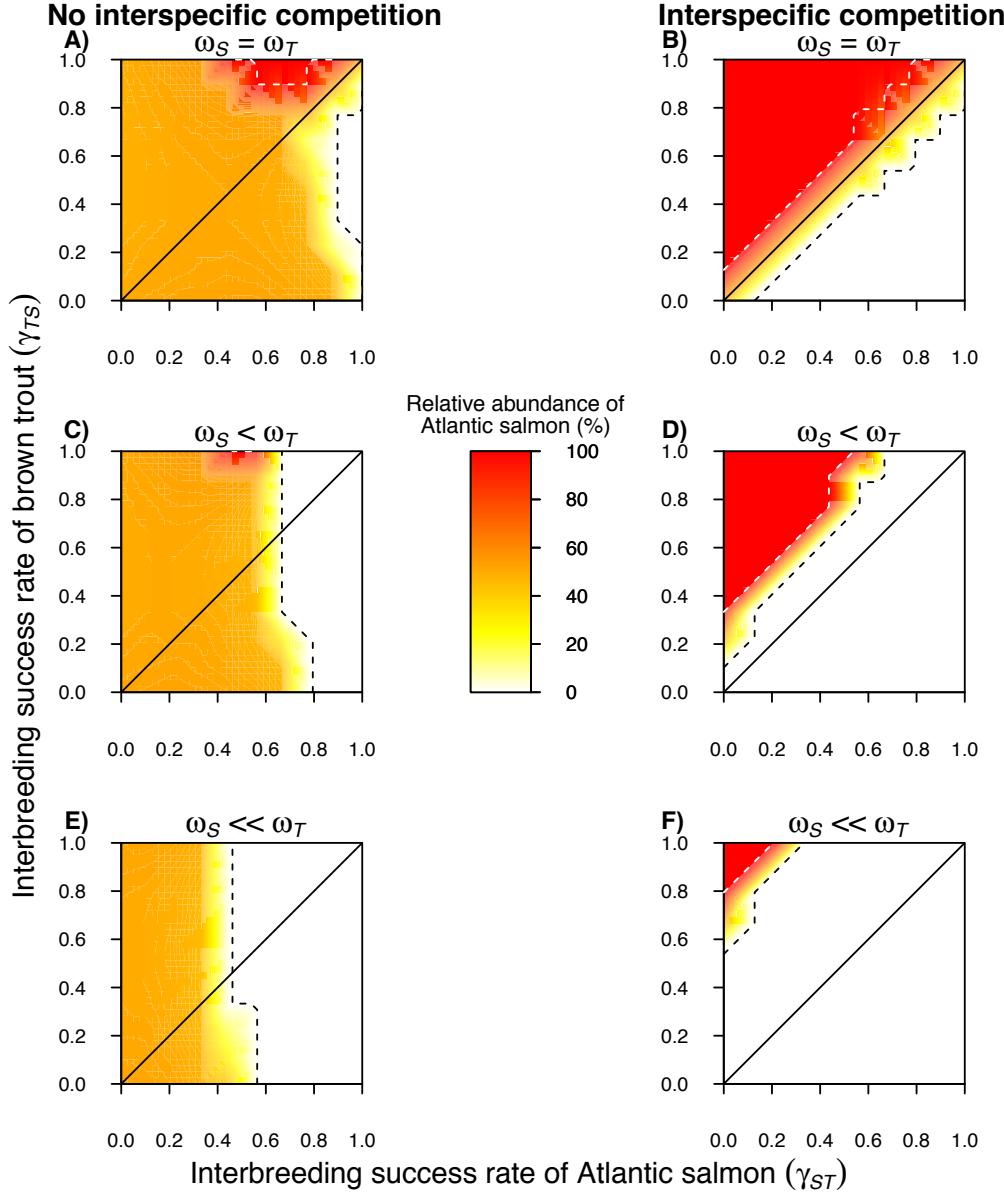


Figure 2.2. Relative abundance of Atlantic salmon (%) as compared to brown trout ($\frac{N_s}{N_s + N_T}$). The diagonal solid lines represent equal interbreeding success rates between Atlantic salmon (γ_{ST}) and brown trout (γ_{TS}). Black or white dotted lines delimit the extinction area of Atlantic salmon and brown trout population, respectively. $\omega_S = \omega_T$ indicates equal fitness for Atlantic salmon ($\omega_S = 1$) and brown trout. $\omega_S < \omega_T$ indicates that Atlantic salmon has a 20% fitness reduction ($\omega_S = 0.8$). $\omega_S \ll \omega_T$ indicates that Atlantic salmon has a 40% fitness reduction ($\omega_S = 0.6$). In a), c), and e), Atlantic salmon and brown trout do not compete. In b), d), and f), Atlantic salmon and brown trout have density-dependent competition. The data presented correspond to the situation after 100 time steps (years).

specific competition in the simulations (Fig. 2.2f), any level of symmetric interbreeding success rates ($\gamma_{ST} = \gamma_{TS}$) or asymmetric rates skewed towards Atlantic salmon ($\gamma_{ST} > \gamma_{TS}$) leads to the displacement of salmon by brown trout, while, when skewed towards brown trout ($\gamma_{ST} < \gamma_{TS}$), it allows coexistence if $\Delta(\gamma_{ST}, \gamma_{TS}) > 0.55$ or a complete displacement of brown trout if $\Delta(\gamma_{ST}, \gamma_{TS}) > 0.8$. Overall, these simulations show that the parasitic disease strongly perturbs the system by threatening salmon, and this effect is enhanced by high interbreeding success rates in salmon or limited by high interbreeding success rates in trout.

The results presented above (Fig. 2.2) remain valid when using the upper and lower limits of the 95% confidence interval of the growth rate (R) and habitat size (V) parameters (Fig. 2.5 and Fig. 2.6, Supporting Information). The results with interspecific competition and symmetrical interbreeding success rates are independent of the changes in R and V . Without interspecific competition, the probability of reaching extinction is inversely proportional to both parameters R and V . We can therefore expect that without competition, the effect of hybridization, combined with the parasitic disease, would be stronger in small rivers supporting smaller and local populations, whereas the effect of hybridization would be negligible in larger rivers, with bigger populations.

We then performed a sensitivity analysis of the system regarding the population growth rate parameter (R), without considering interspecific competition (Fig. 2.3). Under a salmon fitness reduction of 40% ($\omega_S = 0.6$), a higher value of R for all the interacting populations counteracts the negative effects that hybridization produces on the demography of salmon. With higher growth rates, higher interbreeding success rates ($\gamma_{ST} = \gamma_{TS} > 0.4$) are necessary to cause population extinction. Moreover, the dominant or recessive inheritance of resistance to pathogens in hybrids seems to have a more pronounced effect when growth rates are higher. When the trout resistance to pathogens is inherited recessively by hybrids, values of $R = 6$ allow salmon persistence even with a panmictic mate choice ($\gamma_{ST} = \gamma_{TS} = 1$). However, when resistance to pathogens is dominantly or co-dominantly inherited, then salmon extinction occurs (Fig. 2.3a). A value of $R = 12$ generates oscillatory dynamics allowing salmon and hybrids to survive in the community even at high

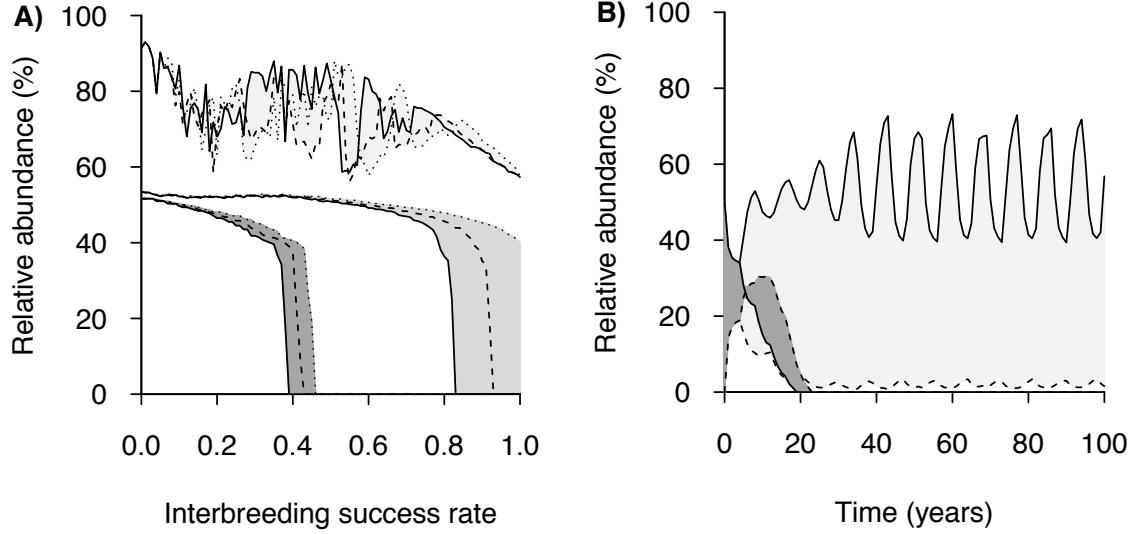


Figure 2.3. Relative abundance of a population of Atlantic salmon affected by a disease ($\omega_S = 0.6$). The abundance is given in percent of the total number of salmonids $\frac{N_S}{N_S + N_T + N_{\frac{1}{2}} + N_{\frac{2}{3}}}$. Brown trout are resistant to disease ($\omega_T = 1$) and are not in competition with Atlantic salmon. (■) $R = 3$; (□) $R = 6$; (▨) $R = 12$. In A) effects of varying yet symmetric interbreeding success rate ($\gamma_{ST} = \gamma_{TS}$); the trout disease resistance is inherited with the following properties: (—) dominantly in hybrids ($\varepsilon_{T\frac{1}{2}} = 1$ and $\varepsilon_{T\frac{1}{2}\frac{2}{3}} = 1$); (···) recessively in hybrids ($\varepsilon_{T\frac{1}{2}} = 0$ and $\varepsilon_{T\frac{1}{2}\frac{2}{3}} = 1$; and (- -) codominantly in hybrids ($\varepsilon_{T\frac{1}{2}} = 0$ and $\varepsilon_{T\frac{1}{2}\frac{2}{3}} = 0$). In B) time series of the relative abundance of Atlantic salmon (—) and hybrid populations (- -) ($(N_{\frac{1}{2}} + N_{\frac{2}{3}})/(N_0 + N_1 + N_{\frac{1}{2}} + N_{\frac{2}{3}})$). The data presented correspond to the situation after 100 time steps (years).

interbreeding success rate ($\gamma_{TS} = 1$), and even if the trout resistance to pathogens is dominantly inherited by hybrid classes (Fig. 2.3a and 2.3b). With $R = 3$, an inflection point is produced at 6 time steps (years), where the number of hybrids exceeds the number of salmon, but both classes become extinct before 23 time steps (years). A minimum of $R = 8$ is required to maintain the population of salmons, whereas values of $R > 14$ generate non-stable equilibrium in the salmonids community (Fig. 2.4). If, in addition to the salmon fitness reduction of 40%, we add interspecific competition in our simulations, this factor drives salmon extinction even without considering interspecific hybridization (data not shown). These results indicate that hybridization alone is unlikely to cause salmon population extinction, but if it occurs in combination with competition and/or with the disease examined here, together they constitute a serious threat for salmon populations.

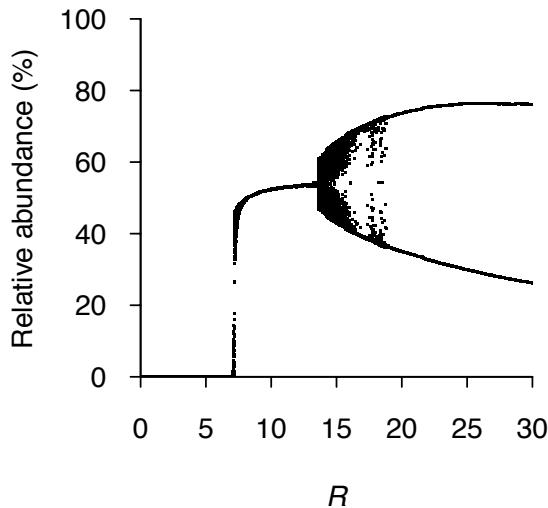


Figure 2.4. Bifurcation diagram of the effect of growth rate (R) on the Atlantic salmon relative abundance. When $R \geq 8$, Atlantic salmons are not threatened; when $R > 15$, then salmon density starts to be chaotic

2.6 Discussion

2.6.1 Distant hybridization

We developed a general model to assess how hybridization between distant species can impact the demography of parental species. This type of hybridization occurs, on one hand, when hybrids are inviable or infertile due to post-zygotic barriers, and the risk to parental species resides in the wasted reproductive effort, as it has been reported in mammals and birds (Rozhnov, 1993; Birkhead and Brilland, 2007). On the other hand, hybrids can be fertile, but their gametes may contain the non-recombined haploid genome of the two parental species (in different gametes) or a single haploid genome as the product of genome exclusion before or during meiosis. Hybrids producing clonal or hemiclonal gametes are common in plants and invertebrates (Mantovani and Scali, 1992; Gugsa et al., 2006). In vertebrates, it has been frequently reported in amphibians, fish and reptiles (Dawley et al., 1987; MaCulloch et al., 1995; Lode, 2001) but not in birds nor in mammals. The model presented herein accounts for all these cases and is therefore useful to study and generate theoretical expectations in a large variety of organisms and biolog-

ical issues. For instance, our model could be implemented to determine the conditions under which populations may reach a stable equilibrium in gynogenetic, parthenogenetic or hybridogenetic systems. It can also serve to understand how different polyploid forms of hybrid origin can persist over large periods of time. In the field of conservation, it is essential to determine the minimum population size and maximum hybridization rate that a species can stand before interspecific hybridization threatens its persistence. The increasing frequency of interspecific hybridization due to anthropogenic causes and global climate change is of growing concern in conservation biology, where efficient tools to project the consequences on the demography of parental species are particularly welcome.

2.6.2 The salmon and trout analysis

In natural conditions, Atlantic salmon and brown trout present low levels of interspecific hybridization, revealing efficient mechanisms of reproductive isolation between both species (Alvarez and Garcia-Vazquez, 2011). However, hybrids are increasingly frequent (Urke et al., 2010), in particular because escaped individuals raised in farms exhibit a relaxed species mate choice (Castillo et al., 2008). In addition, overfishing and diseases have significantly reduced salmon populations locally (Urke et al., 2010). In such conditions, the rare species has more difficulties in finding a conspecific partner and becomes less demanding when looking for a mate, a situation known as the "*desperation hypothesis*" (Hubbs, 1955). This situation favors hybridization, which in turn accelerates species rarity.

Our results show that the asymmetrical interbreeding success rate between Atlantic salmon and brown trout, which might be principally due to mate choice relaxation, will yield different trends depending on the direction and intensity of the asymmetry. A higher interbreeding success rate in brown trout compared to salmon ($\gamma_{ST} < \gamma_{TS}$) produces fewer scenarios with extinction, because the offspring are inviable. In contrast, a higher interbreeding success rate in Atlantic salmon produces more potential situations with extinction, because the hybrid progeny is viable and competes with the progeny of both parental classes. Interestingly, we found that no extinction is expected if the interbreeding success

rate is symmetrical between both species. Nevertheless, according to our simulations, the interbreeding success rate must be very high ($>70\%$) and asymmetrical to drive populations of one of the two species to extinction, which means that in nature, hybridization *per se* is probably not a serious threat. However, this statement changes when hybridization is combined with an additional threat, such as the disease caused by the monogenean *G. salaries* in Atlantic salmon. In this case, an increasing interbreeding success rate of salmon increases its extinction risk.

We also show that salmon populations can reach extinction with low interbreeding success rates, but only when interspecific competition between both species is high. Although there is evidence that brown trout is a strong competitor that displaces Atlantic salmon, interspecific competition is probably not a major risk in natural sympatric populations, as they coexist in different microhabitats (Armstrong et al., 2003). However, allopatric young Atlantic salmon tend to expand their space in the absence of brown trout (Heggenes and Saltveit, 2007), supporting the idea that brown trout outcompete young salmon in parts of its habitat. If one or both species are exotic, then interspecific competition may be enhanced. This is for instance the case in the Kerguelen Island, where both species were introduced, and brown trout is invading and displacing Atlantic salmon, with little hybridization occurring after the very initial contact (Horreo et al., 2011).

The case of Atlantic salmon and brown trout is an example of human-induced environmental changes that have increased the hybridization rate between species that have historically coexisted in sympatry. However, given the low interbreeding success rates registered in the wild (Horreo et al., 2011), we conclude that interspecific hybridization between Atlantic salmon and brown trout is likely not a threat *per se* for the persistence of most populations, except in very extreme situations where the interbreeding is particularly asymmetrical and high for one or both species. Such a situation may be found in rivers dominated by fishes released from farms (Jonsson et al., 2003), as they show highly relaxed mate choice (Youngson et al., 1993). Our case study also reveals that the combined effects of interspecific hybridization with interspecific competition and/or with an additional threat, such as the parasitic disease, might seriously enhance extinction risk. In

the near future, the effects of global climate change will probably call for a revision of our conclusions, as these modifications may alter habitat characteristics, migration patterns, age of maturity, reproduction time and susceptibility to diseases (Jonsson and Jonsson, 2009b). Our model will be the ideal tool to anticipate the impact of climate change on organisms that may undergo distant hybridization.

2.6.3 Model components

As compared to previous models, the one presented herein simultaneously accounts for important ecological, genetic and behavioural parameters like 1) density-dependent competition at the intra- and the inter-specific level; 2) the fact that traits can be inherited in a dominant or recessive way in hybrids; and 3) variable mate choice relaxation between interacting species leading to case specific assortative mating. This renders our model more realistic, more general and also more flexible as compared to previous attempts. Moreover, the components assembled in our model have been previously presented and validated, some being of general use in ecology and demography. The basic formula for calculating the probability M_{ij} that an individual of class i mates with one of class j in equation (2.1), has been proposed and used in essentially the same way as in Ferdy and Austerlitz (2002) and Currat et al. (2008b). The way we calculate the total number of offspring of a given class k , which is given by equation (2.3), is simply the sum of offspring of class k produced by all possible crosses that generate at least a fraction of class k in their progeny, the later being given by equation (2.2). To consider the temporal dynamics of wild adult populations in equation (2.4), we extended a version of the Ricker model (Wilbur, 1976), which is frequently used in the fields of ecology and population dynamics. Our model also takes into account the "*lattice effects*", in equation (2.4), as proposed by Henson et al. (2001), which has been studied and validated by population ecologists. Finally, our model considers the species habitat size, the parameter V_i in our equation (2.4), in the same way as proposed by Henson et al. (2001).

In our case study, we adapted the way of calculating one variable of the model, the interspecific competition coefficient α_{ij} . Because no prior knowledge about possible val-

ues was available, we used a density-dependent form of competition given by equation (2.5), as proposed by Currat et al. (2004). This exemplifies the flexibility of our model, in which several parameters can be substituted by alternative ways of calculation to cope with case-specific characteristics.

2.6.4 Extensions of the model

While applicable to many situations in its current form, our model may be easily extended to cope with more complex or different systems. As an example of possible extension, the demographic regulation may be modified. The Ricker function used here could be changed, even though it has been designed to be used on a wide range of taxa, including fish, amphibians and insects, which are particularly subject to distant hybridization (Henson et al., 2001). A logistic function can be an alternative way of considering demographic growth (Verhulst, 1838), which avoids the overcompensation of the exponential function that keeps adult recruitment low when spawner abundance is high (Wilbur, 1996). It is also possible to use different times to sexual maturity for the different parental species ($\theta_i \neq \theta_j$), which may affect the dynamics of the system. The interbreeding success rate parameter incorporated in the model provides a mean to easily characterize the combination of factors that control interbreeding success, such as mate choice relaxation between different species or hybrid offspring survival. However, future applications could decompose this parameter into the interacting factors that affect the interbreeding success rate. If gonochoric organisms with unequal sex ratio are considered, the model can be simply modified by performing a separate calculation for males and female, where equation (2.1) and equation (2.2) have to be computed with class i corresponding to the subgroup of females (i^f) and class j to the subgroup of males (j^m). In a similar way, it is possible to consider female fecundity variations among parental species and hybrids, while male fecundity remains unchanged. This can be incorporated with the fitness parameter ω_k of equation (2.2), and by performing different calculations for males and females. An additional development could consist of incorporating genetic introgression into the model. However, further and thorough investigations would be needed to extend our model to

include genetic introgression between parental species.

2.6.5 Limitations of the model

The use of the model is limited to the types of interspecific hybridization that do not involve genetic introgression between the parental species, that is, Type 1 and Type 2 (see introduction). The use of this model can also be limited by the amount of available knowledge about basic population and ecological parameters of the species analysed. Our model has parameters for which plausible values are required to produce accurate solutions. However, some parameters can be estimated by a linear or non-linear approach, as in our case study, if enough information about time-series of species demography is available. It is also possible to use our model to understand the role played by a specific parameter in the system by varying this parameter while keeping all other parameters unchanged.

2.6.6 Conclusions

The model presented herein is a tool that opens new and promising path to investigate and understand evolutionary and conservation issues, including the study of the emergence and evolution of hybrid forms and the understanding of the effects of distant hybridization on the demography of parental species. In conservation biology, our model will permit to set out management recommendations by assessing the effects of alternative strategies to reduce extinction risk, or projecting the impact of emerging threats on already affected or yet unaffected species. Moreover, our model is flexible, as it can be easily modified to accommodate additional parameters or alternative functions to better fit to taxon-specific situations. The script of our model is freely available at: <http://genev.unige.ch/montoya-currat/scripts/>. In the implementation presented here, we have highlighted that hybridization of type 1 between Atlantic salmon and brown trout can lead to important demographic changes in the populations, although extinction is predicted only in very peculiar and improbable situations only. The flexibility of our model enabled us to assess the influence of an additional risk factor, a parasitic disease, and showed that the combined effects of

interspecific hybridization and the unequal resistance to pathogens may lead, this time, to the extinction of affected Atlantic salmon populations.

2.7 Acknowledgments

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2.8 Supporting Information

2.8.1 Appendix S1. Estimation of the growth rate (R) and habitat size (V) parameter values by non-linear least square method

As the growth rate (R) and habitat size (V) parameters cannot be easily estimated in the field, we used a non-linear least square method to assess their values in the case of a local population of Atlantic salmon living in sympatry with brown trout. This method was applied to equation (2.4), without considering interspecific competition ($\alpha_{ij} = 0$) and hybridization ($\gamma_{ij} = 0$), using a 30 years time series (1976-2005, Jonsson and Jonsson, 2009a) of smolts (juveniles that are pre-adapted for marine life) abundances for both species in the river Imsa (Norway). Numbers of adults in this river were estimated by considering 7.8 and 12.8% of smolt to adult survival rate for Atlantic salmon and brown trout, respectively (Jonsson and Jonsson, 2011). We evaluated models with different or equal growth rates and habitat size for each species, incorporating Atlantic salmon and brown trout as dummy variables and densities as responses. We used Akaike information criterion corrected by sample sizes (AIC_c) to select the best-fitted combination of parameters (Burnham and Anderson, 2004), which were taken from the model with the lowest

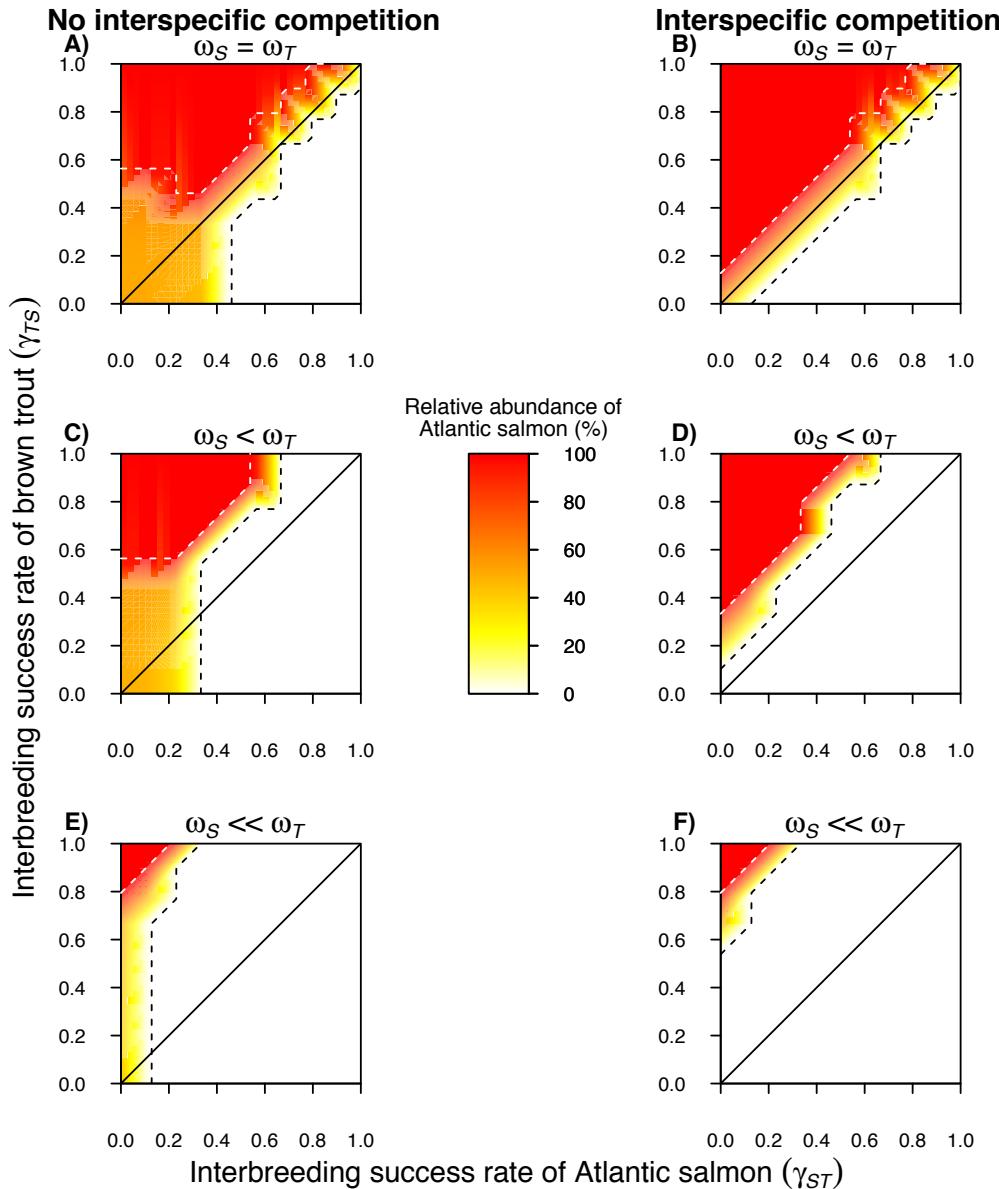


Figure 2.5. Relative abundance of Atlantic salmon (%) as compared to brown trout ($\frac{N_S}{N_S + N_T}$). These results are obtained when using the lower limit of the 95% confident interval of growth rate ($R = 1.63$) and habitat size ($V = 31.4$) (see Fig. 2.2, main text)

AIC_c value.

The best non-linear least square model has equal values of $R = 3$ (SE = 0.7) and $V = 51$ (SE = 10) for both species. This combination of parameters has the minimum AIC_c (Table S2) and is not significantly different from a model with specific values for each species (ANOVA: $F_{2,44} = 0.53$, $P = 0.59$).

Table 2.2. Mating frequencies and relative number of offspring types produced by the inter-crosses among Atlantic salmon (N_S), brown trout (N_T), first-generation hybrids ($N_{\frac{1}{2}}$) and second-generation hybrids ($N_{\frac{2}{3}}$)

Mating pair Female (i) \times Male (j)	Mating frequency (M_{ij})	Relative number of offspring type ($C_{ij,k}$)			
		N_S	$N_{\frac{1}{2}}$	$N_{\frac{2}{3}}$	N_T
$N_T \times N_T$	$\frac{N_T}{\varphi_T}$	0	0	0	1
$N_T \times N_{\frac{1}{2}}$	$\frac{\gamma_{TS} N_{\frac{1}{2}}}{\varphi_T}$	0	0	0	0
$N_T \times N_{\frac{2}{3}}$	$\frac{\gamma_{TS} N_{\frac{2}{3}}}{\varphi_T}$	0	0	0	0
$N_T \times N_S$	$\frac{\gamma_{TS} N_S}{\varphi_T}$	0	0	0	0
$N_{\frac{1}{2}} \times N_T$	$\frac{N_T}{\varphi_{\frac{1}{2}}}$	0	0	0	0
$N_{\frac{1}{2}} \times N_{\frac{1}{2}}$	$\frac{N_{\frac{1}{2}}}{\varphi_{\frac{1}{2}}}$	0	0	0	0
$N_{\frac{1}{2}} \times N_{\frac{2}{3}}$	$\frac{N_{\frac{2}{3}}}{\varphi_{\frac{1}{2}}}$	0	0	0	0
$N_{\frac{1}{2}} \times N_S$	$\frac{N_S}{\varphi_{\frac{1}{2}}}$	0	0	1	0
$N_{\frac{2}{3}} \times N_T$	$\frac{N_T}{\varphi_{\frac{2}{3}}}$	0	0	0	0
$N_{\frac{2}{3}} \times N_{\frac{1}{2}}$	$\frac{N_{\frac{1}{2}}}{\varphi_{\frac{2}{3}}}$	0	0	0	0
$N_{\frac{2}{3}} \times N_{\frac{2}{3}}$	$\frac{N_{\frac{2}{3}}}{\varphi_{\frac{2}{3}}}$	0	0	0	0
$N_{\frac{2}{3}} \times N_S$	$\frac{N_S}{\varphi_{\frac{2}{3}}}$	0	0	0	0
$N_S \times N_T$	$\frac{\gamma_{ST} N_T}{\varphi_S}$	0	1	0	0
$N_S \times N_{\frac{1}{2}}$	$\frac{\gamma_{ST} N_{\frac{1}{2}}}{\varphi_S}$	0	0	0	0
$N_S \times N_{\frac{2}{3}}$	$\frac{\gamma_{ST} N_{\frac{2}{3}}}{\varphi_S}$	0	0	0	0
$N_S \times N_S$	$\frac{N_S}{\varphi_S}$	1	0	0	0

[†] $\phi_S = N_S + \gamma_{ST}(N_T + N_{\frac{1}{2}} + N_{\frac{2}{3}})$; [†] $\phi_T = N_T + \gamma_{TS}(N_S + N_{\frac{1}{2}} + N_{\frac{2}{3}})$; $\phi_{\frac{1}{2}} = \phi_{\frac{1}{2}} = N_S + N_T + N_{\frac{1}{2}} + N_{\frac{2}{3}}$

Table 2.3. Models with equal or different values of growth rate (R) and habitat size (V) for populations of Atlantic salmons (N_S) and brown trouts (N_T). Parameters were adjusted by non-linear least square to an abundance time series data (1976-2005) in the river Imsa (Norway), source: Jonsson and Jonsson (2009a). *** $P < 0.001$.

Model parameters	DF	AIC _c	ΔAIC _c	R ²
$R_S = R_T; V_S = V_T$	44	455.7	0	0.29***
$R_S \neq R_T; V_S = V_T$	43	457.6	1.9	0.29***
$R_S = R_T; V_S \neq V_T$	43	457.9	2.2	0.29***
$R_S \neq R_T; V_S \neq V_T$	42	459.5	3.8	0.23***

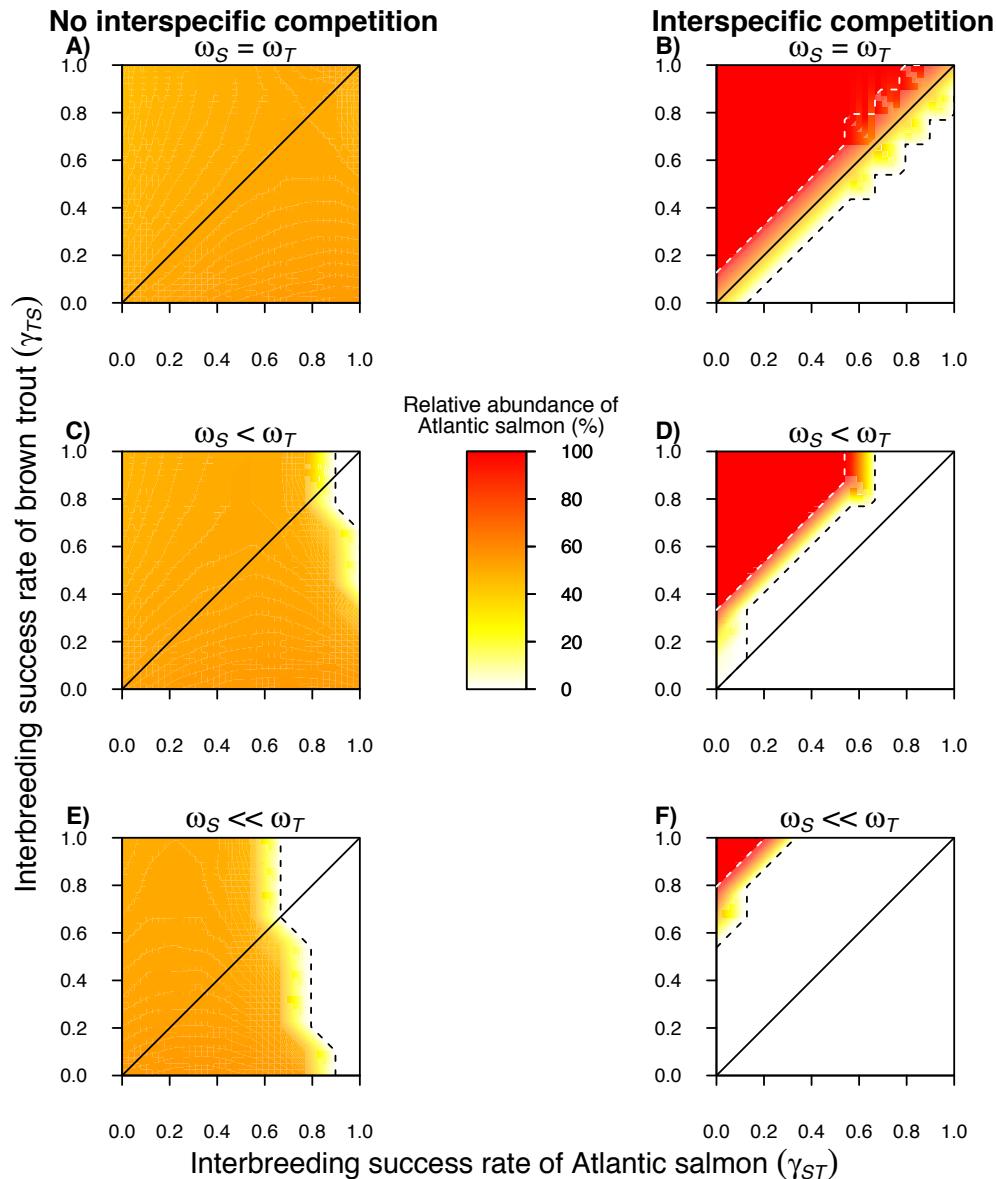


Figure 2.6. Relative abundance of Atlantic salmon (%) as compared to brown trout ($\frac{N_S}{N_S + N_T}$). These results are obtained when using the upper limit of the 95% confident interval of growth rate ($R = 4.37$) and habitat size ($V = 70.6$) (see Fig. 2.2, main text)

CHAPTER 3

Modelling interspecific hybridization with genome exclusion to identify conservation actions: the case of native and invasive *Pelophylax* waterfrogs

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3.1 Project description

In this chapter, we apply our model of distant species hybridization in a case involving hybridization type 2, which comprises fertile hybrids without introgression and the production of clonal or hemiclonal offspring. We illustrate the flexibility of the model by measuring the parameters in a different way than in the previous chapter: i) different sex ratios are incorporated by simulating males and females separately; ii) we propose a general estimation of the growth rate parameter (R) that takes into account the survival at different stages of a life cycle, which are incorporated in a modified version of the Ricker model through the parameter θ ; and iii) we use a different approach to assess the

effect of competition, which was a function in the previous chapter, but here is a fixed value. We use the case of an invasive water frog in Western Europe, showing the different consequences produced by translocations from different geographical origins. This type of hybridization may be facilitated via generating progeny with the invasive genome. This supports the history of extinction that has already been experienced in some parts of Switzerland. A previous classification of human-induced hybridization were previously proposed to set up management conservation programmes (Allendorf et al., 2001), but ignoring this type of hybridization. We include an additional category of fertile hybrids without introgression, stressing the serious extinction risk to native biodiversity that is generated.

Author contributions CSQ collected and analysed the data and drafted the first version of the manuscript. He also participated in the conception and design of the study as well as in the interpretation of the results and the final writing of the manuscript.

3.2 Abstract

Interspecific hybridization occurs in nature but can also be caused by human actions. It often leads to infertile or fertile hybrids that exclude one parental genome during gametogenesis, escaping genetic recombination and introgression. The threat that genome-exclusion hybridization might represent on parental species is poorly understood, especially when invasive species are involved. Here, we show how to assess the effects of genome-exclusion hybridization and how to elaborate conservation actions by simulating scenarios using a model of non-introgressive hybridization. We examine the case of the frog *Pelophylax ridibundus*, introduced in Western Europe, that can hybridize with the native *P. lessonae* and the preexisting hybrid *P. esculentus*, maintained by hybridogenesis. If translocated from Southern Europe, *P. ridibundus* produces new sterile hybrids and we show that it mainly threat *P. esculentus*. Translocation from Central Europe leads to new fertile hybrids, threatening all native waterfrogs. Local extinction is demographically mediated via wasted reproductive potential or via demographic flow through generations

towards *P. ridibundus*. We reveal that enlarging the habitat size of the native *P. lessonae* relative to that of the invader is a promising conservation strategy, avoiding the difficulties of fighting the invader. We finally stress that non-introgressive hybridization should be considered in conservation programs.

3.3 Introduction

Three types of interspecific hybridization can be defined according to the reproductive characteristics of the first generation hybrids: (i) hybridization yielding inviable or infertile offspring; (ii) genome-exclusion hybridization producing F_1 hybrids that exclude one parental genome during gametogenesis and, therefore avoiding genetic introgression between the parental species; and (iii) hybridization generating F_1 hybrids in which genetic recombination between the parental genomes proceeds normally during gametogenesis. The threat to parental species that hybridization with genome exclusion may represent is arguably not due to genetic introgression but can be mediated by a demographic decline in one or both species, yet this phenomenon is poorly understood. In conservation biology, demography is considered of primary importance in determining the viability of wild populations (Lande, 1988).

In addition to the potential threat that interspecific hybridization between native species may represent, especially in the context of global climate change, interspecific hybridization may facilitate biological invasions by accelerating the population decline of native species (Hall and Ayres, 2009). The invasion of exotic species is one of the main threats to biodiversity worldwide, in which competition, predation or even habitat modification by exotic species, can lead native taxa to the brink of extinction (Mack et al., 2000). By modeling interspecific hybridization, it is possible to assess the future consequences on the demography of parental species or hybrid populations and to predict the conditions under which local populations or even a species can reach extinction.

Here, we present an extensive investigation of the possible outcomes on the demography of native species threatened by the introduction of an alien species with which they hybridize, and we project the impact of different changes in the biological setting

to identify effective conservation actions. To this aim, we adapted and implemented a model of interspecific hybridization without genetic introgression that we have recently developed (Quilodrán et al., 2014a). The case study of biological invasion reinforced by non-introgressive hybridization we investigated is the colonization of Western Europe by the waterfrog *Pelophylax ridibundus*, apparently mediated by human activities (Luquet et al., 2011). In France and Switzerland, this waterfrog was introduced during the 20th century for frog leg consumption and for scientific purposes. Since then, this exotic species has been displacing local populations of native waterfrogs probably facilitated by the fact that it can hybridize with the native *P. lessonae*, producing fertile hybridogenetic progeny (Vorburger and Reyer, 2003). This threat to native frogs adds to the global worldwide threat to amphibians caused by human induced climate change (Shoo et al., 2011).

In nature, hybrids between *P. ridibundus* and *P. lessonae* were present in Western Europe before the recent introduction of *P. ridibundus*; they have been named *P. esculentus* and have long been considered as a different species. Early genetic studies revealed the hybrid nature of *P. esculentus*, which likely originated at the time of the last glaciation, about 10,000 years ago, when native populations of *P. ridibundus* were suggested to be present in Western Europe but went subsequently extinct (Vorburger, 2001b). The hybrid *P. esculentus* persisted by hybridogenesis with *P. lessonae* despite the extinction of *P. ridibundus* (Fig. 3.1). In this hybridogenetic system, the hybrid *P. esculentus* develops germ cells that discard the *P. lessonae* genome before meiosis, producing only haploid gametes containing the *P. ridibundus* genome (Anholt et al., 2003). Thus, backcrosses between *P. esculentus* and *P. lessonae* generate only *P. esculentus* hybrids. Crosses between native *P. esculentus* hybrids are unsuccessful likely due to the expression of recessive deleterious mutations (Vorburger and Reyer, 2003). This interesting hybridogenetic system has been named the *L/E* system (Graf, 1986).

The equilibrium of the *L/E* system was disrupted in Western Europe by the anthropogenic introduction of *P. ridibundus* from different places of Central and Southern Europe (Schmeller et al., 2007). It has been recently highlighted that populations of *P. ridi-*

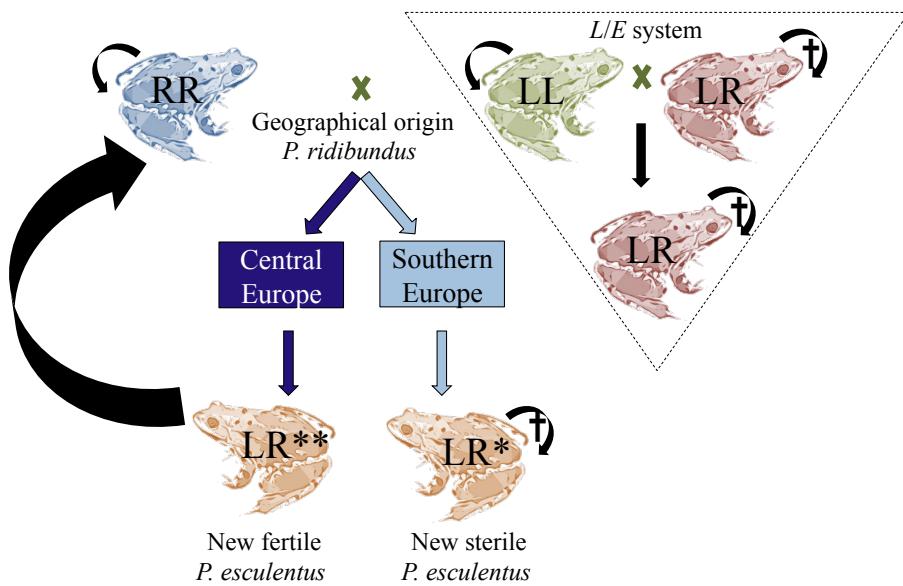


Figure 3.1. Impact of the exotic *P. ridibundus* on the waterfrog *L/E* system of Western Europe. Straight and curve arrows represent heterotypic and homotypic matings, respectively. The black cross symbol means that mating leads to inviable offspring. *LL* = *Pelophylax lessonae*; *RR* = *P. ridibundus*; *LR* = *P. esculentus*; *LR** = new sterile *P. esculentus*; *LR*** = new fertile *P. esculentus* (see main text). Dark and sky grey arrows differentiate new fertile from new sterile hybrids, respectively. The hybrids (*P. esculentus*) were already present in the invaded area and have been persisting by hybridogenesis with *P. lessonae* (the native *L/E* system). Exotic *P. ridibundus* coming from Southern Europe produce new sterile hybrids, whereas when coming from Central Europe, they produce new fertile hybrids, whose offsprings are again *P. ridibundus*.

bundus from different geographical origins differ in the type of offspring they produce (Holsbeek and Jooris, 2010; Plötner et al., 2010). Introduced individuals coming from Southern Europe, when mating with the native *P. lessonae*, produce new *P. esculentus* hybrids that are sterile in all type of crosses (see Fig. 3.1). In contrast, if the parental *P. ridibundus* comes from Central Europe, the resulting *P. esculentus* hybrids are fertile in all type of crosses. The latter situation is explained by the probable absence of recessive deleterious mutations in the genome of *P. ridibundus* coming from Central Europe (Holsbeek and Jooris, 2010).

The introduction of *P. ridibundus* in Western Europe is likely to cause complex interactions and perturbations in the native *L/E* system, and therefore, predicting the risk to resident populations and proposing efficient protection strategies are not trivial tasks. Models that describe the native *L/E* system in Western Europe have already been pro-

posed (Graf, 1986; Hellriegel and Reyer, 2000; Som et al., 2000; Som and Reyer, 2006), but because our model is more general and adaptable, it allows to include the different populations of invasive *P. ridibundus* into the system, with their reproductive specificities. Therefore, by using our model as a tool to simulate different scenarios of invasion and to assess the consequences arising from controlled changes in the biological system, we generated a comprehensive picture of the threats that native frogs may face, we determined the conditions under which native waterfrogs may be at risk, and we identified key factors that can be modified for deploying an efficient conservation strategy.

3.4 Materials and methods

Our aim was to describe and assess the possible outcomes of the invasion of Western Europe by different populations of *P. ridibundus* (*R*) showing different reproductive properties when they hybridize with native *P. lessonae* (*L*) and with the previously present hybrid *P. esculentus* (*E*). For this aim, we adapted (see Chapter 2 for details) the model of distant species hybridization without genetic introgression between parental species that we have recently developed (Quilodrán et al., 2014a). In our simulations, to assure that native frogs reach a stable equilibrium before the invasion of *P. ridibundus*, we let the native *L/E* system evolve for 200 time-steps (years). For the invasion of the exotic *P. ridibundus* populations, and because we do not know the exact initial number of introduced frogs, we simulated a translocation of *P. ridibundus* representing 0.2% of the total frog community, emulating the invasion from a small population source as it is the case for most species translocated by humans (Fitzpatrick et al., 2012). In the model, we used N_L , N_E , N_R to refer to adult frog population sizes (*L* for *P. lessonae*, *E* for *P. esculentus*, and *R* for *P. ridibundus*).

3.4.1 The *L/E* system

In the native *L/E* system, the homotypic mating of *P. esculentus* (*E* × *E*) does not produce viable offspring (Fig. 3.1). Therefore, populations of *P. lessonae* and *P. esculentus* depend

exclusively on the homotypic cross $L \times L$ and on the heterotypic cross $E \times L$, respectively. Assuming equal sex ratio, we used equation (3.1) to calculate the weighted number of breeding events leading to offspring of type *P. lessonae* (η_L), based on equation (3) in Quilodrán et al. (2014a):

$$\eta_{L(t)} = N_{L(t)} \frac{N_{L(t)}}{4\varphi_{L(t)}} \quad (3.1)$$

where $\varphi_{L(t)}$ is a normalization factor such that the proportion of homotypic and heterotypic mating of L is equal to 1 (Chapter 2).

The heterotypic cross between *P. esculentus* and *P. lessonae* produces hybrid offspring with 1:1 sex ratio if the male is *P. lessonae* ($E^f \times L^m$), or only female hybrid offspring if the male is *P. esculentus* ($L^f \times E^m$). This is because *P. esculentus* (both males and females) produces gametes always containing the *R* genome (*P. ridibundus*) with the *X* chromosome (Berger, 1988). Sex determination in these frogs is $XX - XY$ (males being heterogametic). To account for the unequal sex ratio in the offspring type *P. esculentus*, we calculate separately the number of breeding events involving males (η_E^m) and females (η_E^f), using the following equations:

$$\eta_{E(t)}^m = N_{E(t)}^f \frac{\gamma_{EL} N_{L(t)}}{4\varphi_{E(t)}} \quad (3.2)$$

$$\eta_{E(t)}^f = N_{E(t)}^f \frac{\gamma_{EL} N_{L(t)}}{4\varphi_{E(t)}} + N_{L(t)} \frac{\gamma_{LE} N_{E(t)}^m}{2\varphi_{L(t)}} \quad (3.3)$$

The parameter γ represents the interbreeding success rate, as introduced in Quilodrán et al. (2014a). When γ is equal to zero, there is a complete reproductive isolation whereas a value of 1 corresponds to a panmictic reproduction between both species. With any other value of $\gamma \in [0, 1]$, the mating occurs more often between members of the same genotype. Here, γ_{EL} and γ_{LE} are the interbreeding success rate between females E and males L ($E^f \times L^m$) or females L and males E ($L^f \times E^m$), respectively.

3.4.2 The newly-formed hybrids

In order to track the reproductive consequences of the introduced *P. ridibundus* depending on their geographical origin, the population dynamics of new sterile E^* and new fertile hybrids E^{**} were differentiated from that of the old hybrids *P. esculentus* E . For the new hybrids, we assume an equal sex ratio, because E^* and E^{**} are produced by mating between L and R or L and E^* (or E^{**}), and because gametes of new hybrids do not carry exclusively the sexual chromosome X (as it is the case in old *P. esculentus* E). The following equation is used to calculate the weighted number of breeding events resulting in new hybrids E^* :

$$\eta_{E^*(t)} = N_{R(t)}^f \frac{N_{L(t)} \gamma_{RL}}{2\varphi_{R(t)}} + N_{L(t)} \frac{1}{2\varphi_{L(t)}} \left(N_{R(t)}^m \gamma_{LR} + N_{E^*(t)} \omega \gamma_{LE} \right) + N_{E^*(t)} \frac{N_{L(t)} \gamma_{EL} \omega}{4\varphi_{E^*(t)}} \quad (3.4)$$

The same equation is used for new fertile hybrids (E^{**}). The parameter ω represents the fitness of the new hybrids (Quilodrán et al., 2014a), in which zero represents sterile individuals, whereas a value of one corresponds to individuals as fertile as the old *P. esculentus* E . We assumed that new hybrids and old ones have the same demographic parameter values and mating behavior.

3.4.3 The exotic frogs

Breeding events producing males and females *P. ridibundus* (η_R^m , η_R^f) are also calculated separately due to the presence of crosses with old hybrids E , resulting in a sex bias in the offspring population in favor of females. Male and female populations are thus given by equations (3.5) and (3.6), respectively.

$$\begin{aligned} \eta_{R(t)}^m = & N_{R(t)}^f \frac{1}{2\varphi_{R(t)}} \left(N_{R(t)}^m + N_{E^*(t)} \frac{\omega \gamma_{RE}}{2} \right) + N_{E^*(t)}^f \frac{\omega}{2\varphi_{E^*(t)}} \left(N_{R(t)}^m + \frac{N_{E^*(t)}}{2} \right) \\ & + N_{E(t)}^f \frac{1}{2\varphi_{E(t)}} \left(N_{R(t)}^m + N_{E^*(t)} \frac{\omega}{2} \right) \end{aligned} \quad (3.5)$$

$$\begin{aligned}\eta_{R(t)}^f = & N_{R(t)}^f \frac{1}{2\varphi_{R(t)}} \left(N_{R(t)}^m + \left(N_{E(t)}^m + N_{E^*(t)} \frac{\omega}{2} \right) \gamma_{RE} \right) \\ & + N_{E^*(t)}^f \frac{\omega}{2\varphi_{E^*(t)}} \left(N_{R(t)}^m + \left(N_{E(t)}^m + \frac{N_{E^*(t)}}{2} \right) \gamma_{RE} \right) \\ & + N_{E(t)}^f \frac{1}{2\varphi_{E(t)}} \left(N_{R(t)}^m + N_{E^*(t)} \frac{\omega}{2} \right)\end{aligned}\quad (3.6)$$

We used similar demographic and interbreeding success parameter values than those previously published in studies of the *L/E* system in order to find comparable equilibrium states (Hellriegel and Reyer, 2000; Som et al., 2000), see Appendix S1). Then, we introduced *P. ridibundus* into the system. *P. esculentus* was considered to have a panmictic reproduction with *P. lessonae* ($\gamma_{EL} = 1$), while *P. lessonae* was assumed to have 10% of interbreeding success rate with *P. esculentus* ($\gamma_{LE} = 0.1$). We considered the same panmictic reproductive behavior for *P. esculentus* relative to *P. ridibundus* ($\gamma_{ER} = 1$). We explored different levels of interbreeding success rate of the invasive *P. ridibundus* in relation to both native *P. esculentus* (γ_{RE}) and *P. lessonae* (γ_{RL}).

As in equation (4) of Quilodrán et al. (2014a), the temporal dynamics of adult populations is evaluated by adapting a version of the Ricker model, considering the intra- and interspecific density dependent competition during a larval stage (Wilbur, 1976). As incorporated by Henson et al. (2001), we considered the "*lattice effects*", in which the simulated population dynamics could be different from the expected in nature due to the discrete nature of individuals in a population. This effect is introduced in our model through the rounding off operation in equation (3.7):

$$N_{i(t+1)} = \text{round} \left[N_{i(t)} S_i^a + R_i \eta_{i(t-\theta)} e^{\left(-\frac{\eta_{i(t-\theta)} + \sum_{j \neq i} \alpha_{ij} \eta_{j(t-\theta)}}{V_i} \right)} \right] \quad (3.7)$$

where i and j denote a population of L , E , E^* , E^{**} or R . The first term in equation (3.7) characterizes the abundance of adults surviving from the last to the current breeding period, for which is the adult survival probability. The second term represents the surviving progeny until sexual maturity, where θ specifies the time to reach adult age in $t + 1$. The value R_i indicates the number of hatching per breeding pair surviving until maturity (population growth rate). The parameter α_{ij} represents the interspecific compe-

tition between i and j . This parameter can take values ranging from 0 (no competition) to 1, in which case an individual from population j competes with an individual from population i as if it was a member of its own population (j). V_i denotes the habitat size, where $\sum_{i \neq j} \alpha_{ij}/V_i$ delimits the interspecific density-dependent mortality before the sexual maturity stage (Henson et al., 2001).

In nature, the abundance of hybrids relative to the population size of *P. lessonae* varies from 10% to 90% (Tietje and Reyer, 2004). These variations may be related to habitat characteristics. Small ponds with abundant vegetation are favorable to *P. lessonae*; *P. ridibundus* prefers larger ponds with little vegetation and high levels of dissolved oxygen whereas habitats for *P. esculentus* are intermediate between *P. lessonae* and *P. ridibundus* (Holenweg Peter et al., 2002). We simulated several conditions of habitat size available for *P. lessonae* relative to the habitat size available for the exotic *P. ridibundus*: equal size ($V_L = V_R$), 50% greater for *P. lessonae* ($V_L > V_R$) or 50% smaller for *P. lessonae* ($V_L < V_R$). As hybrid's habitat preference is intermediate between the ones of parental species (Holenweg Peter, 2001), we assumed an intermediate habitat size $V_E = (V_L + V_R)/2$ and intermediate competition between hybrids and parental species ($\alpha_{EL} = \alpha_{LE} = \alpha_{ER} = \alpha_{RE} = 0.5$). As *P. ridibundus* and *P. lessonae* live in different habitats, no interspecific competition was assumed between them ($\alpha_{RL} = \alpha_{LR} = 0$) (but see Appendix S2 for an exploration of interspecific competition between both species).

The different abundance registered between both native frogs in the *L/E* system may be also motivated by different fertilities. The clutch size of *P. lessonae* is usually smaller than that of the hybrids *P. esculentus* (Tietje and Reyer, 2004), which are also smaller than the clutch size of *P. ridibundus* (Ivanova and Zhigalski, 2011). To take into account the fertility and the survival rate until maturity, we compute the parameter R_i in equation (3.7) as the product of the clutch size (c_i) and the survival probability across all stages until the age of sexual maturity (b), $\prod_{l=1}^b S_i^l$ as follows:

$$R_i = c_i \prod_{l=1}^b S_i^l \quad (3.8)$$

To calculate the population growth rate parameter, we considered the survival at tad-

poles and metamorphs (S_i^m), and the survival of first and second year juveniles (S_i^{j1}, S_i^{j2}). As the clutch size is strongly correlated with female body size (Schmeller et al., 2007), and knowing that hybrids exhibit intermediate body size between both parental species (Rist et al., 1997), we considered *P. esculentus* females to lay 30% more eggs than *P. lessonae* and 30% less eggs than *P. ridibundus* ($R_L < R_E < R_R$). However, the higher survival of *P. lessonae* tadpoles may reduce (or counterbalance) the initial outnumber of hybrid and *P. ridibundus* tadpoles (Semlitsch and Reyer, 1992). Thus, we also simulated ponds equally productive for all waterfrog ($R_L = R_E = R_R$). The survival of juveniles and adults seems to be similar between *P. lessonae* and *P. esculentus* (Tietje and Reyer, 2004). In the absence of empirical data, we considered these values to be equal among the three waterfrogs (Table 3.1). Values of fecundity and survival were obtained from previous studies (Berven, 1990; Hellriegel and Reyer, 2000; Som et al., 2000; Tietje and Reyer, 2004; Mayer et al., 2013).

3.5 Results

3.5.1 The invasion of *P. ridibundus*

We assessed the consequences of the invasion of *P. ridibundus* coming from different geographic origins with differential capacities to induce hybridogenesis, on the native waterfrog community composed by *P. lessonae* and *P. esculentus*. In the first 200 time-steps (years), the populations of both native frogs reach stable equilibrium with different abundances, depending on the interbreeding success rate of *P. esculentus* (γ_{EL}) and *P. lessonae* (γ_{LE}), the productivity of each population (R_E and R_L), and the habitat size available for each waterfrog (V_E and V_L) (see Appendix S1).

The equilibrium of this hybridogenetic system is disrupted due to the introduction of *P. ridibundus* (Fig. 3.2). We explored an asymmetrical interbreeding success rate between *P. lessonae* and *P. ridibundus* ($\gamma_{RL} \neq \gamma_{LR}$), which could represent, for instance, a different mating preference between both taxa due to body size or mating vocalization. In this first analysis, the reproduction between *P. ridibundus* and *P. esculentus* is considered to be

Table 3.1. List of functions and parameters of the model with default values

Symbol	Definition
N_i	Number of adult individuals of genotypic class i Initial size: $N_L = N_E = 50$; $N_{E^*} = 0$; $N_{E^{**}} = 0$; $N_R = 0$
n_i	Weighted number of mating leading to offspring of class i
R_i	Population growth rate
θ	Time delay from hatching to age maturity in $t + 1$ (two years) $\theta_L = \theta_E = \theta_R = 1$
c	Clutch size $c_L = 1250$; $c_E = 1250 - 1625$; $c_R = 1250 - 2000$
S^m	Survival of metamorphs $S_L^m = 0.02$; $S_E^m = 0.015 - 0.02$; $S_R^m = 0.012 - 0.02$
S^{j1}, S^{j2}	Survival of first and second year juveniles $S_L^{j1} = S_E^{j1} = S_R^{j1} = 0.5$; $S_L^{j2} = S_E^{j2} = S_R^{j2} = 0.4$
S^a	Survival of adults $S_L^a = S_E^a = S_R^a = 0.3$
α	Interspecific competition coefficient $\alpha_{RL} = \alpha_{LR} = 0$; $\alpha_{RE} = \alpha_{ER} = \alpha_{LE} = \alpha_{EL} = 0.5$
V	Habitat size $V_L = 5000$; $V_R = 2500 - 5000$
γ	Interbreeding success rate $\gamma_{EL} = \gamma_{ER} = 1$; $\gamma_{LE} = 0.1$; $\gamma_{RE} = 0 - 1$; $\gamma_{RL} = 0 - 1$; $\gamma_{LR} = 0 - 1$
ω	Fitness of newly-formed hybrids $\omega_E = 0$ or $\omega_E = 1$

panmictic ($\gamma_{RE} = 1$) and all populations are assumed to be equally productive ($R_L = R_E = R_R$).

When *P. ridibundus* comes from Southern Europe ($\omega_{E^*} = 0$), its frequency remains lower than 15% if its mating preference for *P. lessonae* is higher than 2:3 relative to the conspecific mating ($\gamma_{RL} > 0.66$). Some extreme situations are projected in which the exotic frog can replace both native frogs when the heterotypic preference of *P. lessonae* represents about 4:5 of the homotypic mating ($\gamma_{LR} > 0.78$). At this level of hybridization, native frogs can only remain in the community if $\gamma_{RL} > 0.23$. Levels of interbreeding success rate lower than 40% for *P. ridibundus* ($\gamma_{RL} > 0.4$) and 60% for *P. lessonae* ($\gamma_{LR} > 0.6$)

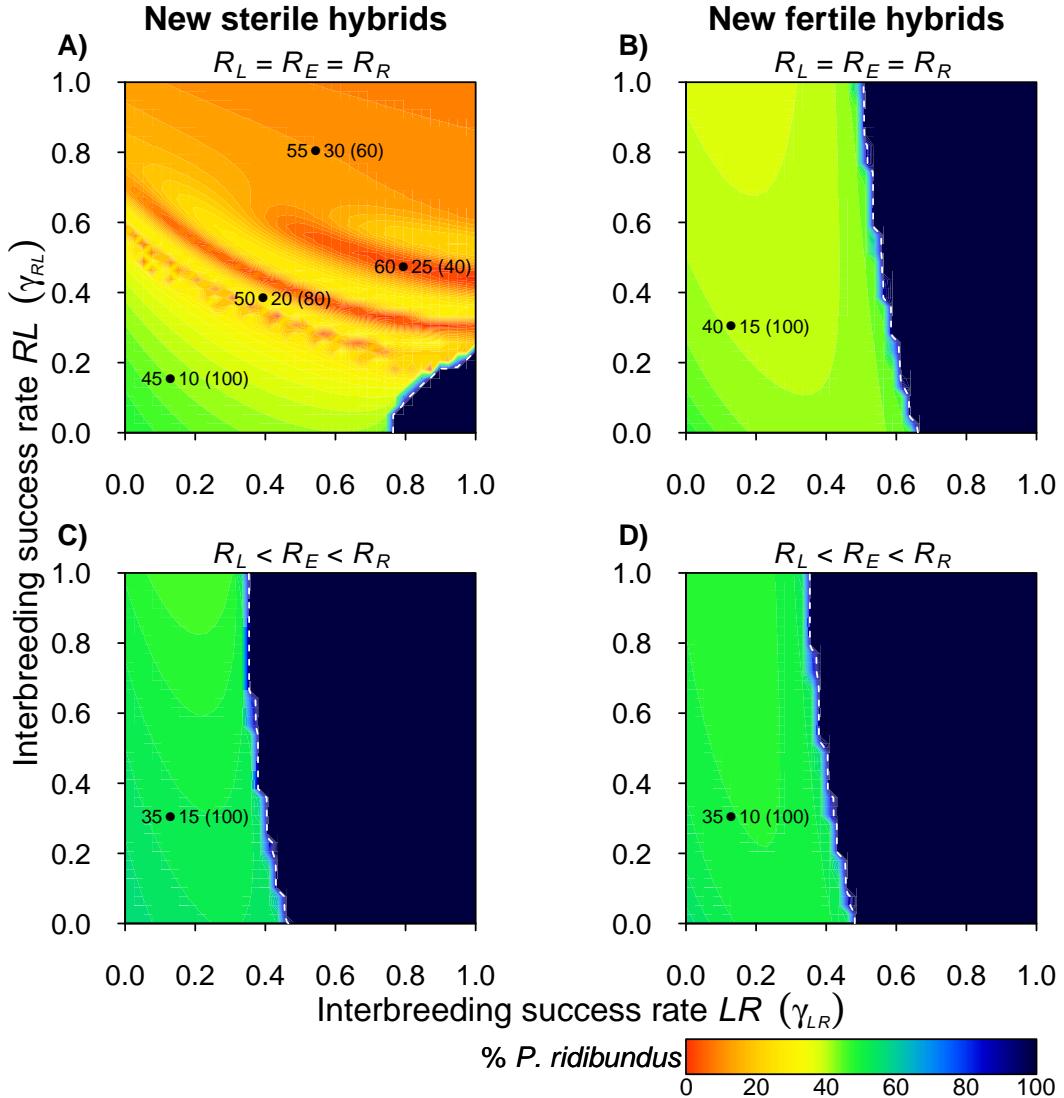


Figure 3.2. Effect of interbreeding success rate between *P. ridibundus* and *P. lessonae* on a waterfrog *L/E* system of Western Europe. a), c) *P. ridibundus* introduced from Southern Europe, producing new sterile hybrids (ω_{E^*}). b), d) *P. ridibundus* introduced from Central Europe, producing new fertile hybrids ($\omega_{E^{**}}$). a), b) Equally productive populations ($R_L = R_E = R_R$); c), d) *P. esculentus* has an intermediate fertility between *P. lessonae* and *P. ridibundus*, the latter being 60% more fertile than *P. lessonae* ($R_L < R_E < R_R$). White dotted lines delimit the exclusive presence of *P. ridibundus* in the system. The colour scale represents the relative abundance of *P. ridibundus*, while the numbers inside the figure denotes the abundance of the other two frogs ($\%L \cdot \%E$) and the percentage of replacement of old by newly-formed hybrids, in brackets. We let the natives *Pelophylax lessonae* and *P. esculentus* interact during 200 time-steps (years) before introducing *P. ridibundus*. Data corresponds to the situation projected after a total of 400 time-steps (years).

cause the extinction of old *P. esculentus* and the collapse of the hybridogenetic system. In this case, the community is composed mostly by *P. lessonae* and *P. ridibundus*, with a marginal population of newly-formed hybrids (E^*) that depends exclusively on the hybridization between both parental species (Fig. 3.2a).

When *P. ridibundus* comes from Central Europe ($\omega_{E^{**}} = 0$), any level of hybridization skewed towards *P. ridibundus* or towards *P. lessonae* ($\gamma_{RL} \neq \gamma_{LR}$) allows the colonization of the exotic frogs in densities of at least 40% (Fig. 3.2b). The extinction of old *P. esculentus* due to the replacement by newly-formed hybrids is always reached. If the proportion of heterotypic matings of *P. lessonae* represents 2:3 of the homotypic matings ($\gamma_{LR} > 0.66$), the extinction of all native frogs is reached and is almost independent from the mate choice relaxation of *P. ridibundus* ($\gamma_{RL} \neq 0$). The invasion of exotic frogs is thus reinforced by the capacity of Central European *P. ridibundus* to produce fertile new hybrids.

When considering a higher number of individuals reaching sexual maturity in *P. ridibundus* and *P. esculentus* than in *P. lessonae* ($R_L < R_E < R_R$), both geographical provenances of the invasive frogs (producing sterile or fertile hybrids) lead to similar results. *P. ridibundus* colonizes the area in frequencies of at least 50%, with old *P. esculentus* always replaced by newly-formed hybrids, and with a community of waterfrogs composed exclusively by *P. ridibundus* if the mate choice relaxation of *P. lessonae* represents more than 50% ($\gamma_{RL} > 0.5$) (Fig. 3.2c and 3.2d). In such scenarios, a more productive population of *P. ridibundus* threatens both native frogs irrespective of the geographical origin or the capacity to induce hybridogenesis.

3.5.2 The effect of available habitat size

The effects of habitat size difference between *P. lessonae* and *P. ridibundus* on the *L/E* system, and the effects due to the interaction among native and exotic frogs were simulated for a period of 200 years (Fig. 3.3). In this analysis we simulated different levels of submerged vegetation and dissolved oxygen favoring one or the other species (see Methods). The aim was to represent a variety of ponds in a given colonized region and to

explore the effect of an increasing mating between the invasive frog and the hybrid *P. esculentus* (γ_{RE}). We assumed an extreme case of symmetrical and panmictic interbreeding success rate between parental taxa ($\gamma_{LR} = \gamma_{RL} = 1$).

Taking into account equally productive populations ($R_L = R_E = R_R$), when the habitat size of *P. ridibundus* is equal or smaller than the one available for *P. lessonae* ($V_L = V_R$ or $V_L > V_R$, Fig. 3.3a) then the new sterile hybrids do not lead to the extinction of native frogs or to a complete replacement of old by newly-formed hybrids. However, a greater habitat size available for *P. ridibundus* ($V_L < V_R$) leads to the extinction of all native frogs, excepting the case in which the reproduction between *P. ridibundus* and the hybrid is panmictic ($\gamma_{RE} = 1$). In this case, the cost of producing sterile hybrids (E^*), replacing 90% of old hybrids *P. esculentus* and competing with the new arrived frogs, restrict the invasion of *P. ridibundus*. A habitat size 55% greater for *P. ridibundus* as compared to *P. lessonae* leads to the extinction of all native frogs, irrespective of the level of interbreeding success rate with the hybrid *P. esculentus* (data not shown). For *P. ridibundus* coming from Central Europe and producing new fertile hybrids ($\omega_{E^{**}}$), a complete extinction of both native frogs is expected if the habitat size of *P. lessonae* is equal or smaller than that available for *P. ridibundus* ($V_L = V_R$ or $V_L < V_R$, Fig. 3.3b). A greater habitat size for *P. lessonae* ($V_L > V_R$) allows the coexistence of all waterfrogs, but a complete replacement of old by newly-formed hybrids (E^{**}) is expected.

In the case of more productive populations of *P. ridibundus* and *P. esculentus* as compared to *P. lessonae* ($R_L < R_E < R_R$), only an invasion of South European *P. ridibundus* (producing new sterile hybrids) and having a smaller habitat size as compared to *P. lessonae* allows the coexistence of all waterfrogs, but 60% of *P. esculentus* is replaced by newly-formed hybrids (E^*) (Fig. 3.3c). In contrast, a displacement of all populations occurs if *P. ridibundus* comes from Central Europe, producing new fertile hybrids (E^{**}), irrespective of the habitat size of the parental species and the interbreeding success rate between *P. ridibundus* and *P. esculentus* (Fig. 3.3d). However, even in this extreme scenario of more productive populations of *P. ridibundus* (producing new fertile hybrids), an habitat size 2.1 times larger for *P. lessonae* allows the coexistence of all waterfrogs, but

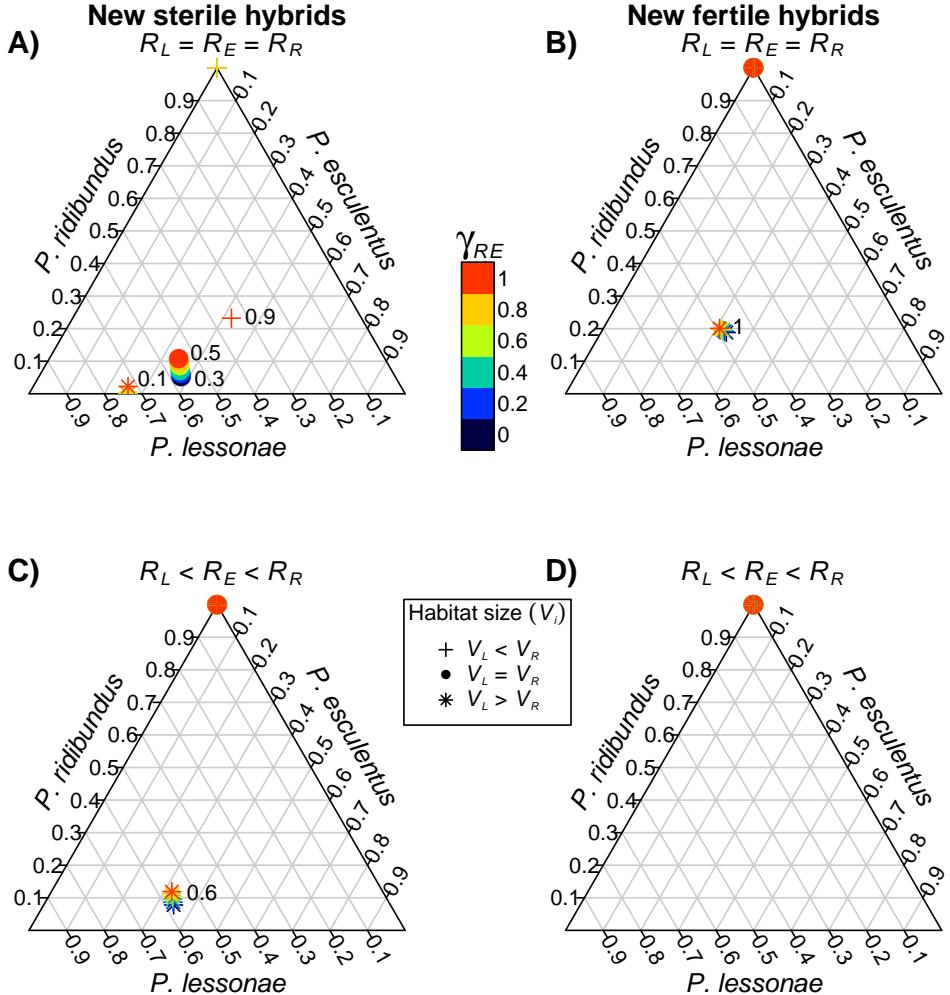


Figure 3.3. Estimated proportion of exotic *Pelophylax ridibundus* and native *P. lessonae* and *P. esculentus* in a *L/E* system of Western Europe. The grey lines inside the triplot indicate the relative abundance of each waterfrog. The horizontal line represents the abundance of *P. ridibundus*, while the left and right side lines represent the abundance of *P. lessonae* and *P. esculentus*, respectively. The color scale represents the interbreeding success rate of *P. ridibundus* with *P. esculentus* (γ_{RE}). The numbers are the proportion of newly-formed *P. esculentus* (see text) within *P. esculentus* population (0 to 1). a), c) *P. ridibundus* introduced from Southern Europe, producing new sterile hybrids ($\omega_{E^*} = 0$). b), d) *P. ridibundus* introduced from Central Europe, producing new fertile hybrids ($\omega_{E^*} = 1$). a), b) Equally productive populations ($RL = RE = RR$); c), d) *P. esculentus* has intermediate fertility between *P. lessonae* and *P. ridibundus*, the latter being 60% more fertile than *P. lessonae* ($RL < RE < RR$). (-) Equal habitat size between *P. lessonae* and *P. ridibundus* ($V_L = V_R$). (+) Habitat size of *P. lessonae* 50% smaller than the one available for *P. ridibundus* ($V_L < V_R$). (*) Habitat size of *P. lessonae* 50% greater than the one available for *P. ridibundus* ($V_L > V_R$). We let the natives *Pelophylax lessonae* and *P. esculentus* interact during 200 time-steps (years) before introducing *P. ridibundus*. Data corresponds to the situation projected after a total of 400 time-steps (years).

with a complete replacement of old by newly-formed hybrids (data not shown). Otherwise, the frog community is composed exclusively by *P. ridibundus* (Fig. 3.3d).

3.6 Discussion

In the present study we used the general model of interspecific hybridization without introgression that we developed recently (Quilodrán et al., 2014a) to analyze and project possible future situations for the native *Pelophylax L/E* system in Western Europe. If we do not consider the recent introduction of *P. ridibundus* in this region, our model gives comparable results with previous studies aimed at understanding the *L/E* system. In particular, we found equilibrium states that are equivalent to those reported by multistage life cycle models (Hellriegel and Reyer, 2000; Som et al., 2000). Moreover, the results obtained with our model are consistent with the suggestion of Holsbeek and Jooris (2010) who anticipated the negative impact of *P. ridibundus* on Western European waterfrogs.

3.6.1 The invasion of *P. ridibundus*

The exotic *Pelophylax ridibundus* is currently replacing native frogs in Western Europe (Vorburger and Reyer, 2003). However, individuals translocated from distinct geographical origins differ in their colonization capabilities and in the mode of invading the waterfrog community (Holsbeek and Jooris, 2010; Plötner et al., 2010). The projections of our model suggest that *P. ridibundus* coming from Southern and from Central Europe are both a threat for the persistence of native waterfrogs in Western Europe. When *P. ridibundus* is introduced from Southern Europe (producing new sterile hybrids), it threatens firstly old *P. esculentus* and also the persistence of the hybridogenetic system, but the whole community of waterfrogs can be threatened if the mate choice preference is skewed towards *P. ridibundus*, or when the invasive frog has a more productive population or a larger habitat size than native frogs. We also showed that *P. ridibundus* coming from Central Europe represents a direct threat for both native frogs in most situations. The inviable offspring production of homotypic matings in *P. esculentus* is critical for the persistence of the *L/E*

system (Hellriegel and Reyer, 2000; Som et al., 2000). With the arrival of *P. ridibundus* from Central Europe, this equilibrium is broken which eventually leads to the collapse of native frogs.

The area invaded by *P. ridibundus* in Western Europe is larger than it was originally predicted (Schmeller et al., 2007). The first observations in Switzerland date back to 1950, and since then, this species has colonized the country with varying local success. Western Switzerland has been invaded more rapidly and native frogs are at edge of extinction, while in Northern and Eastern regions all three taxa are still co-existing (Vorburger and Reyer, 2003). We suggest that these two contrasting situations are due to the introduction of *P. ridibundus* coming from different geographical origins, displaying distinct capacities to induce hybridogenesis.

3.6.2 Conservation action

The results of our simulations show that knowing the provenance of *P. ridibundus* is central to situate the importance of the threat in a management program. However, it is not possible to discriminate the origins of the exotic waterfrogs based on morphology. Nevertheless, it can be done by using bioacoustics measures (Schneider et al., 1993), or by the analysis of genetic markers, for instance the mitochondrial 12s rRNA (Plötner, 1998; Plötner and Ohst, 2001) or the serum albumin intron 1 (SAI1) (Plötner et al., 2009). Crossing experiments is today the best way to recognize the reproductive properties characterizing the geographical origins, but they require infrastructure and are time consuming.

In order to design convenient conservation actions, our model opens the possibility to assess the effects of modifying some parameters of the system. It is thus possible to test and identify the best candidate conservation strategies. Our results indicate that an efficient action could be to increase the habitat size of native frogs relative to the favorable habitat of the exotic frogs. Ponds with submerged vegetation and with medium levels of dissolved oxygen is the preferred habitat of *P. lessonae*, which is also convenient for *P. esculentus*, while *P. ridibundus* performs poorly in such conditions (Holenweg Peter et al., 2002). The identified conservation action directed towards favoring the native species

rather than fighting the invasive one is all the more advantageous since controlling an invasive species, once settled, is extremely difficult and costly (Januchowski-Hartley et al., 2011). Moreover, the suggested action does not involve species identification in the field or in the laboratory, but takes advantage of the difference in the ecological niche between the invasive and native taxa.

Our results indicate that a worse case scenario is when the relative productivity of *P. ridibundus* coming from Central Europe is higher than native waterfrogs, in which case enlarging the habitat size of *P. lessonae* is insufficient to allow the survival of native populations. Even though the clutch size of *P. ridibundus* is known to be greater than that of *P. lessonae*, basic information about the relative number of individuals reaching sexual maturity is still lacking and this knowledge needs to be acquired based on observations in the field before we can assess the realism of this worse scenario. Nevertheless, if we assume that this case is real, by using our model it is possible to determine the amount of *P. ridibundus* that need to be controlled in order to artificially reduce the productivity of *P. ridibundus* up to a level that allows the survival of native species under the condition of an enlarged habitat size for *P. lessonae*. As the species identification is not possible in the field, the control of *P. ridibundus* could be achieved by removing all waterfrogs or their clutch in a determined fraction of the most suitable habitat for *P. ridibundus*. In this way, by using the ecological requirements of the species, it is possible to preferentially remove the invader. However, the knowledge about the difference in habitat suitability between the invasive and native taxa should be locally verified before implementing any eradication program.

3.6.3 Hybrids in conservation policies

We explored the microevolutionary effects of interspecific hybridization without introgression and determined the conditions under which native species might be threatened. In general, hybrids do not fall into protection plans because they are not considered as independent evolutionary lineages (Kraus, 1995). The latter statement may be true if hybrids are inviable or infertile, but not if hybrids generate self-propagating progenies

through parthenogenesis, hybridogenesis or gynogenesis (Kraus, 1995; Christiansen and Reyer, 2009). Polyploid hybrids have been important in the evolution of several plant taxa and the role of hybridization in animal speciation cannot be neglected (Soltis and Soltis, 1999; Choleva et al., 2012). Hybridization between *P. ridibundus* and *P. lessonae* is interesting not only because it is a well-studied case of hybridogenesis but also because populations of only hybrid frogs have been observed in nature (Christiansen and Reyer, 2009), demonstrating the possible emergence of self-sustaining populations. Natural interspecific hybridization is thus a dynamic process with several possible evolutionary outcomes, and natural hybrids are at the center of this process. This gives a conceptual ground explaining why the native hybrid *P. esculentus* should also be protected.

To help prioritizing conservation actions, Allendorf et al. (2001) proposed three different categories of human induced hybridization: (i) complete admixture, (ii) widespread introgression and (iii) hybrids without introgression due to infertile hybrids. In the first two categories, hybridization is a major threat to native species due to genetic introgression. The third category is believed to represent a minor risk because only F_1 individuals are detected in nature and thus, they are generally considered to be infertile, an assumption that can be wrong in an unappreciated proportion (Quilodrán et al., 2014a). Here, we proposed a fourth category in which only F_1 hybrids can be observed into the wild but producing a viable and fertile progeny that may dramatically impact the demography of one or both parental species (Fig. 3.4). These hybrids do not undergo genetic recombination during their gametogenesis as they exclude one or the other parental genome in their germ cells, producing clonal or hemiclonal offspring. Therefore, this kind of hybrids does not mediate nuclear DNA introgression between parental species. As demonstrated here, this type of hybridization could represent a major risk by eventually replacing species via demographic means. In nature, the frequency of this type of hybridization is unknown, but Yakovlev et al. (2000) proposed that it can be the typical situation in hybridization between distantly related fish, which can be frequently seen in some families like the Cyprinidae (e.g. Schmidt et al., 2011). The occurrence of this type of interspecific hybridization in other organisms is probably highly underappreciated, hiding a po-

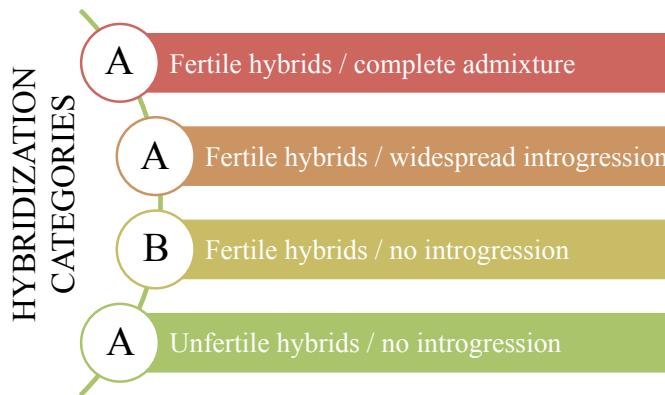


Figure 3.4. Hybridization categories for conservation. A) Classification proposed by Allendorf et al. (2001): i) complete admixture, (ii) widespread introgression and (iii) hybrids without introgression due to infertile hybrids. B) The new category we propose in this study, in which hybrids are fertile, but there is no genetic introgression between parental species because hybrids produce clonal or hemicalonal offspring

tentially important threat to species. We recommend that, in surveys or studies where only F_1 individuals have been detected in nature, the genetic content of the hybrids' gametes should be verified to identify the risk that this interspecific hybridization may convey.

In addition to the conservation considerations discussed above, we believe that our model is a powerful tool for the study of a wide range of theoretical and empirical cases. The code of our model is freely available at: <http://genev.unige.ch/montoya-currat/scripts/> and can be easily modified and adapted to investigate a variety of biological issues in conservation and evolution. For instance, it can be useful to understand the potential impact of inviable or sterile hybridization due to post-zygotic barriers or to assess how different polyploid forms of hybrid origin can persist over large periods of time.

3.7 Acknowledgments

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baobab.unige.ch. We also thank Jean-Luc Falcone for technical advices, Claire Shea and Nicolas Ray for their careful reading of a previous version of this manuscript.

3.8 Supporting Information

3.8.1 Appendix S1. The hybridogenetic system of *Pelophylax lessonae* and *P. esculentus* (L/E system)

The L/E system is composed of *P. lessonae* (*L*) and the hybridogenetic hybrid *P. esculentus* (*E*). To assess the equilibrium states of the L/E system, and to evaluate if our model leads to analogous outcomes than those found in previous studies, we simulated scenarios with different habitat size (V_L and V_E), different population productivity (R_L and R_E), and different interbreeding success rate (γ_{LE} and γ_{EL}). Simulating different habitat sizes is justified because both waterfrogs use different habitats (Holenweg Peter et al., 2002). Simulating different fertilities is grounded on the fact that *P. esculentus* is known to have bigger clutch size than *P. lessonae* (Tietje and Reyer, 2004), although the higher survival rate at tadpole and metamorphic stages in *P. lessonae* may re-equilibrate the final number of individuals reaching sexual maturity in both waterfrogs (Semlitsch and Reyer, 1992). As to variations in the interbreeding success rate, we explored several scenarios in addition to those analyzed in previous studies.

The local abundances of *P. lessonae* (*L*) and *P. esculentus* (*E*) are extremely variable in nature (Tietje and Reyer, 2004). When we simulate $\pm 25\%$ of habitat size differences for each species, population sizes varies from 1:2 to 2:1 for L:E (Fig. 3.5), indicating that the variable abundance observed in nature may be explained by local dissimilar habitat sizes for each waterfrog. Simulations with higher habitat size dissimilarities increase the difference in local abundance between both frogs (data not shown).

The presence of *P. esculentus* in the frog community is highly dependent on the interbreeding success rates between both waterfrogs (γ_{LE} and γ_{EL}). For instance, with a null interbreeding success rate of *P. lessonae* ($\gamma_{LE} = 0$), where its females always mate with its homotypic males, females *P. esculentus* require levels of hybridization of 23% to

40% ($\gamma_{EL} = 0.23 - 0.4$) to persist in the community in every situations (Fig. 3.5b to 3.5f), except when the habitat size of *P. lessonae* is greater than that of *P. esculentus* ($V_L > V_E$) and both frogs are equally productive ($R_L = R_E$). In that later case *P. esculentus* always disappears if the heterotypic mating of *P. lessonae* (γ_{LE}) is close to 0, surviving only if $\gamma_{LE} > 0.05$ and the mate choice of *P. esculentus* is panmictic ($\gamma_{EL} = 1$) (Fig. 3.5a). When the heterotypic mating of *P. lessonae* is greater than 50% ($\gamma_{LE} \geq 0.5$) and that of *P. esculentus* is panmictic ($\gamma_{EL} = 1$), the system collapses in any case, with both frogs reaching extinction (Fig. 3.5).

Our results are comparable to the trends obtained in previous modeling studies of the *L/E* system, namely: 1) the various abundances of *P. lessonae* and *P. esculentus* observed in nature may be explained by different habitat size and/or unequal fertility between both frogs; 2) the *L/E* system can persist with a panmictic mate choice of *P. esculentus* ($\gamma_{EL} = 1$) only if the mate choice relaxation is asymmetrical between both frogs, smaller for *P. lessonae* ($\gamma_{LE} < 1$); 3) a panmictic mate choice of *P. lessonae* ($\gamma_{LE} = 1$) always leads to the collapse of the system (Graf, 1986; Hellriegel and Reyer, 2000; Som et al., 2000). Therefore, with similar variables we get analogous outcomes, but our model allows us to study the effect of different parameters.

Introducing *P. ridibundus* into the *L/E* system

To generate the starting condition of the *L/E* system before the introduction of *P. ridibundus*, we used the conditions most often found in nature, which also correspond to the conditions implemented in previous studies (Graf, 1986; Hellriegel and Reyer, 2000; Som et al., 2000), i.e. a panmictic reproduction of *P. esculentus* ($\gamma_{EL} = 1$) and around 10% of heterotypic mating for *P. lessonae* ($\gamma_{LE} = 0.1$). Under these conditions and with an equal habitat size and fertility between both frogs, *P. lessonae* and *P. esculentus* persist, reaching a stable equilibrium at 60% and 40% of relative densities, respectively (Fig. 3.6, on the left side of the red line).

In the main text, we present various outcomes resulting from the introduction of *P. ridibundus* (R) into the *L/E* system obtained after 200 time-steps (years) following the

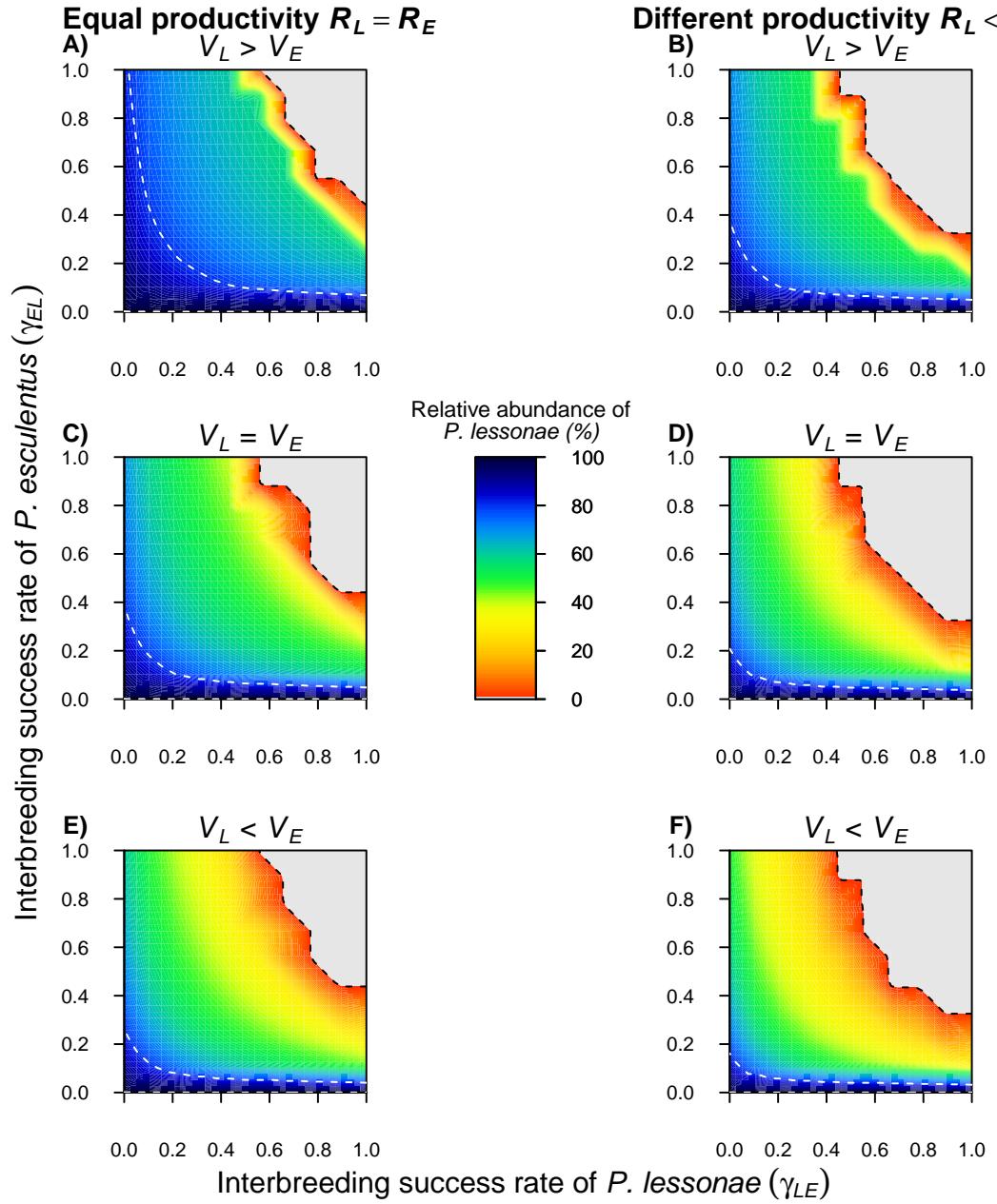


Figure 3.5. Relative abundance of *Pelophylax lessonae* as compared to *P. esculentus*. The dotted white lines delimit the exclusive presence of *P. lessonae*, while the dotted black lines delimit the collapse of the system, in which both native waterfrogs reach extinction. We simulated equally fertile populations ($R_L = R_E$) and also *P. esculentus* 1.3 times more fertile than *P. lessonae* ($R_L < R_E$). We took into account $\pm 25\%$ of different habitat size for both waterfrogs ($V_L < V_E$ or $V_L > V_E$). Parameter values were obtained from the literature (see Table 1, main text). Data are presented after 200 time-steps (years).

translocation of the invasive waterfrog. In the present chapter, we describe the population dynamics of all waterfrogs during this time frame (Fig. 3.6, on the right side of the red bar). The outcomes depend on the geographic origin of *P. ridibundus* because Southern Europe individuals, when mating with *P. lessonae*, produce *P. esculentus* hybrids that are sterile in homotypic crosses, whereas Central Europe individuals produce *P. esculentus* hybrids that are fertile in homotypic crosses (see main text). Here, we consider equal habitat size ($V_L = V_E = V_R$) and equal productivity ($R_L = R_E = R_R$) among waterfrogs, with panmictic mate choices with *P. ridibundus* ($\gamma_{LR} = \gamma_{RL} = \gamma_{RE} = 1$). When *P. ridibundus* comes from Southern Europe, all waterfrogs persist in the community (Fig. 3.6a), with *P. lessonae* having the highest abundances, followed by the new formed hybrids and *P. ridibundus*. These final abundances can dramatically change depending on the parameter values, with, for example, a complete replacement of native frogs by *P. ridibundus* if the interbreeding success rate is highly asymmetrical ($\gamma_{LR} > \gamma_{RL}$) or if *P. ridibundus* and hybrids are considered to be more productive than *P. lessonae* ($R_L < R_E < R_R$) (see other scenarios in the main text). When *P. ridibundus* comes from Central Europe, both native frogs reach extinction (Fig. 3.6b). In this last scenario, the old *P. esculentus* (and the hybridogenetic system) disappears after 30 time-steps while *P. lessonae* reaches extinction after 40 time-steps. Since that moment, the community is composed exclusively of the invasive *P. ridibundus*.

3.8.2 Appendix S2. Introducing competition among parental species

In our analyses we included competition between the hybrid (*P. esculentus*) and the parental species *P. ridibundus* or *P. lessonae* but we did not incorporate interspecific competition between parental species as they use different habitats (Holenweg Peter et al., 2002). However, because both frogs can mate with each other, some competition may be expected, at least during the tadpole stage. We thus simulated also the effect of an increasing interspecific competition between *P. ridibundus* and *P. lessonae* ($\alpha_{RL} = \alpha_{LR} = \alpha$).

We first considered equally productive waterfrog populations (Fig. 3.7). When *P. ridibundus* comes from Southern Europe, producing new sterile hybrids, and with an

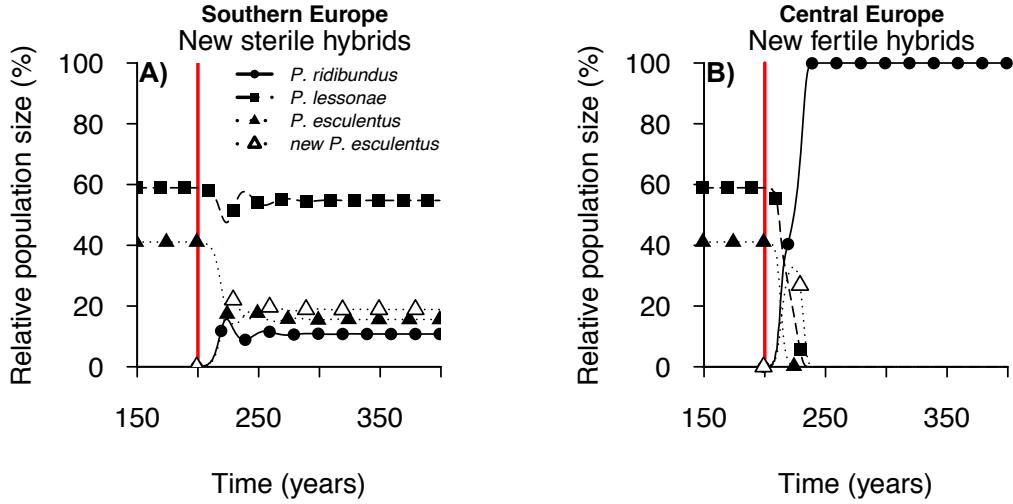


Figure 3.6. Relative population size of waterfrogs in a community of Western Europe. We let the natives *Pelophylax lessonae* and *P. esculentus* interact during 200 time steps (years) before introducing *P. ridibundus* (on the red line). a) New sterile hybrids; b) New fertile hybrids. We assumed panmictic reproduction ($\gamma_{LR} = \gamma_{RL} = \gamma_{RE} = 1$) and equally fertile populations ($R_L = R_E$). Other parameter values are presented in Table 1 (see main text).

interbreeding success rate between parental species of 10% ($\gamma_{RL} = 0.1$; Fig. 3.7a), *P. ridibundus* disappears if both parental species compete for more than 33% of the resources ($\alpha > 0.33$) and if it cannot mate with the hybrids ($\gamma_{RE} = 0$). If the interspecific competition level is lower than 33% ($\alpha < 0.33$), the abundance of *P. ridibundus* increases with decreasing competition. However, if *P. ridibundus* is able to mate with the hybrids ($\gamma_{RE} > 0$), then the abundance of *P. ridibundus* decreases with increasing interspecific competition or tends to stabilize if its interbreeding success rate with the hybrid is greater than 40% ($\gamma_{RE} > 0.4$). When *P. ridibundus* comes from Central Europe, producing new fertile hybrids, its abundance is independent of the heterotypic mating with *P. esculentus* (γ_{RE}). The abundance of *P. ridibundus* remains approximately stable if it uses less than a half of the resources available for *P. lessonae* ($\alpha < 0.5$) whereas it displaces all native frogs if it uses more ($\alpha > 0.5$; Fig. 3.7a).

Similar trends are found when the hybridization between parental species is higher ($\gamma_{RL} = 0.5$; Fig. 3.7b). If the exotic frog comes from Southern Europe, less competition

is required to reduce its abundance up to extinction, or, if they come from central Europe, less competition is required to displace the whole community of native frogs. In this last case, if *P. ridibundus* competes for more than 10% of the resources with *P. lessonae* ($\alpha > 0.1$), both native frogs disappear independently of the heterotypic mating between *P. ridibundus* and the hybrids *P. esculentus* (γ_{RE}) (Fig. 3.7b).

In summary, if we assume interspecific competition between both parental species (α), the abundance of Southern European *P. ridibundus* decreases with increasing competition. At the opposite, competition has a positive effect on the abundance of Central European *P. ridibundus*. With an increased interbreeding success rate between parental species (γ_{RL}), less competition is required for a complete replacement of native frogs by *P. ridibundus* if they come from Central Europe. However, if they come from Southern Europe, an increased hybridization between parental species leads to a decrease of the relative abundance of *P. ridibundus*. The heterotypic mating with hybrids (γ_{RE}) has no effect on the abundance of Central European *P. ridibundus*, but has a positive effect if they come from Southern Europe.

We finally considered a more productive population of *P. ridibundus* and of hybrids than of *P. lessonae* ($R_L < R_E < R_R$), the abundance of *P. ridibundus* increases with increasing competition, up to the replacement of native frogs when competition is strong, and this trend is independent of the geographical origin of *P. ridibundus* and the interbreeding success rate with hybrids (data not shown).

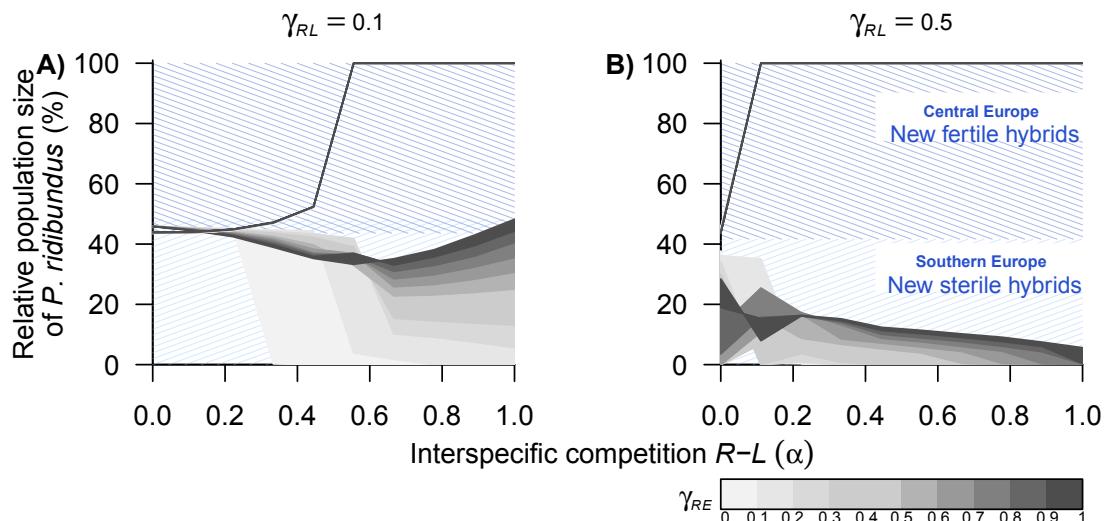


Figure 3.7. Effect of interspecific competition between *P. ridibundus* and *P. lessonae* in the colonization of the waterfrog community by *P. ridibundus* in Western Europe. a) Interbreeding success rate between parental species of 10%; b) Interbreeding success rate between parental species of 50%. We assumed symmetrical interbreeding success rate and competition between parental species ($\gamma_{RL} = \gamma_{LR}$ and $\alpha_{RL} = \alpha_{LR} = \alpha$). Data are presented after 400 time steps (years).

CHAPTER 4

Hybridization with genome exclusion: a highway to extinction

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Unpublished manuscript

4.1 Project description

The main aim of this chapter is to highlight the very fast extinction risk produced by hybridization type 2, which undergoes genome exclusion. It is a phenomenon that is largely underappreciated because it mimics hybridization type 1, with infertile hybrids. We apply the model in a general way, but in using parameter values from our previous application (Chapter 3) about invasive water frogs in Western Europe (*P. ridibundus*), which also produce the same phenomenon when translocated to other places (e.g. *P. perezi* in Spain, Holsbeek and Jooris, 2010). We improve the general model of distant hybridization to incorporate environmental stochasticity. We show that the extinction may be reached in very few generations and that the potential stability of the system is easily disrupted by

changing environmental conditions. Because this hybridization occurs between distant species, which often have differentiated habitat requirements, we propose habitat management as a promising tool to rescue threatened species. We stress the importance of promoting conservation actions when this type of hybridization is achieved.

Author contributions CSQ collected and analysed the data and drafted the first version of the manuscript. He also participated in the conception and design of the study as well as in the interpretation of the results and the final writing of the manuscript.

4.2 Abstract

Human induced habitat changes may lead to the breakdown of reproductive barriers between distantly related species. This phenomenon often results in fertile first-generation hybrids (F_1) that exclude the genome of one parental species during gametogenesis, disabling introgression. The species extinction risk associated to hybridization with genome exclusion has been largely underappreciated because this phenomenon produces only F_1 hybrid phenotype, leading to the misinterpretation that hybrids are sterile and potentially of minor conservation concern. Here, we show that this mode of hybridization may lead to extremely rapid extinction when the process of genome exclusion is unbalanced between the interbreeding species and when the hybridization rate is non-negligible. We find that the coexistence of parental species is possible in some cases of asymmetrical genome exclusion, but show this equilibrium is highly vulnerable to environmental variation. We further demonstrate that expanding the exclusive habitat of the species at risk allows its persistence. Our results highlight the extent of possible extinction risk due to hybridization with genome exclusion and suggest habitat management as a promising conservation strategy. In anticipation of serious threats to biodiversity due to hybridization with genome exclusion, we recommend a detailed assessment of the reproductive status of hybrids in conservation programs.

4.3 Hybridization with genome exclusion

Interspecific hybridization is being enhanced by human-induced disturbances such as habitat modification, species translocation and global climate change (Todesco et al., 2016). The interbreeding between distantly related species often leads to the production of fertile first-generation hybrids (F_1) which produce gametes containing the non-recombined genetic material of one parental species, excluding the genome of the other parent during gametogenesis (e.g. Mee and Taylor, 2012; Som and Reyer, 2006; Tinti and Scali, 1995). Consequently, the offspring of F_1 hybrids is either a pure parental individual or a regenerated F_1 hybrid, depending on the mate (Yakovlev et al., 2000). Hybridization with genome exclusion may result in the extinction of one parental species through its progressive replacement by individuals of the other parental species, a process referred to as "*demographic flow*" between species.

In a hybrid system with genome exclusion no recombination between homologous chromosomes occurs during meiosis and no introgression of nuclear genes take place. F_1 hybrids produce non-recombinant haploid gametes: either a single type of gametes due to the systematic exclusion of one of the parental genomes (non-alternative genome exclusion) or two types of gametes that each contain one of the two parental genomes (Fig. 4.1). Thus, F_1 hybrids clonally transmit the haploid genome of one or both of the parental species. This process may result in hybridogenetic, gynogenetic, parthenogenetic or polyploid forms (Lampert, 2009). Examples are frequently observed in freshwater fishes of the families Atherinidae, Cobitidae, Cyprinidae and Poeciliidae (Schmidt et al., 2011). For example, the hybrids between two North American cyprinids, *Phoxinus eos* and *P. neogaeus*, produce haploid gametes of one of the parental species, thereby potentially regenerating pure, non-hybrid nuclear genomes (Goddard and Schultz, 1993). The regenerated *P. eos* was originally believed to be rare in nature (Binet and Angers, 2005); however, recent studies have revealed the high abundance of such individuals, which replaced all of the original populations of *P. eos* that lived in sympatry with hybrids (Mee and Taylor, 2012). As the original crosses occurred between female *P. neogaeus* and

male *P. eos*, all of the hybrids and regenerated parental species shared the mtDNA haplotypes of *P. neogaeus*; therefore, it is unknown whether a similar replacement has occurred in *P. neogaeus* (Angers and Schlosser, 2007; Mee and Taylor, 2012). Another example involves the *F*₁ hybrids between two European freshwater cyprinids, roach (*Rutilus rutilus*) and bream (*Abramis brama*). These hybrids are known to be fertile (Wood and Jordan, 1987); however, their progeny were long believed to be unfertile due to the absence of post-*F*₁ hybrid phenotypes observed in nature (Hayden et al., 2010; Pitts et al., 1997). However, detailed examination of the gametes produced by *F*₁ hybrids confirmed that they each contain the non-recombined haploid genome of one or the other parental species and could potentially regenerate roach and bream (Yakovlev et al., 2000). In other hybrid systems, *F*₁ hybrids may regenerate only one parental species, as in the hybridization between *Poeciliopsis monacha* and *P. lucida*. *F*₁ hybrids that produce gametes of *P. monacha* restore the *P. monacha* genome when crossing with *P. monacha*, whereas new hybrids are produced when they cross with *P. lucida* (Cimino, 1972). Hybridization with genome exclusion has also been documented in stick insects of the genus *Bacillus* (Mantovani and Scali, 1992), in the fish genus *Squalius* (Crespo-Lopez et al., 2006), and in *Ambystoma* salamanders (Charney, 2012).

Hybridization with genome exclusion occurs in waterfrogs of the genus *Pelophylax*. In Western Europe, hybrids between *P. lessonae* and *P. ridibundus*, currently known as *P. esculentus*, discard the *P. lessonae* genome during gametogenesis and produce gametes that contain the haploid genome of *P. ridibundus*. *F*₁ hybrids are thus regenerated when the hybrids mate with *P. lessonae*. Because the crosses between two hybrids are inviable and as *P. ridibundus* retracted out of Western Europe during the last ice age, the system that comprises *P. lessonae* and the hybrid *P. esculentus* (*L/E* system) has remained in equilibrium for 10,000 years. Recent translocations of *P. ridibundus* from Eastern Europe, where this species occurs naturally, to France and Switzerland during the 20th century are currently destabilizing the *L/E* system. Hybridization between the introduced species and the native ones reinforces the invasive process and may lead to the potential replacement of both native frogs (Holsbeek and Jooris, 2010). In a recent study, we used an original

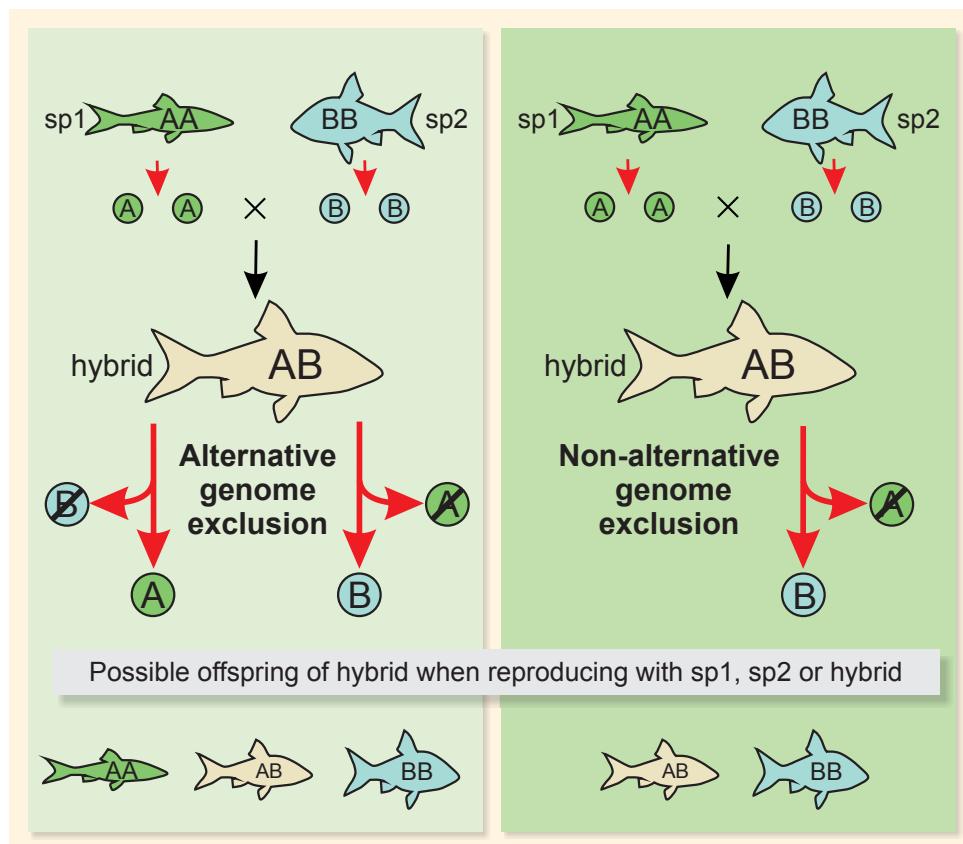


Figure 4.1. Interspecific hybridization with genome exclusion. Interspecific hybridization may lead to the production of fertile hybrids that yield gametes that contain the non-recombined haploid genome of one of the parental species. Circles depict gametes. In the F_1 hybrids, genome exclusion usually happens before or during gametogenesis, producing either a single type of gamete via the systematic exclusion of one parental genome (non-alternative genome exclusion) or two types of gametes, each of which contains one or the other parental genome (alternative genome exclusion). Depending on the type of genome exclusion, either one or both parental species are regenerated by the hybrids in addition to the hybrid itself.

model to assess the conditions under which interspecific hybridization can lead to population extinction; the results provide a means to evaluate the efficiency of conservation actions (Quilodrán et al., 2015). We revealed that enlarging the habitat size of the native *P. lessonae* is a promising conservation strategy that avoids the difficulties of fighting the invader, which cannot be easily recognized morphologically.

4.4 Fast extinction

By modeling interspecific hybridization with genome exclusion between virtual parental species, we project the potential impact of this type of hybridization on species persistence. We adapted our previously published model (Quilodrán et al., 2014a, 2015) to consider diploid organisms with hybrid offspring that undergo different proportions of genome exclusion. We simulated two parental species, coded as 0 and 1, with genomes coded as 00 and 11, respectively. Hybrids either systematically regenerate a single parental species when the proportion of genome exclusion is completely skewed to 0 or 1 or alternate between them with intermediate values of genome exclusion. Values of genome exclusion less than or greater than 0.5 favor the genomes 00 and 11, respectively (see methods in 4.6).

Due to the direct replacement of parental species by hybrid offspring, the extinction of one species can be reached in a few generations if the genome exclusion is completely skewed toward one parental species (Fig. 4.2a). In this case, when hybridization increases to the critical point at which the abundance of hybrids exceeds that of the non-regenerated species, both the hybrids and the non-regenerated species go extinct. At this point, the community is composed exclusively of the species favored by the genome exclusion. In the case where hybrids produce gametes of both parental species in equal proportions, the hybrids reach maximum abundance. When the values of genome exclusion vary between 0.2 and 0.8 and the interbreeding rate between both parental taxa is less than 0.4, all three forms persist in the community. At smaller and larger values of genome exclusion and at higher interbreeding rates, the extinction of the species that is not favored by the genome exclusion occurs rapidly in our simulations (27 generations); this extinction occurs even more rapidly if the genome exclusion is completely skewed toward one species and the interbreeding is panmictic (6 generations).

We assessed the stability of our results when environmental stochasticity is included in the model. Environmental stochasticity was incorporated by varying the temporal autocorrelation of the yearly survival of the offspring (parameter *AC*, see methods in Sup-

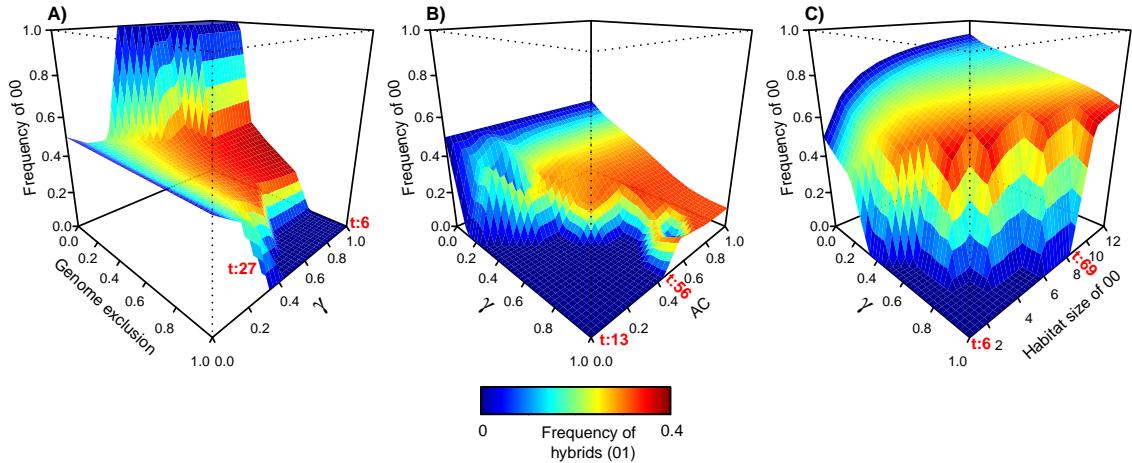


Figure 4.2. Demographic impact of genome exclusion. We simulated two parental species N_0 and N_1 with genomes 00 and 11, respectively. The hybrid $N_{\frac{1}{2}}$ has the genome 01 and generates fertile offspring that undergo genome exclusion. The frequency of hybridization is estimated through the interbreeding success rate parameter " γ ". When $\gamma = 0$, both species are reproductively isolated; reproduction is panmictic when $\gamma = 1$. The frequency of the genome 00 is estimated as $N_0 / (N_0 + N_{\frac{1}{2}} + N_1)$ and that of the hybrid genome 01 as $N_{\frac{1}{2}} / (N_0 + N_{\frac{1}{2}} + N_1)$. A) Proportion of genome exclusion in hybrid offspring; values from 0 to 1 represent systems ranging from completely skewed toward genome 00 to completely skewed toward genome 11. B) Incorporation of stochasticity in the model through the parameter AC (autocorrelation in time); AC values range from 0 to 1 wherein 0 and 1 indicate a completely stochastic model and a totally deterministic one, respectively. We considered a system that is skewed toward one parental species but in which all of the three forms, i.e., the two parental species and the hybrids, can persist in a deterministic and panmictic system (0.75 of genome exclusion favoring genome 11). C) The minimum habitat size required for species of genome 00 to avoid complete extinction when the exclusion is completely skewed toward the species with genome 11 and when reproduction is panmictic between species. Interspecific hybridization with genome exclusion can lead to the extinction of one of the parental species in a few generations (t : number of generations; shown in red). No hybridization between the parental species was simulated during the first 200 generations. Data correspond to a situation projected after a total of 400 generations (see methods in Supporting information).

porting Information), with values ranging from stochastic ($AC = 0$) to completely deterministic environmental changes ($AC = 1$). We considered a case in which the three forms persist in the community even if reproduction is panmictic and genome exclusion is skewed toward one of the parental species (0.75 of genome exclusion, favoring species 1, see Fig. 4.2a). Even if all of the three forms can be found in equilibrium at different abundances in the deterministic model, the species that is not favored by the genome exclusion can reach extinction when environmental stochasticity is incorporated into the model under the same conditions (Fig. 4.2b). Thus, even when the apparent coexistence equilibrium of the three forms can be observed in nature, the long-term output is strongly dependent on environmental variation. Therefore, it is important to consider environmental predictability when projecting the fate of interbreeding species in the context of extreme meteorological events such as those produced by global climate change (Coumou and Rahmstorf, 2012).

We finally considered the worst-case scenario of genome exclusion that is completely skewed in favor of one species to assess the minimum habitat size of the other species that is required to escape extinction (in our simulations, favoring species 1, Fig. 4.2b). We showed that increasing the exclusive habitat for the species that is disadvantaged due to genome exclusion (species 0) lengthens the time span before extinction and may eventually allow the species to persist even when hybridization is at a maximum. In this case, because the reproduction between conspecific or heterospecific partners is similar, the reproductive cost for the species disadvantaged by the genome exclusion is the maximum; thus, extinction can be reached extremely rapidly (6 generations) when the habitat size is equal between species. In that critical case, a habitat size of the threatened species that is nine times larger than that of the favored species may save the threatened species from extinction. Habitat management has already been emphasized as a potential way to rescue species affected by hybridization and genome exclusion (Quilodrán et al., 2015).

In the scenarios examined here, we did not incorporate interspecific competition between parental species because most cases of hybridization with genome exclusion involve distantly related species (Yakovlev et al., 2000) that generally do not compete for

resources. If incorporated into the model when the genome exclusion is slightly skewed in favor of one parental species, interspecific competition leads to the more rapid extinction of both hybrids and the disadvantaged parental species (data not shown).

4.5 Discussion and conclusions

Our results highlight the extreme consequences of hybridization with genome exclusion on species persistence. The direct replacement of a parental species by hybrid offspring may lead to the collapse of one species within a few generations when the exclusion is skewed toward the other species. We thus demonstrate that such kind of hybridization may precipitate a very fast extinction and we show this is strongly facilitated when environmental stability is challenged. The hybridizing species are also more affected by stochastic external stress such as extreme environmental changes. Therefore, the increasing frequency of extreme weather events worldwide (Cai et al., 2014) is an additional threat to the long-term coexistence of some apparently stable hybridogenetic and gynogenetic conditions (e.g. Mee and Otto, 2010; Som and Reyer, 2006).

We also report on actions that can improve species persistence. Because hybridization with genome exclusion is generally observed between distant species (Yakovlev et al., 2000), these species have differentiated habitat requirements (e.g. Holenweg Peter et al., 2002; Toscano et al., 2010). We highlight that taking advantage of these differences and managing the habitat in favor of the handicapped species is an auspicious technique to avoid species loss.

The true incidence of this type of hybridization in nature is unknown. However, approximately 80 taxa of reptiles, amphibians and fishes have been recognized to produce hybrids that undergo genome exclusion (Neaves and Baumann, 2011). Furthermore, we speculate that the incidence of this type of hybridization will increase in the near future because many historically allopatric species are undergoing secondary contact due to human-caused species translocations or the consequences of global climate change, such as habitat modification, changes in migration patterns and changes in the timing of reproduction. Here, we emphasize that the extinction risk is underappreciated because hy-

bridization with genome exclusion generates only hybrids displaying the F_1 phenotype, as in hybridization with hybrid sterility that may be considered of minor conservation concern (Allendorf et al., 2001). Therefore, we urge policy makers and stakeholder managers of conservation programs to include the inspection of the genetic content of the gametes of hybrids where distant species hybridization is occurring and only the F_1 phenotype is observed.

4.6 Acknowledgments

This study was financed by a fellowship from the Center for Advanced Modeling Science (CADMOS) and by grants from the Swiss National Science Foundation (number 31003A_141233 to J.I.M.B. and number 31003A_156853 to M.C.). C.S.Q. acknowledges support from CONICYT-Becas Chile and from the iGE3 student salary award. All computations were performed in the High Performance Computing (HPC) cluster baobab.unige.ch. We thank Carlos Rivera for their comments and suggestions on an earlier version of this manuscript.

4.7 Supporting information

4.7.1 Methods

A general model

Our aim is to assess the threat that interspecific hybridization with genome exclusion may represent for one or both parental species. We adapt a previously published model of interspecific hybridization in which hybrids are unfertile or fertile but do not undergo chromosomal recombination during gametogenesis (Quilodrán et al., 2014a, 2015).

Our model considers diploid organisms without genetic introgression between parental species. Thus, the genome frequency of species 0 is codified as 00, and that of species 1 is codified as 11. Hybrids have the genotype 01. The abundances of the parental species and hybrids are represented by N_0 , N_1 and $N_{1/2}$.

Each genotype class contributes to the next generation by the quotient between the mating frequency of individuals of class i and j and all of the possible mating combinations. The probability M_{ij} for individuals of class i to mate with individuals of class j for all $i, j \in [0, \dots, 1]$ is as follows:

$$M_{ij(t)} = \frac{\gamma_{ij} N_{j(t)}}{\varphi_{i(t)}} \quad (4.1)$$

where $\varphi_i(t)$ is a normalization factor such that $\sum_i M_{ij} = 1$. The parameter γ_{ij} characterizes the interbreeding success rate. It represents a measure of the mating success between individuals of class i and j . When $\gamma_{ij} = 0$, both species are completely isolated, whereas reproduction is panmictic when $\gamma_{ij} = 1$. If $\gamma_{ij} = \gamma ji = \gamma$, the mating preference or fertility success does not differ between the interacting taxa, and the value of γ thus represents a measure of the hybridization frequency (Currat et al., 2008b).

Then, we estimate the number of breeding pairs between i and j that produce offspring k , weighted by the gametes fraction yielding k and the relative fitness of class k , as follows:

$$b_{ij,k(t)} = N_{i(t)} M_{ij(t)} C_{ij,k} \omega_k \quad (4.2)$$

where $C_{ij,k}$ represents the fraction of class k offspring resulting from a reproductive event between classes i and j . The value of ω_k is the relative fitness of offspring k relative to the parental classes i and j . The final weighted number of crosses that produce k is thus estimated as the sum of all the mating pairs that produce individuals of class k .

$$n_{k(t)} = \sum_i \sum_j b_{ij,k(t)} \quad (4.3)$$

The number of individuals who reach sexual maturity after intra- and inter-specific density-dependent effects is computed with an extension of the Ricker model. This function has been demonstrated to be useful for species with a larval stage (Wilbur, 1976) and in which distant hybridization has been frequently observed, i.e., fishes and amphibians.

$$N_{k(t+1)} = \text{round} \left[N_{k(t)} S_k + R_k n_{k-\theta} e^{-\frac{n_{k(t-\theta)} + \sum_{l \neq k} \alpha_{kl} n_{l(t-\theta)}}{V_k}} \right] \quad (4.4)$$

We round off the resulting value of equation (4.4) to take into account the "*lattice effect*", in which unexpected outputs might appear due to the non-continuous but discrete nature of the individuals in a population (Henson et al., 2001). The first term of equation (4.4) denotes the number of adults that survive from one reproductive season to the next, in which S_k is the adult survival of individuals of class k . The second term denotes the number of offspring that survive until sexual maturity, where θ indicates the time to reach maturity in $t + 1$. The parameter α_{kl} denotes the amount of competition between members of different classes relative to the amount of competition achieved by individuals of the same class k . The value of V_k expresses the habitat size as introduced by Henson et al. (2001). Finally, The parameter R_k represents the number of progeny that survives until sexual maturity or the population growth rate. To take into account the survival of offspring at different stages before sexual maturity, we compute the parameter R_k as in equation (8) of Quilodrán et al. (2015):

$$R_k = c_k \prod_{l=1}^b S_k^l \quad (4.5)$$

where c_k is the clutch size and S_k^l is the survival probability across all of the important stages before sexual maturity. More details on our general model can be found in Quilodrán et al. (2014a, 2015).

Implementation

We implement our general model with a theoretical case study of species that undergo interspecific hybridization with genome exclusion. The parameter values are based on an actual case study of waterfrogs on Western Europe that undergo hybridization with genome exclusion that was recently published by Quilodrán et al. (2015).

They correspond to those of *Pelophylax ridibundus* but without overlapping generations (survival of adults set to zero). *Pelophylax ridibundus* is an invasive species that

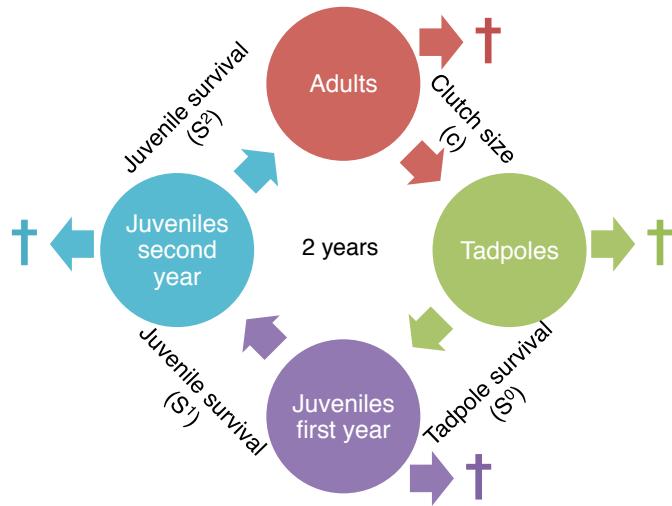


Figure 4.3. Life cycle of the theoretical species described in our model. Individuals take two years to reach sexual maturity. We assume an equal sex ratio and the same parameter values for parental species and hybrids. The parameter values are taken from a case of waterfrogs in Western Europe that undergo hybridization with genome exclusion.

undergoes genome exclusion when it hybridizes with other *Pelophylax* waterfrogs, i.e., *P. perezi* and *P. lessonae* (Holsbeek and Jooris, 2010).

In our theoretical case study, there are three possible forms: two parental species and hybrids, noted as 0, 1 and 1/2. They follow the same code rules described in the model description section.

Individuals take two years to reach sexual maturity after developing from tadpoles and juveniles of first and second year (Fig. 4.1). We assume the same demographic parameter values and equal sex ratios for all of the interacting forms. The reproductive effort between the two parental species is controlled by the interbreeding success rate parameter (γ , see Table 4.1), whereas the reproduction of hybrids is considered to be panmictic with all of the three forms. As hybridization with genome exclusion usually occurs between distantly related species and because hybrids often use intermediate habitats (Hayden et al., 2011; Holenweg Peter et al., 2002), we assume no competition between parental taxa ($\alpha_{01} = \alpha_{10} = 0$) and an intermediate level of parental taxa competition with hybrids ($\alpha_{0\frac{1}{2}} = \alpha_{\frac{1}{2}0} = \alpha_{1\frac{1}{2}} = \alpha_{\frac{1}{2}1} = 0.5$).

Because some species that undergo hybridization with genome exclusion always exclude the genome of one of the two parental species, whereas others non-exclusively

exclude one of either parental genome (Mee and Taylor, 2012; Yakovlev et al., 2000), we introduced a parameter "g" into the model to assess the effect of genome exclusion on different proportions. It simulates scenarios from completely biased exclusion toward a single genome, either 00 or 11 ($g = 0$ or $g = 1$, respectively), to exclusion distributed equally between the two parental genomes ($g = 0.5$). The parameter "g" is thus introduced in equation (4.3). It is defined for all the interacting forms in equations (4.6), (4.7) and (4.8):

$$\begin{aligned} n_{0(t)} = & N_{0(t)} M_{00} + \\ & (1-g) \left(N_{0(t)} M_{0\frac{1}{2}} + N_{\frac{1}{2}(t)} M_{\frac{1}{2}0} + N_{\frac{1}{2}(t)} M_{\frac{1}{2}\frac{1}{2}} \left(\frac{1}{2} + \left| g - \frac{1}{2} \right| \right) \right) \end{aligned} \quad (4.6)$$

$$\begin{aligned} n_{1(t)} = & N_{1(t)} M_{11} + \\ & g \left(N_{1(t)} M_{1\frac{1}{2}} + N_{\frac{1}{2}(t)} M_{\frac{1}{2}1} + N_{\frac{1}{2}(t)} M_{\frac{1}{2}\frac{1}{2}} \left(\frac{1}{2} + \left| g - \frac{1}{2} \right| \right) \right) \end{aligned} \quad (4.7)$$

$$\begin{aligned} n_{\frac{1}{2}(t)} = & N_{0(t)} M_{01} + N_{1(t)} M_{10} + \\ & N_{\frac{1}{2}(t)} M_{\frac{1}{2}\frac{1}{2}} \left(\frac{1}{2} + \left| g - \frac{1}{2} \right| \right) + \\ & g \left(N_{0(t)} M_{0\frac{1}{2}} + N_{\frac{1}{2}(t)} M_{\frac{1}{2}0} \right) (1-g) \left(N_{1(t)} M_{1\frac{1}{2}} + N_{\frac{1}{2}(t)} M_{\frac{1}{2}1} \right) \end{aligned} \quad (4.8)$$

These equations assume Mendelian inheritance and equal fitness values for all three forms (parameters $C_{ij,k} = 1$ and $\omega_k = 1$ in Equation 4.3). Therefore, if the value of g was equal to 0.5, it would be reduced to a case of single biallelic genes.

We are also interested in introducing environmental stochasticity into the model. We incorporate it by adding a temporal dynamic to the growth rate parameter estimated in Equation (4.5) that takes into account the temporal autocorrelation through the yearly survival of juvenile stages as follows:

$$R_{K(t)} = c_k \delta_{(t)} \quad (4.9)$$

where $\delta_{(t)}$ represents the right-hand side of Equation (4.9), which denotes the product of all of the stages before sexual maturity ($\delta_{(0)} = \sum_{l=1}^b S_k^l$). The temporal dynamic is included through a beta distribution with mean $\delta_{(0)}$ and variance $\sigma^2 = (\delta_{(0)} - \delta_{(t)}AC)^2$.

$$\delta_{(t+1)} = \delta_{(t)}AC + (1 - AC)\beta(\delta_{(0)}, \sigma^2) \quad (4.10)$$

The parameter AC characterizes the temporal autocorrelation. It takes values from 0 to 1, with 0 and 1 representing a completely stochastic process and a completely deterministic one, respectively.

We show the result of our implementation in the Figure 4.2 of the main text. We varied different values of hybridization frequency, measured through the interbreeding success rate parameter (γ), to assess its combined effect with different proportions of genome exclusion (g), levels of temporal autocorrelation (AC) and habitat sizes (V) on the frequency of each genome. We simulated 200 generations of independent evolution for each parental species after the onset of hybridization. We present the results after a total of 400 generations.

Table 4.1. List of functions and parameters of the model with default values

Symbol	Definition
N_i	Number of adult individuals of genotypic class i Initial size: $N_0 = N_1 = 50$; $N_{\frac{1}{2}} = 0$
n_i	Weighted number of matings that leads to offspring of class i
R_i	Population growth rate
$\delta_{(t)}$	Product of all of the stages before sexual maturity
AC	Temporal autocorrelation
g	Proportion of exclusion between parental genomes
θ	Time delay from hatching to age at maturity in $t + 1$ $\theta_0 = \theta_1 = \theta_{\frac{1}{2}} = 1$ (two years)
c	Clutch size $c_0 = c_1 = c_{\frac{1}{2}} = 1250$
S^0	Survival of tadpoles $S_0^0 = S_1^0 = S_{\frac{1}{2}}^0 = 0.012$
S^1, S^2	Survival of first- and second-year juveniles $S_0^1 = S_1^1 = S_{\frac{1}{2}}^1 = 0.5$; $S_0^2 = S_1^2 = S_{\frac{1}{2}}^2 = 0.4$
α	Interspecific competition coefficient $\alpha_{01} = \alpha_{10} = 0$; $\alpha_{\frac{1}{2}0} = \alpha_{1\frac{1}{2}} = \alpha_{\frac{1}{2}1} = 0.5$
V	Habitat size $V_0 = V_1 = V_{\frac{1}{2}} = 5000$
γ	Interbreeding success rate $\gamma = \gamma_{01} = \gamma_{10} = 0 - 1$
ω	Fitness of newly formed hybrids $\omega_{\frac{1}{2}} = 1$

CHAPTER 5

Cryptic biological invasions: a general model of hybridization

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5.1 Project description

This chapter presents a full hybridization model to study the very large range of possible outcomes produced when two species admix. The focus is made on hybridization type 3, undergoing genomic mixing and gene flow between parental species, but the other two types of hybridization (i.e genome exclusion and infertile hybrids) can be considered as special cases of this generalized version of the model. We added to our previous model of distant species hybridization the simulation of multiple loci, recognizing the expression of quantitative and qualitative genes and the possibility to explore neutral and selective mechanisms. This generalizes the approach to any hybridization category and to a large range of possible issues in ecology, conservation and evolution. We explore the model by

illustrating changes in the phenotypic landscape produced when genetically distinct organisms hybridize. This is influenced by the effects of additive genes and specific alleles under selection and demographic factors. We highlight the importance of simulating multiple loci instead of a single gene. We also show that the interaction between genetic and demographic factors is important to explain the shape of the phenotypic landscape. We finally stress that genetic swamping may act in very few generations, facilitating biological invasions. We based our simulations on the mallard (*Anas platyrhynchos*), which has been widely translocated by humans, and for which hybridization is a concern in almost their entire distribution.

Author contributions CSQ collected and analysed the data and drafted the first version of the manuscript. He also participated in the conception and design of the study as well as in the interpretation of the results and the final writing of the manuscript.

5.2 Abstract

The dispersal of non-native genes due to hybridization is considered as a cryptic invasion of growing concern in evolutionary biology and conservation. We developed a general model describing the genetic consequences of hybridization, useful for a large range of biological questions. It is the first attempt to concurrently consider multiple loci, quantitative and qualitative gene expression, assortative mating, dominance/recessivity inheritance and density-dependent demographic effects. Natural selection acting on some alleles or genotypes can also be incorporated into the model. Hybridization may produce novel genotypic architectures that depend on the number of genes involved, their direct and indirect interactions, and on the selective pressures acting on each genotype. By using multiple genes, we show that previous modelling approaches based on a single gene may seriously bias conclusions about the effects of hybridization on biodiversity. We also show that it is essential to consider jointly the influence of both genetic and demographic effects to explore the range of potential phenotypes, because demographic factors may either amplify or at contrary balance the genetic effects. By investigating a real case, we

show that invasive species may exclude native taxa not only by direct competition but also indirectly by competition with hybrids. Hybridization may therefore facilitate the invasion of exotic organisms. We highlight that the effects of human-induced hybridization on biodiversity are not necessarily negative by precipitating species loss as it may also increase genetic diversity and the potential of adaptation to changing environmental conditions. Our general model thus represents a powerful tool to explore the effects of hybridization on biodiversity and to investigate specific cases.

5.3 Introduction

Novel breeding opportunities arise when invasive species colonize new areas and interact with related local species. The breakdown of physical reproductive barriers and subsequent hybridization has been considered either as an evolutionary process leading to the emergence of new biodiversity (Mallet, 2007; Brumfield, 2010) or as a threat for local taxa when motivated by human activities (Rhymer and Simberloff, 1996; Allendorf et al., 2001; Vonlanthen et al., 2012).

Hybridization represents the interbreeding between members of genetically distinguishable groups (e.g. from different populations, subspecies, species or genera) (Taylor et al., 2015). Among the possible interactions between species, this process has been referred to as a silent or hidden phenomenon (Currat et al., 2008b; Gómez et al., 2015), with more cryptic effects as compared to other ecological interactions such as predation, competition or parasitism. Although cases of hybridization have increased dramatically in recent years due to the translocation of invasive species or the modification of natural habitats (Fitzpatrick et al., 2012), the long-term consequences of hybridization on the genetics and demography of organisms are poorly understood (Gilman and Behm, 2011). To address this issue, we have recently defined three main types of hybridization based on the reproductive status of F_1 offspring and the evolutionary distance between interacting taxa (see Quilodrán et al., 2014a, 2015). The first two types occur when distantly related species hybridize and are therefore referred to as "*distant hybridization*". The first type is defined by the resulting inviable or infertile hybrids while the second type is characterized

by the production of fertile hybrids but which do not undergo chromosomal recombination during meiosis. The latter type can lead to a variety of possible outcomes, such as polyploid, gynogenetic, partenogenetic or hybridogenetic forms. The third type occurs when species are sufficiently related, so that recombination between homologous chromosomes proceeds in hybrid meiosis, resulting at least partly to the birth of viable and fertile hybrids that mediate genetic introgression from one parental species to the other (referred here to as "*genomic mixing*").

Hybridization involving genomic mixing induces the formation of new genetic architectures. These hybrid organisms may have lower, equivalent or higher fitness than parental individuals (Arnold and Martin, 2010). It has been suggested that the speciation of numerous taxa has been influenced by ancient hybridization events (e.g. Capblancq et al., 2015). Despite this evolutionary role in generating new species, hybridization may also represent an extinction risk with conservation concerns when it is motivated by anthropogenic factors. For instance, the introgression of non-native genes may cause the extinction of native genotypes conferring key local adaptations while introducing maladaptive alleles (Kidd et al., 2009; Todesco et al., 2016). The waste of reproduction effort may reduce the likelihood of population recovery when a taxon is already threatened, which has already limited effective population size (Leonard et al., 2013). Introgression of non-indigenous genes may also change the behaviour of native individuals with unpredictable ecological effects (Ellington and Murray, 2015). Furthermore, the legal status of a threatened and protected species may not be the same for its hybrids, as they may not be considered as protected subjects (Haig et al., 2011; Fitzpatrick et al., 2012).

We previously developed a model to study the first two types of hybridization, which are often observed between distant species. We demonstrated that distant hybridization represents a demographic risk for native species via wasted reproductive effort, either enhancing the effect of additional threats (Quilodrán et al., 2014a), or directly replacing parental species by hybrid offspring (Quilodrán et al., 2015). Here we extended this model in order to incorporate all three types of hybridization, with a specific focus on the third type, which is characterized by process of genomic mixing.

The general model presented here can thus be applied to any type of hybridization and to a large range of biological questions. This approach combines important features of population genetics and population dynamics to explore the potential outputs of a hybrid system. The interaction between genetic and demographic factors may facilitate a rapid extinction risk (e.g. Vonlanthen et al., 2012), but they have rarely been incorporated together in earlier modelling efforts (Hall and Ayres, 2009). Previous attempts at modelling hybridization with genomic mixing have focused in quantitative gene expression, ignoring the influence of density-dependent demographic effects (Ferdy and Austerlitz, 2002; Tanaka, 2010; Kitamoto et al., 2012). The few approaches that have considered density-dependent effects simulate a single locus (Huxel, 1999; Baskett and Gomulkiewicz, 2011; Satake and Araki, 2012). We present the first general model fully addressing six important processes to explore the range of outcomes of hybridization on biodiversity: 1) intra- and inter-specific density-dependent competition; 2) the degree of dominance/recessivity of alleles in hybrids; 3) assortative mating between interacting organisms; 4) simulation of multiple loci; 5) incorporation of quantitative and qualitative gene expressions; and 6) the possibility to simulate both neutral and selective mechanisms.

Using our general model, we first explored the phenotypic landscape that might be observed when genetically distinct organisms hybridize. To better depict the possible consequences, we investigated real cases of hybridization involving the mallard duck (*Anas platyrhynchos*), the world's most common dabbling duck and for which hybridization is a conservation issue in almost its entire geographical distribution (Tubaro and Lijtmaer, 2002). We based our simulations on parameter values assembled from a literature survey. Mallards are holoartic, but they have been introduced in other areas where they interact with closely related taxa, with levels of hybridization and subsequent introgression sufficiently high to threaten local species (e.g. *A. superciliosa*, *A. undulata*, *A. sparsa*, *A. fulvigula*, *A. wyvilliana*, *A. rubripes*) (Mank et al., 2004; Tracey et al., 2008; Fowler et al., 2009; Van Rensburg et al., 2011; Seyoum et al., 2012; Guay et al., 2015). However, hybridization is also a major concern in their original distribution range, where mallards are threatened by introgression with farm-raised individuals (Čížková et al., 2012). Phe-

notypic changes in wild mallards due to the massive release of farm-raised individuals have already been documented (Söderquist et al., 2014). Human releases for hunting and ornamental purposes have changed the genetics, morphology, behaviour and migration of farm-raised ducks (Baratti et al., 2014).

By using our general model, we addressed two main questions about hybridization and cryptic genetic invasions: i) how do interactions between genetics and demography influence the observed phenotypic landscape when hybridization occurs? ii) how can native organisms be threatened by hybridization with an invasive species? We finally illustrate the usefulness of our general model by analysing real situations in which the hybridization of mallards with native species is a conservation concern.

5.4 Material and methods

5.4.1 General description of the model

Our model describes the genetic consequences of the interbreeding between a species (N_1) and a closely related taxon (N_0). Most often, one of the taxa is a new arrived species that hybridizes with a native species. The community is composed of diploid parental organisms, initially differentiated by multiple independent biallelic loci, assuming normal recombination between homologous chromosomes during hybrid meiosis and with case dependent interbreeding rates. We used an approximate hypergeometric model to decompose the possible genotype space in a discrete number of genetic classes, representing the proportions of loci coming from each parental species. This model was originally developed to study additive genes in a discrete number of phenotypes (Doebeli, 1996, 1997; Ferdy and Austerlitz, 2002; Tanaka, 2010), but the approach presented here allows the investigation of specific alleles or genotypes within groups. It is therefore not limited to quantitative characters but extends the method to the analysis of qualitative traits.

The number of independent biallelic loci that determine the reproductive isolation between both species is n_L . In each locus, alleles are denoted by upper case ($AA, BB, CC \dots$) if it comes from N_0 and by lower case if it comes from N_1 ($aa, bb, cc \dots$). We assume

a genotypic space between both taxa ranging between 0 and 1, in which 0 codifies the parental N_0 genotype and 1 the parental N_1 genotype. The number of possible hybrid intervals is defined by $2n_L - 1$. Therefore, N_i for $\frac{1}{2n_L} \leq i \leq 1 - \frac{1}{2n_L}$ are hybrids in which the proportion of upper or lower cases denote the proportion of genes coming from N_0 or N_1 (see Ferdy and Austerlitz, 2002)

The mating frequency of individuals of a given genetic class within or between classes, compared to all possible combinations, determines the contribution of each class to the next generation. Thus the probability M_{ij} for each female of class i to mate with a male of class j , for all $i, j \in [0, \dots, 1]$ is:

$$M_{ij(t)} = \frac{\gamma_{ij} N_{j(t)}}{\varphi_{i(t)}} \quad (5.1)$$

Where φ_i is a normalization factor such that $\sum_i M_{ij} = 1$. In our model, the parameter γ_{ij} represents the interbreeding success rate between individuals of class i and j . When $\gamma_{ij} = \gamma_{ji}$, interbreeding success rate is symmetrical between both classes while it is asymmetrical when $\gamma_{ij} \neq \gamma_{ji}$. When $\gamma_{ij} = \gamma_{ji} = 0$, there is no successful hybridization between i and j , whereas a value of 1 corresponds to a complete panmictic mating (Currat and Excoffier, 2004). Any other value of $\gamma_{ij} \in [0, 1]$ implies that mating is locally non random and reproduction occurs more often between members of class i than between individuals of the different classes i and j . The value of $1 - \gamma_{ij}$ represents thus a measure of assortative mating (see Excoffier et al., 2014; Quilodrán et al., 2014a, 2015). The interbreeding success rate could be considered a fixed parameter among phenotype classes (each γ_{ij} is set a priori), or as a variable that depends on the proportion of genes coming from both parental species. In this latter case, for all $i, j \in [0, \dots, 1]$, the interbreeding success rate is computed as:

$$\gamma_{ij} = \sum_{u=0}^2 \sum_{q=0}^2 \frac{1}{2} \left(2 - |u - q|(1 - \gamma) \right) \frac{f^u f^q \binom{2n_L - 2}{2n_L i - u} \binom{2n_L - 2}{2n_L j - u}}{\binom{2n_L}{2n_L i} \binom{2n_L}{2n_L j}} \quad (5.2)$$

The first section on the left side of equation (5.2) represents the strength of interbreeding between and within genetic classes. Reproduction is panmictic between individuals with the same genotype, but it decreases with the loss of shared loci within and between classes. For instance, the reproduction between two individuals with 50% of shared genes from parental species, in a genotype space defined by five genes ($i = 0.5, j = 0.5, n_L = 5$), would be panmictic if both have the same genome (e.g. "AaBbCcDdEe"), but a leger decrease of interbreeding occurs when the genomes are different (e.g. "AaBbCcDdEe" and "AABBCCcddee"); and a larger decrease when coming from different classes (e.g. $j = 0.2$, "AAbbcccddee"). The values of " u " and " q " represent the frequency of parental genes at a single locus. They take values of 0, 1 and 2 depending on the number of lower case alleles. The second section, on the right side of equation (5.2), is a combinatory factor to take into account all loci in the analysis. The value of " f^u " (and " f^q ") represents the expected genotype frequency under Hardy-Weinberg (HW) equilibrium for each locus (i.e. 1 : 2 : 1 for a biallelic gene, e.g.: $aa : 2Aa : AA$), and it is computed as: $\frac{3 - (-1)^u}{2}$. The frequencies of genetic classes are therefore at HW equilibrium when the reproduction between parental classes is panmictic ($\gamma_{10} = \gamma_{01} = 1$).

Equation (5.2) assumes that gene flow between parental species is symmetrical ($\gamma_{10} = \gamma_{01} = \gamma$). Asymmetrical gene flow between parental species ($\gamma_{10} \neq \gamma_{01}$), due for instance to sex-biased mating preference or sex-biased survival of hybrids, may also be incorporated by setting $\gamma = \gamma_{01}(1 - i)\gamma_{10}i$, with hybrids behaving according to the proportion of genes coming from parental species.

We compute the number of breeding pairs composed of females of class i and males of class j , yielding offspring of class k as:

$$B_{ij,k(t)} = N_{i(t)}M_{ij(t)}C_{ij,k}\omega_k \quad (5.3)$$

Where $C_{ij,k}$ is the proportion of offspring of class k resulting from a reproduction event between individuals of class i and j relative to all progeny produced by ixj . These probabilities were presented by Doebeli (1997), and were modified by Ferdy and Auster-

litz (2002) (in their equations 2, 3 and 4) to work with proportional phenotype classes, as follows:

$$C_{ij,k} = \sum_{g,h \in [0, \dots, 1]} prob_i(g) prob_j(h) b(g, h, k) \quad (5.4)$$

$Prob_i(g)$ is the probability of two individuals belonging to different classes i and g to have an intragenomic overlap, which is the proportion of alleles coming from the same parental species (i.e. the number of loci for which both alleles are lower cases); it is computed as:

$$prob_i(g) = \left[\binom{2n_L}{2n_L g} / \binom{2n_L}{2n_L i} \right]^{2n_L(i-2g)} \binom{n_L - 2n_L g}{s} / \binom{n_L - 2n_L g - s}{2n_L i - 4n_L g - s} \quad (5.5)$$

and $b(g, h, k)$ is the probability that crosses between g and h yield individuals of phenotypic classes k , it is calculated as:

$$b(g, h, k) = \binom{2n_L i - 4n_L g + 2n_L j - 4n_L h}{2n_L k - 2n_L g - 2n_L h} \left(\frac{1}{2} \right)^{2n_L i - 4n_L g + 2n_L j - 4n_L h} \quad (5.6)$$

We introduce the parameter ω_k (equation 5.3), which represents an inherited trait related to fitness in offspring of type k . It could represent the resistance to a particular disease, the relative survival to predation, or any other factor that confers a selective advantage, and that is genetically inherited. The value of ω_k is assumed to be expressed by one independent biallelic locus, in which both parental species are homozygous. Therefore, the expression of this character in the resulting phenotype class k depends on (1) the probability to be heterozygous (ρ_{Aa}) or homozygous (ρ_{AA} or ρ_{aa}) for this locus and (2) the dominance degree of the alleles "A" (ϵ_A) or "a" (ϵ_a). For individuals of class $k \in [0, \dots, 1]$, it is computed as:

$$\omega_k = \Omega_A \rho_{AA,k} + (\varepsilon_A \Omega_A + \varepsilon_a \Omega_a) \rho_{Aa,k} + \Omega_a \rho_{aa,k} \quad (5.7)$$

With $\varepsilon_A + \varepsilon_a = 1$. For instance, if $\varepsilon_A = 1$ and $\varepsilon_a = 0$, a character carrying the "A" allele is dominant while a character carrying the "a" allele is recessive. If $\varepsilon_A + \varepsilon_a = 0.5$, both characters are codominant. The values of Ω_A and Ω_a are parameters that represent the relative fitness at the allelic level, in which the allele with the highest fitness has $\Omega = 1$, while the other one is expressed as a fraction relative to 1.

The probability of being homozygous for an upper case allele "A" (ρ_{AA}) for any individual of class i , with n_L number of genes, is calculated as:

$$\rho_{AA,i}^{n_L} = \binom{2n_L - 2}{2n_L i} / \binom{2n_L}{2n_L i} \quad (5.8)$$

Similarly, the probability to be heterozygous for the allele "A" (ρ_{Aa}) for any individual of class i is:

$$\rho_{Aa,i}^{n_L} = \binom{2n_L - 2}{2n_L i - 1} / \binom{2n_L}{2n_L i} \quad (5.9)$$

Finally, the probability to be homozygous for the allele "a" (ρ_{aa}) for any individual of class i is computed as:

$$\rho_{aa,i}^{n_L} = \binom{2n_L - 2}{2n_L i - 2} / \binom{2n_L}{2n_L i} = 1 - \rho_{Aa} - \rho_{AA} \quad (5.10)$$

The equations 5.8, 5.9 and 5.10 can be used to add a selective advantage in a second gene or to recognize a specific genotype in the range of possible genetic classes. The probability of a class i to carry a specific genotype is computed as:

$$\rho_{genotype,i} = \prod_{m=1}^{n_L} \rho_{allele, \frac{2n_L i - \Delta_{allele}}{2(n_L + 1 - m)}}^{n_L + 1 - m} \quad (5.11)$$

Where ρ_{allele} denotes the probability to be homozygous (ρ_{AA} or ρ_{aa}) or heterozygous (ρ_{Aa}) for upper cases or lower case alleles at the position of the gene m . The parameter Δ_{allele} represents the subtraction of lower case alleles at the previous genes. It subtracts 2, 1 or 0 alleles depending on the genetic characteristics of the previous gene $m - 1$, i.e. aa, Aa, AA , respectively. For instance, the probability to have a genotype "AABbCcddEe" in the phenotype class 0.5 (on a target genome with five genes), would be computed as:

$$\rho_{AA, \frac{5}{10}}^5 \rho_{AA, \frac{5}{8}}^4 \rho_{AA, \frac{4}{6}}^3 \rho_{AA, \frac{3}{4}}^2 \rho_{AA, \frac{1}{2}}^1.$$

The final number of offspring of type i is then calculated as the addition of all breeding events leading to the same type of genotype class i , as follows:

$$n_k(t) = \sum_{i,j \in [0, \dots, 1]} B_{ij,k(t)} \quad (5.12)$$

To evaluate the temporal dynamics of adult populations after intra and interspecific density-dependent competition, we used a logistic regulation (Currat et al., 2008b). We take into account the "lattice effect" described by Henson et al. (2001), in which the final outcome could be perturbed by the non-continuous nature of the number of individuals in a given population. This is incorporated through the rounding off of the following recursion equation:

$$N_{i(t+1)} = round \left[n_{i(t)} \left[1 + r_i \left(k_i - \sum_{j \in [0, \dots, 1]} \alpha_{ij} n_j \right) \middle/ K_i \right] \right] \quad (5.13)$$

Where K_i represents the carrying capacity and r_i the growth rate *per capita* of the i^{th} genetic class. The value of α represents the intra- (α_{ii}) and inter-class competition effects (α_{ij}). This value is usually set to 1 for intraspecific competition of parental organisms (α_{00}

or α_{11}). Therefore, zero represents no competition for environmental resources, while a full competition is achieved with a value of 1. Those values may either be fixed for each class, or may depend on local population densities (see Excoffier et al., 2014), or being conditional to the genomic overlap from parental species. In this last case, the values of α_{ij} may be computed the same way as parameter γ_{ij} in equation (5.2).

In the simulations that we present in this paper we used interbreeding (γ) and competition (α) depending on the proportion of loci coming from the parental classes 0 and 1. In the case of competition, parental organisms may or may not be in competition for environmental resources ($\alpha \neq 0$ or $\alpha = 0$, respectively), but full competition will always be acting on individuals of the same genotype, and for hybrids of different genetic classes, which level will depend on the proportion of shared loci.

5.4.2 Model exploration

Because various previously developed models focused on one single locus (e.g. Huxel, 1999; Baskett and Gomulkiewicz, 2011; Satake and Araki, 2012), we first assessed the influence of the number of simulated genes on the time needed to reach outcomes at equilibrium, defined as the moment when frequencies of all classes are stable in two consecutive generations. We also estimated the deviation to the Hardy-Weinberg (HW) equilibrium at the time when simulations reach frequencies at equilibrium.

We explored the expression of particular locus (i.e. qualitative expression) and additive genes (i.e. quantitative expression), emerging when two genetically distinct individuals hybridize. We first focused in a virtual quantitative trait influenced by additive neutral genes. In this case, the genotypic classes, with different proportions of genes from parental species, can therefore be considered as phenotypes expressed from the additive genes. We used our model to assess the range of possible phenotypes susceptible to be observed (i.e. landscape). We then incorporated purifying selection in a specific gene to explore its qualitative effect in the phenotypic landscape.

We also examined the influence of different population size (i.e carrying capacities) and competitive abilities between parental species on the phenotypic landscape and eval-

uate the risk of species extinction by genetic swamping that can be reached with the combined effects of genetic and demographic factors incorporated here.

5.4.3 Hybridization with mallards

The demographic parameter values are based on a previous publication characterizing the population dynamic of mallards, with 40-years of systematic census surveys (Table 5.1) (see Sæther et al., 2008). We used these parameters to explore our model, but the results are based in two different situations for which hybridization with mallards have conservation concerns.

We first addressed the change on the phenotypic landscape resulting from the hybridization of two genetically distinct taxa. This is a theoretical approach, but it may fit with some observations on mallards, which have experienced phenotypic changes due to introgression with human selected farm-raised conspecifics. The farm-mallards are massively released for hunting and ornamental purposes and participate in approximately 67% of all yearly breeding pairs in Europe (Champagnon et al., 2013). The invasion of farm-mallard genes in the wild have changed the morphology of wild mallards, which have a more "goose-like" bill than their ancestors (Söderquist et al., 2014). This theoretical exploration of phenotypic landscape, based in demographic parameters obtained from mallard populations, may bring some light to explain the effects of genetic introgression as expressed by bill size changes.

We secondly examined the situation in which mallards, which have been translocated to different regions in the world, are seriously threatening local species by genetic introgression. One of the most emblematic cases is the grey duck (*A. superciliosa*) in New Zealand, where mallards were introduced for hunting at the end of the 19th and early 20th century (Dyer and Williams, 2010). Several populations of grey duck are already extinct and most current individuals have a hybrid ancestry (Guay et al., 2015). In the 80's, Gillespie (1985) estimated the proportion of the total population with pure native genome to be 4.5%, the proportion of grey duck-like hybrids at 11.7%, and mallard-like hybrids at more than 60%. He recognized seven phenotypic categories among hybrids and pure

parental individuals. To examine this case of extreme introgression level we adapted the parameters of our model by assuming that the phenotypic differentiation is the product of additive genes. We also considered a similar population growth rate in both taxa, and we tried to estimate other demographic and genetic parameter values that best explain the invasion of mallards and the decline of the native species. We simulated the genetic interaction to begin in 1910, when the feral population of mallards was established (Dyer and Williams, 2010). We focused on the parameters of competition and carrying capacity because the competitive exclusion of native taxa by invasive mallards has been documented previously (e.g. Kirby et al., 2004; Williams and Basse, 2006). We thus explored different values of interbreeding success rate (γ), competition (α) and carrying capacity K to find the combination of values that best explain the history of colonization and hybridization of mallards in New Zealand, using the abundances reported by Gillespie (1985) as references. The best-explained scenario was selected as one with the minimal mean absolute error between observed and predicted values, computed as: $\sum |x_{predicted} - x_{observed}| / n$. We then used this best-explained scenario to project 50 additional generations of interbreeding in order to investigate future consequences. All simulations were performed using *R* (R Development Core Team, 2015).

5.5 Results

5.5.1 Effects of the number of genes considered

We first assessed the influence of the number of simulated genes on the time to reach frequencies in equilibrium and measure the deviation to HW equilibrium at this time (Fig. 5.1). We performed these simulations without incorporating the density-dependent demographic effects of equation (5.13) in order to get relative frequencies, illustrating the performance of the model independently of specific demographic values.

We found that equilibrium is reached after various amount of time depending on the number of genes considered and especially on the level of interbreeding success rate (γ). Simulations with a single locus are extremely influenced by γ . When comparing single

Table 5.1. List of main functions and parameters used in our general hybridization model.

Notation	Definition
<i>List of function</i>	
N_i	Number of adult individuals of phenotypic class i
M_{ij}	Mating probability between phenotypic classes i and j
$b_{ij,k}$	Number of mating ixj resulting in offspring of type k
$C_{ij,k}$	Probability of mating ixj to produce offspring of types k
ω_i	Effect of inherited characters on fitness of individuals of class i
$\rho_{Aa,i}$	Probability of class i to be heterozygous for the allele "A"
η_k	Total number of offspring of class k
<i>Demographic parameters^a</i>	
K	Carrying capacity
r	Growth rate <i>per capita</i>
α	Competition
Intercross parameters	
η_L	Number of independent biallelic loci
γ	Interspecific success rate
Ω_A	Relative fitness of allele "A" in relation to the alternative form "a"
ε_A	Dominance degree of the allele "A"

a. Demographic parameter values of carrying capacity and growth rate were fixed according to previous simulations based on a 40-years survey of mallards ($K = 118.8$, $r = 1.3$) (see Sæther et al., 2008).

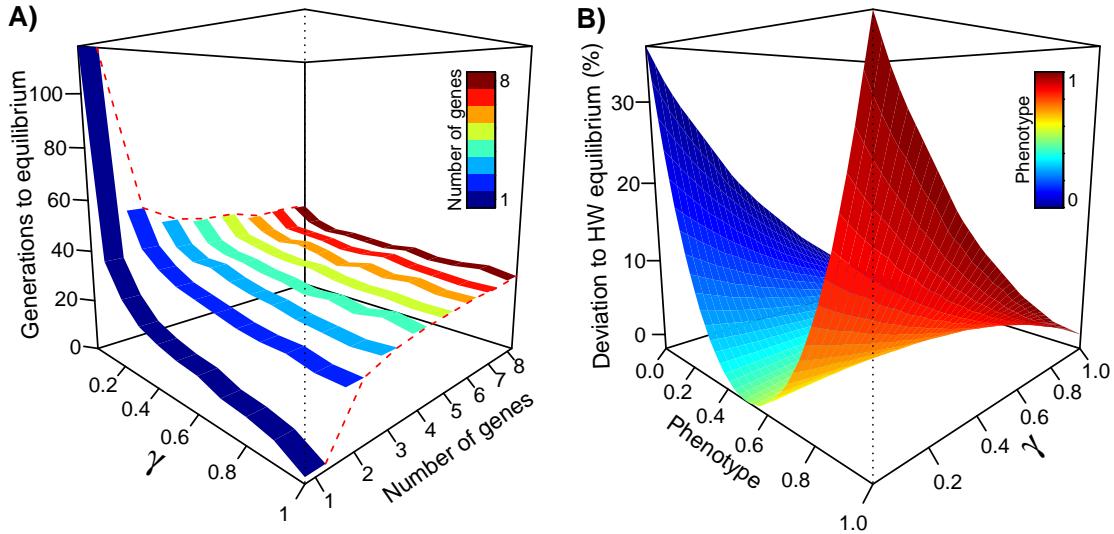


Figure 5.1. Simulation results when multiple genes are considered in the model. a) Effect of the number of genes and interbreeding success rate (γ) on the time to reach frequencies in equilibrium; b) Influence of interbreeding success rate (γ) on the deviation from Hardy-Weinberg (HW) equilibrium of five biallelic genes (simulations with one, two or three genes are available on supporting information, see Fig. 5.6). We explored various level of interbreeding success rate, from rare hybridization success ($\gamma = 0.01$) to a panmictic mating system ($\gamma = 1$). The data presented are those after 150 generations of genomic mixing.

locus simulations with those having more than three genes, a small value of γ ($\gamma = 0.01$) tends to increase the number of generations to reach the equilibrium by ~ 1.8 times while panmictic reproduction ($\gamma = 1$) tends to decrease the number of generations needed by > 10 times. The number of generations needed to reach frequencies in equilibrium is stable when more than two genes are considered in the simulations, especially with γ larger than 0.2 (Fig. 5.1a). There is still approximately 0.3 to 0.4 times of difference to reach equilibrium when using two genes or more than three genes.

The deviation to HW equilibrium at the time of frequencies in equilibrium is also affected by the interbreeding success rate (Fig. 5.1b). We illustrate this result using a quantitative character depending on five biallelic genes (from red to blue in Fig. 5.1b). A maximum deviation of approximately 40% is reached with a small interbreeding success rate ($\gamma = 0.01$) if the phenotype values are extreme (0.0 or 1.0), with an asymptotic decrease with increasing values of interbreeding. Similar results are found with two sim-

ulated genes or more (Fig. 5.6, supporting information). However, the deviation is much higher with a single biallelic gene (Fig. 5.6, supporting information). These results highlight the importance of considering multiple genes in the simulations when the number of genes involved in a given character is unknown and that three genes seems to be a good approximation for multiple genes.

5.5.2 Exploration of the phenotypic landscape

The phenotypic landscape of an additive trait is extrapolated using five biallelic genes. We incorporate the density dependent effects of equation (5.13) in this analysis using parameters drawn from the population dynamics of mallards. These ducks have experienced phenotypic changes due to hybridization with genetically distinct farm-raised individuals released for hunting or ornamental purposes. In our simulations, we let the two parental taxa N_0 and N_1 evolve independently during the first 100 generations, then demographic and genetic interactions among the two taxa were simulated for an additional 150 generations. Depending on the case analyzed, the parental taxa may or may not be in competition for environmental resources. However, in all cases, we let competition go on among individuals of the same class and among other classes according to the fraction of shared parental loci.

Without competition between parental taxa and with identical demographic parameters, the expected phenotypic landscape depicts a Gaussian-like shape with higher abundance in the most heterologous class (0.5, Fig. 5.2a). This pattern is perturbed by asymmetrical carrying capacities between parental taxa and by competition. The phenotype with highest abundance shifts towards class 1 when adding 50% more carrying capacity to parental class 1 ($K_1 = 1.5K_0$, Fig. 5.2b). The optimum is still present in individuals with hybrid genomes, but in those with more genes shared with parental class 1. Importantly, even though there is no competition between parental taxa, class 0 and hybrids with more alleles shared with it, are almost extinct due to the competitive exclusion of hybrids with more alleles shared with taxon 1. When adding competition between parental taxa, parental class 0 and all hybrid categories become extinct and the community is thus com-

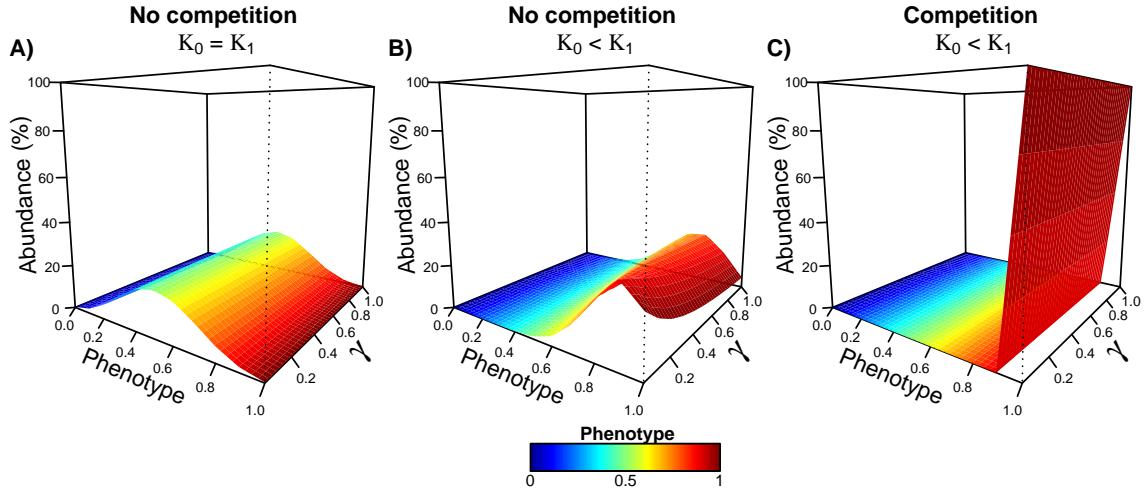


Figure 5.2. Density-dependent demographic parameters influencing the landscape of observed phenotypes. The phenotypic landscape is extrapolated from the contribution five additive genes ($\eta_L = 5$). We show the effect of the presence or absence of interspecific competition ($\alpha_{01} = \alpha_{10} = 1$ or $\alpha_{01} = \alpha_{10} = 0$) with equal or unequal carrying capacities between the two parental species ($K_1 = K_0$ or $K_1 = 1.5K_0$). We explored various levels of interbreeding success rate, from rare hybridization success ($\gamma = 0.01$) to a panmictic mating system ($\gamma = 1$). The data are presented after 100 generations of independent evolution and 150 generations of genomic mixing (250 total generations).

posed exclusively by individuals of class 1 (Fig. 5.2c). Overall, these results show that hybridization may exclude a native species having a demographic disadvantage compared to the other taxon. This effect is indirect through the hybrids in absence of competition between parental taxa and stronger if there is competition between them, in both cases facilitating the invasion of non-native genes.

5.5.3 Adding Selection

We incorporated the effect of purifying selection by decreasing the fitness (ω) of individuals carrying a specific allele " a ", originally present in parental class 1. We decrease the fitness of this allele by 30% ($\Omega_a = 0.7$ and $\Omega_A = 1$). This may represent the effect of higher susceptibility to a disease or any other negative selective pressure.

We first assumed that parental classes are not in competition for environmental re-

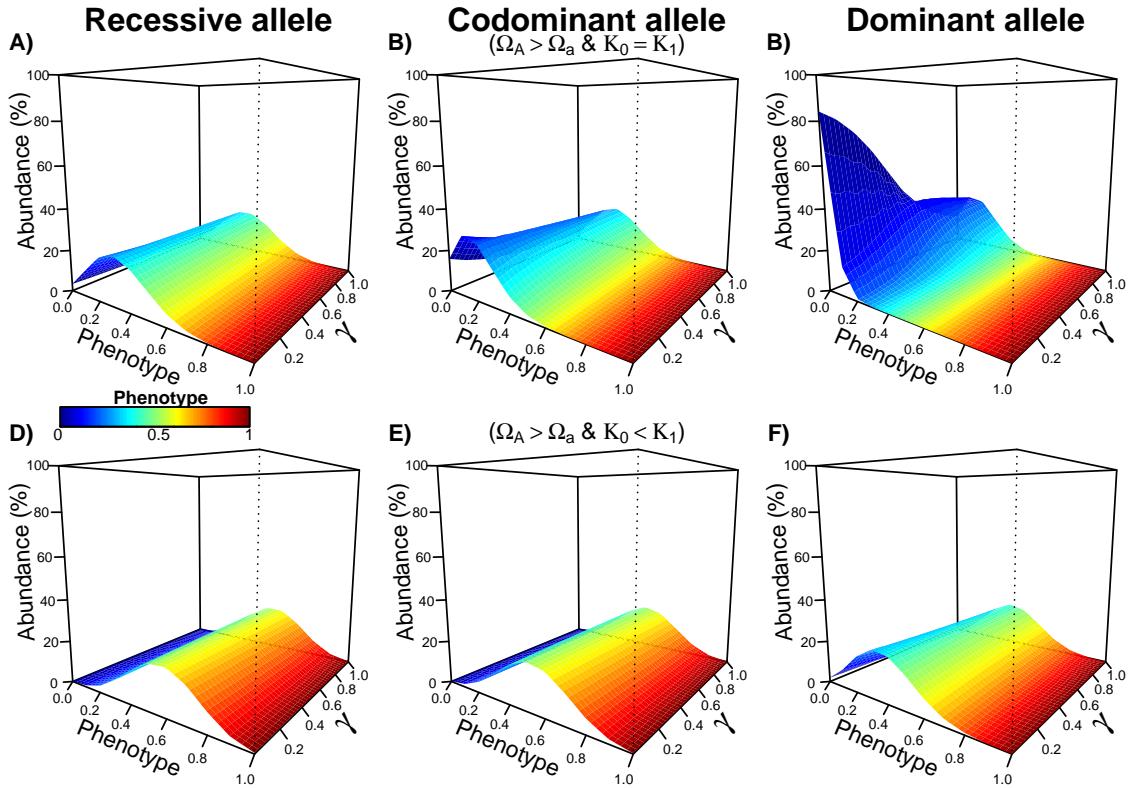


Figure 5.3. Effects of a deleterious allele "a" with fitness reduced by 30%. The phenotypic landscape is extrapolated from five additive genes ($nL = 5$). There is no interspecific competition ($\alpha_{01} = \alpha_{10} = 0$) and carrying capacity may either be equal or unequal between the interacting taxa ($K_1 = K_0$ or $K_1 = 1.5K_0$). a) Allele "a" is recessive ($\varepsilon_a = 0$); b) allele "a" is co-dominant ($\varepsilon_a = 0.5$); c) allele "a" is dominant ($\varepsilon_a = 1$). Simulations incorporating interspecific competition ($\alpha_{01} = \alpha_{10} \neq 0$) are available on supporting information (see Fig. S2). We explored various levels of interbreeding success rate, from rare hybridization success ($\gamma = 0.01$) to a panmictic mating system ($\gamma = 1$). The data are presented after 100 generations of independent evolution and 150 generations of genomic mixing (250 total generations).

sources ($\alpha_{01} = \alpha_{10} = 0$). When carrying capacity is equal between both parental taxa and the allele "a" is recessive ($\varepsilon_a = 0$), the maximum abundances are found in the hybrid classes close to class 0. Increasing the interbreeding success rate shifts this optimum approximately 10% away from class 0, towards more heterologous classes (from 0.3 to 0.4) (Fig. 5.3a). This effect is stronger with co-dominant alleles ($\varepsilon_a = 0.5$). The maximum frequency is found in classes with closer ancestry to class 0 than previously ($i \sim 0.1$) and the interbreeding success rate moves this optimum to about 20% (to $i \sim 0.3$) when the reproduction is panmictic ($\gamma = 1$) compared to a low interbreeding rate ($\gamma = 0.01$) (Fig.

5.3b). When this allele is dominant ($\varepsilon_a = 1$) and the interbreeding success rate is small ($\gamma = 0.01$), the maximum abundance is found in parental class 0 (~80%), but increasing values of interbreeding success rate shifts this optimum away from class 0 of about 10%, to heterologous hybrid classes with values around 0.1 (Fig. 5.3c). Whatever the scenarios of dominance/recessivity inheritance for allele "*a*", individuals of class 1, initially carrying this allele, and those with a close genotype become extinct. A deleterious allele carried by one species thus brings this species to the verge of extinction despite admixture with another species that does not carry this deleterious allele.

The effect of purifying selection in allele "*a*" may be counterbalanced by a demographic advantage given to the species originally carrying this allele ($K_1 = 1.5K_0$). The number of hybrid classes with more genes shared with 1 slightly increases with a larger interbreeding success rate, for all scenarios of dominance/recessivity inheritance, even if parental class 1 is still rare in the whole community (Fig. 5.3d, 5.3e and 5.3f).

Using the same settings as before (with species 1 having a higher carrying capacity and being affected by purifying selection in allele "*a*"), we added competition between parental taxa (Fig. 5.7, supporting information). Hybrid categories with the highest proportion of genes shared with 1 are favoured when allele "*a*" is recessive or when it is co-dominant with higher values of interbreeding success rate ($\gamma > 0.3$). However, there is still a complete exclusion of individuals of class 1 when allele "*a*" is dominant and interbreeding success rate is smaller than 90% ($\gamma < 0.9$). In this case only class 0 is present in the community. Completely opposite results can be obtained when adding even more carrying capacity to species of class 1 ($K_1 = 2K_0$). Individuals of this parental class are able to completely exclude all other categories, independently of the dominance/recessivity inheritance of the deleterious allele "*a*" (Fig. 5.7, supporting information).

We illustrate the relation between interspecific competition (α) and reduced allelic fitness in Figure 5.4a. In this simulation, the parental species of class 1 has twice the carrying capacity than the species of class 0 ($K_1 = 2K_0$), but is affected by various levels of fitness reduction in a co-dominant allele "*a*". Individuals of class 1 are the most abundant in the community if the reduction in fitness is smaller than 20% ($\Omega_A > 0.8$)

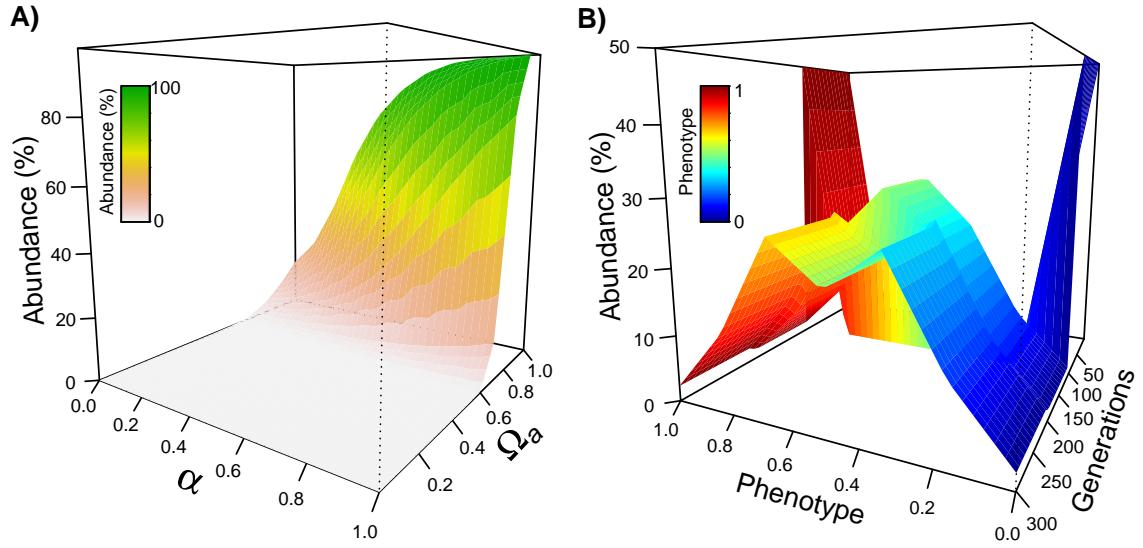


Figure 5.4. Purifying selection. a) Combined effect of interspecific competition ($\alpha_{01} = \alpha_{10} = \alpha$) and purifying selection on the abundance of a parental species of class "1" with higher carrying capacity ($K_1 = 2K_0$), but affected by reduced fitness on allele "a" ($\eta_L = 5$, data exposed after 100 generations of independent evolution and 150 generations of genomic mixing); b) forward simulations of the abundance of two parental species (classes 0 and 1), which have experienced independent evolution during 100 generations before hybridization starts. A lethal genotype ("AaBbCc") appears in generation 200 ($\eta_L = 3$). The interbreeding is panmictic ($\gamma = 1$).

and the competition between parental taxa is higher than 70% ($\alpha > 0.7$). The competitive advantage of having higher carrying capacity does not compensate for a reduction in fitness over 40% ($\Omega_A < 0.6$), in which case species of class 1 become extremely rare in the community (Fig. 5.4a). These results stress that both genetics and demography are important to shape the observed phenotypic landscape and its optimum and that one may either increase or cancel the effects of the other.

The landscape of possible phenotypes is unimodal in the previous simulations, but multimodal optima are also possible. To illustrate this we used our model to recognize a specific genotype within a phenotypic class (Fig. 5.4b). We additionally simulate two taxa in competition and differentiated by three biallelic genes. Both species were allopatric during the first 100 generations. The phenotypic landscape turns into a Gaussian-like distribution after a few generations of panmictic interbreeding ($\gamma = 1$). In generation 200, the genotype "AaBbCc" starts to be lethal in our simulations and the phenotypic land-

scape turns into a bimodal shape (Fig. 5.4b). Other multimodal forms can be obtained by adding various lethal genotypes or more than a single allele with reduced fitness. This whole exploration phase demonstrates how useful can be our model to study the outcomes of many potential complex situations of hybridization involving many evolutionary factors.

5.5.4 Fitting observed values of hybridization between mallards and grey ducks

We applied our model to the colonization history of mallards in New Zealand, where they hybridize with native grey ducks. This last species was abundant at the beginning of the 20th century but today is seriously threatened. The decrease of this native species and the appearance of hybrid phenotypes are well documented. There are seven phenotypes previously defined by morphology that we assume are the expression of three additive genes (i.e. $2\eta_L + 1$) and for which the relative frequencies are documented. The aggressive competition and the use of generalist habitats have been documented in invasive mallards. In order to explain the observed hybrid frequencies, we thus set full interspecific competition of mallards ($\alpha_{mallard} = 1$) to assess the carrying capacity (K) and the amount of interspecific competition performed by the native species (α_{native}).

We first estimated the carrying capacity that best explains the invasion of mallards to be between 1.5 to twice that of the grey duck species, leaving all other parameters free to vary (Fig. 5.5a). We then set the carrying capacity of mallards to be twice as large as that of grey ducks (best estimation) for the subsequent simulations, because it presents the minimum mean absolute error in explaining the observed hybrid frequencies (<7%). Second, we estimated that high values of interbreeding success rate ($\gamma > 0.4$) and high asymmetrical competition between native and invasive species ($\alpha_{native} \ll \alpha_{mallard}$) are necessary to explain the invasion of mallards in New Zealand. The best combination of parameters supports an absence of competition from grey duck to mallard ($\alpha_{native} = 0$) and 70% of interbreeding success rate between both taxa (Fig. 5.5b).

We used these estimated parameter values to explore the phenotypic evolution due

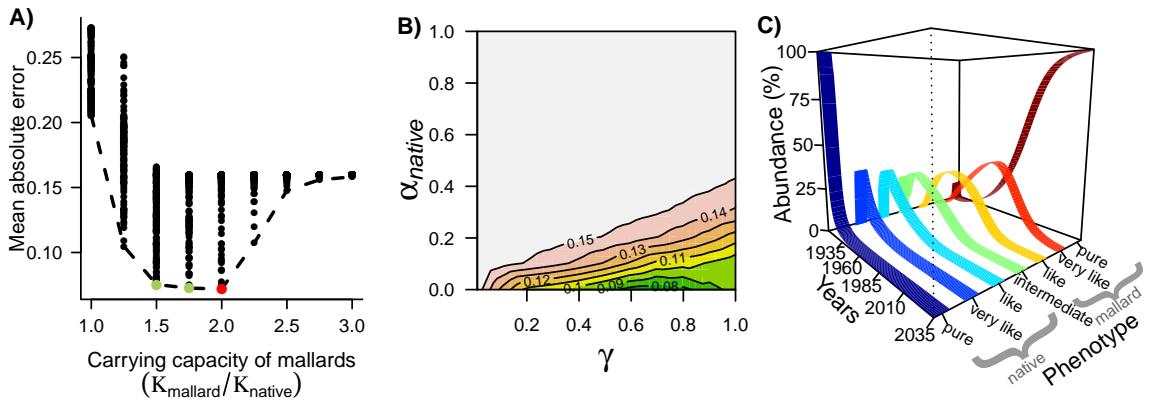


Figure 5.5. Demographic declines of a native species. Simulations are based on the colonization history of mallards in New Zealand (*Anas platyrhynchos*) where they seriously threaten the native grey duck (*Anas superciliosa*). We evaluated different values of carrying capacity (K), interspecific competition exerted by the native species (α_{native}) and interbreeding success rate (γ) to minimize the error when fitting observed abundance values. There are seven documented phenotypes due to hybridization between mallards and grey ducks. We assume these phenotypes are the product of three additive genes ($\eta_L = 3$, see Methods). a) Relative carrying capacities of mallards to explain the colonization time in New Zealand (red point minimize the error with observed values); b) mean absolute error when fixing the best estimated carrying capacity of mallards (two times larger) and varying the value of competition (α_{native}) and interbreeding success rate (γ) (the dark green values minimize the error: $\alpha_{\text{native}} = 0$ and $\gamma = 0.7$); we explored various levels of interbreeding success rate, from rare hybridization success ($\gamma = 0.01$) to a complete panmictic mating system ($\gamma = 1$); c) forward simulation using the best combination of genetic and demographic parameters that explain the invasion of mallards in New Zealand. Simulations with alternative carrying capacities (green points in Fig. 5.5a) are presented in supporting information (see Fig. 5.8).

to the invasion of mallards since 1910, when a stable feral population was first observed (Fig. 5.5c), to the present and project it until 2035. The native species is dominant at the beginning of the simulations, but hybrids with a proportion of shared genes closer to the native species become quite abundant ($\sim 25\%$) in a few generations. They were in competition with the native species provoking an asymptotical population decrease through time. These hybrids also started to disappear in favour of other hybrid classes with a proportion of shared genes closer to mallards. An explosion in the abundance of mallards occurred when the native duck was already rare, due to competition with hybrids.

Similar results are obtained when performing these simulations with the best combination of parameters for carrying capacities 1.5 and 1.75 times larger for mallards (Fig. 5.8, supporting information). The hybrids with genotypes closer to the native species are the first that start to be abundant, but also the first to decline after the colonization of mallards. The final projections 20 years from now always result in the exclusion of the native species and hybrids by mallards. These simulations illustrate the potential of hybridization as a process that facilitates biological invasions.

5.6 Discussion

5.6.1 Development of a general model of hybridization

We developed a general model of hybridization that can be applied to a large range of ecological and evolutionary case studies. Here the main focus of the model is placed on genomic mixing and the appearance of new hybrid phenotypes, but it could also allow the study of outbreeding depression due to apparition of infertile hybrids or the production of polyploidy and hybridogenetic forms (see Quilodrán et al., 2014a, 2015)

The new general model was developed by using our previously published model of hybridization between distant species to which we incorporated a modified version of the approximate hypergeometric model, originally developed to study intraspecific quantitative genetic characters (Doebeli, 1996, 1997). Our general approach allows for the study of interspecific genetic interactions and the recognition of specific alleles or genotypes within genetic classes, leading to the incorporation of both quantitative and qualitative gene expression. Therefore, further applications of our model are not limited to quantitative phenotypes, and can be extended to the proportion of parental genomes, assessing the effects of additive genes and the influence of specific loci. In this last case, models involving only genotypes can be highly computationally demanding due to the number of genotypic classes increasing exponentially with the number of loci (2^{nL}). Our approach thus simplifies the simulation of any number of genes by hugely reducing the number of possible classes to $(2n_L + 1)$ and by recognizing the alleles or genotypes of specific

interest.

Other applications of the approximate hypergeometric model have assessed the effect of hybridization between genetically distinct groups on quantitative traits (e.g. Ferdy and Austerlitz, 2002; Tanaka, 2010). However, our model is the first to incorporate density-dependent demographic effects, recognize target genotypes or alleles and incorporate dominance/recessivity inheritance. These are major improvements that allowed us to examine the effect of selection in our analysis. We illustrated the effect of deleterious alleles, but the influence of positive and balancing selection may also be explored in future studies.

5.6.2 Incorporation of multiple genes in the simulations

Despite the main influence of population dynamic on the outcomes of hybridization with genomic mixing, only a few previous approaches have incorporated density-dependent effects, mainly taking into consideration a single biallelic gene (Baskett and Gomulkiewicz, 2011; Satake and Araki, 2012). Simulations with a single gene may reveal general patterns (e.g. Huxel, 1999), but we showed here that they significantly bias conclusions about the ecological and evolutionary consequences of hybridization. By simulating multiple genes, we demonstrated that deviation to Hardy-Weinberg equilibrium and the time to reach frequencies in equilibrium may be affected by the number of simulated genes, obtaining more stable patterns when simulating more than two genes. This may seriously affect the estimation of risk of parental species extinction and the time to reach it. It is thus important to simulate multiple genes when aiming to investigate processes with an unknown number of genes involved.

5.6.3 Genomic mixing and conservation

The new genetic composition due to hybridization between genetically distinct organisms may influences the appearance of new genotypic architectures. The number of observed phenotypes depends on the amount of additive genes influencing quantitative traits or in the dominance/recessivity of qualitative gene expression. The shape of the phenotypic

landscape depends on a combination of demographic factors (e.g. carrying capacities and competition) and genetics (e.g. dominance/recessivity inheritance and selection in specific alleles or genotypes). We demonstrated that these novel phenotypes may be fixed in the community replacing one or both pure parental genotypes by a hybrid swarm or progressively disappearing, thereby facilitating the invasion of one of the parental genotypes. Moreover, we demonstrated that the influence of detrimental alleles might be counterbalanced by larger carrying capacities or higher competitive skills. A mixture of both genetic and demographic effects is thus important to explain the optimum phenotypes susceptible to be observed in the field. The complementary effect between demographic decline and speciation reversal due to genomic mixing is potentially important to explain the influence of hybridization in species loss (Vonlanthen et al., 2012). This type of process may be explored using our model. Further application may help to fill the gap between population dynamics and population genetics, disciplines that have been recognized to complement each other but that have evolved separately (Hall and Ayres, 2009).

5.6.4 Wild and farm-raised mallards

The appearance of novel hybrid phenotypes has been observed in mallards (Champagnon et al., 2010; Söderquist et al., 2014). The release of farm-raised individuals, which have experienced human driven selection, produced a rapid morphological change in the bill size of wild animals since the beginning of the releases around 35 years ago (Champagnon et al., 2010). These new types of mallards have a more "*goose-like*" bill than their ancestors (Söderquist et al., 2014). The farm-raised ducks seem to have higher mortality and lower breeding success (Osborne et al., 2010; Champagnon et al., 2012). However, according to our simulations, this rapid morphological change can be simply explained by the massive release of farm-raised ducks without invoking any reduction of hybrid fitness or specific genotype selection. In Europe, the release of ducks by humans is so enormous that it may artificially increase the farm-raised duck carrying capacity. Our simulations showed that a sufficiently high carrying capacity might fix hybrid phenotypes even when they have a relatively smaller fitness. The population of breeding wild mallards in Europe

represents 4.5 million breeding pairs, but 3 million are released from farms (Champagnon et al., 2013). Nonetheless, to achieve the real consequence of hybridization in conservation biology, further studies must define what a new "*goose-like*" bill (or any other new phenotype) represents, assessing the effects on fitness and on the net ecological interaction with other organisms (e.g. trophic niche).

5.6.5 Consequences of mallard invasion in New Zealand

We showed that the appearance of hybrids might threaten native taxa and even facilitate a biological invasion. Mallards have been widely translocated by humans, successfully colonizing new areas and producing hybrids that seriously threaten native taxa. This is the case with grey ducks in New Zealand, but also occurs with other species such as: the yellow-billed duck (*A. undulata*), African black duck (*A. sparsa*) in Southern Africa (Van Rensburg et al., 2011), Pacific black duck (*A. superciliosa rogersi*) in Australia (Guay and Tracey, 2009), Florida mottled duck (*A. fulvigula*), American black duck (*A. rubripes*) and Hawaiian duck (*A. wyvilliana*) in North America (Mank et al., 2004; Fowler et al., 2009; Seyoum et al., 2012). The Anatidae family is well known to have extremely high levels of hybridization, covering more than a half of recognized avian hybrids and much of which are fertile (Tubaro and Lijtmaer, 2002).

Our results suggest that mallards have taken advantage of hybridization to succeed a rapid expansion in novel areas. Their aggressive interspecific competition and their capacity to exploit new resources related to human-disturbed environments (Kirby et al., 2004; Williams et al., 2005; Williams and Basse, 2006) provide mallards with higher opportunities to displace native taxa by direct competition or indirectly through competition with hybrids. In New Zealand, there is no evidence of decreased hybrid fertility between grey ducks and mallards (Guay et al., 2014). Our simulations estimate a competitive pressure first exerted by grey-like hybrids and then by mallard-like hybrids and mallards themselves. The final expectation is the extinction of grey ducks and hybrids in favour of mallards. Even though these simulations were based on frequencies observed during the 80's (Gillespie, 1985), while grey ducks are currently no more considered as game

species but as an endangered one (Rhymer, 2006; Robertson et al., 2013), our simulations fit well with present-day observations. Grey ducks are extremely rare, with some populations being already extinct and the majority of individuals are mallard-like hybrids or pure mallards (Williams and Basse, 2006; Baker et al., 2014; Guay et al., 2014). The current extinction risk is so high that the most efficient strategy would be to translocate the few remaining grey ducks to an offshore island without mallards (Rhymer et al., 2004; Guay et al., 2014).

A similar extinction process was experienced by grey ducks inhabiting Lord Howe Island, on the east coast of Australia. Mallards self-colonized the island in 1963, presumably from New Zealand, igniting the complete extinction of pure grey duck (Tracey et al., 2008). In mainland Australia, mallards were also introduced for hunting and hybridization has since been recognized as a threat for the Australian Pacific black duck (*A. supersiliosa rogersi*), but the extent of this hybridization is unknown (Guay and Tracey, 2009). The results of our simulations project that the ecological and genetic displacement of native species by mallards may be produced in very few generations. It is thus a priority for further studies to assess the current hybridization level in Australia and to control the feral population of mallards, in order to not repeat the history of extinction experienced in Howe Island and New Zealand.

5.6.6 New opportunities brought by hybridization

The novel genetic architecture visible in our phenotypic landscapes may also represent the increase of genetic diversity brought by hybridization. We exposed different situations in which theoretical parental taxa admix and generate new hybrid individuals that may be found at high frequencies. If those hybrids do not have an important decrease on fitness or a change in ecological functions of parental organisms, because they are phylogenetically closely related, hybridization may simply represents an increase of genetic diversity. Additionally, we differentiated parental phenotypes with a colour pattern (blue or red). However, the range of colours may also represent specific niches, with one potentially available to be colonized by these new hybrid organisms (e.g. green), in which case

hybridization is potentially driving new potential opportunities of adaption and evolution (e.g. Leducq et al., 2016).

Hybridization occurs naturally among many plant and animal taxa and is considered an important source of evolutionary change (Fredrickson and Hedrick, 2006). The exact number of species that hybridize is unknown, but approximately 25% of plants and 10% of animals are known to hybridize with another related species (Mallet, 2007). Determining whether hybridization cases are natural or human induced is a high priority in conservation biology (Allendorf et al., 2001). In this last case, the loss of important local adaptations due to genetic swamping, the behavioural change influencing ecological interactions, and the reduced likelihood of population recovery due to reduced reproductive value, may certainly represent a serious threat for native species (Rhymer and Simberloff, 1996; Todesco et al., 2016). However, even when hybridization is induced by human, it is not necessarily negative for native biodiversity. Indeed, hybridization is a source of genetic diversity that may be important for adaptation to changing environmental conditions, particularly to prevent the negative effects of habitats that are modified by humans. In our case study, interspecific hybridization with invasive mallards is mainly considered a detrimental threat for native species, but the occurrence of novel adaptation possibilities has already been proposed for the North American mottled duck (*Anas fulvigula*), which has increased its genetic diversity due to hybridization with mallards (Peters et al., 2014). The negative or positive effect of hybridization on biodiversity is therefore not only determined by human actions, but also by the resulting consequence on fitness and alterations in key ecological interactions. Assisted hybridization may eventually represent a conservation management tool to facilitate local adaption to climate change (Aitken and Whitlock, 2013; Taylor et al., 2015) or to rescue small populations affected by inbreeding depression (Todesco et al., 2016). Our model could thus be an ideal tool in the future to assess the exact resulting effects of hybridization on biodiversity.

5.7 Conclusions

The development of our general model opens new research opportunities in ecology, conservation and evolution. This is the first approach combining density-dependent demographic effects with quantitative and qualitative multigenic simulations. Through simulations based on our model, we highlighted the potential appearance of novel genetic architectures that may subsequently disappear or be fixed in the community. These novel genotypes may threaten native taxa or be a source of genetic diversification potentially leading to adaptation to new environmental conditions. Our case study was based on mallards, but further studies with specific parameter values may explore the effect of hybridization on any diploid organism. The R script of our modelling approach is freely available at: <http://genev.unige.ch/montoya-currat/scripts/>. It is easily modifiable to fit particular case studies or to investigate other theoretical questions about hybridization. Further studies may for instance consider hybridization success rate as a variable instead of a fixed parameter, which may depend on demographic frequencies or given environmental conditions. More complex demographic models, incorporating environmental and demographic stochasticity, can also been envisaged in order to maximize the likelihood to explain historical datasets (e.g. Lande et al., 2006; Coulson et al., 2011). New hybridization opportunities induced by humans are expected for the near future either due to the invasion of translocated species (Baker et al., 2014), domesticated animals (e.g. Leonard et al., 2013; Nussberger et al., 2014) and genetically modified organisms (e.g. Oke et al., 2013) or due to the range expansion of species induced by climate change (e.g. Gómez et al., 2015; Taylor et al., 2015). This general model of hybridization represents therefore an important instrument for the development of conservation strategies and for the understanding of processes behind the emergence and evolution of new species.

5.8 Acknowledgments

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5.9 Supporting Information

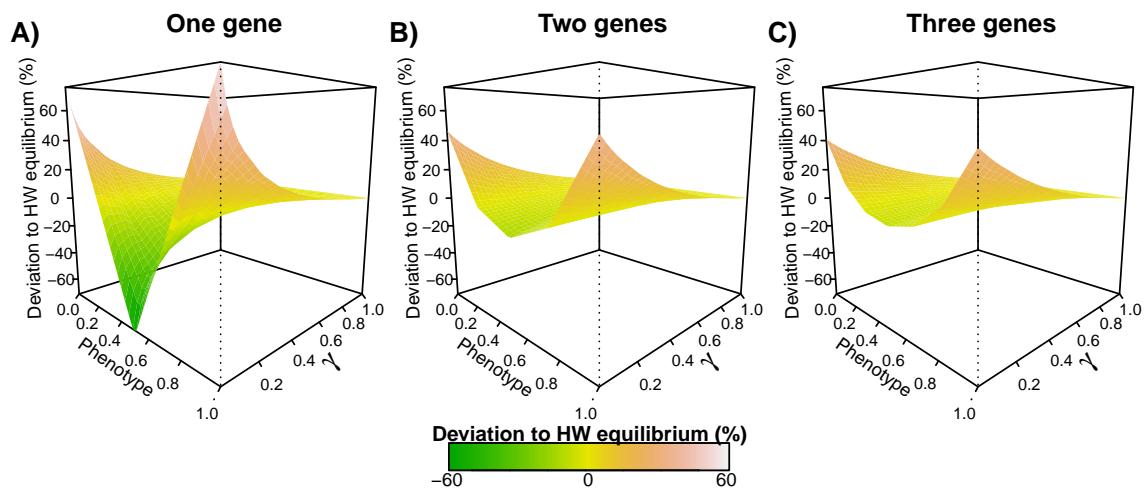


Figure 5.6. The effect of different number of simulated genes on the deviation to the Hardy-Weinberg (HW) equilibrium reached at the time of frequencies in equilibrium. We explore values of interbreeding success rate ranging from rare hybridization success ($\gamma = 0.01$) to a panmictic mating system ($\gamma = 1$). The data are exposed after 150 generations of genomic mixing.

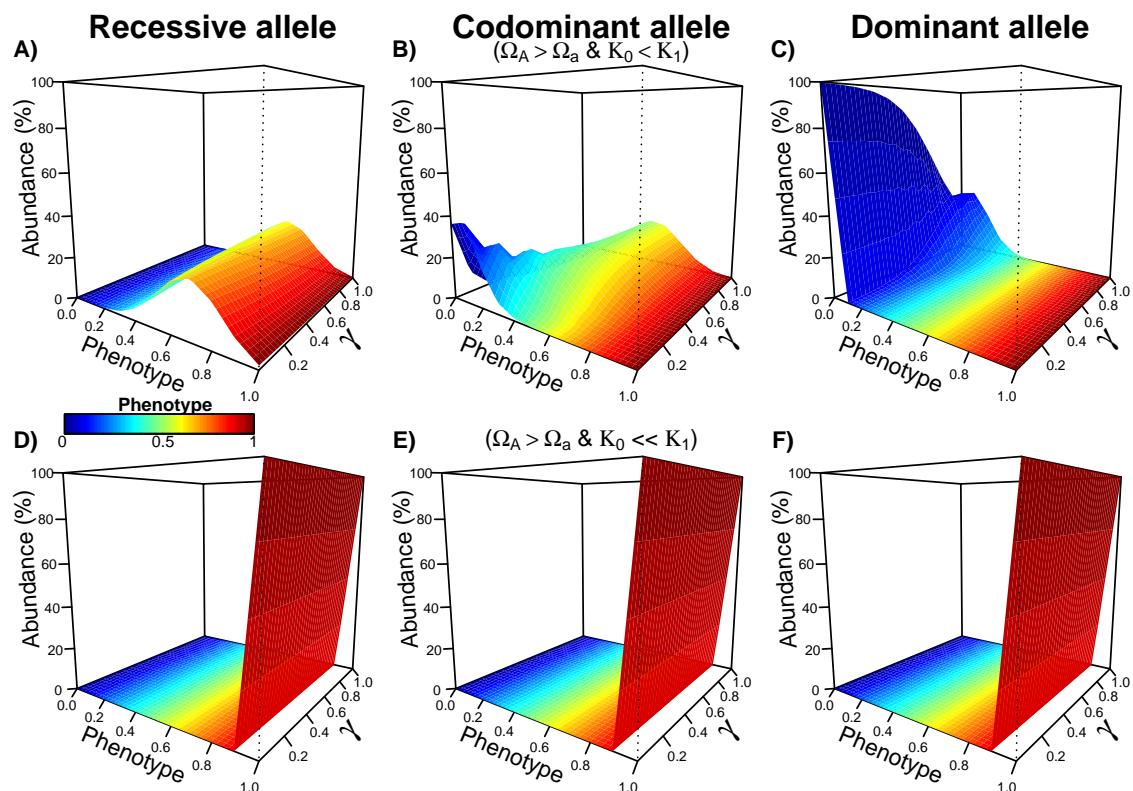


Figure 5.7. Effects of a deleterious allele "a" with fitness reduced by 30%. There is interspecific competition between parental taxa ($\alpha_{01} = \alpha_{10} \neq 0$). The parental species with reduced allelic fitness (species of class 1) has higher or much higher carrying capacities than the other parental species (class 0) ($K_1 = 1.5K_0$ and $K_1 = 2K_0$). The results are obtained after 100 generations of independent evolution and 150 generations of genomic mixing (250 total generations).

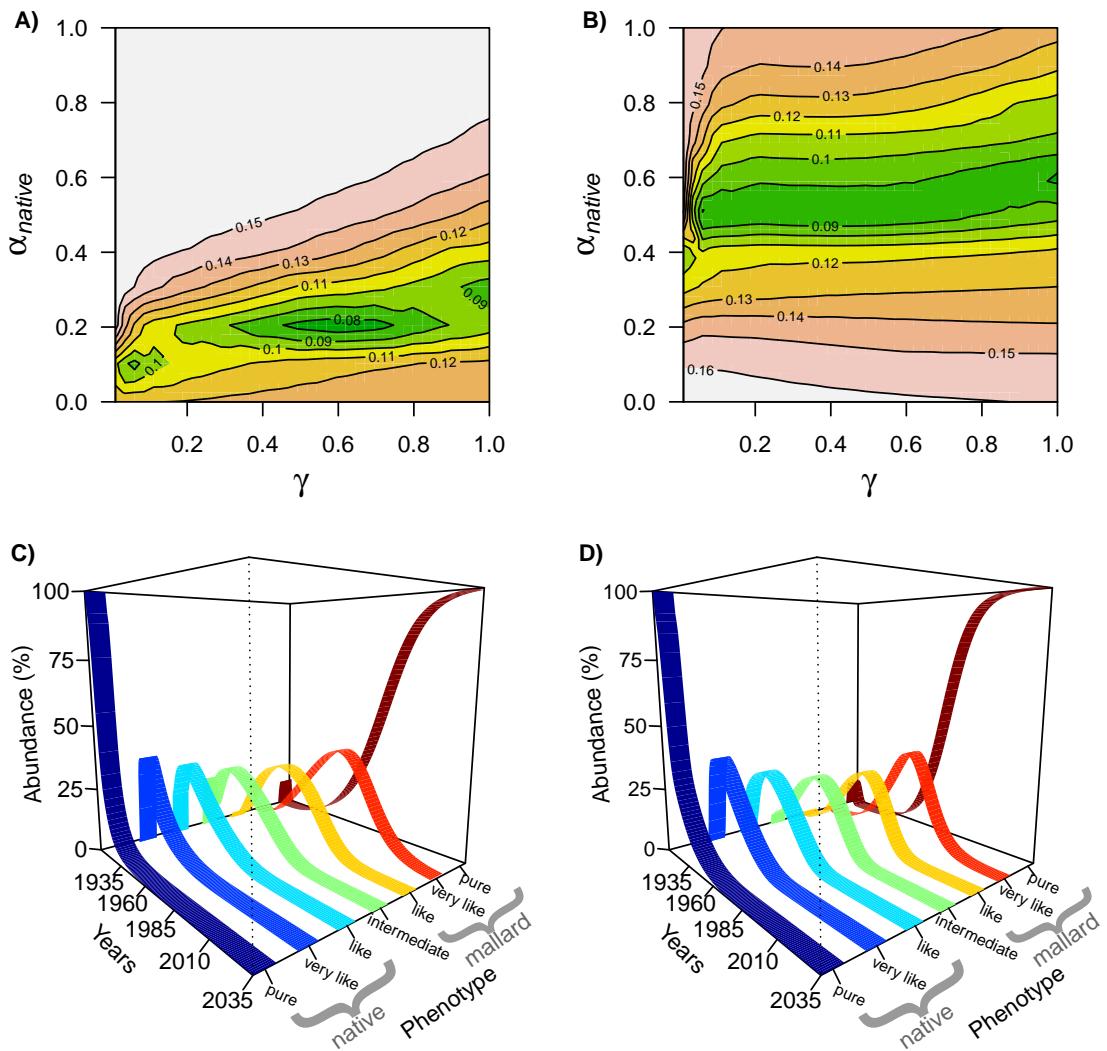


Figure 5.8. Parameter values and forward simulations when using alternative combinations of carrying capacities to explain the observed colonization of mallards (*Anas platyrhynchos*) in New Zealand. a) and c) carrying capacity of mallard 1.75 times larger than the one of the native species; b) and d) carrying capacity of mallard 1.5 times larger than the one of the native species.

CHAPTER 6

Models of hybridization during range expansions and their application to recent human evolution

Laurent Excoffier, **Claudio S. Quilodrán**, Mathias Currat Published in: *Cultural Developments in the Eurasian Paleolithic and the Origin of Anatomically Modern Humans* (2014) pp:122-137

6.1 Project description

The aim of this chapter is to present a new hybridization model that was implemented in the software SPLATCHE 2 Ray et al. (2010), which is a programme for simulating genetic diversity in a spatially explicit framework. This project was initiated by professor Laurent Excoffier in order to answer criticisms that were recently published by Zhang (2014). The argument against the software focused on the hybridization model and on the conclusion of Currat et al. (2008b), which documented a general pattern of asymmetrical hybridization, which was much greater for the invasive than in the local species, even when the interbreeding rate is low. This new model does not have the concerns referred

to by Zhang (2014) and confirms the conclusion of Currat et al. (2008b). Zhang (2014) did not consider his results in a spatial expansion context, and it is this process that is driving the observed asymmetrical introgression. We use the same scenarios as used by Currat et al. (2008b), concerning a theoretical species expanding in competition with a local species, but using the new hybridization model. We additionally simulate the same scenarios of Currat and Excoffier (2011), concerning the hybridization between Neanderthals and modern humans, but simulated with the previous version of SLATCHE 2. We show that the new model of hybridization needs a slightly higher interbreeding rate in order to explain the same level of introgression, but where the main conclusions remain valid.

Author contributions CSQ performed the simulations and participated in the design of the study, in the interpretation of the results and in the revision of the manuscript.

6.2 Abstract

The history of modern human is likely to have consisted in a series of range expansions from Africa that led to the settlement of the whole world. During these expansions, modern humans have been in contact with other hominins and hybridized with them. However, the location and the extent of these admixture events are largely unknown. We describe here a general model of hybridization occurring when a species colonizes the territory of another one. We show that a massive and asymmetric introgression from the local species into the invading species is expected for neutral markers, even if admixture is symmetric at the time of the hybridization. We discuss the implication of this process for the potential introgression of archaic genes into the gene pool of modern humans.

6.3 Introduction

Several lines of genetic, archeological and paleontological evidence suggest that anatomically modern humans (*Homo sapiens*) colonized the world in the last 60,000 years by a

series of migrations originating from Africa (e.g. Liu et al., 2006; Handley et al., 2007; Prugnolle et al., 2005; Ramachandran et al., 2005; Li et al., 2008; Deshpande et al., 2009; Mellars, 2006; Lahr and Foley, 1998; Gravel et al., 2011; Rasmussen et al., 2011). With the progress of ancient DNA analysis, it has been shown that archaic humans hybridized with modern humans outside Africa. Recent direct analyses of fossil nuclear DNA have revealed that 1-4 percent of the genome of Eurasian has been likely introgressed by Neanderthal genes (Green et al., 2010; Reich et al., 2010; Vernot and Akey, 2014; Sankararaman et al., 2014; Prüfer et al., 2014; Wall et al., 2013), with Papua New Guineans and Australians showing even larger levels of admixture with Denisovans (Reich et al., 2010; Skoglund and Jakobsson, 2011; Reich et al., 2011; Rasmussen et al., 2011). It thus appears that the past history of our species has been more complex than previously anticipated (Alves et al., 2012), and that modern humans hybridized several times with local hominins during their expansion out of Africa, but the exact mode, time and location of these hybridizations remain to be clarified (Alves et al., 2012; Wall et al., 2013). In this context, we review here a general model of admixture during range expansion, which lead to some predictions about expected patterns of introgression that are relevant to modern human evolution.

6.4 Simulation of spatial expansions with interbreeding

We have developed the SPLATCHE program (Ray et al., 2010) to simulate the genetic diversity of one or several samples in a spatially explicit landscape having been colonized from one or several introduction points. This framework allows one to study the pattern of neutral genetic diversity expected after a range expansion into an empty or an occupied habitat, with or without interaction and competition between invading and local species. Neutral diversity can be easily modelled if the past demographic history of a species is known, thanks to recent progress in coalescent theory (see e.g. Wakeley, 2009, for a review). Even though the precise history of a species is rarely known with good accuracy, one has often information on the geographic distribution of the species, as well as on current and past environmental data. This information can be approximately translated

into demographic information, such as local carrying capacities or local migration rates, which can differ in various environments (Ray et al., 2008; Ray and Excoffier, 2009), and be then used to simulate genetic diversity. The simulation of genetic diversity is done in two distinct steps in the SPLATCHE framework. A first step consists in forward simulations of the above mentioned demographic parameters, and a second step consists in backward coalescent simulations (Kingman, 1982) of genetic diversity conditional on demographic information recorded in the first step.

In Figure 6.1A and 6.1B, we illustrate two time-points of the forward simulation of the expansion of a species in the territory of another one. At the beginning of such simulations, we assume that some areas are already occupied by a local species. A new invading species appears at an arbitrary position. We model the overlap of these species by making them evolve in two different layers (see Fig. 6.1C), where subpopulations (demes) of a given layer (species) can exchange migrants with neighboring demes of the same layer, but also interbreed with individuals of the other species that are present at the same location, and which thus result in admixture events. The invading population can send migrants to empty neighboring demes of its layer, which are then logically filled to their carrying capacity, and which can send further migrants to adjacent demes, thus progressively colonizing the whole world (see Fig. 6.1A, 6.1B).

In some previous work (Currat and Excoffier, 2004, 2011; Currat et al., 2008b), we have developed a model of interaction between the local and the invading based on the following two principles. 1) The rate of interbreeding was assumed to be density-dependent. At any location, the probability of a successful introgression event was thus defined as $A = \gamma(2N_L N_I)/(N_L + N_I)^2$, where N_L and N_I are the current deme densities of the local and invasive species, respectively. 2) We then assumed that following the admixture, AN_L genes from the local species introgress the invasive species, and AN_I genes would flow in the other direction at each generation. In this model, the parameter γ is a general measure of the strength of barriers to gene flow between species. We do not explicitly model the nature of these barriers, but they could be either prezygotic (and γ could for instance be considered as a measure of disassortative mating), postzygotic (and γ would be a measure

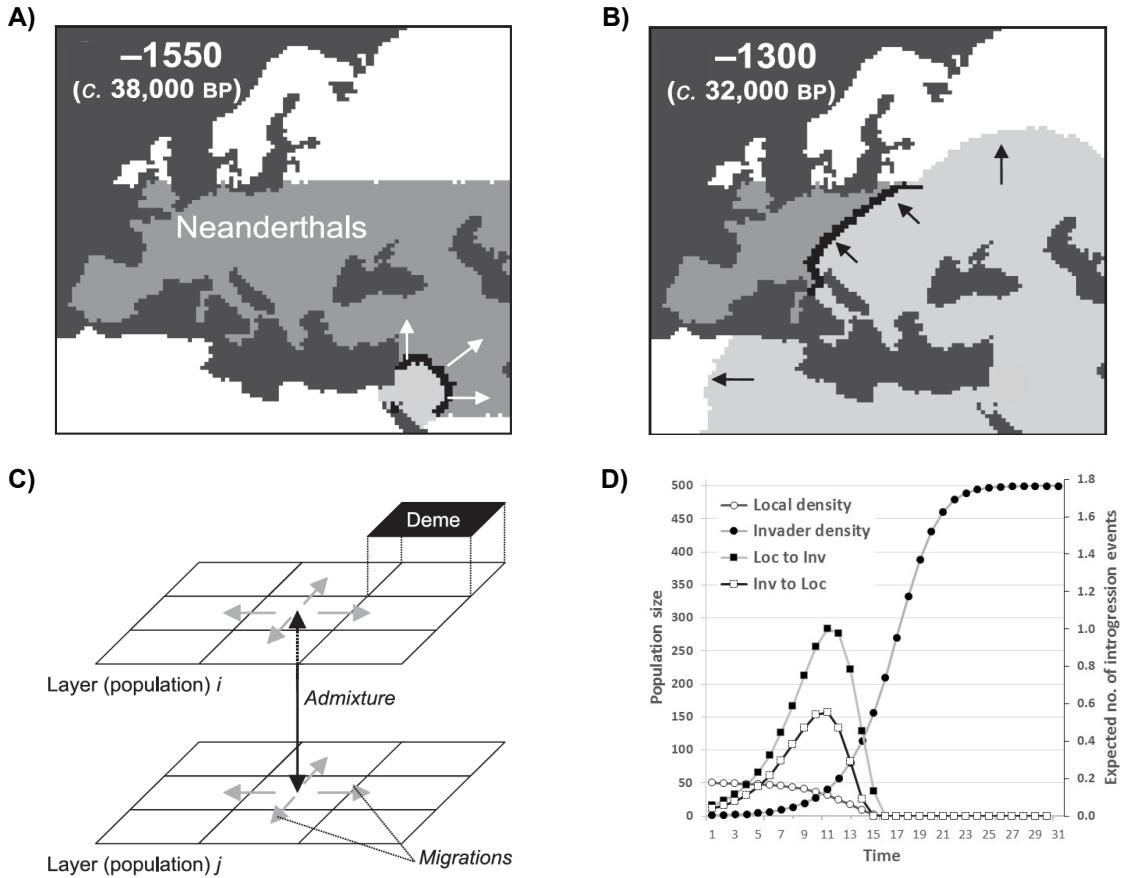


Figure 6.1. Representation and properties of a range expansion process with local interbreeding and competition with a local species. (A-B) Schematic representation of the range expansion of modern humans into Europe and Middle-East, assumed to be already occupied by a Neanderthal subdivided population (adapted from Currat et al. (2008a)). Expansion was assumed to have started 1600 generations ago (~40,000 years ago) from the Sinai Peninsula, and expanded concentrically from this location in the Middle-East and into Europe. Dark grey area represents locations with Neanderthals only. Light grey area represents locations with modern humans only. Black area represents locations where Neanderthals and modern human coexist and have the possibility to interbreed, which is at the edge of the modern human expansion wave. (C) Schematic simulated interaction between Neanderthals and modern humans. Humans and Neanderthals are assumed to occupy two different population layers. Within layers, migrants can be exchanged between neighboring subpopulations (demes). Between layers, members of the two species can interbreed if they occupy the same location. (D) Illustration of the local demographic and introgression dynamics. We plot the evolution of population densities and introgression events over time at a given location of the lattice using demographic parameters from scenario C1 described in Table 1, $\gamma = 4\%$, except that there was no migration from neighbouring demes for simplicity. At generation zero, the local species is at carrying capacity, and an invading species with a higher carrying capacity appears.

of the fitness of the hybrid individuals), or any combination of factors preventing the successful mating of members of both species (Currat and Excoffier, 2011). In any case, a value of 0 corresponds to a total absence of interbreeding between the two species, a value of 1 corresponds to random mating between the two species, and any value in between implies that mating is locally non-random between the two species. Deme density in the invasive is then updated as $N_I' = N_I(1 - A) + AN_L$ to take interbreeding into account, and is then further updated to reflect logistic regulation, competition and migration, and a similar update is performed in the local species (see Currat and Excoffier, 2004, 2011; Currat et al., 2008b, for more details). A major result from this model is that it predicts that the genome of the invading species should be massively introgressed by that of the local species if interbreeding success measured by γ is larger than a few % ($>2\%$ Currat et al., 2008b). Using this model, Currat and Excoffier (2011) showed that the level of 1-3% Neanderthal nuclear introgression observed in contemporary Eurasians and the complete absence of Neanderthal mtDNA introgression in modern humans (Currat and Excoffier, 2004) were compatible with very low levels of interbreeding success ($\gamma < 2\%$).

6.5 A new model of admixture

This model of admixture has been recently criticized (Zhang, 2014) on the ground that introgression was locally asymmetric, as $AN_L > AN_I$, implying a much larger level of introgression from the local to the invasive species in the initial phase of the invasion (see Figure 2B in Currat et al. (2008b), because invading populations have typically low densities on their margins. Zhang (2014) then claimed that this initial asymmetry could induce a final large introgression asymmetry, but he neither checked his claim in the context of a spatial range expansion nor in a model involving interspecific competition. It would thus appear useful to check if asymmetric introgression would also occur during range expansions if introgression was locally more symmetric. To address this point, we have implemented a new model of hybridization in SPLATCHE that we detail below.

The new model first posits that each of the N_I^* newborn individuals in the invasive population must have one parent coming from the same population. Then assuming local

random mating between populations, the probability that the other parent originates from the same population is $N_I/(N_I + N_L)$, where N_I and N_L are the diploid population sizes at the previous generation. Similarly, the probability that the other parent comes from the local population and therefore that the individual is a hybrid is $N_L/(N_I + N_L)$. Therefore the expected number of introgression events from the local to the invasive population per generation is $S_{LI} = \gamma N_I^* N_L / (N_I + N_L)$, which is similar to the equation used by Zhang (2014) to define the number of admixed individuals except that N_I^* is used here instead of N_I in Zhang (2014). We show in Figure 6.1D the dynamics of this model at a given arbitrary location on the invading wave front where admixture can occur (shown as a black strip on Figures 6.1A and 6.1B). We plot the densities of the two species and the expected number of interbreeding events in both directions. In brief, the invading species has a higher carrying capacity, which allows it to grow initially in our model that includes competition between the two species. It grows logistically until it reaches its own carrying capacity (250 diploids in Fig. 6.1D). The local species that is initially at carrying capacity (25 diploids in Fig. 6.1D) suffers from competition with the invading species, and progressively declines until it goes extinct (Shigesada and Kawasaki, 1997) in line with recent models of Neanderthal decline (e.g. Banks et al., 2008a). Introgression events will initially be very rare in both species, but will increase to reach a maximum when the two species have the same density. Introgressions from the local to the invading species will nevertheless be slightly more frequent than in the reverse direction, as $N_I^* N_L > N_L^* N_I$ since the local population is declining and the invasive population is increasing. Note that the asymmetry in introgression increases in this model with the intrinsic growth rate r (equal to 0.5 in both species in Fig. 6.1D). This dynamics implies that i) the invading species will be mostly introgressed at low density, ii) introgression can occur in both direction but the invading genes having introgressed the local population cannot be observed if the local population goes extinct iii) a gene introgressing the invading population will be found in multiple copies when the invading species has reached carrying capacity. It follows that with recurrent introgression events occurring at the wave front during the whole range expansion, the original gene pool of the invading population should become increasingly

diluted (Chikhi et al., 2002), and we would still expect to see a massive introgression in the territories newly colonized by the invading species unless the hybrids are heavily counter-selected (Currat et al., 2008b; Excoffier et al., 2009).

6.6 Introgression levels as a function of interbreeding success

We checked the predictions of our admixture model with spatially explicit simulations. We thus simulated a range expansion in a two dimensional stepping-stone world of 50x50 demes, where an expansion started 1500 generations ago from the lower left corner into a world already filled by a local species. We studied the same 7 scenarios C1 to C7 defined in Table 6.1, which were already studied in Currat et al. (2008b). The final introgression rates in the invasive species for the old and new models of admixture are presented in Figure 6.2 for these 7 scenarios. We see that the results are qualitatively similar, but only differ quantitatively. A larger interbreeding success rate (γ) is needed to lead to the same level of final introgression with the new model assuming a more symmetric introgression rate between populations. However, if γ exceeds 10%, the invasive species is massively introgressed by the local species, except for scenario C5, which assumes that the carrying capacity of the invasive species is 100 times larger than that of the local species. Overall, we see in Table 6.2 that under the new model, we need just to double the interbreeding success to reach the same level of final introgression as compared to the old admixture model. It implies that our main conclusion, that a massive introgression of local genes into the invasive population is expected when interbreeding is not very rare, remains valid under the new model with symmetric admixture. In more details, we see in Figure 6.2 that when the invading species is not much more abundant than the local species, high levels of introgression already occur for very low levels of interbreeding (see cases C6 and C7 in Fig. 6.2). Overall, the final level of introgression is positively correlated with the size of the local population (compare cases C2 and C3), and negatively correlated with the size of the invading population (compare cases C1 and C2 or C4 and

Table 6.1. Parameters of the simulated invasion scenarios studied in a simple square world of 50 x 50 demes, initially entirely filled by a local species. The source of the invasion is arbitrarily located in deme at position <5; 5>. K : Carrying capacity expressed in number of genes or haploid individuals. K_m : Number of genes sent to neighboring demes of the same species at carrying capacity. Each generation, a given gene has probability m to migrate to neighboring demes. In all scenarios, the intrinsic rate of growth (r) was set to 0.5.

Scenario	Local species		Invasive species	
	K	K_m	K	K_m
C1	50	1	500	10
C2	50	1	5000	100
C3	500	10	5000	100
C4	50	10	500	100
C5	50	10	5000	1000
C6	50	1	100	10
C7	500	10	1000	100

C5 in Fig. 6.2). Introgression is also favored when gene flow between adjacent demes is restricted (compare cases C1 and C4, C1 and C6, as well as C2 and C5). This makes sense, because genes introgressed from the local population at the wave front will compete with migrant genes from the invading populations if gene flow is high, and will be thus less amplified by the logistic growth. Therefore, intraspecific gene flow protects against interspecific introgression, a phenomenon that has been confirmed when comparing levels of introgression in species with sex-biased dispersal, where genetic markers preferentially transmitted by the dispersing sex very generally show lower levels of introgression than other markers (Petit and Excoffier, 2009).

6.7 A spatially explicit model of admixture between Neanderthals and modern humans

On their road out of Africa, anatomically modern humans (AMH) met various archaic humans, such as Neanderthals, Denisovans and probably others. Very little is known about the exact nature of the interactions between AMH and Neanderthals and virtually nothing about interactions with Denisovans. Simulation is thus an invaluable tool to in-

Table 6.2. Interbreeding success values (γ) necessary to obtain 20, 40 or 80% of introgression in the invasive species with the new admixture model described above and the old one defined in Currat et al. (2008b). Demographic scenarios C1-C7 are described in Table 6.1.

Demographic	Final introgression								
	20%			40%			80%		
	Scenarios	new	old	factor ^a	new	old	factor ^a	new	old
C1	0.012	0.006	1.95	0.015	0.010	1.54	0.035	0.021	1.64
C2	0.014	0.008	1.75	0.027	0.014	1.95	0.059	0.034	1.72
C3	0.004	0.002	1.91	0.008	0.004	2.20	0.019	0.009	2.22
C4	0.021	0.013	1.60	0.032	0.018	1.82	0.072	0.038	1.93
C5	0.028	0.018	1.51	0.047	0.028	1.68	0.120	0.060	2.00
C6	0.010	0.004	2.65	0.014	0.007	2.07	0.029	0.013	2.25
C7	0.004	0.002	2.52	0.008	0.003	2.69	0.019	0.007	2.85

a. factor is the ratio between new and old γ values

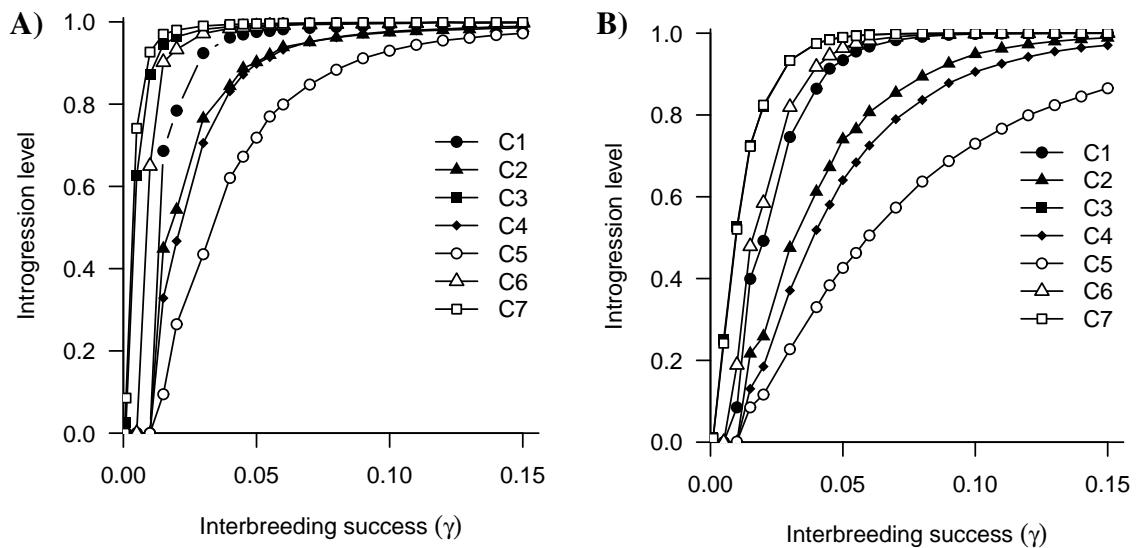


Figure 6.2. Proportion of genes introgressed into a given species as a function of the level of successful interbreeding (γ), assuming that the two species compete for local resources. Reported introgression levels were obtained as averages over 10,000 simulations. For each coalescent simulation, we sample 40 genes in 25 equally spaced demes of the invading population and measured introgression rate as the total fraction of genes that originated from the local population. Simulation parameters for cases C1-C7 are described in Table 6.1. A: Results from the admixture model described in Currat et al. (2008a). B: Results of the new admixture model for the same parameter values.

vestigate the effects admixture and competition on genetic diversity in a spatially dynamic context. The main interest of spatially-explicit simulation compared to previous mathematical models is that progressive admixture in time and space can be simulated between Neanderthals and AMH. It has been shown that a continuous interbreeding over space and time between Neanderthals and AMH in Eurasia may well explain the current patterns of genetic introgression (Currat and Excoffier, 2011). First, it was shown that the absence of Neanderthal type of mitochondrial DNA in contemporary human population is compatible with an extremely low interbreeding success rate (parameter γ) between AMH and Neanderthals (Currat and Excoffier, 2004). The analysis of the draft genome of NE suggests between 2 and 3% of Neanderthal DNA in the genome of contemporary non-Africans (Prufer et al., 2014; Green et al., 2010). Recent simulations have confirmed that less than 2% of interbreeding success is compatible with this observation (Currat and Excoffier, 2011) and consequently with an absence of mitochondrial introgression. Such low levels of interbreeding would correspond to about 200 or 300 successful hybridization events between Neanderthals and AMH over all their coexistence period (at least 10 KY in Europe, more in the Near-East) and over all their area of overlap. Such rare hybridization events are in line with results of Neves and Serva (2012) obtained under a different approach.

Here we reestimate the possible extent of admixture between AMH and Neanderthals using the new model of hybridization presented above, where gene flow is more symmetric between the two populations. Details about the demographic scenarios may be found in Currat and Excoffier (2011) but are summarized in Table 6.3. In a few words, we examined three alternative possible areas of hybridization between Neanderthals and AMH: A) an extended zone until the Altai mountains where the eastern Neanderthals remains has been found (Krause et al., 2007; Prufer et al., 2014); A'') an intermediate zone over the area where the presence of Neanderthals is well documented; A''') a restricted hybridization zone in the Middle-East only (Green et al., 2010). For each scenario with different values of parameter (Table 6.3), we performed 10,000 independent simulations and computed the proportion of Neanderthal introgression in one sample located in France and one in

China, which corresponds to the location of real samples previously analysed in Green et al. (2010). We consider a simulation compatible with the observation only if it gives a Neanderthal introgression rate between 2 and 3% in both Europe and Asia, as inferred in Green et al. (2010). Figure 6.4 shows the likelihoods obtained for different values of interbreeding success rate (γ) and different scenarios. Our new series of simulations confirm our previous results in showing that the extended hybridization zone A is significantly more likely than smaller areas A' and A'' (Fig. 6.4A, Table 6.3). It thus suggests on the one hand that Neanderthal have probably occupied a very large area over Asia, probably reaching the south of Siberia, and on the other hand that there was a strong reproductive isolation between them since our most likely estimates of interbreeding success are only around 1% (Table 6.3). We then performed ten additional versions of scenario A (see Table 6.3), in order to explore the influence of the various parameters on the results. We investigated various population densities in AMH (scenario B, C and C'), various migration (D) and growth rates (E), and various levels of heterogeneity in population densities, both in AMH and Neanderthals (F, F', F'', G and G'). Overall, all the simulations compatible with the observed data simulate an interbreeding success rate γ smaller than 3% (Fig. 6.4, Table 6.3), slightly higher than our previous estimate of 2% (Curran and Excoffier, 2011). However, if we add another condition for considering a simulation as compatible with the observation, that introgression is higher in Asia than in Europe as recently proposed using a more detailed analysis of the Neanderthal genome (Wall et al., 2013), then γ is again estimated to be below 2% (results not shown). Those simulations thus demonstrate that the reported pattern of Neanderthal introgression in AMH is compatible with a strong reproductive isolation corresponding to a few hundreds of successful hybrids between Neanderthals and AMH, and this for the whole interaction period and the whole geographic overlap between these two species.

Table 6.3. Demographic parameters of the simulated spatially explicit scenarios of hybridization between modern humans and Neanderthals.

Models	K_N^a	K_H^b	r^c	m_N^d	m_H^e	Estimated interbreeding success ^f	Model A relative probability ^{g h}
A. Large Neanderthal range	200	800	0.8	0.1	0.2	0.0092	[0.0050-0.0160]
A'. Restricted Neanderthal range	200	800	0.8	0.1	0.2	0.0116	[0.0032-0.0215]
A''. Hybridization in Middle-East only	200	800	0.8	0.1	0.2	0.0130	[0.0028-0.0228]
B. Large K	400	1600	0.8	0.1	0.2	0.0070	[0.0040-0.0120]
C. Small K	100	400	0.8	0.1	0.2	0.0159	[0.0058-0.0254]
C'. Very small K	25	100	0.8	0.1	0.2	0.0498	[0.0386-0.0713]
D. Small m	200	800	0.8	0.05	0.1	0.0092	[0.0040-0.0163]
E. Small r	200	800	0.4	0.1	0.2	0.0067	[0.0040-0.0110]
F. Variable KH	200	200-1600	0.8	0.1	0.2	0.0095	[0.0040-0.0167]
F'. Variable KH and KN (correlated)	50-400	200-1600	0.8	0.1	0.2	0.0092	[0.0040-0.0167]
F''. Variable KH and KN (uncorrelated)	50-400	200-1600	0.8	0.1	0.2	0.0099	[0.0040-0.0169]
G. K 4x higher in ME	200 (50)	800 (200)	0.8	0.1	0.2	0.0226	[0.0097-0.0364]
G'. K 2x higher in ME	200 (100)	800 (200)	0.8	0.1	0.2	0.0138	[0.0058-0.0239]

a. Neanderthal carrying capacity

b. Human carrying capacity

c. Intrinsic rate of growth

d. Migration rate between Neanderthal demes

e. Migration rate between human demes

f. Maximum likelihood estimates of interbreeding success (γ) between humans and Neanderthals are reported with limits of a 95% CI shown within brackets.

g. Probability of scenario A relative to the other scenarios computed from weighted AIC's computed as a weighted AIC $w_m = e^{-\frac{1}{2}AIC_m} / \left(e^{-\frac{1}{2}AIC_m} + e^{-\frac{1}{2}AIC_A} \right)$

(Burnham and Anderson, 1976), where AIC_m is Akaike Information Criterion (Akaike, 1974) of the alternative scenario m computed as $AIC = 2k - 2\ln(L)$, with k being the number of estimated parameters (here $k = 1$) and L being the maximum likelihood of the model.

h. Hybridization occurs for about 80 generations in the Middle-East



Figure 6.3. Simulated landscape used in our simulations. The union of the dark green and brown zones represents the conventionally assumed Neanderthal range (Klein, 2003) (scenario A' in Table 6.3), whereas the violet zone represents a larger range, including the Altai mountains where Neanderthals remains have been recently identified. The brown zone represents an even more restricted area of potential hybridization in the Middle East (scenario A'' in Table 6.3). The grey zone is the Himalayan range where migrations have been disallowed. The dark green dot is an arbitrary place of origin for the expansion out of Africa, and the two red dots are the locations of the two samples where introgression is measured (Paris, France and Beijing, China). In our simulations, the continental areas have been divided into square cells (cell size=deme area=100 x 100 km²) where a human and a Neanderthal local population could potentially coexist, compete and exchange migrants. Adapted from Currat and Excoffier (2011).

6.8 Discussion

Our model of continuous but limited interbreeding between Neanderthals and AMH over the whole Neanderthal range can nicely explain most currently documented patterns of human-Neanderthal ancestry: a limited and relatively uniform introgression level in Eurasia (Green et al. 2010), potentially higher in East-Asia (Wall et al., 2013); a Neanderthal introgression in AMH but not the opposite direction (Green et al., 2010); an absence of mitochondrial introgression (Krings et al., 1997); signals of introgression in areas where Neanderthal apparently never existed (Green et al., 2010). Moreover, our model leads to very similar results over a wide range of parameters values and it is parsimonious since it does not require additional factors to explain observations that are difficult to account for by a model of single admixture in the Middle East (Green et al., 2010); Reich et al.

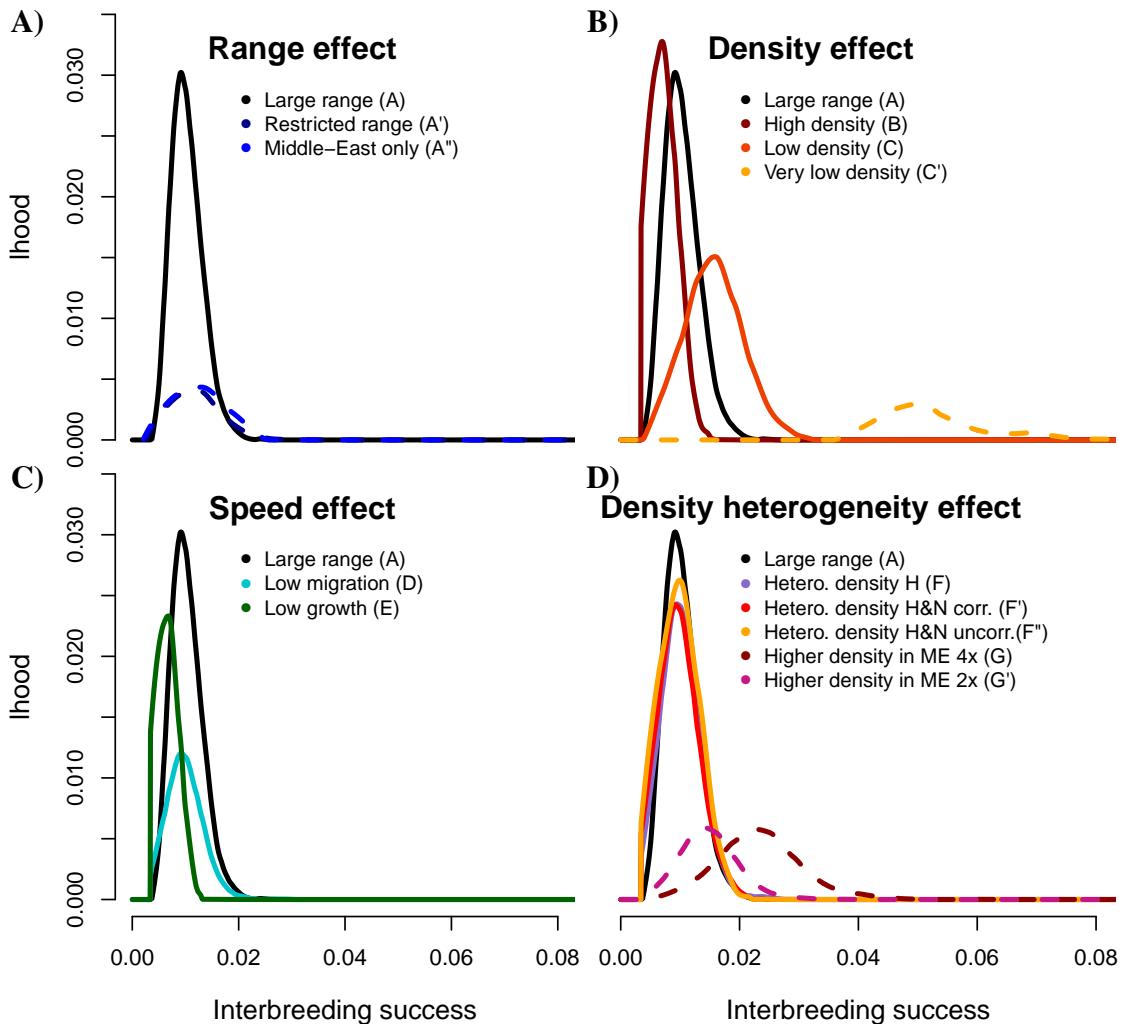


Figure 6.4. Distribution of the proportion of simulations (among 10,000) resulting in Neanderthal introgression levels compatible with observations (1.9% -3.1%, (Reich et al., 2010)) in both French and Chinese samples. Each likelihood curve corresponds to a different demographic scenario described in Table 6.3 and Figure 6.3. Results were obtained by assuming a deme area of 100 x 100 km². Solid lines correspond to scenarios that are equally likely (within 2 AIC units from the scenario with the highest likelihood), whereas scenarios shown with a dotted line have an associated AIC more than 2 units larger, and thus cannot be considered as equally well supported by the data.

2011), such as the absence of more recent admixture in Europe despite a documented and prolonged period of interaction (e.g. Mellars, 2011). Using our spatially-explicit model, we found that observed low levels of Neanderthal ancestry in Eurasians are compatible

with a very low rate of interbreeding (<3%), which could be due to a strong assortative mating or to a reduced fitness of the hybrids, or to a combination of these two factors. Our model additionally suggests that those rare admixture events occurred over a wide European and Asiatic range, beyond the Middle East, after the split of Europeans and Asians, and thus in different places in Europe and Asia. However our model is not able to define the precise past distribution of Neanderthals, but it suggests that it was of comparable size in Asia and in Europe at the time of the spread of AMH. Interestingly, recent studies of the distribution of genomic regions of Neanderthal origins in Europeans and Asians (Sankararaman et al., 2014; Vernot and Akey, 2014) have led to results compatible with the prediction of our spatially explicit model of admixture with competition between the two species. Indeed, it was shown that 1) European and Asian genomes harboured different Neanderthal introgressed segments, suggesting several and independent admixture events in the two continents, and 2) large genomic regions were deprived of any introgressed Neanderthal segments suggesting the potential role of selection to have prevented admixture in these regions, implying a lower fitness of hybrid individuals.

Another important result of our new series of simulations is to show that symmetrical interbreeding between two species can result in final asymmetrical introgression due to the different demographic dynamics of the local and the invasive species. Indeed, in our model, Neanderthals are considered as being at demographic equilibrium while AMH are expanding demographically and spatially. There should have been a continuous incorporation of Neanderthals genes at the wave front of the AMH expansion, combined with a relatively high probability for those genes to be spread by gene surfing (Klopfenstein et al., 2006). This continuous input process can explain why few successful hybridization events are sufficient to result in 2-3% of final introgression in the genome of non-Africans. What happens at the front of the human expansion wave is thus critical for determining the final introgression levels. It is also important to realize that our model implicitly assumes that some sexual or classical selection against hybrids occurred during the expansion process. However, things could have been even more complicated since expanding populations have been recently shown to build some genetic load (Peischl et al., 2013) and thus see

their fitness reduced with distance from the source of the expansion. The build-up of an expansion load could thus leave room for adaptive introgression to occur, and several genomic regions showing very high frequencies of Neanderthal segments have already been flagged (Sankararaman et al., 2014), even though some of these segments could have increased by chance during the expansion process by gene surfing.

6.9 Acknowledgments

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CHAPTER 7

Introgression during density-dependent range expansion: European wildcats as a case study

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Unpublished manuscript

7.1 Project description

In this project we present two new models of density-dependent dispersal during spatial range expansion. Recent studies have highlighted the importance of incorporating such types of dispersal, but they are purely ecological, and the few attempts including a genetic admixture are density-independent. We compare our results with the simulations of Currat et al. (2008b) concerning the spreading of an invasive species that is hybridizing with a native species, without interspecific competition. We did not consider competition because it allows the coexistence of both species and we can therefore measure the expected asymmetrical introgression levels, which are higher in the invasive species Currat et al. (2008b). We show that the qualitative expectation of Currat et al. (2008b) remains

valid under different dispersion modes, but the results differ quantitatively in terms of colonization time and level of introgression. We illustrate the usefulness of this approach by applying it to a recent range expansion of European wildcats in the Jura region, which for 25 years were considered to be extinct. The population has recovered recently, but hybridization with domestic cats is the main current threat. This example illustrates that the invasive species under the expectation of Currat et al. (2008b) is not necessarily non-indigenous and may also represent local species, either naturally expanding their home range or recolonizing area losses by human disturbances. We show that a model that is more adapted to territorial species increases the likelihood to explain current introgression levels, allowing the projection of the extinction risk for the near future. Further efforts to prevent current hybridization have to be implemented in order to preserve the European wildcat species in the Swiss Jura.

Author contributions CSQ collected and analysed the data and drafted the first version of the manuscript. He also participated in the conception and design of the study as well as in the interpretation of the results and the final writing of the manuscript

7.2 Abstract

The dynamics of range expansion needs to be considered when assessing the genetic consequences of invasive organisms spreading and interbreeding with native taxa. Models of hybridization during range expansion have been recently developed but assume dispersal to be independent from local population densities. However, organisms may disperse because they are attracted by conspecifics, or to the contrary, because they prefer depopulated areas. These behaviours are referred to as positive or negative migratory responses towards conspecifics. Here, through spatially explicit simulations, we assess the effects of various modes of density-dependent dispersal during range expansion on the genetic introgression between two interacting species. We find a massive introgression of genes from the local species into the invasive species with all modes of dispersal, even when hybridization rate is relatively low. This trend represents a general expectation for neu-

tral genes, independently of the mode of dispersal of the invasive species. However, the various modes of spatial dispersion differ in colonization times and rate of introgression. Invasive individuals attracted by conspecifics need more time to colonize the whole area and are more introgressed by local genes, while the opposite is found for solitary or territorial individuals. We applied our simulation framework to the real case of European wildcats and domestic cats that hybridize in the Jura region, by analysing autosomal, mtDNA and Y-chromosome genetic markers. The adequacy between real and model-simulated data increases up to 30% when using a more solitary mode of dispersion for wildcats instead of gregarious dispersion, in accordance with the ecological knowledge for this species. Then, using our best-fitting model, we project that wildcats might rapidly reach extinction in the Jura area due to interbreeding with domestic cats if the situation remains unchanged. The models of density-dependent dispersal modes we present here are thus powerful tools for conservation and evolutionary studies, their application improving the predictive power of models of species range expansion.

7.3 Introduction

Organisms may expand or shift their geographical range as a consequence of translocation, modifications of habitat and climate change (e.g. Brown et al., 2010). Among the interactions that take place during range expansions, interspecific hybridization is of growing concern in both evolutionary and conservation biology. This is the consequence of the emergence of new overlaps in breeding period and place, leading to hybridization between historically allopatric species with incomplete reproductive barriers, breaking their independent evolution (Arnold and Martin, 2010).

The resulting introgression between the interacting species is influenced by the dynamic of range expansion (e.g. Johannesen et al., 2006; Garcia et al., 2011; Ren et al., 2012). The invasive species usually arrives with few individuals while the local species may be considered at demographic equilibrium. This demographic imbalance at the wave front of the invasive range expansion results in asymmetric introgression between both species, with massive genes coming from the local to the invasive. This asymmetrical

pattern was demonstrated by Currat et al. (2008b) by using genetic simulations and an extensive literature survey.

Models aiming at studying the genetic consequences of species range expansion have been developed, but assume dispersal to be independent from local population densities ((Currat et al., 2008b; Excoffier et al., 2014)). This is not necessarily true for species that utilize indications from conspecifics as attracting or repulsive signals for entering a given area (Quilodrán et al., 2014b). Density-negative dispersal, or avoidance of populated areas, may be observed in territorial species with aggressive interactions (e.g. Aguillon and Duckworth, 2015), while density-positive dispersal, or attraction, may be observed in gregarious species with colonial behaviour (e.g. Szostek et al., 2014). The classical model of density-dependent distribution considers territorial species as avoiding conspecifics (Fretwell and Lucas, 1969), but alternative examples showed that they can also be attracted, for instance in migratory songbirds looking for suitable patches for survival or mating (Rushing et al., 2015). Recent studies have highlighted the critical importance to incorporate density-dependent dispersal when investigating the consequence of species range expansion (Altwegg et al., 2013; Bocedi et al., 2014; Ponchon et al., 2015). However, those ecological works did not incorporate the genetic dimension. Here, we assess the influence of positive and negative density-dependent dispersal during range expansion on the level of genetic introgression between interbreeding native and invasive organisms.

We exemplified the importance of incorporating density-dependent dispersal in the models by using European wildcats (*Felis silvestris silvestris*) as a case study. The European wildcats were widely distributed across Europe (Sommer and Benecke, 2006), but habitat loss and hunting reduced their populations to near extinction during the 19th and 20th centuries (Stahl and Artois, 1994). Yet, conservation actions helped to increase the population in some parts of Europe (e.g. Say et al., 2012). European wildcat is still listed as an endangered species in the Red List of various countries, the major threat being hybridization with domestic cats (*Felis s. catus*) (Yamaguchi et al., 2015). Here, we restrict our analysis to the Jura region, in Switzerland, where wildcats were virtually extinct in the middle of 20th century, with no observations of individuals between 1943 and 1968 (Nuss-

berger et al., 2007). The Swiss federal game law protected this species in 1962 (Duell and Agosti, 1994) and new observations in the Jura Mountains have been made since then. Several observations have been registered in the 90's (Dötterer and Bernhart, 1996), with an increasing trend in recent years (Nussberger et al., 2014), evidencing a range expansion of wildcats. A genetic characterisation of the interbreeding between both cats in this area is available (Nussberger et al., 2013; Nussberger, 2013; Nussberger et al., 2014). We used this example of recent range expansion and the associated genetic data to illustrate the improvement on predictive power when spatial dispersal behaviour is incorporated into models of species range expansion with hybridization. We then used the most likely model to explain the current amount of introgression, as identified through simulations, in order to project future scenarios of introgression between wild and domestic cats in the Jura region.

7.4 Materials and Methods

7.4.1 Simulation of range expansion with hybridization

In order to simulate the range expansion of an invasive species into an empty area or into a territory already occupied by another local species, with or without genetic admixture, we used a modified version of the program SPLATCHE 2 (Ray et al., 2010). This software was designed to simulate neutral genetic diversity in a spatially explicit landscape. The simulations are done in two steps: 1) a forward simulation of demographic parameters; and 2) a backward coalescence simulation, conditioned on the demographic information of the first step, in order to compute the proportion of introgressed genes between species (see Currat et al., 2004).

SPLATCHE 2 is simulating the evolution of a series of interconnected demes during a given number of generations. The distribution range of a single species is represented as one grid of demes arranged in a stepping-stone manner, while two different species are represented by two superimposed grids, one for each of them. Gene flow between neighbouring demes belonging to the same grid represents migration and is regulated by the

parameter m (migration rate), while gene flow between superimposed demes belonging to different grids represents hybridization between species and is regulated by the parameter γ (interbreeding success rate). Within each deme, population density is logically regulated using the parameters r (growth rate) and K (carrying capacity). Interspecific competition between two simulated species can be incorporated by using the Lotka-Volterra approach (Volterra, 1928; Lotka, 1932). More information about algorithms is available in Ray et al. (2010), but the admixture mode was implemented following a version improved by Excoffier et al. (2014).

Admixture between species is simulated in every deme, in which N_i and N_j are diploid population sizes of the two species at the previous generation ($t - 1$). In the current generation (t), considering panmictic reproduction within demes, newborn individuals \dot{N}_i have a probability $\frac{N_i}{N_i + N_j}$ to have parental ascendance from the same species (i) and a probability $\frac{N_j}{N_i + N_j}$ to be a hybrid, with one parent coming from the species j . Therefore, the expected number of admixtures resulting in a transfer of genes j into the species i is $A_{ji} = \frac{\gamma \dot{N}_i \dot{N}_j}{N_i + N_j}$ where γ is a parameter measuring the strength of barriers to gene flow between both species and is called interbreeding success rate. A value of zero indicates no interbreeding between both species, a value of 1 indicates that the reproduction is panmictic between the species, and any intermediate value implies that mating is non-random among both species (Currat and Excoffier, 2004, 2011; Quilodrán et al., 2014a, 2015).

We followed the simulation scheme of Currat et al. (2008b) in order to investigate how density-independent dispersal affects their conclusions about asymmetrical introgression between both species (which was shown to be massive for the invasive species). We thus used a two dimensional square space of 100 x 100 demes, in which an invasive species started a range expansion 1,500 years ago from the centre of the grid. At the onset of the expansion, the area is already occupied by a local species, which can hybridize with the invasive one at various rate corresponding to γ . We then performed 10,000 backward coalescent simulations for each demographic scenario in order to assess the final proportion of introgressed genes on each species, sampling 40 genes in 25 equally

Table 7.1. Simulated scenarios with parameter values. They represent the expansion of invasive organisms in an area occupied by a local species without interspecific competition. These scenarios are the same as the ones explored by Currat et al. (2008b) with density-independent dispersal. K is the carrying capacity and K_m the number of emigrants sent to neighbour demes when carrying capacity is reached. The intrinsic growth rate (r) is fixed to 0.5 in all scenarios. Scenarios incorporating interspecific competition are shown in supporting information (7.8).

Scenario	Local species		Invasive species	
	K	K_m	K	K_m
NC1	50	10	50	10
NC2	500	10	500	10
NC3	500	100	500	100
NC4	50	10	500	100
NC5	500	100	50	10

spaced demes.

We explored scenarios assessing the effect of different carrying capacities (K) and number of migrants among neighbour demes (K_m). We present five scenarios without competition between species (NC, Table 7.1), while seven scenarios with competition (C) are presented in supplementary material (Table 7.3, supporting information). We did this choice because NC scenarios allow coexistence of both species and introgression could thus be computed in both local and invasive organisms. The invasive species has a competitive advantage due to larger carrying capacity, driving local species to extinction in scenarios C. In this last case, interbreeding occurred exclusively at the edge of the wave of expansion, in which both species still coexist. Without competition, both species are supposed to use different niche and can therefore coexist and interbreed until the end of our simulations. All scenarios NC and C are identical to those of Currat et al. (2008b), except regarding the mode of dispersal (see below).

7.4.2 New models of density-dependent dispersal

Organisms may disperse because they are attracted by conspecifics, or conversely because they prefer depopulated areas. We implemented two models of dispersal to reflect those behaviours, referred to as positive or negative migratory responses toward conspecifics. For all models, the proportion of individuals emigrating from each deme at each genera-

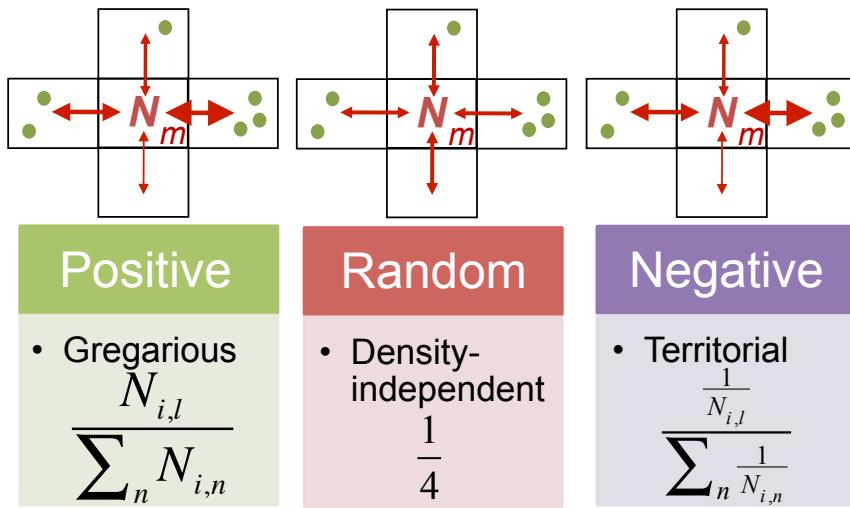


Figure 7.1. Models of density-dependent dispersal implemented in the modified version of SPLATCHE 2. Green dots represent individuals in each neighbour deme. The width of the arrows denotes the amount of migrants sent from the central deme. The migration probability of species i in time t to neighbour demes was considered to be either dependent (negative and positive models) or independent of neighbour densities (random model). The values of l and n represent one of the four available neighbour demes.

tion is defined by the migration rate m . However, the direction of emigrants varies among models (Fig. 7.1). In the original version of SPLATCHE 2, the migratory probabilities are density independent and are equal toward each neighbouring deme (random model in Fig. 7.1). This model was used by Currat et al. (2008b) and denotes our null hypothesis to test the effect of positive and negative density-dependent dispersal. For those two last models, the migratory probability from a deme i to a deme l of the same species (grid) depends on the densities in the neighbouring demes as shown on Fig 7.1. The positive model is computed as: $\frac{N_{i,l}}{\sum_n N_{i,n}}$, where n represents the number of neighbour demes. It simulates the more gregarious or social behaviour of individuals attracted by conspecifics. The negative model is computed as: $\frac{1}{\sum_n \frac{1}{N_{i,n}}}$, characterizing the more territorial or solitary behaviour of individuals avoiding conspecifics during spatial dispersal.

7.4.3 Application to European wildcats

We applied our approach to the case of hybridization between wildcats and domestic cats in the Jura Mountains (Switzerland). We assumed a recent range expansion of European wildcats in this area, where they were considered to be virtually extinct for 25 years, but increasing observations have been registered since a change of policy in 1962. This period of range expansion represents 17 generations in our simulations (with a generation time of three years for cats). We thus simulated this recent range expansion to illustrate how the incorporation of spatial dispersal behaviour increases the explanatory and the predictive power.

We simulated an array of 256 demes of 25 km^2 , roughly representing the Swiss Jura region ($\sim 6,400 \text{ km}^2$). In this landscape, 16 demes represent habitat exclusively suitable for wildcats, 48 demes are potentially shared by both wildcats and domestic cats, while the remaining 192 demes are exclusively used by domestic cats. About $1,600 \text{ km}^2$ are suitable for wildcats (Nussberger et al., in prep).

The values of demographic parameters and observed introgression are based on Nussberger (2013). The genetic information is extracted from 68 autosomal nuclear SNP-markers, four mtDNA SNP-markers and two Y-chromosome SNP-markers. All SNPs are highly differentiated between both species of cats (Nussberger et al., 2013). We consider a single population of wildcats found in the Jura on both side of the political border between France and Switzerland (Table 7.2).

We assessed the likelihood of each model of spatial dispersal (positive, negative or random) to explain the observed introgression levels between both cats. This computation is done independently for all three marker-categories (autosomal, mitochondrial and Y chromosome). We computed a dummy variable evaluating whether simulated introgression belong to a confidence interval around the observed values (Table 7.2). We used this variable as the response in a generalized additive model (GAM) with binomial error. GAM is a regression method that allows incorporating the non-linear effect of the interbreeding success rate parameter (γ), which is used as explanatory variable. We used the predicted values of the three dispersal models (random, positive and negative) as the like-

Table 7.2. Observed genetic introgression and parameter values used in the case study of hybridization between European wildcats and domestic cats in the Jura region. Data obtained from Nussberger (2013).

	Wildcat	Domestic cat
Genetic introgression		
Autosomal	7-18%	0-5%
mtDNA	9-22%	0-3%
Y-chromosome	0-9%	0%
Model parameters		
Generation time (years)	3	3
Interbreeding success rate (γ)	0-0.4	0-0.4
Growth rate (r)	0.5	0.7
Migration rate (m)	0.18	0.18
Carrying capacity (K)	12	70

lihood to explain the introgression observed in the field. The goodness of fit between the alternative scenarios and the data was compared by means of AIC (Akaike Information Criterion), defined as $AIC = 2k - 2\ln(L)$, where k is the number of estimated parameters (here, equal to 1) and L the maximum likelihood of the model (Akaike, 1974). We considered models with a $\Delta AIC < 2$ as equivalent ones (see Currat and Excoffier, 2011, for a similar method).

7.5 Results

7.5.1 Speed of range expansion

We first modelled a single species invading a large unoccupied area of 10,000 demes (Fig. 7.2). The mode of density-dependent dispersal influences the speed of the range expansion. Organisms that tend to avoid areas already occupied by conspecific (negative model) lead to a faster expansion, while organisms attracted by conspecific (positive model) are slower to colonize the whole area when compared with density-independent dispersal (random model). The mode of dispersal also affects the number of individuals in each deme, with higher and lower densities at the wave front of range expansion for the negative and positive model, respectively.

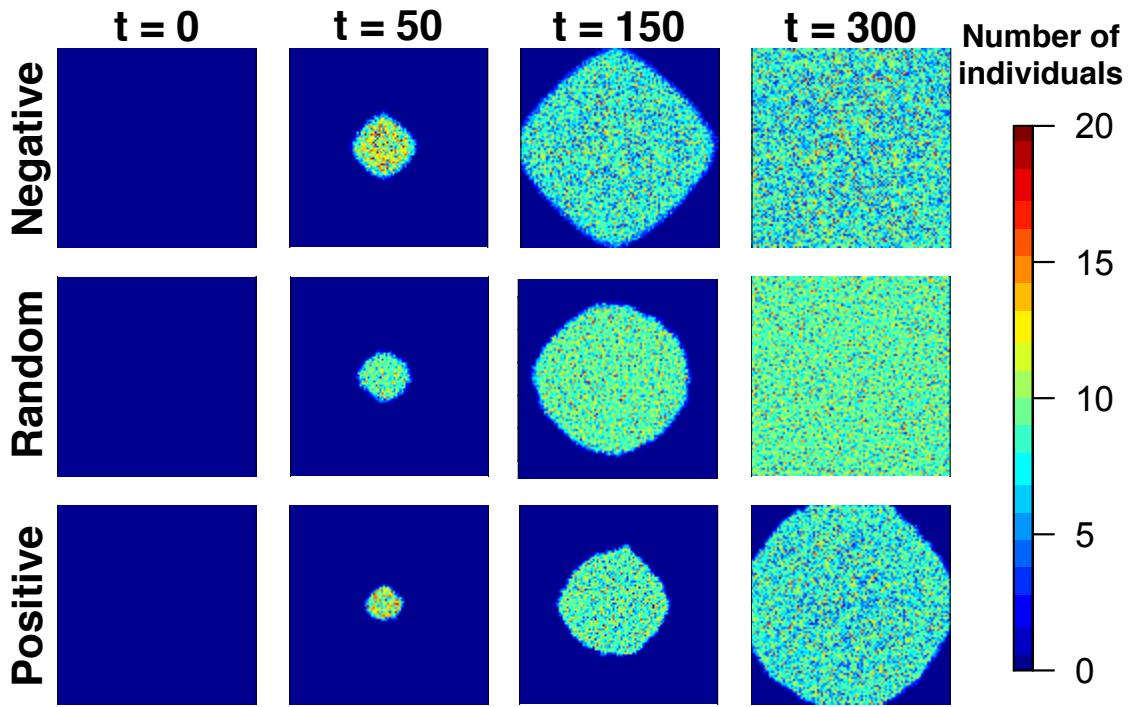


Figure 7.2. Range expansion of a theoretical species with different models of dispersal. The square space is composed of 10,000 demes. Population density in each deme is logistically regulated with a carrying capacity of 20 individuals (K). The intrinsic growth rate (r) is fixed to 0.5. The corresponding time is shown at the top of each column (t = number of generations). All expansion starts at $t = 0$ in the centre deme.

7.5.2 Genetic introgression

Once the species has colonized the whole area, we let it evolve until generations 1,000 and it is thereafter considered as the local species. A second species was then introduced in the centre of the area and colonizes it. This invasive species may hybridize with the local one at various rates regulated by the value of γ (Fig. 7.3). Both species coexist and admix in the absence of interspecific competition. For all three models of spatial dispersal (i.e. positive, negative and random migratory response to conspecifics), we found that reciprocal introgression occurs at very low levels of interbreeding, but introgression starts to be asymmetrical toward the invasive species with higher γ values. A massive introgression of local genes in the invasive species is obtained at relatively low γ ($> 5\%$), due to the demographic dynamic. Introgression level in the invasive species is positively

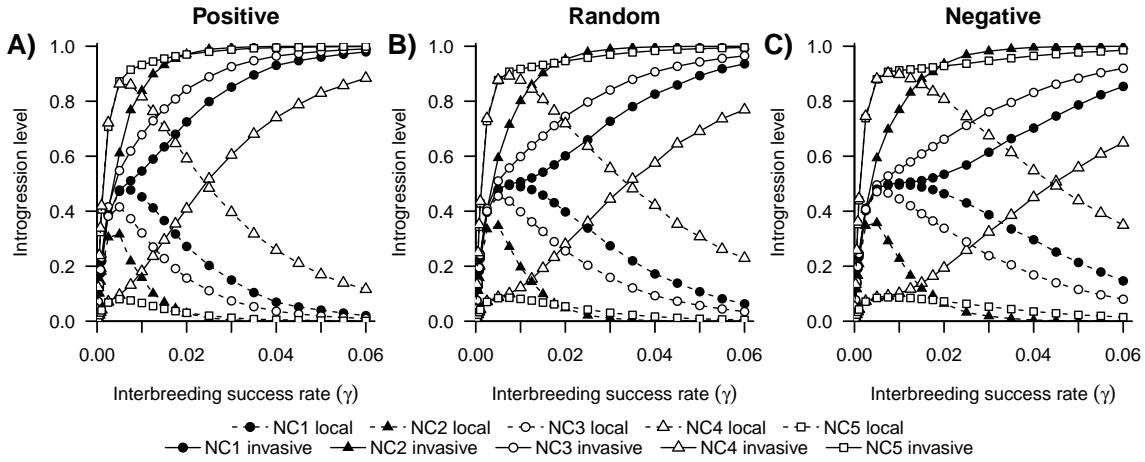


Figure 7.3. Effect of interbreeding success rate on the proportion of introgressed genes in a theoretical invasive and local species taken from the square world described in Fig. 7.2. Different models of spatial dispersal are presented: A) Positive (density-dependent), B) random (density-independent), C) Negative (density-dependent). At the onset of the invasive expansion, the local species occupied the whole area and then interact with the invasive during 1,500 years. Introgression values are average over 10,000 stochastic simulations.

correlated with the local density (compare scenarios NC1 vs NC5) whereas negatively correlated with invasive density (scenarios NC1 vs NC4) and migration rate (scenarios NC2 vs NC3). Local introgression of invasive genes follows the opposite trend. At very low frequency of interbreeding (γ), introgression of genes is found to be larger in the species with the smaller density (NC4 and NC5), even when it is the local one (NC4), due to the scarcity of interbreeding events during the period of range expansion which consequently do not affect the introgression level. However, as soon as the probability of interbreeding exceeds 5%, all scenarios result in a massive introgression of local genes in the invasive species. The massive introgression of neutral genes in the invasive organisms is thus dependent on a value of interbreeding success rate (γ) big enough to result in interbreeding events occurring at the front of the range expansion wave.

Although the positive and negative models of spatial dispersal exhibit the same general trend than the random model, they show some quantitative differences. To get equal introgression levels in both species, a lower interbreeding rate (γ) is required for the positive model (Fig. 7.3A) as compared with the random model (Fig. 7.3B), and higher for the

negative model (Fig. 7.3C). For instance, scenario NC4, in which the invasive species is much more abundant than the local one, requires around 4% of interbreeding to start having more introgression in the invasive species than in the local one for the random model, while it needs around 3% of interbreeding for the positive and 5% for the negative. In other words, when invasive individuals are attracted by conspecific (positive model), this leads to more introgression in the invasive species and less in the local one, by comparison to random dispersal, whereas the opposite occurs when invasive individuals are repulsed by conspecific (negative model). To depict this result we computed the differences in the level of genetic introgression between both models of density-dependent dispersal and the random model (Fig. 7.4). All models are equivalent at low frequency of interbreeding. The differences reach a maximum between 2% to 4% of interbreeding success rate (γ). Higher interbreeding success rates tend to homogenize the results of all three models due to the near complete introgression of genes from the local to the invasive species (see Fig. 7.3). Scenarios with the higher local densities (NC2, NC5 and NC3) show the smallest differences between both density-dependent models and the random model. At a given frequency of interbreeding (γ), with the positive model, the invasive species is more introgressed and the local one is less introgressed than expected with the random model (Fig. 7.3A and 7.3B). However, the negative model exhibits the opposite trend, where the local species is much more introgressed and the invasive species is less introgressed than expected with the random model (Fig 7.3C and 7.3D).

Similar results were found when interspecific competition is incorporated in the simulations (see Appendix S1, supporting information). In these simulations, the invasive species progressively replaces the local one due to competition of resources and higher carrying capacity. Even if the local species is demographically extinct at the end of a simulation, their genes can still be found in the genome of invasive organisms when the interbreeding rate is large enough. Here again, the density-dependent models of spatial dispersal (positive and negative) show the same general trend than the random model, with the same patterns of differences as described above for the non-competition scenarios.

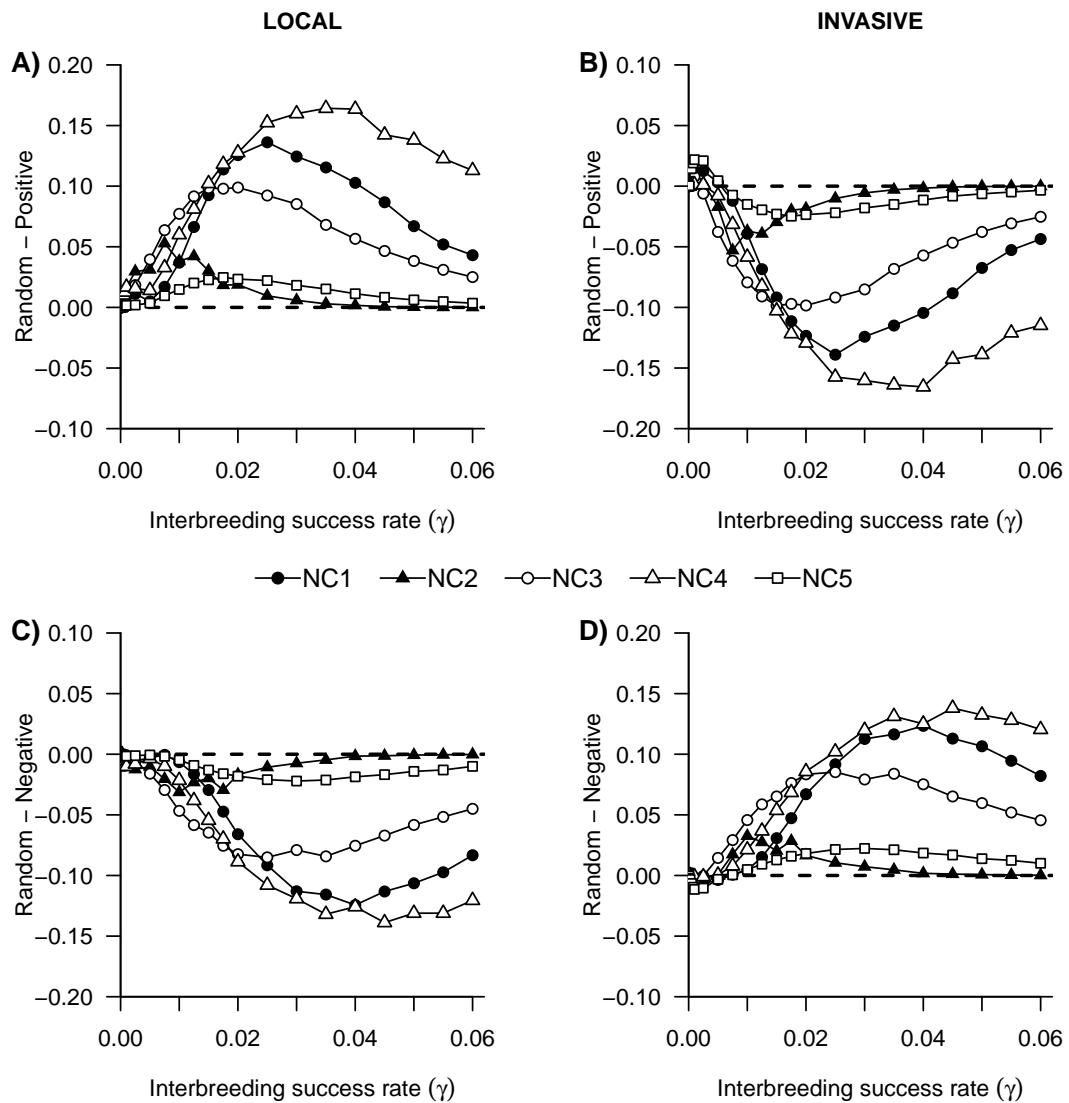


Figure 7.4. Differences in the proportion of introgressed genes of positive and negative model compare to the random model of spatial dispersal. At the onset of the invasive expansion, the local species occupied the whole area and then interact with the invasive during 1,500 years. A) and C) represent the differences for local organisms; B) and D) represent the differences for the invasive species. Values are average over 10,000 simulations.

7.5.3 Case study: European wildcats and domestic cats

We applied the three different models of spatial dispersal on a real case of hybridization between European wildcats and domestic cats in the Jura region. Massive introgression

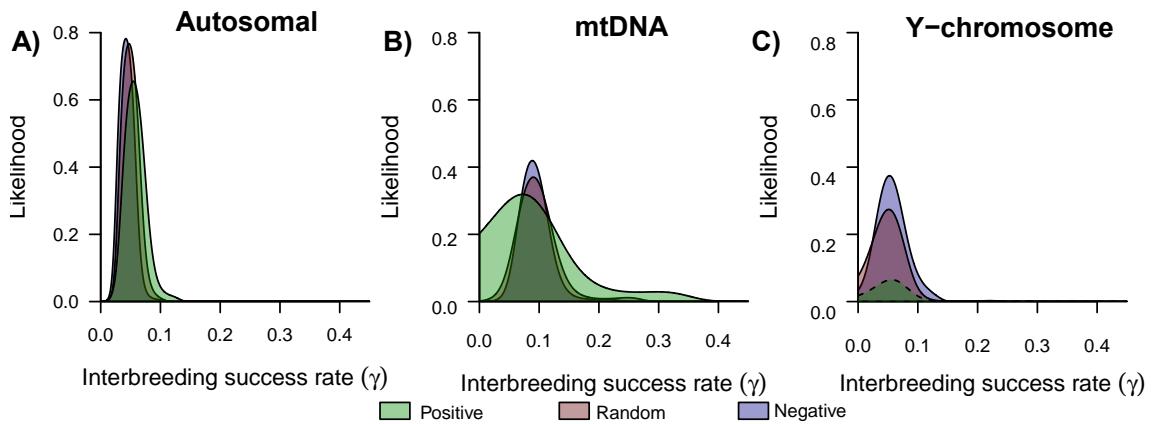


Figure 7.5. Likelihood of the three models of spatial dispersal in explaining the observed introgression between European wildcats and domestic cats. Various interbreeding success rate applied to three kinds of genetic markers are presented. The dotted borderline represents $\Delta\text{AIC} > 2$ when comparing the density-dependent models of spatial dispersal (negative and positive) with the density-independent one (random).

of domestic cat genes is found in European wildcats, whereas almost no introgression of wildcat genes is found in domestic cats (Table 7.2). Wildcats were considered to be nearly extinct, but the implementation of new policies for conservation helped to increase the number of individuals. A recent range expansion during the last 50 years (~ 17 generations) may have influenced new genetic interactions with domestic cats.

Our results show that the negative density-dependent model of spatial dispersal is consistently the most likely explanation for the current introgression of genes between both cats across all genetic markers (Fig 7.5). The likelihood of simulations to explain field observations increases by 13% for autosomal markers (Fig 7.5A), 10% for mtDNA (Fig 7.5B) and 31% for the Y-chromosome (Fig 7.5C) when comparing with the worse model of spatial dispersal (positive-density). However, for Autosomal and mtDNA, the difference between the three models is not significant ($\Delta\text{AIC} < 2$). Nevertheless, the positive model applied on the Y-chromosome is significantly less likely when compared with the random ($\Delta\text{AIC} = 2.9$) and with the negative model ($\Delta\text{AIC} = 3.5$).

The most likely values of interbreeding success rate (γ) range between 4% and 9% considering all markers and models of spatial dispersal. Those values explain much more

observed introgression when applied to the autosomal markers as compared to the mtDNA and Y-chromosome markers (Fig 7.5). An interbreeding rate of around 5% explains a maximum of 80% of introgression for the autosomal markers when using the negative model (Fig 7.5A), and a minimum of 6% on the Y-chromosome when using the positive model (Fig 7.5C). For mtDNA, a higher value of interbreeding success rate is needed to explain a maximum of introgression, a γ around 7% for the positive and 9% for the random and negative models is needed to explain 30% and 40% of the introgression between both cats, respectively (Fig 7.5B).

7.5.4 Projection of future wildcats introgression by domestic cats

We then projected the evolution of introgression between both cats under the conditions for hybridization found today. We simply added more generations to our most likely scenario, the negative model (Fig 7.6), keeping the demographic parameter values equal to those used to explain the current introgression (Table 7.2). The most likely values of interbreeding rate for each marker were used to simulate further generations (equal to 4.2% for autosomal, 9% for mtDNA and 5.2% for Y-chromosome, see Table 7.4 in supporting information).

Figure 7.6 shows the amount of introgression projected through time in wild and domestic cats. The current time is represented as a vertical dotted line. The main expectation is that wildcats will progressively be more introgressed by domestic cat genes in further generations, until being massively introgressed. Their genetic pool is supposed to be composed of 50% of genes coming from domestic cats at the 34th, 9th, and 23rd generations for the autosomal (Fig 7.6A), mtDNA (Fig 7.6B) and Y-chromosome (Fig 7.6C), respectively. In only 28 generations, more than 80% of their genes are expected to be derived from domestic cats at the mtDNA level (the most introgressed marker). More generations are needed for other genetic markers to reach similar levels of introgression (108 generations for autosomal and 66 for Y-chromosome). The expected introgression is not linear, faster introgression is expected during the first decades, with wildcat genes being nearly fully replaced by domestic genes in further generations (Fig 7.6). In hundred years, we

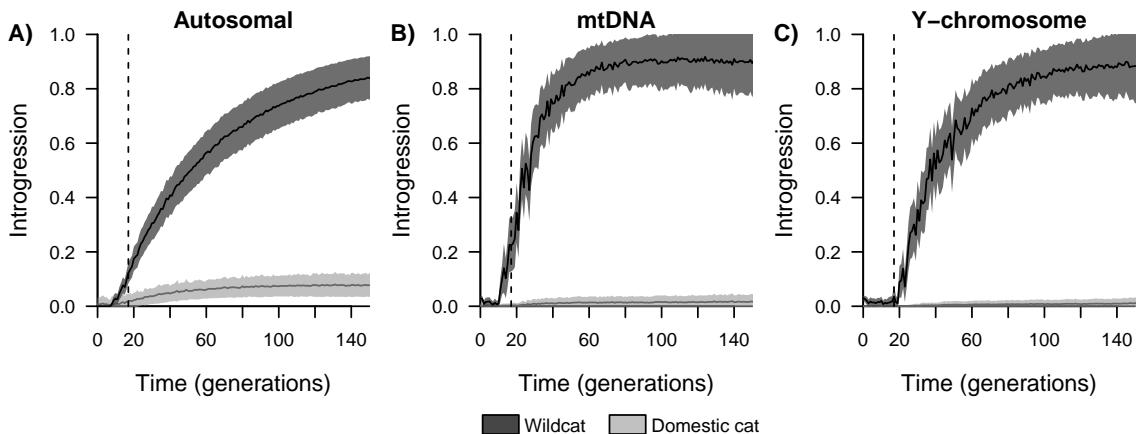


Figure 7.6. Projected introgression level through time between European wildcats and domestic cats. Values are presented by using the negative density-dependent model of spatial dispersal (mean \pm SD). The vertical dotted lines denote present time. Values on the right side of the dotted line represent the projection for future generations. They follow current conditions of demographic parameters, keeping the most likely value of interbreeding success rate for each marker (see Table 7.4, supporting information). Values are averages over 10,000 simulations.

predict that 50% of autosomal genes in wildcats will be introgressed from domestic cats, as well as 82% of their mtDNA and 62% of their Y-chromosome genes.

At the expected time of (near) extinction of wildcats, we show that a small proportion of wildcat genes are expected to remain in the pool of domestic cats. The maximum is presented by autosomal markers with a proportion of $8 \pm 0.5\%$ (mean \pm CI at 95%), but even for the Y-chromosome, which currently shows no introgression of genes on domestic cats, we expect a proportion of around $1.3 \pm 0.2\%$ of wildcat genes in the domestic cat (Fig 7.6).

Similar general trends of highly asymmetrical and massive introgression of genes in the wildcats are obtained when making predictions with the random and positive models (Fig. 7.8, see Supporting information). The random model is equivalent to the negative, but the positive needs more time for the mtDNA and Y-chromosome to reach similar values of introgression. For instance, 25 and 31 generations are needed to show 50% of introgressed genes on the mtDNA and Y-chromosome, respectively. This means around 48 additional years (~ 75 in total) for the mtDNA and 24 years for the Y-chromosome

(~93 in total) to project similar results as the ones obtained with the negative model.

7.6 Discussion

7.6.1 Density dependent dispersion and range expansion

Dispersal is a major process for both the successful colonization of a species naturally expanding their home range or for those settling new areas in response to human activities (Wilson et al., 2009). It is important to have accurate modelling tools to predict when and how an invasion might succeed; attempts to reverse or control the negative effects of human-translocated species on local biodiversity can be extremely costly and difficult (Hauser and McCarthy, 2009). The introduction of exotic species is usually recognized as being ecologically detrimental for native taxa, either due to direct predation, competition or modification of habitat, but also due to the genetic impact of hybridization (Hall et al., 2006). Hybridization has been shown to have the potential to facilitate biological invasions and result in the decline of native genotype or the extinction of one or both parental species (Quilodrán et al., 2015).

The use of social signals during dispersion is widely documented in animals, such as territorial or colonial birds (Kivelä et al., 2014), mammals (McGuire et al., 2009), reptiles (Spiegel et al., 2015), amphibians (González-Bernal et al., 2014), fishes (Bett and Hinch, 2015) and even invertebrates (Donahue, 2006). The presence of conspecifics can play a positive, negative or neutral effect when individuals are seeking habitat for survival or reproduction (Muller, 1998). We highlight the importance of incorporating behavioural responses toward conspecifics when projecting the dynamics of ecological and genetic interactions during range expansion.

Improving the predictive power of range expansion models, as we did here, is crucial to understand better how species respond to current and rapid environmental changes (Ponchon et al., 2015). In fact, dispersal can be a key adaptive response to global climate change, in which individuals can escape locally degraded environments and colonize new suitable areas (Travis et al., 2013). In that case, new biodiversity can be produced either

because populations become allopatrically structured or by making contact with sister species. Hybridization is also an evolutionary force that has been acting in the speciation process of several taxa (Brumfield, 2010). However, it has also been presented as a mechanism for "*speciation reversal*" when breaking the independent evolution of recent separated groups (Vonlanthen et al., 2012). The zone of hybridization can move in space and time when influenced by a changing climate, but the evolutionary consequences on local biodiversity are uncertain (Buggs, 2007). There is strong evidence of extreme weather changes in recent years, namely on patterns of heat waves and precipitation, that have been linked to human influences (Coumou and Rahmstorf, 2012). New ecological and genetic interactions are thus likely to be produced in the near future.

7.6.2 Asymmetrical introgression is the general expectation for neutral genes

Previous studies have highlighted the importance of density-dependent dispersal in ecology and evolution, but they did not consider genetic aspects (e.g. Altweig et al., 2013; Boedi et al., 2014; Ponchon et al., 2015). Our work is thus the first to study the genetic dimension of density-dependent migration during range expansion of an invasive species. For this, we developed two new models of density-dependent dispersal during range expansion to study their influence on genetic introgression between local and invasive species when hybridization between them is possible. Here we computed introgression levels with and without competition for environmental resources using the same demographic scenarios as in Currat et al. (2008b). Our results show that their main conclusion of a massive introgression of neutral genes in the invasive species, even when the frequency of interbreeding is very low, and asymmetrical compared to the introgression in the local species, remains valid with both models of density-dependent dispersal. Our results are closer to the ones presented by Excoffier et al. (2014) as compared to those of Currat et al. (2008b) because we used the same admixture model as in Excoffier et al. (2014), which is better adapted to hybridization. Our two density-dependent models present qualitatively similar trends, but a greater frequency of interbreeding (γ) is needed

under negative and a smaller one under positive density-dependent dispersal to get results similar to those obtained with random density-independent dispersion.

This general pattern of introgression between a native and an invasive species undergoing range expansion thus represents a null expectation for neutral genetic markers. Deviations from this neutral model are possible when selection is acting on genes conferring varying fitness and spreading between both species (Whitney et al., 2006). In addition, neutral polymorphisms may become advantageous in a new genetic or environmental setting (e.g. Montoya-Burgos, 2011), making the outcomes more difficult to predict. Sex-biased gene flow, due for instance to a behavioural response to new phonotypical traits, producing asymmetrical mating preferences (Meyer et al., 2006; While et al., 2015), or due to sex-biased survival of hybrids (Bundus et al., 2015), may also disturb this null expectation.

7.6.3 Density-dependent dispersal influences demographic and introgression patterns

We show that negative or positive density-dependent response toward conspecifics affects both the colonization dynamics and the pattern of introgression between interacting species. Altwegg et al. (2013) found a qualitatively similar result in terms of colonization time, in which colonization of a given area occurs much faster for negative density-dependent emigration than for positive. In addition, densities of the invasive species are lower at the wave front with positive and higher for negative dispersal.

The quantity of introgression also differs when comparing both models to one completely independent of densities (random dispersal). For a given value of interbreeding success rate (γ), the amount of introgression in the invasive species is lower under negative and higher under positive density-dependent dispersal. This result is influenced by the slower colonization time resulting from the positive model, which lengthens the overall cohabitation period and maximizes the effect of the wave front to amplify introgression (Currat et al., 2008b). In addition, the low density populations at the wave front receive less migrants from behind under the positive model, which is favourable for in-

trogression to occur (Petit and Excoffier, 2009). The opposite trend is observed in the local species, with larger introgression under negative density-dependent dispersal and lower under positive density-dependent dispersal. This is influenced by the faster range expansion under negative density-dependent dispersal and the demographic imbalance between both species, in which the rarest species is more likely to hybridize with a more abundant one (Hubbs, 1955). The local species is in demographic equilibrium, thus the invasive one, arriving with few individuals and escaping their conspecifics under negative density-dependent dispersal, have higher probability to find a heterospecific partner during the breeding period (McCracken and Wilson, 2011). Individuals from the core of expansion tend to migrate in periphery attracted by the lower densities. Introgression in the invasive species is therefore limited by the larger gene flow coming from the core (Petit and Excoffier, 2009). Consequently, invasive populations are growing more quickly and the probability for the local organisms to receive invader genes by hybridization also increases. Our series of simulations highlight the difficulty to predict the genetic outcomes resulting from interacting processes, namely migration, demographic growth and hybridization. It underlines the usefulness of computer simulations to study such complex systems.

7.6.4 Negative density-dependent dispersal explains better introgression in European Wildcats

Wildcats were considered to be almost extinct in the Swiss Jura, but policy changes and new legislation allowed significant recovery of the population during the last 50 years (Nussberger et al., 2014). They are still considered a threatened species in several countries in Europe, with the primary risk being hybridization with domestic cats (Yamaguchi et al., 2015). We thus applied the three models of spatial dispersal in the case of hybridization between European wildcats and domestic cats in order to evaluate which model was the most likely in explaining the observed introgression. The expected model given our ecological knowledge was the negative migratory response.

The negative model was consistently the most likely one to explain the observed hy-

bridization in nature, but we cannot absolutely reject the random density-independent model. It is interesting to note that even within the short time frame of our simulations (17 generations, \sim 50 years), we are able to reject the positive model of density-dependent dispersal and to improve the goodness of fit by 30% using the negative model for Y chromosome data. Allowing more time for ecological and genetic interactions may probably increase the power to differentiate among models of spatial dispersal.

Wildcats are solitary individuals and their home ranges rarely overlap, almost never for females (Biró et al., 2004). They associate exclusively for mating (Sunquist and Sunquist, 2002), and may thus disperse avoiding agonistic encounters due to territorial behaviour between individuals (Corbett, 1979). Our negative model is more accurate for this type of behaviour, in which territorial individuals avoid conspecifics during dispersal, increasing the probability of mating with a heterospecific during breeding period — in this case domestic cats, which are less territorial. Domestic cats can either live alone, in groups or a mixture of this life style (Corbett, 1979). They are distributed worldwide, associated with humans as pets or for controlling agricultural pests (Turner, 2000). Domestic cats were brought into Europe already by the Romans (Faure and Kitchener, 2009). Thus, domestic cats, including feral cats, were already present when wildcats started the re-colonization in the 20th century. The interbreeding success rate (γ) that best explains observed introgression is estimated around 5% for the autosomal and Y-chromosome markers. Higher values are required for mtDNA (\sim 9%). Male wildcats display more explorative spatial behaviour when looking for a partner than females (Daniels et al., 2001). They are therefore more likely to be involved in a heterospecific mating. This behaviour contributes to explain the observed higher introgression and the higher interbreeding rate in mitochondrial genes compare to the Y-chromosome.

7.6.5 Consequences of hybridization between European Wildcats and domestic cats

The pattern of asymmetrical and larger introgression in wildcats may seem counterintuitive. The null expectation presented by Currat et al. (2008b) and confirmed by our

simulations anticipated higher introgression in the invasive species. Indeed, the invasive is not always non-indigenous and the local is not necessarily a native taxa. In this case, we are dealing with a recolonization of lost territory by wildcat at the expense of the non-indigenous domestic cats. The recent range expansion of this threatened species represents a success for conservation management, but hybridization with domestic cats suggest that the policy should be amended to better control both feral and domestic animals in the area suitable for colonization by wildcats.

The projections of our simulation indicate more than 25% of mtDNA introgression in less than a decade and 50% in less than 30 years. For autosomal and Y-chromosome markers, this extremely high level of introgression may be reached in about 100 and 70 years, respectively. At this level of introgression it will be hard to define what those hybrids represent. Note that this expectations are based on the assumption that current parameters are constant over time and for neutral genes only.

The consequences of the hybridization on European wildcats are still poorly explored. Major issues are known for the consequences on fitness, behaviour and interaction with other organisms in the ecosystem. It is critical to establish the level of introgression at which a genetic rescue is still possible and to define if those hybrids displaying key ecological behaviour would be also subject of protection.

Domestic cats carry genotypes that differ from all other subspecies of wildcats (Driscoll et al., 2009). They were domesticated roughly 9,500 years ago from a distinct subspecies of Near East origin (*Felis s. lybica*) (Driscoll et al., 2007). The consequences of hybridization are uncertain, and the effects are not necessarily limited to the concerned taxa, as reduction of fitness due to outbreeding depression (e.g. Muhlfeld et al., 2009) or competition with hybrids (e.g. Ryan et al., 2009), but might also have broader ecological impacts. Hybrids may exhibit different environmental requirements and behaviour, reflecting intermediate phenotypes compared to parental taxa. The domestication process produced morphological changes in size and colour of domestic cats (Daniels et al., 2001), but also altered rate of reproduction, disease resistance and behaviour (Oliveira et al., 2008a). For instance, Darwin noticed a smaller intestine in domestic cats compared to that of wildcats,

a change attributed to the introduction of kitchen scraps to an otherwise strictly carnivorous diet (Darwin, 1868). Domestic cats are social and tolerant of people while wildcats are territorial and cryptic (Driscoll et al., 2009). Domestic cats have thus phenotypic and genetic variation and a legacy of domestication related to human activities. It is difficult to predict the impact of these traits introduced in the wildcat populations.

It is still possible to genetically differentiate between wildcats and domestic cats in Switzerland and other part of Europe, such as Portugal, Italy and Germany (Lecis et al., 2006; Oliveira et al., 2008b; Eckert et al., 2010; Nussberger et al., 2013). However, much higher introgression has been found in Hungary and Scotland (Beaumont et al., 2001; Lecis et al., 2006). Our simulations project a similarly high level of introgression in Switzerland if the current state of hybridization remains the same in the near future. With such high levels of introgression it is important to understand the ecological niche of these hybrids to enable conservation measures based on ecosystem function rather than morphological attributes (Daniels and Corbett, 2003). Meanwhile preventing further hybridization is a priority. Sterilization of free-ranging domestic cats, such as those on farms, as well as the control of feral individuals, are two measures that can be implemented in the short time. Even if these measures are laborious tasks, they may be less economically- and ecologically-costly than reversing the negative effects of hybridization (e.g. Saari et al., 2014).

7.6.6 Conclusion

A massive introgression of genes from a local species into a species invading its range is expected for neutral genes, whatever the mode of spatial dispersal. Our models of spatial dispersal differ quantitatively in terms of colonization time and level of introgression between local and invasive species, but the general trend first observed by Currat et al. (2008b) is confirmed by all our simulations. However, the quantitative differences highlighted here may be significant when one wants to study the genetic consequences of range expansions on specific organisms, as illustrated with the increasing likelihood of the most adequate model of spatial dispersion in our case study on European wildcats. In-

cluding density-dependent dispersal, as we did here, may improve the predictive power of models of range expansion. Our modelling approach strongly suggests that hybridization should then be actively hindered in order to preserve functional ecology and morphological attributes of European wildcats. Our spatially explicit approach constitutes a valuable tool in evolutionary and conservation biology that can be used in a variety of biological issues, including the set-up of management recommendations for threatened species and the study of past and future evolution of interacting taxa.

7.7 Acknowledgments

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7.8 Supporting Information

We simulated seven scenarios of an invasive species colonizing the area of a local one using the same parameters and conditions than the ones used by Currat et al. (2008*b*), that is, with hybridization and interspecific competition between the species. The seven scenarios differ by the carrying capacities (K) and the number of migrants (K_m) sent to neighbour demes at each generation (Table 7.3). Interspecific competition coefficient (α_{ij}) was not fixed, it was assumed to be density-dependent ($\frac{N'_j}{N'_i+N'_j}$) (Currat and Excoffier, 2004). The area represents a theoretical world of 10,000 demes, in which both species are being interacting during 1,500 generations (see main text for further details about the method). In the scenarios we examined, the invasive species progressively replace the local one because it is more competitive for environmental resources and has a higher carrying capacity (Fig. 7.7). Even if the local species reaches extinction at the end of the simulation, its genes are still found in the invasive genome if enough interbreeding is not prevented. More than

Table 7.3. Parameter values for the 7 scenarios of an invasive species in range expansion in an area occupied by a local species with interspecific competition. These scenarios are identical to those in Currat et al. (2008b). K is the carrying capacity and K_m the number of emigrants sent to neighbour demes when carrying capacity is reached. The intrinsic growth rate (r) is fixed to 0.5 in all scenarios.

Scenario	Local species		Invasive species	
	K	K_m	K	K_m
C1	50	1	500	10
C2	50	1	5000	100
C3	500	10	5000	100
C4	50	10	500	100
C5	50	10	5000	1000
C6	50	1	100	10
C7	500	10	1000	100

80% of local genes compose the genome of the invasive species when interbreeding success rate γ is higher than 15%. The number of local genes found in the invasive species is negatively correlated with the density of the invasive (compare scenarios C2 and C4 vs C6 and C7). In other words, the higher the invasive population density, the lower the amount of introgressed local genes in the invasive population. The level of introgression is also negatively correlated with the number of migrants sent to neighbouring demes, even if the density of the invasive is much higher than the local species (see scenario C1 and C3 vs C5) as reported by Petit and Excoffier (2009). These observed trends are consistent across all three models of spatial dispersal but a lower interbreeding success rate (γ) is needed in the positive model (Fig. 7.7A) to show equivalent results as in the random model of dispersal (Fig. 7.7B). To the contrary, a higher interbreeding success rate (γ) is required in the negative model of dispersal (Fig. 7.7C) to display similar introgression levels than in the random models of dispersal. The resulting differences on introgression levels between the density-independent (random) and the density-dependent models of spatial dispersal (positive and negative) are therefore equivalent to the ones obtained without competition, presented in the main text (Fig. 7.3).

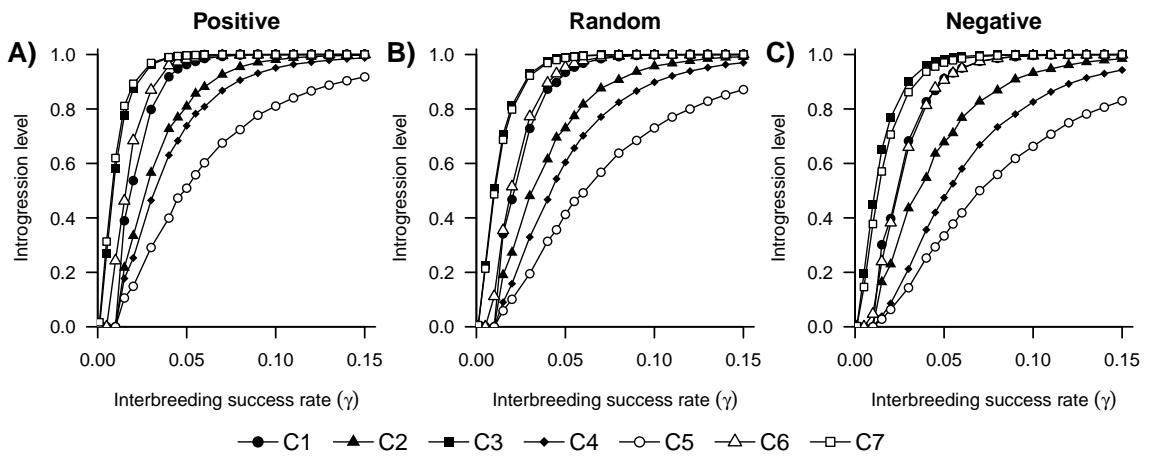


Figure 7.7. Effect of interbreeding success rate on the proportion of introgressed genes in a theoretical invasive species taken from the square world described in Fig. 7.2 of the main text. There is interspecific competition between both species. Different models of spatial dispersal are presented: A) Positive (density-dependent), B) random (density-independent), C) Negative (density-dependent). At the onset of the invasive expansion, the local species occupied the whole area and then interact with the invasive during 1,500 years. Introgression values are average over 10,000 stochastic simulations.

Table 7.4. Maximum value of likelihood and estimated interbreeding success rate for the three model of spatial dispersal applied to different genetic markers. The ΔAIC compare the most likely model in explaining the introgression between European wildcat and domestic cats.

Marker	Model	ΔAIC	Maximum likelihood	Interbreeding success rate (γ)
Autosomal	Negative	-	0.78 (0.76-0.80)	0.042 (0.038-0.046)
	Random	0.04	0.77 (0.75-0.78)	0.047 (0.043-0.052)
	Positive	0.35	0.66 (0.64-0.67)	0.054 (0.049-0.059)
mtDNA	Negative	-	0.42 (0.40-0.44)	0.089 (0.081-0.096)
	Random	0.25	0.37 (0.35-0.39)	0.090 (0.082-0.099)
	Positive	0.55	0.32 (0.31-0.33)	0.073 (0.056-0.089)
Y-chr	Negative	-	0.37 (0.36-0.39)	0.052 (0.044-0.060)
	Random	0.62	0.27 (0.26-0.29)	0.051 (0.042-0.061)
	Positive	3.50	0.06 (0.05-0.07)	0.056 (0.041-0.071)

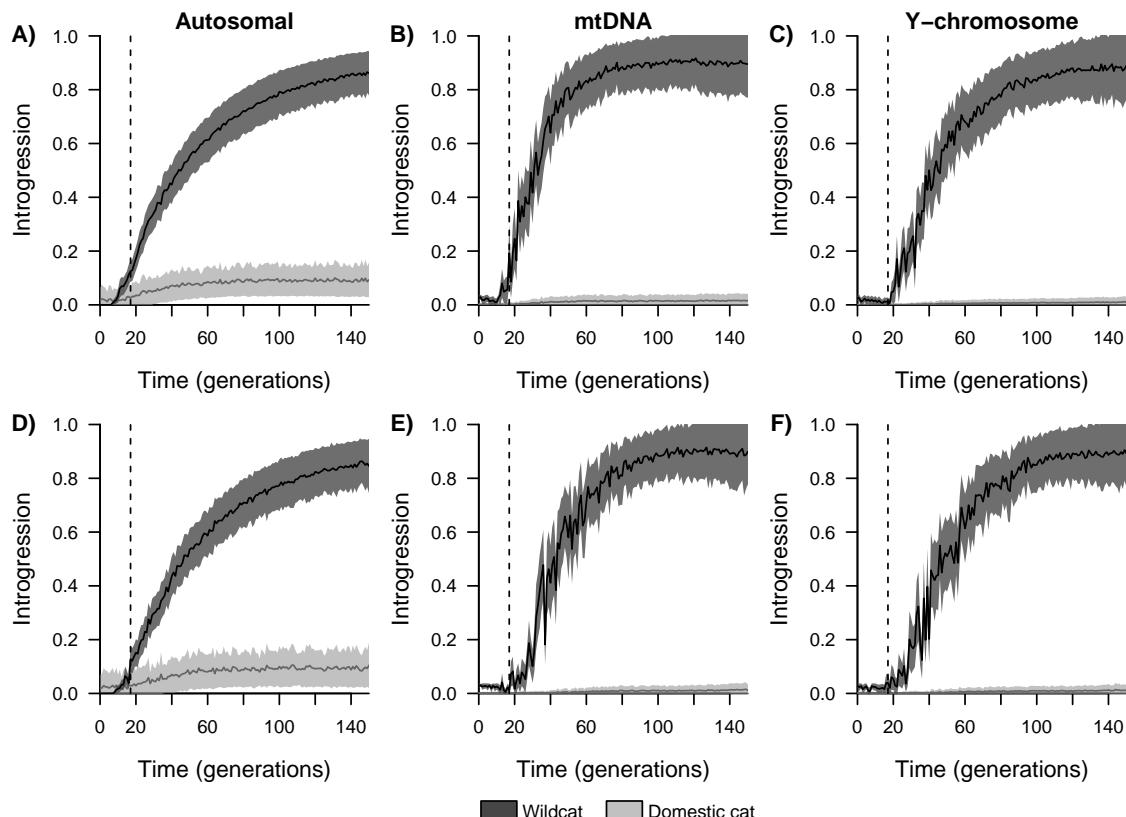


Figure 7.8. Projected introgression level through time between European wildcats and domestic cats. Values are presented by using the random (A, B and C) and positive (D, E, F) models of spatial dispersal (mean \pm SD). The vertical dotted lines denote present time. Values on the right side of the dotted line represent the projection for future generations. They follow current conditions of demographic parameters, selecting the most likely value of interbreeding success rate for each marker and model of spatial dispersal (see Table 7.4).

CHAPTER 8

General discussion

8.1 Types of hybridization

I defined three main types of hybridization that I used as a framework for the understanding of the ecological and evolutionary consequences of hybridization. On the one hand, they consist of hybridizations without gene flow between parental species, either because hybrids are inviable or infertile (Type 1) or because one parental genome is excluded during the gametogenesis of F_1 hybrids (Type 2). On the other hand, it characterizes interbreeding in which homologous chromosomes recognize themselves during meiosis, resulting in gene flow and consequent introgression between parental organisms (Type 3). The type 1 and type 2 are usually occurring when distantly related species hybridize, whereas type 3 is often observed in the reproduction between more closely-related taxa. The models of hybridization were based on this classification and were applied to very different case studies in order to draw a general picture of the effects of hybridization on biodiversity (Fig. 8.1).

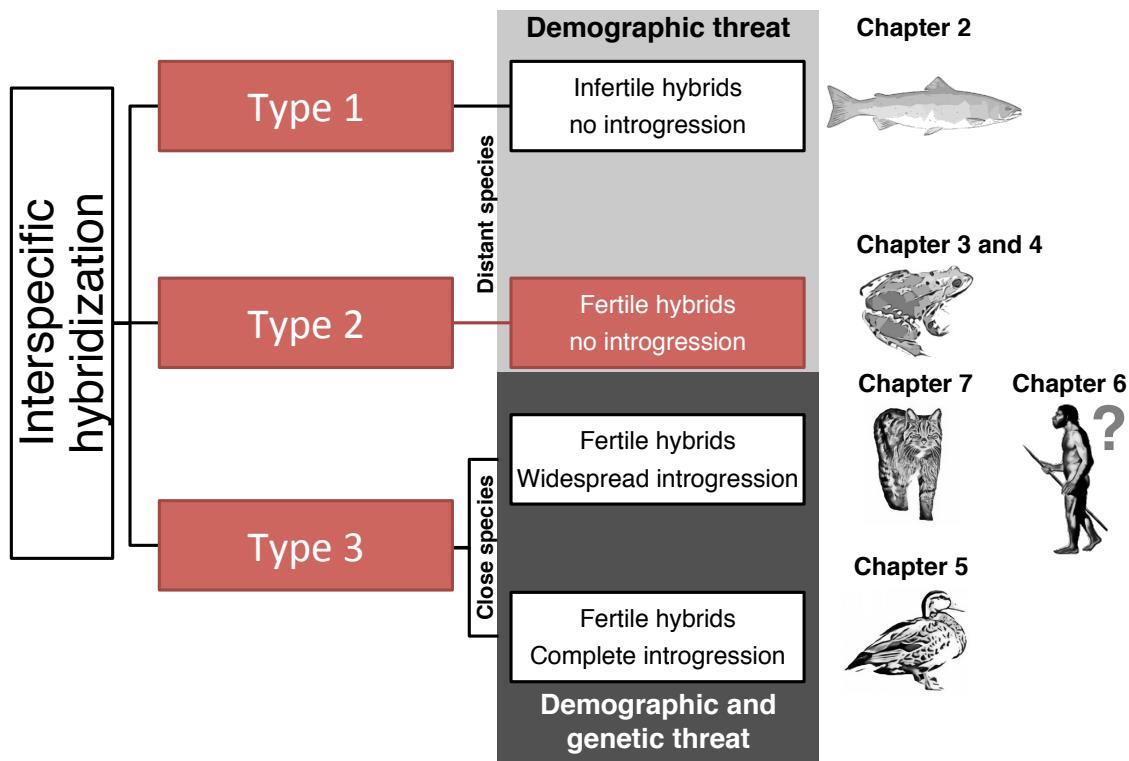


Figure 8.1. We identified three types of hybridization (red boxes), which were used as a framework to develop our modelling approaches. They were applied to real case studies within the different chapters of this thesis. A previous classification of human-induced hybridization to guide conservation actions is shown in the white boxes (see Allendorf et al., 2001)

8.2 Modelling interspecific hybridization

The progressive enrichment of the modelling complexity presented along the different chapters of my PhD thesis manuscript depicts the various types of hybridization and their consequences on biodiversity. I gave a particular emphasis on deciphering the situations leading to possible extinctions of native species when hybridization occurs with invasive species (Chapters 2, 3, 4, 5 and 7). I also investigated the influence of selection acting on alleles that can flow between interbreeding species (Chapter 5) and examined how neutral genes with hybrid ancestry may remain at high frequencies in a recipient species (Chapter 7), even when the other species is already extinct (Chapter 6). The results obtained by using the series of models developed during my PhD thesis exemplifies the large range of

biological issues that can be investigated, highlighting that these models form a valuable toolbox in ecology, conservation and evolution.

8.2.1 General model

The first model I developed was a mathematical description of the process of hybridization of type 1 and type 2, also referred to as distant hybridization. The resulting model was much more general in describing these types of hybridization than previous efforts, as they were aimed at analysing very specific cases (Graf, 1986; Rodriguez, 1996; Hellriegel and Reyer, 2000; Som et al., 2000; Som and Reyer, 2006). The previous models have illustrated the influence of assortative mating (e.g. Som et al., 2000) or the effect of density-dependent competition (e.g. Hellriegel and Reyer, 2000). To these two processes I added the critical effects of dominance/recessivity inheritance in hybrids (Chapters 2 and 3). This allowed me to study inherited traits affecting the fitness and the stability of a variety of hybrid systems. Later on, I additionally incorporated environmental stochasticity (Chapter 4), refining the model for further studies in aiming to explore the combined effects of hybridization and changing environmental conditions that are driven by climate change.

I then improved the model of distant species hybridization to include hybridization of type 3, i.e. with genetic introgression between parental species (Chapter 5). Previously proposed models have covered many aspects of this kind of hybridization (Huxel, 1999; Ferdy and Austerlitz, 2002; Tanaka, 2010; Baskett and Gomulkiewicz, 2011; Satake and Araki, 2012), but they either have ignored the effect of density-dependent competition (Ferdy and Austerlitz, 2002; Tanaka, 2010), or if considering it, they have focused on the effect of a single gene (Huxel, 1999; Baskett and Gomulkiewicz, 2011; Satake and Araki, 2012). The new model, presented in Chapter 5, is much more general than the models that were previously proposed, as it fully incorporates: density-dependent competition, assortative mating, dominance/recessivity inheritance and multiple gene simulations, in which it is possible to recognize quantitative and qualitative gene expression and the effect of neutral and selective mechanisms. I showed the importance of simulating multiple loci

instead of single genes in order to obtain accurate results. For instance, previous models focusing on a single gene may uncover correct general patterns (e.g. Huxel, 1999), but they may lead to seriously biased conclusions about the effects on biodiversity, namely when projecting the time to extinction with unknown number of involved genes. I also showed that the combined effects of demographic and genetic factors is critical to explain the abundance of hybrid phenotypes, where demographic conditions may counterbalance the effect of selection in single or additive alleles (Chapter 5). Modelling the effects of multiple genes, but ignoring the effect of density-dependence, may therefore fail in explaining the phenotypic or genotypic landscape resulting from hybridization between genetically distinct organisms (e.g. Ferdy and Austerlitz, 2002; Tanaka, 2010).

8.2.2 Simulation of spatial dynamics

Spatially explicit simulations have shown that after a successful invasion, introgression of neutral genes is expected to be higher in the invasive species than in the local species, and those genes may persist even if the local species is extinct (Currat et al., 2008b). This pattern was recently criticized due to potential inconsistencies in the hybridization model used to demonstrate it (Zhang, 2014). In Chapter 6, I collaborated to the development of a more realistic hybridization model to evaluate this criticism, proving that it is the interbreeding in the wave front of a range expansion that is determining this general expectation for neutral alleles and not asymmetry in the hybridization model. In Chapter 7, I revealed that this pattern persists, whatever the mode of spatial dispersal of the interacting species (attracted or repulsed by conspecifics), demonstrating the robustness and generality of this result.

I participated to the modification of the current version of the software SPLATCHE 2 (Ray et al., 2010), a tool to simulate genetic diversity and ecological interactions in a spatially explicit context (Currat et al., 2004). It resulted to the improvement of the hybridization model and the incorporation of two different modes of spatial dispersals. The new version is thus a more realistic approach for simulating the interbreeding between species (Chapter 6), and is much more adapted for the colonization and spread of invasive

organisms with territorial or more social behaviours (Chapter 7). I showed that density-dependent dispersal influences the colonization time and the resulting level of introgression between local and invasive taxa. The incorporation of these characteristics increases the likelihood of explaining the past evolution, but potentially also improves the power in projecting future scenarios (Chapter 7). There are other available tools to simulate genetic diversity in a spatially explicit context (e.g. Meirmans, 2011; Rebaudo et al., 2013; Delli-cour et al., 2014), but the improvement brought to the algorithm of SPLATCHE 2 makes it the only software which incorporates the behaviour of spatial dispersal, which is an es-sential property to explain the consequences of the expansion of invasive species on local biodiversity (Chapter 7). The importance of dispersal behaviour during range expansion has being stressed by purely ecological studies (e.g. Altwegg et al., 2013; Bocedi et al., 2014; Ponchon et al., 2015), being previously ignored in population genetics.

8.2.3 Complementary approaches

I investigated the effects of introgressive hybridization through two different kinds of model: first, a general model to study all hybridization types (Chapter 5) and second, through the use of spatially explicit simulations (Chapters 6 and 7). The first attempt allows the monitoring of multiple genes by exploring the combined effects of natural seเลction, neutral genes and demographic factors. I have developed this approach allowing the incorporation of many evolutionary parameters, being computationally quite demand-ing. The second approach is an improvement of an existing programme (SPLATCHE 2), which simulates spatial dynamics (population geographic location and migration) in a very computationally efficient way, but has less flexibility in terms of evolutionary factors that may be incorporated. For instance, it does not allow the recognition of specific genes under selection and is restricted to neutral processes. However, it incorporates spatial dynamics, a critical feature to assess the effect of invasive species that have experienced range expansion and that hybridize with local organisms. Further studies may use one of the approaches depending on the characteristics of the hybrid system. The first approach may be preferred when introgression is not related to the issue of interest or, when gene

flow is of interest but the main aim is to recognize particular alleles under selection or to examine the result of additive gene expressions. The second approach may be preferred when the spatial dynamics is an important process to be incorporated and selection is not a main focus.

Both approaches allow the examination of general questions about hybridization and biodiversity, but they are restricted by the availability or the acquisition of enough information to provide a good estimation of the parameter values, which is often a difficult task. However, the increasing advances in molecular tools allowing the analysis of large quantities of genetic data (e.g. Sanchez-Mazas et al., 2012; Chen et al., 2016), the development of new approaches to estimate demographic parameters from abundance time-series (e.g. Simmonds and Coulson, 2015), and the novel computational tools to solve numerical problems (e.g. Chopard et al., 2014) may reduce this limitation in the near future.

8.3 Demographic effects (Type 1 and Type 2)

The first type of hybridization does not result in introgression, because offspring are inviable or infertile, being sometimes considered as a minor risk related to introgressive hybridization (e.g. Gese et al., 2015). However, I showed in Chapter 2 that this type of hybridization represents an extinction risk when the loss of reproductive value enhances a demographic decline for one (or both) parental species. The reasons could be either because rare populations meet more abundant populations and therefore waste reproductive efforts, or because additional threats are cumulated, such as a disease. I exemplified this through the case of the admixture between Atlantic salmon (*Salmo salar*) and brown trout (*Salmo trutta*), for which I showed that hybridization alone is not a threat for the persistence of these species, but it could lead to the extinction of some local populations of salmon that are already threatened by a parasitic disease. This type of hybridization does not produce new diversity because hybrids are infertile, but it may cause the extinction of some taxa.

The second type of hybridization results in fertile hybrids but the introgression is prevented because their offspring are clonal or hemiclonal, transmitting the genome of a sin-

gle parental species. I showed that the effect of this kind of hybridization on biodiversity is potentially much more important than previously thought. In Chapter 3 and Chapter 4, I showed that the extinction of native species and the invasion of exotic organisms might be reached in very few generations. This was illustrated by a case study between Western European water frogs, for which the invasive species has already colonized and completely replaced native frogs since their introduction around 60 years ago (Vorburger and Reyer, 2003; Holsbeek and Jooris, 2010; Quilodrán et al., 2015). I highlighted that by having a result that emulates the result of hybridization type 1 (i.e. only displaying F_1 phenotypes), hybridization type 2 may represent an underappreciated way to very fast extinction (Chapter 4). We thus urge stakeholders of conservation programmes to include the examination of hybrid gametes when distant species hybridization is occurring and only F_1 phenotypes are detected. Because this type of hybridization is often observed between distant species (Yakovlev et al., 2000), which frequently have highly differentiated habitat requirement (e.g. Holenweg Peter et al., 2002; Armstrong et al., 2003; Hayden et al., 2011), I propose that habitat management would be the most effective action to avoid the extinction of native organisms, even more so when the interacting taxa are difficult to recognize by their morphology (e.g. Holsbeek and Jooris, 2010).

The first and second types of hybridization represent a demographic rather than a genetic threat of species loss. This is driven by wasted reproductive effort, either due to infertile hybrids, on the first type, or due to offspring that clonally transmit the non-indigenous genome, on the second type. Hybridization type 2 may additionally favour the production of a unique parental genome and facilitate a rapid replacement of one parental species through hybrid offspring (i.e. demographic flow). The extinction risk is determined by demographic swamping, in which the level of population growth rate of the threatened species is not enough for species persistence (Wolf et al., 2001).

Despite the fact that the first type may be considered as an evolutionary dead-end, because of the absence of gene flow between parental species (Allendorf et al., 2001), the second type may represent evolutionary opportunities by generating self-reproducing polyploidy forms (Christiansen and Reyer, 2009). For instance, in our example on Euro-

pean Water frogs (Chapter 3), *P. esculentus* is a hemiclonal hybrid that originated from the mating between *P. ridibundus* and *P. lessonae*, and was regenerated by hybridogenesis. Self-reproducing hybrids have been observed, in which the appearance of the triploid frog reproduces as the parental species and continues to reproduce in its absence (Som and Reyer, 2006; Christiansen et al., 2010). This demonstrates the potential of hybridization type 2 in generating self-sustaining populations and cryptic speciation. The speciation by polyploidy is rarely observed in animals but is frequently observed in plants (Liu, 2010; Ainouche and Wendel, 2014).

8.4 Demographic and genetic effects (Type 3)

The third type of hybridization defines the interbreeding with gene flow between parental organisms leading to genetic introgression, often occurring between more closely-related taxa (Chapters 5, 6 and 7). This type of hybridization may result in two different effects on biodiversity, either a genetic and demographic risk of species extinction (Todesco et al., 2016), or the opportunity of adaptation and evolution of novel diversity (Arnold and Martin, 2010). The development of new molecular tools has revealed numerous cases of species that are carrying genes of hybrid ancestry (e.g. Hailer et al., 2012; Li et al., 2016; Schumer et al., 2016), suggesting that the role in evolution of this type of hybridization has been much more important than previously thought (Mallet, 2007), even for our own evolutionary history (Huerta-Sánchez et al., 2014; Kuhlwilm et al., 2016; Simonti et al., 2016).

I showed that the new genetic architectures produce a landscape of possible phenotypes that are explained by both genetic (e.g. dominance/recessivity inheritance, selection) and ecologic factors (e.g. carrying capacities, competition) (Chapter 5). The illustration of the complementary effect of population genetics and population dynamics is important because both fields have largely evolved independently (Hall and Ayres, 2009), demonstrating here the importance of considering their joint influences. I also showed that these hybrids may replace native species in a few generations, facilitating biological invasions (e.g. Guay et al., 2014). The main threats of species loss are therefore driven by

two different but potentially complementary mechanisms: genetic swamping, in which one species is replaced by hybrids (Todesco et al., 2016), and demographic swamping, in which maladaptive hybrids reduce the population growth and precipitate the extinction (Wolf et al., 2001).

8.5 Assiguation to a type of hybridization

These three types of hybridization constitute a useful guideline for the understanding of the genetics and/or demographics effects of hybridization on biodiversity. However, to determine one of these types in a specific real system is not always an easy task to achieve, especially when it regards the past evolution of already extinct organisms or when it regards the projection of long-term effects. For instance, we considered hybridization between *Homo Neanderthalensis* and *Homo sapiens* of type 3, in order to explain the estimated level of introgression of Neanderthal ancestry into modern humans (2-3%, Chapter 6). In this case, an extremely rare interbreeding rate is sufficient to explain the reported level of observed introgression (Currat and Excoffier, 2011). This corresponds to between 200 and 300 admixture events over their whole cohabitation zone and time, during more than 10,000 years in Europe and Asia (see Annex). However, the hybrids were probably mostly infertile, as suggested by the low level of nuclear introgression in modern humans (Green et al., 2010; Reich et al., 2010; Wall et al., 2013), the absence of shared mitochondrial DNA (Mason and Short, 2011) and a highly differentiated Y-chromosome that support at least male offspring sterility (Mendez et al., 2016). If the resulting offspring were mostly infertile, the current fraction of the genome introgressed may be the results of a very small introgression, probably originally found in females, which may have largely increased in frequency driven by the range expansion of modern humans, acting as an invasive species under the expectation of Currat et al. (2008b) and confirmed in chapters 6 and 7. Mostly infertile hybrids, but with very low introgression, are also observed in our example of hybridization Type 1, between Atlantic salmon and brown trout (Castillo et al., 2007). I neglected this introgression because I was interested in the short-term effect of hybridization producing extinction risk, but it would not be the case when projecting

evolutionary long-term effects, even more when concerning range expansions, in which case it would be considered and simulated as type 3.

8.6 Conservation priorities

8.6.1 Categories of Allendorf et al. (2001)

Allendorf et al. (2001) already proposed categories of hybridization that are widely used to prioritize conservation actions when hybridization is induced by anthropogenic factors (e.g. Winkler et al., 2011; Meraner et al., 2013). Those authors also considered three categories, but which are defined in a different way to our original classification (Fig. 8.1): i) sterile hybrids (no introgression), ii) widespread introgression and iii) complete admixture. Indeed, they ignore the effect of fertile hybrids without introgression (our hybridization type 2), which is, potentially, the category that may induce the faster extinction risk (Chapter 4). Additionally, the infertility of hybrids (our hybridization type 1) is often seen as a less problematic concern related to the other two types of hybridization (e.g. Gese et al., 2015). However, this is not necessarily true when hybridization type 1 interacts with demographic imbalance or competition between species or hybrids; or when additional threats are at play (Chapter 2). Importantly, Allendorf et al. (2001) considered the anthropogenic motivation as a *sine qua non* condition to distinguish the conservation issues of hybridization. I highlight here that interspecific hybridization, even when induced by humans, is potentially representing a source of genetic variation, potentially useful to rescue species that are affected by inbreeding depression and to increase the likelihood of potential adaptation to climate change. Recent studies have even proposed the use of assisted hybridization as a conservation tool for the rescue of species that are confronted by changing environmental conditions (Aitken and Whitlock, 2013; Gómez et al., 2015; Hamilton and Miller, 2016).

8.6.2 Novel conservation priorities

The classification of Allendorf et al. (2001) has been extremely useful during the past 15 years, but the wider understanding of the impact of hybridization on biodiversity that has been brought by more recent studies, allowed us to bring a novel view to the priorities for conservation (Fig. 2). Given our classification, the conservation priorities are also found in human-induced hybridization, but this is not the single cut-off to delimit them. Indeed, hybridization type 1, with infertile hybrids, and hybridization type 3, with fertile hybrids and introgression, should not represent a priority when they are not interacting and cumulating with other threats such as demographic decline or the disruption of ecological functions. I thus suggest that the resources and efforts to protect biodiversity may be redirected either to other conservation issues or other threatened organisms. Hybridization type 3 may even be used as a conservation tool to increase genetic diversity and opportunities of adaptation, but it has to be implemented carefully (Amos and Balmford, 2001; Kovach et al., 2016). The potential fitness loss and the detrimental ecological effects of hybridization have first to be evaluated, and this is often difficult to achieve (e.g. Ellington and Murray, 2015). I propose that phylogenetically closer taxa with similar ecological requirements may offer some guidelines for assisted hybridization as a tool in conservation (Fig. 8.2). In this case, where organisms are evolutionarily close and share similar ecologies, and when the local species is on brink of extinction, the hybrids may also represent a subject of protection for conservation programmes, even when hybridization is caused by anthropogenic factors.

Hybridization type 1 is a major conservation concern when interacting with demographic decline, either because two species with high density-imbalance interbreed or because it amplifies additional risks in populations that are already threatened (Chapter 2). Hybridization type 2 is always a threat that may disrupt ecological equilibriums in very few generations (Chapter 3). Actions of conservation have to be implemented in the short-term to avoid the extremely rapid extinction risk (Chapter 4). Hybridization type 3 is also a priority when affecting key ecological interactions, either because enhancing demographic decline (e.g. introgression of maladaptive alleles) or because it is changing

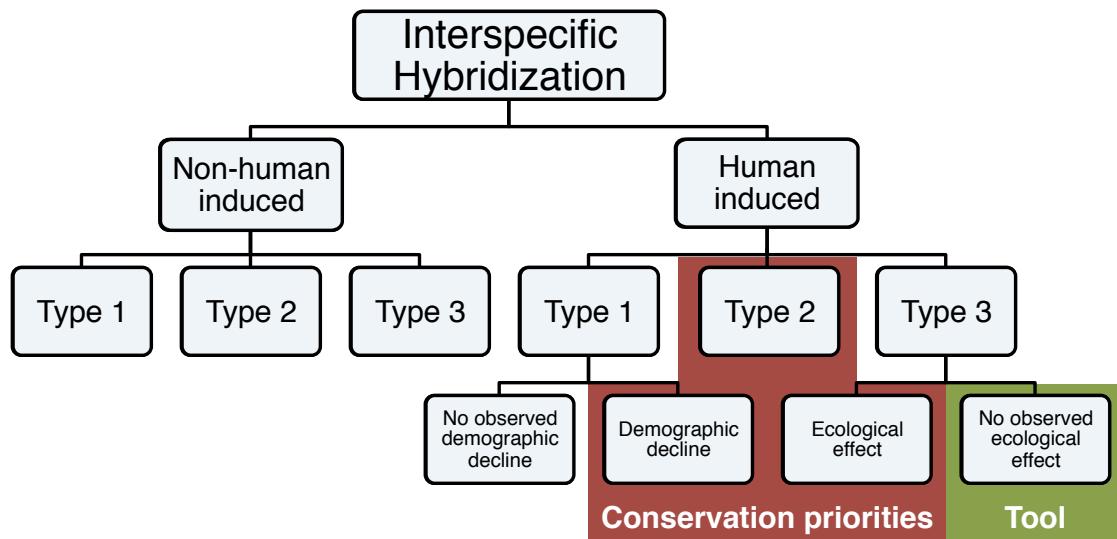


Figure 8.2. The three defined types of hybridization may be driven, or not driven, by human activities. Type 1 (inviable or infertile offspring, no introgression), type 2 (fertile offspring, no introgression), type 3 (fertile offspring, introgression). The conservation priorities to avoid biodiversity loss are colour highlighted in red and basically represent human-induced hybridization that produces demographic decline or ecological disequilibrium. A potential tool to increase genetic diversity is colour highlighted in green.

the behaviour of wild individuals (e.g. Chapter 5, Kidd et al., 2009; Ellington and Murray, 2015). All of these cases of hybridization may facilitate biological invasions and represent a risk of species loss (Fig. 8.2). The occurrences of these types of hybridization have grown enormously due to human activities, and the rate is expected to be higher in the near future due to climate change (Taylor et al., 2015; Todesco et al., 2016).

8.7 Breaking paradoxes

Hybridization that influences both the loss and the creation of new biodiversity may seem paradoxical at a first glance. The loss of native biodiversity is certainly an issue related to conservation biology when it is induced by anthropogenic factors under the conditions exposed in Fig. 8.2 and in the previous sub-chapter. However, hybridization type 3, and potentially also type 2, had influenced the evolution of several species of hybrid origins (e.g. Brumfield, 2010; Capblancq et al., 2015; Li et al., 2016), participating in the cre-

ation of novel biodiversity. This is therefore not a real paradox, but an intrinsic property of hybridization, which may drive the extinction of native species and at the same time stimulate the apparition of new species.

A potentially more problematic view arises under the light of the biological species concept, which does not make room for interspecific hybridization (Arnold and Martin, 2010). However, semipermeable barriers between genetically, morphologically or ecologically distinct organisms have motivated a large debate about species and hybridization (e.g. Rundle et al., 2001; Mallet, 2007, 2008; Behie and Oxenham, 2015). This discussion is not superfluous for conservation biology because it delimits the unit of protection (Fitzpatrick et al., 2015). This is a debate that is not only a matter for biologists, but also for scientists of very different domains, as well as politicians who define legal aspects of wildlife protection (Soulé, 1985). In this sense, Pasachnik et al. (2010) propose that whatever else a species is, in the field of conservation it should be a group of organisms deserving legal protection because its extinction would constitute a meaningful loss of biodiversity. The evolution of biodiversity represents a continuity, in which speciation processes may occur slowly or relatively fast, but where they will always be having a lapse in uncertainty (Gould, 1992). Conservation biology may therefore consider the level of uncertainty due to hybridization by protecting biodiversity as a dynamic system, which is not focused on reproductive isolation to delimit discrete units, but on the sum of features for which the loss of certain organisms may represent a detrimental effect on biodiversity.

8.8 Conclusions and perspectives

The models of hybridization that are developed in the different chapters of my PhD thesis represent, all together, an important toolbox to assess the extent of the consequences of hybridization on biodiversity. These models may be applied to evaluate extinction risk, but also at long-term timescales to generate theoretical evolutionary expectations. The general model of hybridization presented here may be used for a very large range of biological issues, from the reproduction between distantly- to closely-related taxa, incorporating important genetic and demographic properties, which were not fully incorporated

in previous models (e.g. Huxel, 1999; Ferdy and Austerlitz, 2002; Tanaka, 2010; Satake and Araki, 2012). I applied this model to polyploid (Chapter 2) and diploid organisms (Chapters 3, 4 and 5), but further studies may extent the analysis to haploid forms. In this sense, the hypergeometric phenotypic model (Doebeli, 1997), which I modified to study hybridization type 3 by incorporating interspecific mating and recognizing specific loci and genotypes of interest, is also available for haploid organisms (Doebeli, 1996) and may bring some light for further improvement of the general model. In chapter 5, I demonstrated the importance of simulating multiple loci when exploring the effects of hybridization on biodiversity. Because I showed that the time to reach frequencies in equilibrium and the deviation to Hardy-Weinberg equilibrium are stable when simulating three or more genes, three genes may therefore represent a minimum number of loci to assess the effect of hybridization with an unknown number of involved genes. The R scripts of our general model are easy adaptable to further theoretical questions or particular case studies and are freely available to the scientific community at URL: <http://genev.unige.ch/montoya-currat/scripts/>.

The improved version of the software SPLATCHE 2 also offers a more realistic and flexible tool than alternative programmes (e.g. Meirmans, 2011; Rebaudo et al., 2013; Dellicour et al., 2014) to study the effects of hybridization in a spatially-explicit context. It can be used in a variety of further studies that aim to assess the effects of spatial dynamic and genetic diversity when hybridization is at play, but is currently restricted to the simulation of neutral genes. Currat et al. (2015) recently proposed a program allowing the simulation of genetic lineage under selection, but do not incorporate hybridization. We may thus imagine joining in the future the genetic properties of our general model of hybridization to the spatially explicit approach, which may therefore represent an valuable new tool to investigate the effect of adaptive introgression in a spatial explicit context.

The three types of hybridization defined during this work constitute an important framework to understand the ecological and evolutionary consequences of hybridization. This allowed me to identify the situations in which those different types of hybridization may represent potential species loss and issues in conservation biology. The conservation

priorities established in Fig. 8.2 are not delimitated only by the human induced origin of hybridization, contrary to the original classification of Allendorf et al. (2001), but by the disruption of key ecological interactions driven by genetic and demographic factors. This highlight that hybridization, even when induced by anthropogenic factors, may also represent a subject of protection. It may eventually enhance the likelihood of adaptation to environmental changing conditions or to increase genetic diversity of taxa affected by inbreeding depression. This classification notably incorporates the effect of hybridization type 2, which was previously underappreciated, or even ignored (Allendorf et al., 2001). I propose that it should be considered as a potential highway to extinction, and thus deserves high priority in conservation programs. I believe that the conservation priorities emerging from my research represent a novel view to guide the development of programs aiming at protecting biodiversity, not as a fixed picture of wildlife, but as a dynamic evolutionary system.

CHAPTER 9

Annex

9.1 Simulations of human dispersal and genetic diversity

9.1.1 Project description

This project is a review of modelling approaches that are currently available for studying the dispersal of modern humans during their spread out of Africa. We list different programmes for simulating genetic diversity, with a special focus on spatially explicit simulations and on the new version of the software SPLATCHE (as modified in Chapter 6). We also performed new simulations, leading to the larger introgression levels of Neanderthal ancestry in modern populations of East Asia than in Europe, as recently observed by Wall et al. (2013). We confirm that a low interbreeding rate between modern humans and Neanderthals is sufficient to explain the current introgression level. We emphasize the flexibility of spatially explicit modelling approaches in order to take advantage of the very last scientific advances, offering a powerful framework for the study of evolution.

Author contributions CSQ performed all the simulations and participated in the design of the study, in the interpretation of the results and in the revision of the manuscript.

9.1.2 Introduction

Homo sapiens is a highly mobile species. From its likely place of origin in Africa, it colonized the entire planet in less than 50,000 years. This early colonization phase was constrained by geographic and environmental boundaries (coastlines, mountains, forests), but also by the presence of other archaic *Homo* species (Neanderthals, Denisovans, *H. erectus*), who were present in most of the old world (Veeramah and Hammer, 2014). Given the fossil record, Africa and the Near-East have been occupied by anatomically modern humans (AMH) before Asia, Europe and the Americas (e.g. Henn et al., 2012). The most supported scenario for the origin of our own species is often termed "*Recent African Origin*" (RAO) and proposes an emergence of AMH in East Africa between 200 and 100 kya (Higham et al., 2010), followed by a rapid spread toward the rest of the world starting around 60 kya (Henn et al., 2012), which led to a full replacement of all archaic human forms. The initial version of RAO has recently been challenged by the sequencing of the Neanderthal and Denisovan genomes (Green et al., 2010; Reich et al., 2010; Prufer et al., 2014) and by statistical analyses of existing genomic data sets (Wall et al., 2013). These studies support the existence of a relatively low genetic contribution of archaic forms in current non-African humans, which probably arose through hybridization after the exit out of Africa. These new analyses changed the old RAO paradigm to a scenario one could call "*RAO with hybridization*" (Stringer, 2014). However, very little is known on the exact extant of the interactions between AMH and Neanderthals (NE) and even less with other archaic populations.

Despite this general RAO scenario, many unknowns still exist on the migration routes followed by our ancestors. The exact dates of colonization of many regions of the world are also uncertain simply because old fossils are rare or absent in many regions, even though such an absence is not a proof that these regions have not been colonized by early humans. Consequently, several alternative hypotheses have been proposed to explain the colonization of different regions of the world (Veeramah and Hammer, 2014). For instance, at least three main possible routes of migration have been proposed to explain the diffusion of AMH from Africa to East Asia and Oceania: a coastal "*southern route*"

along the coast of the Pacific Ocean (Macaulay et al., 2005); a second more continental route in the south of Himalaya (Rasmussen et al., 2011), and another migration route North of the Himalaya (Di and Sanchez-Mazas, 2011).

The dispersal of AMH out of Africa has been probably triggered by a combination of various factors such as new abilities or opportunities (due technological advances or cultural changes), climatic variation and demographic pressure (Powell et al., 2009; Eriksson et al., 2013; Lahr and Foley, 1998). In any case, this initial global dispersal has been followed by many additional migrations, at various times and geographic scales. Climate variation played an important role in promoting those migrations through several mechanisms: first, the sea level was about 120 m below the current level during cold periods, which created many land bridges between continents and previously isolated islands (e.g. British Isles, New Guinea, Beringia); second, glaciers and ice caps extended over much larger areas during cold periods (Ray and Adams, 2001) making them uninhabitable; third, vegetation cover has also significantly changed with temperature variations, displacing towards refugia (Hewitt, 2000) most animals and plants that were food sources for humans (Banks et al., 2008b). In addition, at the beginning of the Holocene, most human populations have passed through a major economic and cultural transition in different parts of the world, switching from a hunter-gatherer to a food production lifestyle (Bellwood, 2001). This change corresponds to the appearance of plant and animal domestication, pottery, and of sedentary lifestyle and probably involved demographic increases and large-scale migrations (Zvelebil, 2001). Finally, sedentarized human populations continued to exchange migrants until present time and additional waves of migration took place around the world during the historical period, but probably at a smaller scale (Sokal, 1991).

Ongoing short range migrations have left traces in the genome of contemporary humans (Ray et al., 2005), which shows a strong concordance between geography and genetics in most parts of the world (e.g. Novembre et al., 2008). For these reasons, it seems necessary to take into account the spatial constraints on the dispersal of modern humans when they colonized the planet. However, it is still very difficult to consider these popula-

tion dynamics when analysing genomic data, as envisioned models quickly become very complex and are difficult to parameterize and test. Fortunately, modelling and computer simulations of complex evolutionary scenarios can be used to produce realistic models of human migration over time and space and to assess their impact on current genetic and genomic diversity. Thanks to a regular increase in computer power and to the development of efficient algorithms and realistic models, simulation approaches have become essential to study human evolution. In this review, we shall describe the main modelling approaches used to study the effect of human dispersal on genetic diversity at the global or continental scale, with a focus on spatially-explicit simulations. We shall also present and comment their major contributions to our understanding of human evolution and discuss future developments.

9.1.3 Modelling and simulating human dispersal

The modelling and simulation of evolutionary scenarios using computer programs consist of a combination of mathematical models defined by a series of parameters. Typically, three different approaches have been used to simulate human dispersal in a geographic landscape: forward diffusion models, forward individual based simulations, and forward demographic coupled with backward genetic simulations. Diffusion approaches are based on a set of spatially explicit differential equations specifying density and diffusion (migration) parameters in a continuous space. They are extensions of Fisher's approach to model the wave of advance of advantageous genes in one dimension (Fisher, 1937). Fisher's models have since been extended to model the colonisation of different continents in two dimensions (e.g. Steele et al., 1998; Fort et al., 2004; Martino et al., 2007; Fort and Pujol, 2008) or to the spread of cultures or technologies in already settled habitats (Fort and Méndez, 1999; Ackland et al., 2007). These diffusion models have also been refined to take into account the heterogeneity of the habitat (see Steele, 2009, for a review). Note that these models can mainly predict colonization times or the spread of beneficial variants in an already colonized habitat, and they have been coupled to the generation of genetic data only very recently (Barton et al., 2013*b,a*).

Individual-based or agent-based simulations are the most flexible way to simulate genetic data, as they allow one to simulate very specific behaviours, such as sex-specific reproductive success or migration, age-specific mortality or migration rates. They are usually performed in discrete demes positioned on a one-dimensional (e.g. Fix, 1997; Eswaran et al., 2002, 2005; Ramachandran et al., 2005) or two-dimensional lattice (Rendine et al., 1986; Barbujani et al., 1995; Deshpande et al., 2009; Itan et al., 2009; Rasteiro et al., 2012) corresponding to stepping-stone models, but they can be extended to 2D hexagonal demes (e.g. Eriksson and Manica, 2012) enabling a more realistic spatial diffusion process (Lavrentovich et al., 2013). Individual-based simulations also allow one to simulate loci under arbitrarily complex selection models (Fix, 1996; Itan et al., 2009; Currat et al., 2010; Peischl et al., 2013) fully or partially linked with neutral loci (e.g. Chadeau-Hyam et al., 2008). However, this complexity has a cost in terms of computing power and time, implying that a small number of individuals and populations can be modelled, even though the rescaling of mutation, migration rates and selection coefficients can allow one to model large populations with a smaller number of individuals (e.g. Chadeau-Hyam et al., 2008). Another drawback of forward approaches is that one needs to define starting conditions, or to wait that some demo-genetic equilibrium has been reached before starting recording the simulations. Nevertheless, these models have been applied to very interesting problems in human evolution, ranging from the spread of Neolithic farmers into Europe and their interaction with local hunter-gatherers (Rendine et al., 1986; Barbujani et al., 1995; Rasteiro et al., 2012; Rasteiro and Chikhi, 2013), the expansion out of Africa, either with (Eswaran et al., 2002, 2005) or without (Ramachandran et al., 2005; Deshpande et al., 2009) hybridization, or to the estimation of the geographical origin of beneficial mutations in European populations (Itan et al., 2009).

Despite their great flexibility, forward individual-based simulations can sometimes be very slow and require a lot of memory, since they simulate all the individuals of many populations. A way to solve these problems is to use forward simulations to simulate the demography of the populations, and then coalescent approaches to simulate their genetic diversity. These approaches have typically been implemented in the SPLATCHE soft-

ware (see Currat et al., 2004; Ray et al., 2010, and details below) or in simpler 1 D serial founder effect models (DeGiorgio et al., 2011), and a similar approach has been used to simulate genetic data linked to a site under selection (Ewing and Hermisson, 2010). One usage of these modelling approaches is to generate genetic data for various alternative hypotheses (therefore various combinations of values assigned to the parameters), in order to evaluate which is the scenario most (or less) compatible with the observed genetic data and thus to perform model choice. They can also be used to describe and study evolutionary processes and to estimate demographic or genetic parameters. In the latter case, simulations can be coupled with Bayesian inference procedures such as the approximate Bayesian computation (Beaumont et al., 2002; Wegmann et al., 2010) to estimate demographic parameters under various evolutionary scenarios.

9.1.4 Realistic simulation with spatially-explicit simulations

Here we focus on spatially-explicit simulation of human dispersal and their genetic diversity. By spatially-explicit, we mean that the simulation of populations or individuals takes into account their geographic position. The stepping-stone model (Kimura, 1953), which consists in an array of cells in one or two dimensions is the most commonly used spatially-explicit model. Here, the location of each population is defined by its coordinates and because migrants are only exchanged between neighbouring populations, the effective amount of gene flow between two populations is inversely related to their distance on the grid. This leads to genetic isolation by distance (IBD) (Wright, 1943), a process that played an important role in human evolution (Morton, 1977, 1982), and which largely explains the correspondence between geography and genetic variation in extent human populations (e.g. Novembre et al., 2008). Note that very detailed geographic (e.g. continental contours) and environmental (e.g. mountains, deserts) information can be used in spatially-explicit simulations, which is facilitated by the use of geographic information system (GIS). Note that spatially explicit simulations can also be done by specifying an arbitrary migration matrix between all pairs of populations in a model, as implemented in programs like SIMCOAL and FASTSIMCOAL (Excoffier et al., 2000; Laval and Ex-

coffier, 2004; Excoffier and Foll, 2011) or in MS (Hudson, 2002). However, in this case the migration matrix can become huge and difficult to set up for models with complex geographic features, and therefore we will not discuss these programs below. In Table 9.1, we give a list of other spatially-explicit simulation models and programs that have been used or could potentially be used in the context of human dispersal. Since their exact implementation varies from one model to the other, we redirect the readers to the original papers to get details about their underlying methodology. However, we illustrate below the implementation of the main key elements of a spatially-explicit simulation framework through the program SPLATCHE that we have developed.

9.1.5 SPLATCHE: an example of spatially-explicit simulation program

The program SPLATCHE is able to translate environmental information into genetic diversity (Currat et al., 2004; Ray et al., 2010). The simulations are done in two phases: during the first forward part, the demography and dispersal of a species can be simulated from one or several origins, taking into account environmental information. In a second phase, the molecular genetic diversity of one or several samples drawn from the population simulated during the first phase can be generated.

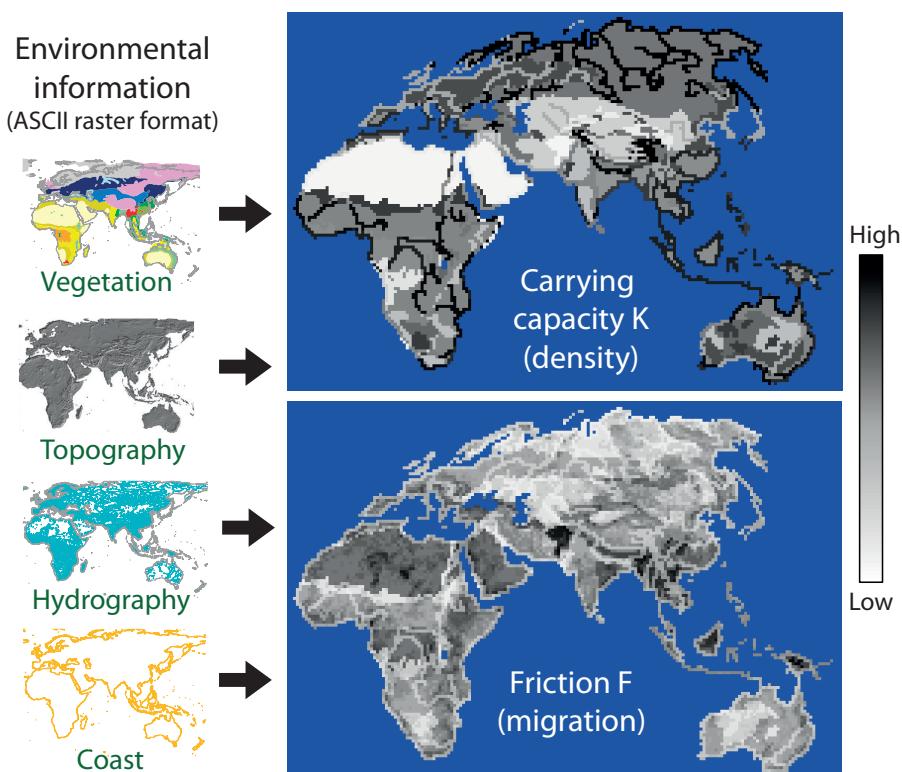


Figure 9.1. Schematic representation of the incorporation of environmental information in SPLATCHE. The influence of various environmental factors, such as vegetation, hydrography, topography and coastlines, are translated into two demographic parameters: carrying capacity K which affects population densities; Friction F which affects migration.

Table 9.1. List of spatially-explicit computer programs (white lines) and studies (greyed lines) where human dispersal and genetic diversity can or have been modelled, respectively. If the program is available online, the URL is given, as well as the Operating System (W/M/L for Windows/Mac OSX/Linux) on which the program runs.

Program name (if available) and short model description	Related references	Available version	Dimension	OS (language)
EASYPOL: Individual based computer program for population genetics simulations. http://www.unil.ch/dee/en/home/menuninst/software-dataset/software/easypop.html	Balloux (2001)	Ver. 2.0.1 2006	2D	W/M (C)
SPLATCHE: Simulation of demography and resulting molecular diversity for a wide range of evolutionary scenarios, taking into account environmental heterogeneity. Coalescent. http://www.splatche.com	Currat et al. (2004) Ray et al. (2010)	Ver. 2.01 2012	2D	M/L (C++)
NEMO: A stochastic, individual based, genetically explicit and stochastic simulation program designed to study the evolution of life history/phenotypic traits and population genetics. http://nemo2.sourceforge.net/ .	Guillaume and Rougemont (2006)	Ver. 2.2.0 2011	2D	W/M/L (C++)
QUANTINEMO: An individual-based program for the analysis of quantitative traits with explicit genetic architecture potentially under selection in a structured population. http://www2.unil.ch/popgen/softwares/quatinemo/	Neuenschwander et al. (2008)	Ver. 1.0.4 2011	2D	W/M/L (C++)
CDPOP: Individual based spatially-explicit simulator of gene-flow in complex landscapes. http://cel.dbs.umt.edu/cms/index.php/software/cdpop	Landguth and Cushman (2010)	Ver 1.2 2014	2D	W/M/L (Python)

GINKGO: Agent-based forward-time simulation to produce gene genealogies for multiple populations in a spatially-explicit and environmentally-heterogeneous framework. http://phylo.bio.ku.edu/ginkgo/index.html	Sukumaran and Holder (2011)	Ver. 3.9.0 2010	2D	W/M/L (C++)
MARLIN: Program to create, run, analyse, and visualize spatially explicit population genetic simulations. http://www.bentleydrummer.nl/software/software/Marlin.html .	Meirmans (2011)	Ver. 1.0 2009	2D	M (C)
DIM SUM: Stand-alone Java program for the simulation of population demography and individual migration, recording ancestor-descendant relationships. http://code.google.com/p/bio-dimsum	Brown et al. (2011)	Ver. 0.91 2010	2D	W/M/L (Java)
SIMADAPT: Spatially explicit, individual-based, landscape-genetic simulation model to represent evolutionary processes and population dynamics in changing landscapes. http://www.openabm.org/model/3137/version/8/view	Rebaudo et al. (2013)	Ver. 8 2013	2D	W/M/L (NetLogo)
PHYLOGEOSIM: Simulation of DNA sequences under a model of coalescence on a 2-dimensional grid of populations. http://ebe.ulb.ac.be/ebe/PhyloGeoSim.html	Dellicour et al. (In prep)	Ver. 1.0 (in prep)	2D	W/M/L (Java)
Simulation of the demic diffusion model of human expansion. Based on the model of the wave of advance of advantageous genes Fisher (1937)	Sgaramella-Zonta and Cavalli-Sforza (1973) Cavalli-Sforza and Hewlett (1982) Rendine et al. (1986) Edmonds et al. (2004) Ramachandran et al. (2005)	-	2D	-
Simulation of microevolution in European populations, incorporating genetic drift and gene flow (isolation by distance).	Barbujani et al. (1995)	-	2D	-

Analytical dynamic colonization population-genetics model in a one-dimensional habitat, based on model published in Austerlitz et al. (1997).	Liu et al. (2006)	-	1D	-
Serial founder effect model. Expansion in one-dimensional array of populations, each with the same carrying capacity.	Deshpande et al. (2009)	-	1D	-
Flexible computer simulation model to explore the spread of lactase persistence, dairy-ing, other subsistence practices and unlinked genetic markers in Europe and western Asia's geographic space.	Itan et al. (2009)	-	2D	-
SELECTOR: Forward simulation program to study diploid individuals within a spatially explicit framework. Simulation of allele frequencies at neutral or selected loci.	Currat et al. (2010)	-	2D	-
CISGeM: Climate Informed Spatial Genetic Models. Spatially explicit stepping-stone model divided into hexagonal cells.	Eriksson and Manica (2012) Eriksson et al. (2013)	-	2D	-
SINS: Forward simulation of individuals through time and space.	Rasteiro et al. (submitted)	-	2D	-

Spatial structure: A digital map in ASCII raster format is used for the spatial specifications of the simulations. It represents the geographical contour of the region of interest with a geographic projection adapted to the representation of surfaces (Ray, 2003). Additional information, such as vegetation cover, terrain, sea coast or rivers may also be incorporated in the program using the same file format. The map is divided in geographic cells that are characterized by their coordinates and possibly by environmental characteristics. The dimension of the cell (usually identical for all cells) can be of arbitrary size and represent a real geographic distribution. For studying human dispersal, cells of 50x50 km^2 (e.g. Currat and Excoffier, 2005) or 100x100 km^2 are usually used (e.g. Currat and Excoffier, 2011) depending on the desired resolution and on the computational constraints (more cells implies more computing time). Sizes of this magnitude seem to be adequate to represent subpopulations of hunter-gatherers (Cavalli-Sforza and Hewlett, 1982; Hewlett et al., 1982; Gronenborn, 1999; Anderson and Gillam, 2000). The environmental characteristics of each cell (vegetation, altitude, coastal area, river, etc.) may be directly used to compute two demographic variables, the carrying capacity K and the friction rate F (Fig. 9.1). It is possible to take into account the uncertainty of these parameters by performing multiple simulations with different parameter values and by doing sensitivity analyses (Ray et al., 2008). Each cell contains one deme, which represents a sub-unit of the whole population (or species) under study, or alternatively, two demes representing two interacting species or populations (see Box 9.1.7 and Fig. 9.2 for details).

Time: a single simulation consists in recording the density of all demes and the number of migrants exchanged between demes during a fixed number of generations (parameter t).

Dispersal and migration: a migration probability (parameter m) for individual genes to move between (neighbouring) demes. This probability is constant in SPLATCHE but can be different during the dispersion phase and at demographic equilibrium in other programs (e.g. Deshpande et al., 2009; Eriksson et al., 2013). This basic migration scheme may be altered in different ways:

- By using friction values (parameter F), which represent the difficulty of crossing

a cell depending on its specific environmental characteristics. Higher F values assigned to a given cell generally imply less migrants entering it (Ray et al., 2008). This parameter can be used for instance to favour movements along coastlines or rivers, or to the opposite, to use rivers, hills, deserts or mountains as barriers to gene flow.

- By allowing for long-distance dispersals (Ray et al., 2010), occurring at a given rate (parameter λ) and at various distances (parameter d).
- By directing migration specifically into a given direction (Arenas et al., 2012), e.g. towards the South during glaciation or to the North during a post-glacial colonization.

Demographic dynamics: deme density is usually logically regulated, reflecting intra-deme competition for resources. The increase in density is controlled by the growth rate (parameter r) and the maximum number of individuals that may be sustained by the cell (the carrying capacity, parameter K). This last parameter may reflect the influence of the environment (e.g. different vegetation types leading to different K) or the type of culture or economy (e.g. food production versus hunter-gathering techniques). Heterogeneous environments can also be considered in the dispersion model (Wegmann et al., 2006).

Generation of genetic data: SPLATCHE is using a coalescent approach (Kingman, 1982; Hudson, 1990) to reconstruct backward in time the genealogy of a series of sampled genes. For neutral loci, the virtual genetic diversity obtained at the end of a simulation is constrained by the demography of the simulated population and possibly by a mutation and recombination model that depends on the type of simulated genetic data (e.g. allele frequencies or molecular data).

The combination of the various elements described above allows one to construct and simulate realistic scenarios of human dispersal and testing those using genetic data. For instance, the genetic consequences of a range expansion (demographic increase linked to a geographical spread), bottleneck, population contraction to refuge area(s), interactions between populations (competition and admixture) or a combination of those processes, can be investigated using this general approach.

9.1.6 Main results and discussion

The simulation of human dispersal offers a powerful tool to study the evolution of our species, and it complements other methodological approaches. Most of the early models for the simulation of human dispersal have been developed in the context of the peopling history of Europe (Rendine et al., 1986; Barbujani et al., 1995; Currat and Excoffier, 2005; Arenas et al., 2013), but we focus here only on simulations of human dispersal at the global scale. The first realistic attempts (Ray et al., 2005; Liu et al., 2006) to simulate worldwide dispersal showed an excellent fit between the predictions of the models and real data, confirming that models explicitly incorporating demography and geography were powerful to make inferences on human peopling history. This has been recently confirmed by a recent study incorporating Pleistocene climatic variation (Eriksson et al., 2013), which showed that climatic change had a significant impact on human dispersal and the establishment of current genetic diversity.

Genes surfing the waves of expansion

An important result brought by the simulation of human dispersal was to explain the mechanisms by which genetic diversity progressively decreases with distance from Africa: a series of founder effects during the range expansion of human populations (Ramachandran et al., 2005; Deshpande et al., 2009). The same mechanism has also been proposed to explain clinal genetic patterns in Europe (Barbujani et al., 1995; Currat and Excoffier, 2005). The process of decreasing diversity along a colonization route was extensively described and demonstrated theoretically by a series of spatially-explicit simulations performed in a 2-dimensional stepping-stone (Deshpande et al., 2009). This effect results from a phenomenon called "*allele surfing*" (Edmonds et al., 2004; Klopstein et al., 2006), which describes how the frequency of a neutral allele can dramatically increase during a population expansion due to pure neutral demographic effects. Surfing is a stochastic process that only applies to a relatively small number of alleles from the source population or to new mutations appearing during the expansion, but it has important evolutionary consequences (Excoffier and Ray, 2008; Petit and Excoffier, 2009). Simulations have

shown that the frequency of surfing varies depending on the demographic parameters of the population (Klopfenstein et al., 2006). The probability of surfing increases with the growth rate (parameter r) while it inversely decreases with the carrying capacity (K) and the migration rate (m). This gene surfing process has been identified theoretically by spatially-explicit simulations before being confirmed by empirical studies, both in yeasts and bacteria (Hallatschek et al., 2007) and by a survey of the recent human colonization of the Saguenay Lac Saint-Jean in Quebec (Moreau et al., 2011). This finding shows that neutral evolutionary processes can produce patterns identical to those expected under the action of positive selection (i.e. an allele present at very high frequency in the final population). It thus challenged the view that large differences between populations such as those observed at some loci between Africans and non-Africans were due to ongoing selection (Currat et al., 2006).

Hybridization during expansion

On their road out of Africa, AMH met various archaic human forms, such as Neanderthals (NE), Denisovans (DE) and probably others (Prufer et al., 2014). Very little is known about the exact nature of the interactions between AMH and NE and virtually nothing with DE. Simulation is thus an inestimable tool to assess, in a spatially dynamic context, the effects on genetic diversity of at least two kinds of interactions: admixture and competition. The main interest of spatially-explicit simulation compared to previous mathematical models is that progressive admixture in time and space can be simulated between NE and AMH, instead of instantaneous merging of two panmictic populations (Nordborg, 1998; Serre et al., 2004).

Spatially-explicit simulations have shown that continuous interbreeding over space and time between NE and AMH during the spread out of Africa of the latter, may well explain the current patterns of genetic introgression. First, it has been shown that the absence of Neanderthal type of mitochondrial DNA in contemporary human population is compatible with an extremely low interbreeding success rate (parameter γ in Box 1) between AMH and Neanderthal (Currat and Excoffier, 2004). It was shown (Currat and

Excoffier, 2011) that less than 2% of interbreeding success rate (γ) is compatible with the observed presence of 2 to 3% of Neanderthal DNA in the genome of contemporary non-Africans (Green et al., 2010; Reich et al., 2010; Wall et al., 2013). Such a low level of introgression could be due to only about 200-300 successful hybridization events between NE and AMH over their whole cohabitation period (at least 10 Ky in Europe, even more in the Near-East) and over all their area of overlap. Recent new estimations using a more symmetrical hybridization model (Excoffier et al., 2014) and considering in the estimation procedure that NE introgression is higher in Asia than in Europe (Wall et al., 2013), has produced similar results with an estimate γ of less than 3% (Box 2). These results thus demonstrate that the reported pattern of NE introgression in extent modern Humans is compatible with a strong reproductive isolation between AMH and NE. In addition, spatially-explicit simulations suggest that the hybridization between AMH and NE occurred over a large geographic zone covering Western and Central Asia, and probably reaching southern Siberia. The analysis was not able to precisely delineate the Neanderthal occupation zone, but it suggested that it could be as big in Asia as in Europe at the time of the spread of AMH (Currat and Excoffier, 2011).

Limitations and Future developments

One sensitive point of any modelling approach is the choice of the parameter values, which may be difficult for some parameters. For instance, demographic parameters for prehistoric populations (densities, growth and migration rates) are often difficult to evaluate and the mutation rate for the studied loci might not be known precisely (Gibbons, 2012). To somehow circumvent this problem, a thorough examination of the literature is necessary to establish possible intervals of parameter values. For instance, density estimates may come from ethnographic comparisons (e.g. Pennington, 2001) or long-term estimation (Biraben, 1979), while growth and migration rates may be derived using estimates of colonization times in different continental areas (Currat and Excoffier, 2004, 2005; Ray et al., 2005; Currat and Excoffier, 2011). The simulation approach then allows an extensive exploration of the parameter space and the validation of plausible values.

Compared to deterministic mathematical models, computer simulations have the advantage of considering stochastic processes in the analyses, which could play an important role in the evolution of humans, as in the case of the gene surfing phenomenon described above. A benefit of the simulation approach is that models can be improved step by step by adding new elements and new information brought by scientific discoveries (Currat and Silva, 2013).

Another advantage of realistic simulations of human dispersal is their ability to integrate various sources of information, such as genetics, archaeology and environment. This feature could be very useful in the near future as new types of data are regularly produced. For instance, in the last decades, it has been increasingly possible to extract DNA from fossil remains and this technical advance has been widely used in the study of human evolution. Computer simulations should allow one to analyse the increasing number of genomic data retrieved from ancient specimens (Sanchez-Quinto et al., 2012; Skoglund et al., 2012, 2014), which should be especially powerful when combined with modern DNA. Moreover, computer simulations could be used to check if selection has favoured the introgression of some genes of archaic origin (Caspermeyer, 2014; Ding et al., 2013). Finally, computer simulation could be used to understand the relation between Denisovans, Southeast Asians and Oceanians (Reich et al., 2011), but the lack of spatial information about the exact ancestral Denisovan range makes it a challenging task.

9.1.7 Conclusion

Computer simulations are a powerful tool to study the effects of population dynamics on the genetic diversity of populations. It has been shown that properly considering the spatial dynamics of populations can drastically change the interpretation of empirical data. For instance, a spatial expansion does not show the same typical bell-shaped mitochondrial mismatch distribution than a pure demographic expansion in a panmictic population, but rather a multimodal mismatch distribution when migration rates between demes are small to moderate (Ray et al., 2003; Excoffier, 2004).

All in all, spatially-explicit simulations support a relatively simple scenario of global

human dispersal out of Africa with very rare interbreeding events with archaic humans over a large geographic range. They revealed that observed low levels of Neanderthal ancestry in Eurasians are compatible with a very low rate of interbreeding (<3%) and that those rare and distinct admixture events occurred also after the split of Europeans and Asians over a wide European and Asiatic range, well beyond the Middle-East. A spatially explicit model of population expansion with continuous but limited interbreeding explains most observed patterns of human genomic diversity, such as: i) a recent single origin (Stewart and Stringer, 2012), ii) decreasing genetic diversity from Africa (Prugnolle et al., 2005); iii) limited and relatively uniform Neanderthal introgression in Eurasia (Green et al., 2010), larger in East Asia than in Europe (Wall et al., 2013), iv) introgression asymmetry between NE and AMH (Green et al., 2010), v) lack of mitochondrial introgression (Serre et al., 2004; Reich et al., 2010), vi) introgression in areas where Neanderthal never existed (Green et al., 2010), vii) more than one hybridization event with archaic humans (Wall et al., 2013). Spatially-explicit simulation of human dispersal thus provides a simple but powerful framework for the interpretation of genomic data, with considerable room for improvements and extensions.

9.1.8 BOX 1 Simulation of interactions between two populations

The program SPLATCHE offers the possibility to study the interactions between two populations (e.g. hunter-gatherers and Neolithic farmers) or two species (e.g. NE and AMH) in a spatially-explicit framework (Ray et al., 2010). It simulates two demes per geographic cell, each of them representing one population (Fig. 9.2), and the simulated world can thus be seen as two superimposed layers of demes. SPLATCHE considers two kinds of interaction between interacting populations or species: competition and admixture (Fig. 9.2).

Competition is simulated using a classical Lotka-Volterra model (Lotka, 1932), which is an extension of the logistic regulation model. The density of one species is directly constrained by the density of the other one, assuming that both are in competition for local resources (e.g. habitat, food). Competition coefficients (α) are used to reflect the

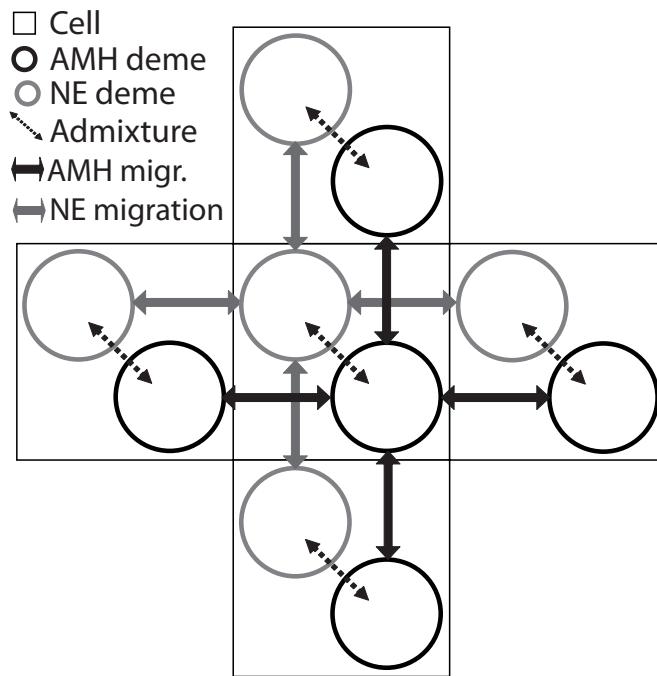


Figure 9.2. Schematic representation of a spatially-explicit modelling of two interacting populations. The whole area under study is divided into geographic cells, which each contain two demes representing two interacting populations (for example AMH and NE). Demes of the same population belonging to neighbouring cells can exchange migrants while admixture (gene flow) can occur between demes within the same cell.

intensity of this kind of interactions and can be different in the two populations, i.e. due to a competitive advantage of one over the other. The competition coefficients α can be fixed to a specific value, such as 1, which means that an individual of the rival population exerts as much competitive pressure as an individual belonging to the same population. Alternatively, α can be density dependent (Curran and Excoffier, 2005), i.e. computed as $\alpha_{ij} = N_j / (N_i + N_j)$, where α_{ij} represents the effect of competition of an individual of population j on an individual of population i and N_i and N_j are the densities of both populations in the cell. In that case, the strength of competition between both populations evolves over time and the most numerous one has a competitive edge over the less numerous one. Under this model, if the carrying capacities (K) between the two populations are sufficiently different, as it is assumed for AMH over NE (Curran and Excoffier, 2004, 2011), then the one with the lower K will eventually go extinct due to competition.

Admixture is simulated by local gene flow between the two demes belonging to the

same cell and it can be regulated by an interbreeding success rate (parameter γ). If γ is equal to 0 then there is no gene flow between the two populations. If γ is equal to 1, there is random mating between them. Lower values of γ imply the existence of barriers to gene flow between the two species, which can be either pre-zygotic (e.g. cultural avoidance, disassortative mating) or post-zygotic due to lower hybrid fitness or a combination of those various factors. In previous studies, we implemented a model of density-dependent gene flow between AMH and NE (Currat and Excoffier, 2004, 2011). A new admixture model has been recently implemented in SPLATCHE, which is fully symmetrical when both species are at demographic equilibrium and which is more accurate for the description of interspecific hybridization than the previous model (Excoffier et al., 2014). In this new model, each N'_i newborn individual in a population i has at least one parent belonging to population i . Then, assuming random mating the probability that the second parent originated from population j is simply computed as $N_j/(N_i + N_j)$, where N_i and N_j are the densities of both populations in the previous generation. Thus, the expected number of gene flow events (introgressions) from population j to i at each generation is defined as:

$$S_{ij} = \gamma N'_i \frac{N_j}{2(N_i + N_j)} \quad (9.1)$$

This new admixture model gives results qualitatively and quantitatively very similar to the previous one (Excoffier et al., 2014).

9.1.9 BOX 2 Estimation of hybridization between Neanderthals and AMH

In order to investigate hybridization between Neanderthals and AMH, we explored a series of scenarios of human dispersal out of Africa into Eurasia, with various demographic parameters, hybridization and competition zones and varying intensities of admixture. We redirect the readers to the original article for exact details on those alternative scenarios (Currat and Excoffier, 2011). In all examined scenarios, Neanderthals is assumed to be at demographic equilibrium in its entire range at the beginning of the simulation,

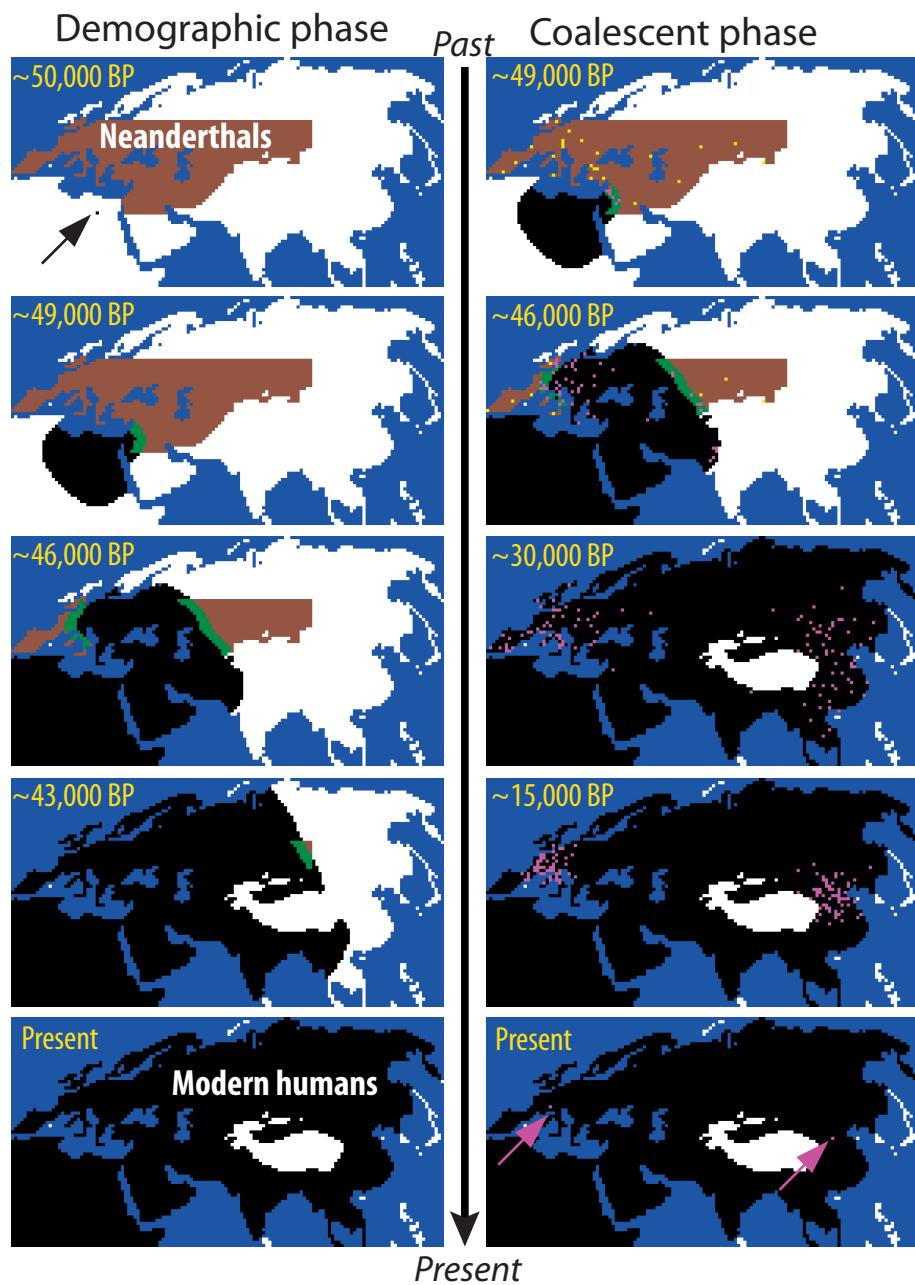


Figure 9.3. Example of the simulation of the dispersal of AMH out of Africa and the progressive disappearance of NE that inhabited an extended area in Eurasia. Black arrow represents the origin of AMH and pink arrows the current sampled locations. White represents empty cells, brown cells are occupied by NE only, black the cells are occupied by AMH only and green represents the zone where NE and AMH coexist. Left panel shows the demographic forward phase and right panel shows the coalescent backward phase. Pink and yellow dots on the right panel represent at any time the location of lineages ancestral to the AMH sampled genes in AMH and NE demes, respectively. The parameters used for the simulations are those of scenario A in Table 9.2.

while AMH is expanding demographically and spatially (Fig. 9.3). Various sizes of Neanderthal occupation zone where hybridization with AMH occurred were tested, ranging from the Middle-East only to a wider area extending to southern Siberia (Fig. 9.3). During the AMH expansion, admixture can occur and Neanderthals disappear due to competition with AMH. At the end of a simulation, the proportion of Neanderthal ancestry is measured in modern human genomes in Europe and in East Asia and compared to the reported levels of 2-3% (Reich et al., 2010). For each of the 13 envisioned scenarios, we performed 10,000 coalescent simulations and we computed the proportion of those simulations that were compatible with the observation. In our new study, a simulation was declared compatible if it resulted in 2-3% of Neanderthal ancestry in both Europe and East Asia and if Neanderthal introgression was slightly larger in East Asia than in Europe (as recently shown in Wall et al. (2013)). Figure 9.4 and Table 9.2 show the interbreeding rates obtained with this new series of simulations. They confirm previous results (Currat and Excoffier, 2011; Excoffier et al., 2014), as very few successful hybridization events ($\gamma < 3\%$) over a wide Eurasian range are sufficient to result in 2-3% of introgression in non-Africans. Such a low hybridization rate is sufficient to explain current Neanderthal introgression because the few Neanderthal genes that are incorporated continuously at the wave front of the AMH expansion tend to be amplified by the surfing phenomenon (Currat et al., 2008b). Indeed, a few introgression events occurring in an invading deme on the wave front can result in many more introgressed copies, because these introgressions usually occur when the invading deme is still growing and has not reached its carrying capacity. Second, AMH pioneers are recruited at the front of the expansion and consequently have a higher probability to propagate their genes (including recently introgressed Neanderthal genes) further away in the expanding population. Rare but continuous interbreeding events during the expansion of AMH over a large Neanderthal Eurasian range is thus a simple and efficient model to explain patterns of Neanderthal ancestry in current genomes.

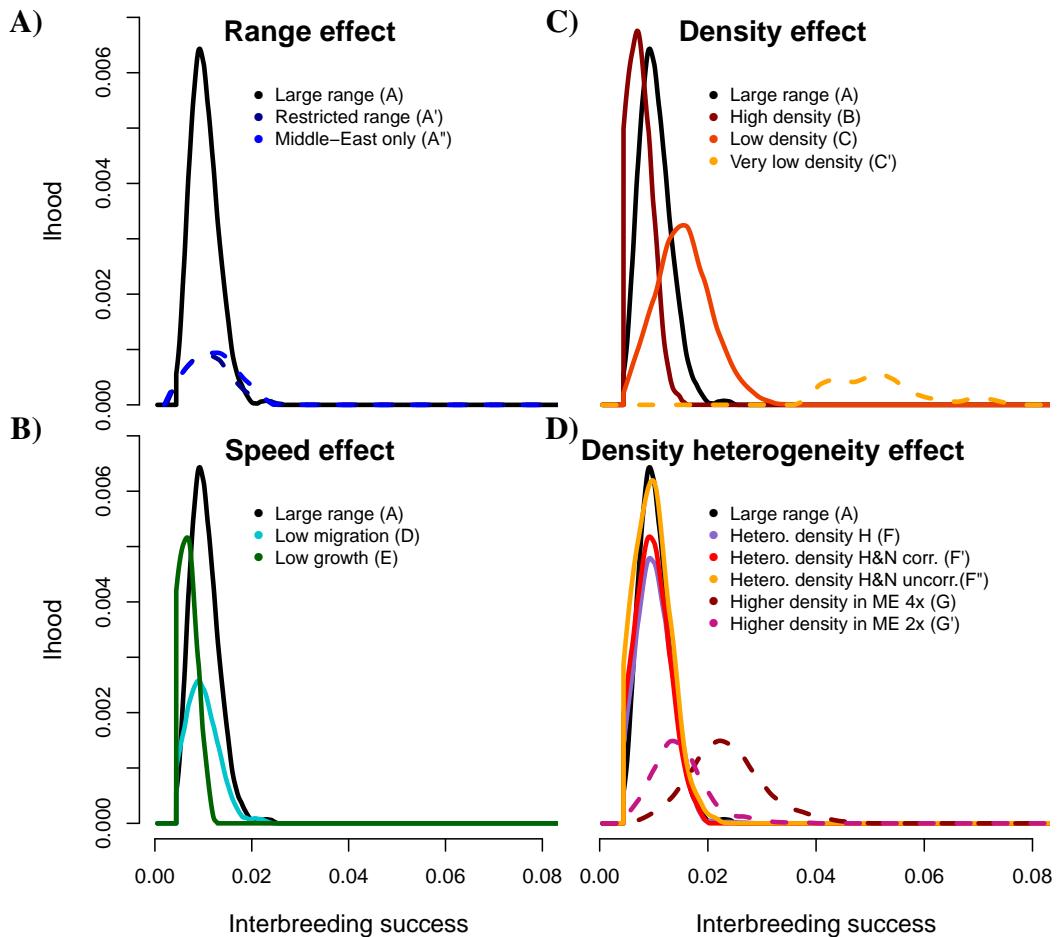


Figure 9.4. Distribution of the proportion of simulations (among 10,000) resulting in Neanderthal introgression levels higher in the Chinese sample but still compatible with observations (1.9–3.1% in both French and Chinese samples). Each likelihood curve corresponds to a different demographic scenario described in Table 9.2. Results were obtained by assuming a deme area of 100 x 100 km². Solid lines correspond to scenarios that are equally likely (within 2 AIC units from the scenario with the highest likelihood), whereas scenarios shown with a dotted line have an associated AIC more than 2 units larger, and thus cannot be considered as equally well supported by the data (details of the estimation procedure may be found in Currat and Excoffier (2011)).

Table 9.2. Demographic parameters, interbreeding rate estimates and relative probabilities of the simulated scenarios.

Models	K_N ¹	K_H ²	r ³	m_N ⁴	m_H ⁵	Colonization time ⁶	Estimated interbreeding success ⁷	Model A relative probability ^{7,8}
A. Large Neanderthal range	200	800	0.8	0.1	0.2	220	0.0093	[0.0049-0.0159]
A'. Restricted Neanderthal range	200	800	0.8	0.1	0.2	220	0.0105	[0.0031-0.0213]
A''. Hybridization in Middle-East only	200	800	0.8	0.1	0.2	180 ⁹	0.0126	[0.0027-0.0224]
B. Large K	400	1600	0.8	0.1	0.2	220	0.0070	[0.0044-0.0121]
C. Small K	100	400	0.8	0.1	0.2	220	0.0155	[0.0054-0.0259]
C'. Very small K	25	100	0.8	0.1	0.2	240	0.0519	[0.0380-0.0731]
D. Small m	200	800	0.8	0.05	0.1	290	0.0091	[0.0044-0.0163]
E. Small r	200	800	0.4	0.1	0.2	300	0.0066	[0.0044-0.0109]
F. Variable K_H	200	200-1600	0.8	0.1	0.2	220	0.0093	[0.0044-0.0169]
F'. Variable K_H and K_N (correlated)	50-400	200-1600	0.8	0.1	0.2	220	0.0093	[0.0044-0.0163]
F''. Variable K_H and K_N (uncorrelated)	50-400	200-1600	0.8	0.1	0.2	220	0.0098	[0.0044-0.0165]
G. K 4x higher in ME	200 (50)	800 (200)	0.8	0.1	0.2	220	0.0222	[0.0105-0.0369]
G'. K 2x higher in ME	200 (100)	800 (200)	0.8	0.1	0.2	220	0.0135	[0.0056-0.0229]

1. Neanderthal carrying capacity

2. Human carrying capacity

3. Intrinsic rate of growth

4. Migration rate between Neanderthal demes

5. Migration rate between human demes

6. Approximate time (in generations) for the colonization of Europe from the Middle-East estimated from the simulations. This statistic is determined by the growth and migration rates, and varies also slightly with the hybridization rate.

7. Maximum likelihood estimates of interbreeding success between humans and Neanderthals are reported with limits of a 95% CI within brackets.

8. Probability of scenario A relative to the other scenarios computed from weighted AIC's (see Material and Methods).

9. Hybridization occurs for about 80 generations in the Middle-East

CHAPTER 10

Literature Cited

- Abbott, R. J. 1992. Plant invasions, interspecific hybridization and the evolution of new plant taxa. *Trends in Ecology & Evolution* **7**:401–405.
- Ackland, G. J., M. Signitzer, K. Stratford, and M. H. Cohen. 2007. Cultural hitchhiking on the wave of advance of beneficial technologies. *Proceedings of the National Academy of Sciences* **104**:8714–8719.
- Aguillon, S. M., and R. A. Duckworth. 2015. Kin aggression and resource availability influence phenotype-dependent dispersal in a passerine bird. *Behavioral Ecology and Sociobiology* **69**:625–633.
- Ainouche, M. L., and J. F. Wendel, 2014. Polyploid speciation and genome evolution: Lessons from recent allopolyploids, Pages 87–113 . Springer.
- Aitken, S. N., and M. C. Whitlock. 2013. Assisted gene flow to facilitate local adaptation to climate change. *Annual Review of Ecology, Evolution, and Systematics* **44**:367.
- Akaike, H. 1974. A new look at the statistical model identification. *Automatic Control, IEEE Transactions on* **19**:716–723.

10. Literature Cited

- Allendorf, F. W., R. F. Leary, P. Spruell, and J. K. Wenburg. 2001. The problems with hybrids: setting conservation guidelines. *Trends in Ecology & Evolution* **16**:613–622.
- Altwegg, R., Y. C. Collingham, B. Erni, and B. Huntley. 2013. Density-dependent dispersal and the speed of range expansions. *Diversity and Distributions* **19**:60–68.
- Alvarez, D., and E. Garcia-Vazquez. 2011. Maintenance of asymmetric hybridization between Atlantic salmon (*Salmo salar*) and brown trout (*Salmo trutta*) via postzygotic barriers and paternal effects (vol 68, pg 593, 2011). *Canadian Journal of Fisheries and Aquatic Sciences* **68**:952–952.
- Alves, I., A. Sramkova Hanulova, M. Foll, and L. Excoffier. 2012. Genomic data reveal a complex making of humans. *PLoS Genet* **8**:e1002837.
- Amos, W., and A. Balmford. 2001. When does conservation genetics matter? *Heredity* **87**:257–265.
- Anderson, D. G., and J. C. Gillam. 2000. Paleoindian colonization of the Americas: implications from an examination of physiography, demography, and artifact distribution. *American Antiquity* pages 43–66.
- Angers, B., and I. J. Schlosser. 2007. The origin of *Phoxinus eos-neogaeus* unisexual hybrids. *Molecular Ecology* **16**:4562–4571.
- Anholt, B. R., H. Hotz, G. D. Guex, and R. D. Semlitsch. 2003. Overwinter survival of *Rana lessonae* and its hemiclonal associate *Rana esculenta*. *Ecology* **84**:391–397.
- Arenas, M., O. Francois, M. Currat, N. Ray, and L. Excoffier. 2013. Influence of admixture and paleolithic range contractions on current European diversity gradients. *Mol Biol Evol* **30**:57–61.
- Arenas, M., N. Ray, M. Currat, and L. Excoffier. 2012. Consequences of Range Contractions and Range Shifts on Molecular Diversity. *Molecular Biology and Evolution* **29**:207–218.
- Armstrong, J. D., P. S. Kemp, G. J. A. Kennedy, M. Ladle, and N. J. Milner. 2003. Habitat requirements of Atlantic salmon and brown trout in rivers and streams. *Fisheries Research* **62**:143–170.
- Arnold, M. L., and N. H. Martin. 2010. Hybrid fitness across time and habitats. *Trends in Ecology & Evolution* **25**:530–536.
- Arriaga, L., E. Huerta, R. Lira-Saade, E. Moreno, and J. Alarcón. 2006. Assessing the risk of releasing transgenic *Cucurbita* spp. in Mexico. *Agriculture, ecosystems & environment* **112**:291–299.
- Austerlitz, F., B. JungMuller, B. Godelle, and P. H. Gouyon. 1997. Evolution of coalescence times,

10. Literature Cited

- genetic diversity and structure during colonization. *Theoretical Population Biology* **51**:148–164.
- Baker, J., K. J. Harvey, and K. French. 2014. Threats from introduced birds to native birds. *Emu* **114**:1–12.
- Bakke, T. A., A. Soleng, and P. D. Harris. 1999. The susceptibility of Atlantic salmon (*Salmo salar* L.) x brown trout (*Salmo trutta* L.) hybrids to *Gyrodactylus salaris* Malmberg and *Gyrodactylus derjavini* Mikailov. *Parasitology* **119**:467–481.
- Balloux, F. 2001. EASYPop (version 1.7): A computer program for population genetics simulations. *Journal of Heredity* **92**:301–302.
- Banks, W. E., F. d'Errico, A. T. Peterson, M. Kageyama, A. Sima, and M.-F. Sánchez-Goñi. 2008a. Neanderthal extinction by competitive exclusion. *PLoS One* **3**:e3972.
- Banks, W. E., F. d'Errico, A. T. Peterson, M. Vanhaeren, M. Kageyama, P. Sepulchre, G. Ramstein, A. Jost, and D. Lunt. 2008b. Human ecological niches and ranges during the LGM in Europe derived from an application of eco-cultural niche modeling. *Journal of Archaeological Science* **35**:481–491.
- Baratti, M., N. Baccetti, M. Cordaro, A. Mori, and F. Dessì-Fulgheri. 2014. Investigating the puzzling genetic structure of mallard populations (*Anas platyrhynchos* L.) in Italy. *European Journal of Wildlife Research* **61**:81–89.
- Barbujani, G., R. R. Sokal, and N. L. Oden. 1995. Indo-European origins: a computer-simulation test of five hypotheses. *Am J Phys Anthropol* **96**:109–32.
- Barton, N., A. Etheridge, and A. Véber. 2013a. Modelling evolution in a spatial continuum. *Journal of Statistical Mechanics: Theory and Experiment* **2013**:P01002.
- Barton, N. H., A. M. Etheridge, J. Kelleher, and A. Véber. 2013b. Genetic hitchhiking in spatially extended populations. *Theoretical population biology* **87**:75–89.
- Barton, N. H., and G. M. Hewitt. 1985. Analysis of hybrid zones. *Annual Review of Ecology and Systematics* **16**:113–148.
- Baskett, M. L., and R. Gomulkiewicz. 2011. Introgressive hybridization as a mechanism for species rescue. *Theoretical Ecology* **4**:223–239.
- Beaumont, M., E. Barratt, D. Gottelli, A. Kitchener, M. Daniels, J. Pritchard, and M. W. Bruford. 2001. Genetic diversity and introgression in the Scottish wildcat. *Molecular ecology* **10**:319–336.

10. Literature Cited

- Beaumont, M. A., W. Zhang, and D. J. Balding. 2002. Approximate Bayesian Computation in Population Genetics. *Genetics* **162**:2025–2035.
- Behie, A. M., and M. F. Oxenham. 2015. Taxonomic tapestries: The threads of evolutionary, behavioural and conservation research. ANU Press.
- Bellard, C., P. Cassey, and T. M. Blackburn. 2016. Alien species as a driver of recent extinctions. *Biology letters* **12**:20150623.
- Bellwood, P. 2001. Early Agriculturalist Population. *Annu. Rev. Anthropol.* **30**:181–207.
- Berger, L. 1988. On the origin of genetic systems in european water frog hybrids. *Zoologica Poloniae* **35**:5–32.
- Berven, K. A. 1990. Factors affecting population fluctuations in larval and adult stages of the wood frog (*Rana sylvatica*). *Ecology* **71**:1599–1608.
- Bett, N. N., and S. G. Hinch. 2015. Attraction of migrating adult sockeye salmon to conspecifics in the absence of natal chemical cues. *Behavioral Ecology* page arv062.
- Binet, M. C., and B. Angers. 2005. Genetic identification of members of the *Phoxinus eos-neogaeus* hybrid complex. *Journal of Fish Biology* **67**:1169–1177.
- Biraben, J. 1979. Essay on the evolution of numbers of mankind. *Population* **34**:13–25.
- Birkhead, T. R., and J. P. Brillard. 2007. Reproductive isolation in birds: postcopulatory prezygotic barriers. *Trends in Ecology & Evolution* **22**:266–272.
- Biró, Z., L. Szemethy, and M. Heltai. 2004. Home range sizes of wildcats (*Felis silvestris*) and feral domestic cats (*Felis silvestris f. catus*) in a hilly region of Hungary. *Mammalian Biology-Zeitschrift für Säugetierkunde* **69**:302–310.
- Bocedi, G., D. Zurell, B. Reineking, and J. M. Travis. 2014. Mechanistic modelling of animal dispersal offers new insights into range expansion dynamics across fragmented landscapes. *Ecography* **37**:1240–1253.
- Brown, J. M., K. Savidge, and E. J. McTavish. 2011. DIM SUM: demography and individual migration simulated using a Markov chain. *Mol Ecol Resour* **11**:358–63.
- Brown, R. M., R. A. Nichols, C. G. Faulkes, C. G. Jones, L. Bugoni, V. Tatayah, D. Gottelli, and W. C. Jordan. 2010. Range expansion and hybridization in Round Island petrels (*Pterodroma* spp.): evidence from microsatellite genotypes. *Molecular Ecology* **19**:3157–3170.
- Brumfield, R. T. 2010. Speciation genetics of biological invasions with hybridization. *Molecular Ecology* **19**:5079–5083.

10. Literature Cited

- Buffon, G. L. L. 1753. *Histoire naturelle, générale et particulière: avec la description du Cabinet du Roi*. Imprimerie Royale, Paris.
- Buggs, R. J. A. 2007. Empirical study of hybrid zone movement. *Heredity* **99**:301–312.
- Bundus, J. D., R. Alaei, and A. D. Cutter. 2015. Gametic selection, developmental trajectories, and extrinsic heterogeneity in Haldane's rule. *Evolution* **69**:2005–2017.
- Burnham, K., and D. Anderson. 1976. Mathematical models for nonparametric inferences from line transect data. *Biometrics* **32**:325–336.
- Burnham, K. P., and D. R. Anderson. 2004. Multimodel inference - understanding AIC and BIC in model selection. *Sociological Methods & Research* **33**:261–304.
- Cai, W., S. Borlace, M. Lengaigne, P. Van Rensch, M. Collins, G. Vecchi, A. Timmermann, A. Santoso, M. J. McPhaden, and L. Wu. 2014. Increasing frequency of extreme El Niño events due to greenhouse warming. *Nature Climate Change* **4**:111–116.
- Capblancq, T., L. Després, D. Rioux, and J. Mavárez. 2015. Hybridization promotes speciation in Coenonympha butterflies. *Molecular Ecology* **24**:6209–6222.
- Caspermeyer, J. 2014. Sunlight Adaptation Region of Neanderthal Genome Found in up to 65% of Modern East Asian Populations. *Molecular biology and evolution* page msu003.
- Castillo, A. G. F., F. Ayllon, P. Moran, J. I. Izquierdo, J. L. Martinez, E. Beall, and E. Garcia-Vazquez. 2008. Interspecific hybridization and introgression are associated with stock transfers in salmonids. *Aquaculture* **278**:31–36.
- Castillo, A. G. F., E. Beall, P. Moran, J. L. Martinez, F. Ayllon, and E. Garcia-Vazquez. 2007. Introgression in the genus *Salmo* via allotriploids. *Molecular Ecology* **16**:1741–1748.
- Cavalli-Sforza, L. L., and B. Hewlett. 1982. Exploration and mating range in African Pygmies. *Annals of human genetics* **46**:257–270.
- Chadeau-Hyam, M., C. J. Hoggart, P. F. O'Reilly, J. C. Whittaker, M. De Iorio, and D. J. Balding. 2008. Fregene: simulation of realistic sequence-level data in populations and ascertained samples. *Bmc Bioinformatics* **9**:364.
- Champagnon, J., P.-A. Crochet, J. Kreisinger, D. Čížková, M. Gauthier-Clerc, G. Massez, P. Söderquist, T. Albrecht, and M. Guillemain. 2013. Assessing the genetic impact of massive restocking on wild mallard. *Animal Conservation* **16**:295–305.
- Champagnon, J., M. Guillemain, J. Elmberg, K. Folkesson, and M. Gauthier-Clerc. 2010. Changes

10. Literature Cited

- in Mallard *Anas platyrhynchos* bill morphology after 30 years of supplemental stocking. *Bird Study* **57**:344–351.
- Champagnon, J., M. Guillemain, J. Elmberg, G. Massez, F. Cavallo, and M. Gauthier-Clerc. 2012. Low survival after release into the wild: assessing “the burden of captivity” on Mallard physiology and behaviour. *European Journal of Wildlife Research* **58**:255–267.
- Charney, N. D. 2012. Relating hybrid advantage and genome replacement in unisexual salamanders. *Evolution* **66**:1387–1397.
- Chen, J., J. Rozowsky, T. R. Galeev, A. Harmanci, R. Kitchen, J. Bedford, A. Abyzov, Y. Kong, L. Regan, and M. Gerstein. 2016. A uniform survey of allele-specific binding and expression over 1000-Genomes-Project individuals. *Nature Communications* **7**.
- Chikhi, L., R. A. Nichols, G. Barbujani, and M. A. Beaumont. 2002. Y genetic data support the Neolithic demic diffusion model. *Proc Natl Acad Sci U S A* **99**:11008–13.
- Choleva, L., K. Janko, K. De Gelas, J. Bohlen, V. Slechtova, M. Rabova, and P. Rab. 2012. Synthesis of clonality and polyploidy in vertebrate animals by hybridization between two sexual species. *Evolution* **66**:2191–2203.
- Chopard, B., J. Borgdorff, and A. Hoekstra. 2014. A framework for multi-scale modelling. *Philosophical Transactions of the Royal Society of London A: Mathematical, Physical and Engineering Sciences* **372**:20130378.
- Christiansen, D. G., C. Jakob, M. Arioli, S. Roethlisberger, and H.-U. Reyer. 2010. Coexistence of diploid and triploid hybrid water frogs: population differences persist in the apparent absence of differential survival. *BMC ecology* **10**:14.
- Christiansen, D. G., and H. U. Reyer. 2009. From clonal to sexual hybrids: genetic recombination via triploids in all-hybrid populations of water frogs. *Evolution* **63**:1754–1768.
- Cimino, M. C. 1972. Egg-production, polyploidization and evolution in a diploid all-female fish of genus *Poeciliopsis*. *Evolution* **26**:294–306.
- Čížková, D., V. Javůrková, J. Champagnon, and J. Kreisinger. 2012. Duck’s not dead: Does restocking with captive bred individuals affect the genetic integrity of wild mallard (*Anas platyrhynchos*) population? *Biological Conservation* **152**:231–240.
- Colliard, C., A. Sicilia, G. F. Turrisi, M. Arculeo, N. Perrin, and M. Stöck. 2010. Strong reproductive barriers in a narrow hybrid zone of West-Mediterranean green toads (*Bufo viridis* subgroup) with Plio-Pleistocene divergence. *BMC Evolutionary Biology* **10**:1.

10. Literature Cited

- Corbett, L. K., 1979. Feeding ecology and social organization of wildcats (*Felis silvestris*) and domestic cats (*Felis catus*) in Scotland. Thesis, University of Aberdeen.
- Coulson, T., D. R. MacNulty, D. R. Stahler, R. K. Wayne, and D. W. Smith. 2011. Modeling effects of environmental change on wolf population dynamics, trait evolution, and life history. *Science* **334**:1275–1278.
- Coumou, D., and S. Rahmstorf. 2012. A decade of weather extremes. *Nature Climate Change* **2**:491–496.
- Coyne, J. A., and H. A. Orr. 1989. Patterns of speciation in *Drosophila*. *Evolution* pages 362–381.
- Coyne, J. A., and H. A. Orr. 1997. "Patterns of speciation in *Drosophila*" revisited. *Evolution* **51**:295–303.
- Cracraft, J., 1983. Species concepts and speciation analysis, Pages 159–187 . Springer.
- Crespo-Lopez, M. E., T. Duarte, T. Dowling, and M. M. Coelho. 2006. Modes of reproduction of the hybridogenetic fish *Squalius alburnoides* in the Tejo and Guadiana rivers: An approach with microsatellites. *Zoology* **109**:277–286.
- Crossman, C. A., L. G. Barrett-Lennard, and E. B. Taylor. 2014. Population structure and inter-generic hybridization in harbour porpoises *Phocoena phocoena* in British Columbia, Canada. *Endangered Species Research* **26**:1–12.
- Currat, M., and L. Excoffier. 2004. Modern humans did not admix with Neanderthals during their range expansion into Europe. *Plos Biology* **2**:2264–2274.
- Currat, M., and L. Excoffier. 2005. The effect of the Neolithic expansion on European molecular diversity. *Proceedings of the Royal Society B-Biological Sciences* **272**:679–688.
- Currat, M., and L. Excoffier. 2011. Strong reproductive isolation between humans and Neanderthals inferred from observed patterns of introgression. *Proceedings of the National Academy of Sciences of the United States of America* **108**:15129–15134.
- Currat, M., L. Excoffier, W. Maddison, S. P. Otto, N. Ray, M. C. Whitlock, and S. Yeaman. 2006. Comment on "Ongoing adaptive evolution of ASPM, a brain size determinant in homo sapiens" and "microcephalin, a gene regulating brain size, continues to evolve adaptively in humans". *Science* **313**:–.
- Currat, M., P. Gerbault, D. Di, J. M. Nunes, and A. Sanchez-Mazas. 2015. Forward-in-Time, Spatially Explicit Modeling Software to Simulate Genetic Lineages Under Selection. *Evolutionary bioinformatics* **Suppl** **2**:27–39.

10. Literature Cited

- Currat, M., E. S. Poloni, and A. Sanchez-Mazas. 2010. Human genetic differentiation across the Strait of Gibraltar. *BMC Evol Biol* **10**:237.
- Currat, M., N. Ray, and L. Excoffier. 2004. SPLATCHE: a program to simulate genetic diversity taking into account environmental heterogeneity. *Molecular Ecology Notes* **4**:139–142.
- Currat, M., N. Ray, and L. Excoffier, 2008a. Genetic simulations of population interactions during past human expansions in Europe. Pages 37–47 in S. Matsumura, P. Forster, and C. Renfrew, editors. *Simulations, Genetics and Human Prehistory - A Focus on Islands*. McDonald Institute for Archaeological Research, Cambridge.
- Currat, M., M. Ruedi, R. J. Petit, and L. Excoffier. 2008b. The hidden side of invasions: Massive introgression by local genes. *Evolution* **62**:1908–1920.
- Currat, M., and N. M. Silva. 2013. Investigating European genetic history through computer simulations. *Human heredity* **76**:142–153.
- Daniels, M. J., M. A. Beaumont, P. J. Johnson, D. Balharry, D. W. Macdonald, and E. Barratt. 2001. Ecology and genetics of wild-living cats in the north-east of Scotland and the implications for the conservation of the wildcat. *Journal of Applied Ecology* **38**:146–161.
- Daniels, M. J., and L. Corbett. 2003. Redefining introgressed protected mammals: when is a wildcat a wild cat and a dingo a wild dog? *Wildlife Research* **30**:213–218.
- Darwin, C. 1859. *On the Origin of Species by Means of Natural Selection, or Preservation of Favoured Races in the Struggle for Life*. John Murray, London.
- Darwin, C. 1868. *The variation of animals and plants under domestication*. O. Judd.
- Dasmahapatra, K. K., J. R. Walters, A. D. Briscoe, J. W. Davey, A. Whibley, N. J. Nadeau, A. V. Zimin, D. S. T. Hughes, L. C. Ferguson, S. H. Martin, C. Salazar, J. J. Lewis, S. Adler, S. J. Ahn, D. A. Baker, S. W. Baxter, N. L. Chamberlain, R. Chauhan, B. A. Counterman, T. Dalmay, L. E. Gilbert, K. Gordon, D. G. Heckel, H. M. Hines, K. J. Hoff, P. W. H. Holland, E. Jacquin-Joly, F. M. Jiggins, R. T. Jones, D. D. Kapan, P. Kersey, G. Lamas, D. Lawson, D. Mapleson, L. S. Maroja, A. Martin, S. Moxon, W. J. Palmer, R. Papa, A. Papanicolaou, Y. Pauchet, D. A. Ray, N. Rosser, S. L. Salzberg, M. A. Supple, A. Surridge, A. Tenger-Trolander, H. Vogel, P. A. Wilkinson, D. Wilson, J. A. Yorke, F. R. Yuan, A. L. Balmuth, C. Eland, K. Gharbi, M. Thomson, R. A. Gibbs, Y. Han, J. C. Jayaseelan, C. Kovar, T. Mathew, D. M. Muzny, F. Ongeri, L. L. Pu, J. X. Qu, R. L. Thornton, K. C. Worley, Y. Q. Wu, M. Linares, M. L. Blaxter, R. H. Ffrench-Constant, M. Joron, M. R. Kronforst, S. P. Mullen, R. D. Reed, S. E.

10. Literature Cited

- Scherer, S. Richards, J. Mallet, W. O. McMillan, C. D. Jiggins, and C. Heliconius Genome. 2012. Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. *Nature* **487**:94–98.
- Dawley, R. M., R. J. Schultz, and K. A. Goddard. 1987. Clonal reproduction and polyploidy in unisexual hybrids of *Phoxinus eos* and *Phoxinus eogaeus* (pisces, cyprinidae). *Copeia* pages 275–283.
- DeGiorgio, M., J. H. Degnan, and N. A. Rosenberg. 2011. Coalescence-time distributions in a serial founder model of human evolutionary history. *Genetics* **189**:579–593.
- Dellicour, S., O. Hardy, and P. Mardulyn. In prep. PhyloGeoSim 1.0. A program to simulate the evolution of DNA sequences under a spatially explicit model of coalescence. .
- Dellicour, S., C. Kastally, O. J. Hardy, and P. Mardulyn. 2014. Comparing phylogeographic hypotheses by simulating DNA sequences under a spatially explicit model of coalescence. *Molecular biology and evolution* **31**:3359–3372.
- Deshpande, O., S. Batzoglou, M. W. Feldman, and L. L. Cavalli-Sforza. 2009. A serial founder effect model for human settlement out of Africa. *Proceedings of the Royal Society B-Biological Sciences* **276**:291–300.
- Devos, Y., R. S. Hails, A. Messéan, J. N. Perry, and G. R. Squire. 2012. Feral genetically modified herbicide tolerant oilseed rape from seed import spills: are concerns scientifically justified? *Transgenic research* **21**:1–21.
- Di, D., and A. Sanchez-Mazas. 2011. Challenging views on the peopling history of East Asia: the story according to HLA markers. *American journal of physical anthropology* **145**:81–96.
- Ding, Q., Y. Hu, S. Xu, J. Wang, and L. Jin. 2013. Neanderthal introgression at chromosome 3p21. 31 was under positive natural selection in East Asians. *Molecular biology and evolution* page mst260.
- Dobzhansky, T. 1937. *Genetics and the Origin of Species* (Classics of Modern Evolution Series). Columbia University Press.
- Dobzhansky, T. 1970. *Genetics of the evolutionary process*. Columbia University Press New York.
- Doebeli, M. 1996. Quantitative genetics and population dynamics. *Evolution* **50**:532–546.
- Doebeli, M. 1997. Genetic variation and the persistence of predator-prey interactions in the Nicholson-Bailey model. *Journal of Theoretical Biology* **188**:109–120.

10. Literature Cited

- Donahue, M. J. 2006. Allee effects and conspecific cueing jointly lead to conspecific attraction. *Oecologia* **149**:33–43.
- Dötterer, M., and F. Bernhart. 1996. The occurrence of wildcats in the southern Swiss Jura Mountains. *Acta Theriologica* **41**:205–210.
- Driscoll, C. A., D. W. Macdonald, and S. J. O'Brien. 2009. From wild animals to domestic pets, an evolutionary view of domestication. *Proceedings of the National Academy of Sciences* **106**:9971–9978.
- Driscoll, C. A., M. Menotti-Raymond, A. L. Roca, K. Hupe, W. E. Johnson, E. Geffen, E. H. Harley, M. Delibes, D. Pontier, and A. C. Kitchener. 2007. The Near Eastern origin of cat domestication. *Science* **317**:519–523.
- Duelli, P., and D. Agosti. 1994. Rote Listen der gefährdeten Tierarten der Schweiz. BUWAL, Bundesamt für Umwelt, Wald und Landschaft.
- Dyer, J., and M. Williams. 2010. An introduction most determined: Mallard (*Anas platyrhynchos*) to New Zealand. *Notornis* **57**:178–195.
- Eckert, I., F. Suchentrunk, G. Markov, and G. B. Hartl. 2010. Genetic diversity and integrity of German wildcat (*Felis silvestris*) populations as revealed by microsatellites, allozymes, and mitochondrial DNA sequences. *Mammalian Biology-Zeitschrift für Säugetierkunde* **75**:160–174.
- Edmonds, C. A., A. S. Lillie, and L. L. Cavalli-Sforza. 2004. Mutations arising in the wave front of an expanding population. *Proc Natl Acad Sci U S A* **101**:975–9.
- Ellington, E. H., and D. L. Murray. 2015. Influence of hybridization on animal space use: a case study using coyote range expansion. *Oikos* **124**:535–542.
- Ellstrand, N. C., S. M. Heredia, J. A. Leak-Garcia, J. M. Heraty, J. C. Burger, L. Yao, S. Nohzadeh-Malakshah, and C. E. Ridley. 2010. Crops gone wild: evolution of weeds and invasives from domesticated ancestors. *Evolutionary Applications* **3**:494–504.
- Ellstrand, N. C., P. Meirmans, J. Rong, D. Bartsch, A. Ghosh, T. J. de Jong, P. Haccou, B.-R. Lu, A. A. Snow, and C. Neal Stewart Jr. 2013. Introgression of crop alleles into wild or weedy populations. *Annual Review of Ecology, Evolution, and Systematics* **44**:325–345.
- Ellstrand, N. C., and K. A. Schierenbeck. 2000. Hybridization as a stimulus for the evolution of invasiveness in plants? *Proceedings of the National Academy of Sciences* **97**:7043–7050.
- Eriksson, A., L. Betti, A. D. Friend, S. J. Lycett, J. S. Singarayer, N. von Cramon-Taubadel, P. J.

10. Literature Cited

- Valdes, F. Balloux, and A. Manica. 2013. Late Pleistocene climate change and the global expansion of anatomically modern humans. *Proceedings of the National Academy of Sciences of the United States of America* **109**:16089–16094.
- Eriksson, A., and A. Manica. 2012. Effect of ancient population structure on the degree of polymorphism shared between modern human populations and ancient hominins. *Proc Natl Acad Sci U S A* **109**:13956–60.
- Eswaran, V., G. Clark, H. Harpending, K. Rosenberg, E. Trinkaus, M. Wolpoff, J. Zilho, and V. Eswaran. 2002. A Diffusion Wave out of Africa: The Mechanism of the Modern Human Revolution? 1. *Current Anthropology* **43**:749–774.
- Eswaran, V., H. Harpending, and A. R. Rogers. 2005. Genomics refutes an exclusively African origin of humans. *J Hum Evol* **49**:1–18.
- Ewing, G., and J. Hermisson. 2010. MSMS: a coalescent simulation program including recombination, demographic structure and selection at a single locus. *Bioinformatics* **26**:2064–2065.
- Excoffier, L. 2004. Patterns of DNA sequence diversity and genetic structure after a range expansion: lessons from the infinite-island model. *Molecular Ecology* **13**:853–864.
- Excoffier, L., and M. Foll. 2011. Fastsimcoal: a continuous-time coalescent simulator of genomic diversity under arbitrarily complex evolutionary scenarios. *Bioinformatics* **27**:1332–1334.
- Excoffier, L., M. Foll, and R. Petit. 2009. Genetic Consequences of Range Expansions. *Annual Review in Ecology, Evolution, and Systematics* **40**.
- Excoffier, L., J. Novembre, and S. Schneider. 2000. SIMCOAL: A general coalescent program for the simulation of molecular data in interconnected populations with arbitrary demography. *J. Heredity* **91**:506–510.
- Excoffier, L., C. S. Quilodrán, and M. Currat. 2014. Models of hybridization during range expansions and their application to recent human evolution. Pages 122–137 in A. Derevianko and M. Shunkov, editors. *Cultural Developments in the Eurasian Paleolithic and the Origin of Anatomically Modern Humans*. Department of the Institute of Archaeology and Ethnography SB RAS, Novosibirsk, Russia.
- Excoffier, L., and N. Ray. 2008. Surfing during population expansions promotes genetic revolutions and structuration. *Trends Ecol Evol* **23**:347–51.
- Faure, E., and A. C. Kitchener. 2009. An archaeological and historical review of the relationships between felids and people. *Anthrozoös* **22**:221–238.

10. Literature Cited

- Ferdy, J. B., and F. Austerlitz. 2002. Extinction and introgression in a community of partially cross-fertile plant species. *American Naturalist* **160**:74–86.
- Fisher, R. A. 1937. The wave of advance of advantageous genes. *Annals of Eugenics* **7**:355–369.
- Fitzpatrick, B. M., J. A. Fordyce, M. L. Niemiller, and R. G. Reynolds. 2012. What can DNA tell us about biological invasions? *Biological Invasions* **14**:245–253.
- Fitzpatrick, B. M., M. E. Ryan, J. R. Johnson, J. Corush, and E. Carter. 2015. Hybridization and the species problem in conservation. *Curr. Zool* **61**:204–214.
- Fix, A. G. 1996. Gene frequency clines in Europe: demic diffusion or natural selection? *Journal of the Royal Anthropological Institute* pages 625–643.
- Fix, A. G. 1997. Gene frequency clines produced by kin-structured founder effects. *Human biology* pages 663–673.
- Fort, J., and V. Méndez. 1999. Reaction-diffusion waves of advance in the transition to agricultural economics. *Physical Review E* **60**:5894.
- Fort, J., and T. Pujol. 2008. Progress in front propagation research. *Reports on Progress in Physics* **71**:086001.
- Fort, J., T. Pujol, and L. L. Cavalli-Sforza. 2004. Palaeolithic populations and waves of advance. *Cambridge Archaeological Journal* **14**:53–61.
- Fowler, A. C., J. M. Eadie, and A. Engilis Jr. 2009. Identification of endangered Hawaiian ducks (*Anas wyvilliana*), introduced North American mallards (*A. platyrhynchos*) and their hybrids using multilocus genotypes. *Conservation Genetics* **10**:1747–1758.
- Franco-Trecu, V., C. Abud, M. Feijoo, G. Kloetzer, M. Casacuberta, and P. Costa-Urrutia. 2016. Sex beyond species: the first genetically analyzed case of intergeneric fertile hybridization in pinnipeds. *Evolution & Development* **18**:127–136.
- Frankham, R., J. D. Ballou, M. R. Dudash, M. D. Eldridge, C. B. Fenster, R. C. Lacy, J. R. Mendelson, I. J. Porton, K. Ralls, and O. A. Ryder. 2012. Implications of different species concepts for conserving biodiversity. *Biological Conservation* **153**:25–31.
- Fredrickson, R. J., and P. W. Hedrick. 2006. Dynamics of hybridization and introgression in red wolves and coyotes. *Conservation Biology* **20**:1272–1283.
- Fretwell, S. D., and H. L. Lucas. 1969. On territorial behavior and other factors influencing habitat distribution in bird. I. Theoretical development. *Acta Biotheoretica* **19**:16–36.
- Fuchs, E. J., A. M. Martínez, A. Calvo, M. Muñoz, and G. Arrieta-Espinoza. 2016. Genetic

10. Literature Cited

- diversity in *Oryza glumaepatula* wild rice populations in Costa Rica and possible gene flow from *O. sativa*. *PeerJ* **4**:e1875.
- Galbreath, P. F., and G. H. Thorgaard. 1995. Sexual maturation and fertility of diploid and triploid Atlantic salmon x brown trout hybrids. *Aquaculture* **137**:299–311.
- Garcia, M. G., R. S. Silva, M. A. Carnielo, J. W. Veldman, A. A. B. Rossi, and L. O. de Oliveira. 2011. Molecular evidence of cryptic speciation, historical range expansion, and recent intraspecific hybridization in the Neotropical seasonal forest tree *Cedrela fissilis* (Meliaceae). *Molecular Phylogenetics and Evolution* **61**:639–649.
- Garcia-Vazquez, E., F. Ayllon, J. L. Martinez, J. Perez, and E. Beall. 2003. Reproduction of interspecific hybrids of Atlantic salmon and brown trout in a stream environment. *Freshwater Biology* **48**:1100–1104.
- Garcia-Vazquez, E., J. Perez, F. Ayllon, J. L. Martinez, S. Glise, and E. Beall. 2004. Asymmetry of post-F-1 interspecific reproductive barriers among brown trout (*Salmo trutta*) and Atlantic salmon (*Salmo salar*). *Aquaculture* **234**:77–84.
- Gese, E. M., F. F. Knowlton, J. R. Adams, K. Beck, T. K. Fuller, D. L. Murray, T. D. Steury, M. K. Stoskopf, W. T. Waddell, and L. P. Waits. 2015. Managing hybridization of a recovering endangered species: The red wolf *Canis rufus* as a case study. *Current Zoology* **61**:191–205.
- Gibbons, A. 2012. Turning back the clock: slowing the pace of prehistory. *Science* **338**:189–191.
- Gillespie, G. D. 1985. Hybridization, introgression, and morphometric differentiation between Mallard (*Anas platyrhynchos*) and Grey Duck (*Anas superciliosa*) in Otago, New Zealand. *The Auk* pages 459–469.
- Gilman, R. T., and J. E. Behm. 2011. Hybridization, species collapse, and species reemergence after disturbance to premating mechanisms of reproductive isolation. *Evolution* **65**:2592–2605.
- Goddard, K. A., and R. J. Schultz. 1993. Aclonal reproduction by polyploid members of the clonal hybrid species *Phoxinus eos-neogaeus* (Cyprinidae). *Copeia* pages 650–660.
- Gómez, J. M., A. González-Megías, J. Lorite, M. Abdelaziz, and F. Perfectti. 2015. The silent extinction: climate change and the potential hybridization-mediated extinction of endemic high-mountain plants. *Biodiversity and Conservation* pages 1–15.
- González-Bernal, E., G. P. Brown, and R. Shine. 2014. Invasive cane toads: Social facilitation depends upon an individual's personality. *PloS one* **9**:e102880.
- Gottelli, D., C. Sillero-Zubiri, G. D. Applebaum, M. S. Roy, D. J. Girman, J. Garcia-Moreno,

10. Literature Cited

- E. A. Ostrander, and R. K. Wayne. 1994. Molecular genetics of the most endangered canid: the Ethiopian wolf *Canis simensis*. *Molecular Ecology* **3**:301–312.
- Gottelli, D., C. Sillero-Zubiri, J. Marino, S. Funk, and J. Wang. 2013. Genetic structure and patterns of gene flow among populations of the endangered Ethiopian wolf. *Animal Conservation* **16**:234–247.
- Gould, S. J. 1992. What is a species. *Discover* **13**:40–44.
- Graf, J. D. 1986. Population genetics of the *Rana esculenta* complex: a model. *Studies in herpetology* pages 175–180.
- Grant, B. R., and P. R. Grant. 2008. Fission and fusion of Darwin's finches populations. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* **363**:2821–2829.
- Gravel, S., B. M. Henn, R. N. Gutenkunst, A. R. Indap, G. T. Marth, A. G. Clark, F. Yu, R. A. Gibbs, P. Genomes, and C. D. Bustamante. 2011. Demographic history and rare allele sharing among human populations. *Proc Natl Acad Sci U S A* **108**:11983–8.
- Gray, A. K., M. A. Evans, and G. H. Thorgaard. 1993. Viability and development of diploid and triploid salmonid hybrids. *Aquaculture* **112**:125–142.
- Green, R. E., J. Krause, A. W. Briggs, T. Maricic, U. Stenzel, M. Kircher, N. Patterson, H. Li, W. Zhai, M. H. Fritz, N. F. Hansen, E. Y. Durand, A. S. Malaspinas, J. D. Jensen, T. Marques-Bonet, C. Alkan, K. Prüfer, M. Meyer, H. A. Burbano, J. M. Good, R. Schultz, A. Aximu-Petri, A. Butthof, B. Hober, B. Hoffner, M. Siegmund, A. Weihmann, C. Nusbaum, E. S. Lander, C. Russ, N. Novod, J. Affourtit, M. Egholm, C. Verna, P. Rudan, D. Brajkovic, Z. Kucan, I. Gusic, V. B. Doronichev, L. V. Golovanova, C. Lalueza-Fox, M. de la Rasilla, J. Fortea, A. Rosas, R. W. Schmitz, P. L. Johnson, E. E. Eichler, D. Falush, E. Birney, J. C. Mullikin, M. Slatkin, R. Nielsen, J. Kelso, M. Lachmann, D. Reich, and S. Paabo. 2010. A draft sequence of the Neandertal genome. *Science* **328**:710–722.
- Gronenborn, D. 1999. A variation on a basic theme: the transition to farming in southern central Europe. *Journal of world prehistory* **13**:123–210.
- Groves, C. 2012. Species concept in primates. *American journal of primatology* **74**:687.
- Guay, P., A. Taysom, R. Robinson, and J. Tracey. 2014. Hybridization between the Mallard and native dabbling ducks: causes, consequences and management. *Pacific Conservation Biology* **20**:41–47.

10. Literature Cited

- Guay, P.-J., and J. Tracey. 2009. Feral Mallards: a risk for hybridisation with wild Pacific Black Ducks in Australia? *Victorian Naturalist*, The **126**:87.
- Guay, P.-J., M. Williams, and R. W. Robinson. 2015. Lingering genetic evidence of North American mallards (*Anas platyrhynchos*) introduced to New Zealand. *New Zealand Journal of Ecology* **39**:103–109.
- Gugsa, L., A. K. Sarial, H. Lorz, and J. Kumlehn. 2006. Gynogenic plant regeneration from unpollinated flower explants of *Eragrostis tef* (Zuccagni) Trotter. *Plant Cell Reports* **25**:1287–1293.
- Guillaume, F., and J. Rougemont. 2006. Nemo: an evolutionary and population genetics programming framework. *Bioinformatics* **22**:2556–2557.
- Haig, S. M., W. M. Bronaugh, R. S. Crowhurst, J. D'Elia, C. A. Eagles-Smith, C. W. Epps, B. Knaus, M. P. Miller, M. L. Moses, S. Oyler-McCance, W. D. Robinson, and B. Sidlauskas. 2011. Genetic applications in avian conservation. *Auk* **128**:205–229.
- Hailer, F., V. E. Kutschera, B. M. Hallström, D. Klassert, S. R. Fain, J. A. Leonard, U. Arnason, and A. Janke. 2012. Nuclear genomic sequences reveal that polar bears are an old and distinct bear lineage. *Science* **336**:344–347.
- Hails, R. S. 2000. Genetically modified plants—the debate continues. *Trends in Ecology & Evolution* **15**:14–18.
- Haines, M. L., A. Moussalli, D. Stuart-Fox, N. Cleemann, and J. Melville. 2014. Phylogenetic evidence of historic mitochondrial introgression and cryptic diversity in the genus *Pseudemoia* (Squamata: Scincidae). *Molecular phylogenetics and evolution* **81**:86–95.
- Halas, D., and A. M. Simons. 2014. Cryptic speciation reversal in the *Etheostoma zonale* (Teleostei: Percidae) species group, with an examination of the effect of recombination and introgression on species tree inference. *Molecular phylogenetics and evolution* **70**:13–28.
- Hall, R. J., and D. R. Ayres. 2009. What can mathematical modeling tell us about hybrid invasions? *Biological Invasions* **11**:1217–1224.
- Hall, R. J., A. Hastings, and D. R. Ayres. 2006. Explaining the explosion: modelling hybrid invasions. *Proceedings of the Royal Society B-Biological Sciences* **273**:1385–1389.
- Hallatschek, O., P. Hersen, S. Ramanathan, and D. R. Nelson. 2007. Genetic drift at expanding frontiers promotes gene segregation. *Proc Natl Acad Sci U S A* **104**:19926–30.

10. Literature Cited

- Hamilton, J. A., and J. M. Miller. 2016. Adaptive introgression as a resource for management and genetic conservation in a changing climate. *Conservation Biology* **30**:33–41.
- Handley, L. J., A. Manica, J. Goudet, and F. Balloux. 2007. Going the distance: human population genetics in a clinal world. *Trends Genet* **23**:432–9.
- Hauser, C. E., and M. A. McCarthy. 2009. Streamlining ‘search and destroy’: cost-effective surveillance for invasive species management. *Ecology Letters* **12**:683–692.
- Hayden, B., A. Massa-Gallucci, J. Caffrey, C. Harrod, S. Mariani, M. O’Grady, and M. Kelly-Quinn. 2011. Trophic dynamics within a hybrid zone - interactions between an abundant cyprinid hybrid and sympatric parental species. *Freshwater Biology* **56**:1723–1735.
- Hayden, B., D. Pulcini, M. Kelly-Quinn, M. O’Grady, J. Caffrey, A. McGrath, and S. Mariani. 2010. Hybridisation between two cyprinid fishes in a novel habitat: genetics, morphology and life-history traits. *Bmc Evolutionary Biology* **10**:11.
- Heggenes, J., and S. J. Saltveit. 2007. Summer stream habitat partitioning by sympatric Arctic charr, Atlantic salmon and brown trout in two sub-arctic rivers. *Journal of Fish Biology* **71**:1069–1081.
- Hellriegel, B., and H. U. Reyer. 2000. Factors influencing the composition of mixed populations of a hemiclonal hybrid and its sexual host. *Journal of Evolutionary Biology* **13**:906–918.
- Henn, B. M., L. L. Cavalli-Sforza, and M. W. Feldman. 2012. The great human expansion. *Proc Natl Acad Sci U S A* **109**:17758–64.
- Henson, S. M., R. F. Costantino, J. M. Cushing, R. A. Desharnais, B. Dennis, and A. A. King. 2001. Lattice effects observed in chaotic dynamics of experimental populations. *Science* **294**:602–605.
- Hewitt, G. M. 2000. The genetic legacy of the quaternary ice ages. *Nature* **405**:907–913.
- Hewitt, G. M. 2011. Quaternary phylogeography: the roots of hybrid zones. *Genetica* **139**:617–638.
- Hewlett, B., J. M. Van De Koppel, and L. L. Cavalli-Sforza. 1982. Exploration ranges of Aka pygmies of the Central African Republic. *Man* pages 418–430.
- Higham, T., R. Jacobi, M. Julien, F. David, L. Basell, R. Wood, W. Davies, and C. B. Ramsey. 2010. Chronology of the Grotte du Renne (France) and implications for the context of ornaments and human remains within the Chatelperronian. *Proceedings of the National Academy of Sciences of the United States of America* **107**:20234–9.

10. Literature Cited

- Hindar, K., and T. Balstad. 1994. Salmonid culture and interspecific hybridization. *Conservation Biology* **8**:881–882.
- Hindar, K., I. A. Fleming, P. McGinnity, and A. Diserud. 2006. Genetic and ecological effects of salmon farming on wild salmon: modelling from experimental results. *Ices Journal of Marine Science* **63**:1234–1247.
- Holenweg Peter, A. K. 2001. Dispersal rates and distances in adult water frogs, *Rana lessonae*, *R. ridibunda*, and their hybridogenetic associate *R. esculenta*. *Herpetologica* **57**:449–460.
- Holenweg Peter, A. K., H. U. Reyer, and G. A. Tietje. 2002. Species and sex ratio differences in mixed populations of hybridogenetic water frogs: The influence of pond features. *Ecoscience* **9**:1–11.
- Holsbeek, G., and R. Jooris. 2010. Potential impact of genome exclusion by alien species in the hybridogenetic water frogs (*Pelophylax esculentus* complex). *Biological Invasions* **12**:1–13.
- Horreo, J. L., F. Ayllon, J. Perez, E. Beall, and E. Garcia-Vazquez. 2011. Interspecific Hybridization, a Matter of Pioneering? Insights from Atlantic Salmon and Brown Trout. *Journal of Heredity* **102**:237–242.
- Hubbs, C. L. 1955. Hybridization between fish species in nature. *Systematic Zoology* **4**:1–20.
- Hudson, R. R. 1990. Gene genealogies and the coalescent process. Oxford University Press, oxford.
- Hudson, R. R. 2002. Generating samples under a Wright-Fisher neutral model of genetic variation. *Bioinformatics* **18**:337–8.
- Huerta-Sánchez, E., X. Jin, Z. Bianba, B. M. Peter, N. Vinckenbosch, Y. Liang, X. Yi, M. He, M. Somel, and P. Ni. 2014. Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. *Nature* **512**:194–197.
- Hughes, J., and D. W. Macdonald. 2013. A review of the interactions between free-roaming domestic dogs and wildlife. *Biological Conservation* **157**:341–351.
- Huxel, G. R. 1999. Rapid displacement of native species by invasive species: effects of hybridization. *Biological Conservation* **89**:143–152.
- Huxley, J. 1942. Evolution. The Modern Synthesis. Evolution. The Modern Synthesis. .
- Itan, Y., A. Powell, M. A. Beaumont, J. Burger, and M. G. Thomas. 2009. The origins of lactase persistence in Europe. *PLoS Comput Biol* **5**:e1000491.
- Ivanova, N. L., and O. A. Zhigalski. 2011. Demographic Features of Populations of the Marsh

10. Literature Cited

- Frog (*Rana ridibunda* Pall.) Introduced into Water Bodies of the Middle Urals. Russian Journal of Ecology **42**:400–406.
- Jansson, H., and T. Ost. 1997. Hybridization between Atlantic salmon (*Salmo salar*) and brown trout (*S. trutta*) in a restored section of the River Dalalven, Sweden. Canadian Journal of Fisheries and Aquatic Sciences **54**:2033–2039.
- Januchowski-Hartley, S. R., P. Visconti, and R. L. Pressey. 2011. A systematic approach for prioritizing multiple management actions for invasive species. Biological Invasions **13**:1241–1253.
- Johannesen, J., B. Johannesen, E. Griebeler, I. Baran, M. Tunc, A. Kiefer, and M. Veith. 2006. Distortion of symmetrical introgression in a hybrid zone: evidence for locus-specific selection and uni-directional range expansion. Journal of evolutionary biology **19**:705–716.
- Johnsen, B. O., and A. J. Jensen. 1991. The gyrodactylus story in norway. Aquaculture **98**:289–302.
- Jonsson, B., and N. Jonsson. 2009a. Migratory timing, marine survival and growth of anadromous brown trout *Salmo trutta* in the River Imsa, Norway. Journal of Fish Biology **74**:621–638.
- Jonsson, B., and N. Jonsson. 2009b. A review of the likely effects of climate change on anadromous Atlantic salmon *Salmo salar* and brown trout *Salmo trutta*, with particular reference to water temperature and flow. Journal of Fish Biology **75**:2381–2447.
- Jonsson, B., and N. Jonsson. 2011. Ecology of Atlantic salmon and brown trout: habitat as a template for life histories. Fish and Fisheries Series, Springer-Verlag, Dordrecht.
- Jonsson, N., B. Jonsson, and L. P. Hansen. 2003. The marine survival and growth of wild and hatchery reared Atlantic salmon. Journal of Applied Ecology **40**:900–911.
- Kidd, A., J. Bowman, D. Lesbareres, and A. Schulte-Hostedde. 2009. Hybridization between escaped domestic and wild American mink (*Neovison vison*). Molecular Ecology **18**:1175–1186.
- Kierzkowski, P., L. Pasko, M. Rybacki, M. Socha, and M. Ogielska. 2011. Genome dosage effect and hybrid morphology - the case of the hybridogenetic water frogs of the *Pelophylax esculentus* complex. Annales Zoologici Fennici **48**:56–66.
- Kimura, M. 1953. "Stepping-stone" model of population. Annual Report of National Institute of Genetics **3**:62–63.
- Kingman, J. 1982. The coalescent. Stoch. Proc. Appl. **13**:235–248.

10. Literature Cited

- Kirby, R. E., G. A. Sargeant, and D. Shutler. 2004. Haldane's rule and American black duck x mallard hybridization. *Canadian Journal of Zoology* **82**:1827–1831.
- Kitamoto, N., A. Kaga, Y. Kuroda, and R. Ohsawa. 2012. A model to predict the frequency of integration of fitness-related QTLs from cultivated to wild soybean. *Transgenic research* **21**:131–138.
- Kivelä, S. M., J.-T. Seppänen, O. Ovaskainen, B. Doligez, L. Gustafsson, M. Mönkkönen, and J. T. Forsman. 2014. The past and the present in decision-making: the use of conspecific and heterospecific cues in nest site selection. *Ecology* **95**:3428–3439.
- Klein, R. G. 2003. Paleoanthropology. Whither the Neanderthals? *Science* **299**:1525–7.
- Klopfstein, S., M. Currat, and L. Excoffier. 2006. The fate of mutations surfing on the wave of a range expansion. *Molecular biology and evolution* **23**:482–490.
- Konishi, M., and K. Takata. 2004. Impact of asymmetrical hybridization followed by sterile F-1 hybrids on species replacement in *Pseudorasbora*. *Conservation Genetics* **5**:463–474.
- Kovach, R. P., G. Luikart, W. H. Lowe, M. C. Boyer, and C. C. Muhlfeld. 2016. Risk and efficacy of human-enabled interspecific hybridization for climate-change adaptation: response to Hamilton and Miller (2016). *Conservation Biology* **30**:428–430.
- Kraus, F. 1995. The conservation of unisexual vertebrate populations. *Conservation Biology* **9**:956–959.
- Krause, J., L. Orlando, D. Serre, B. Viola, K. Prüfer, M. P. Richards, J. J. Hublin, C. Hanni, A. P. Derevianko, and S. Paabo. 2007. Neanderthals in central Asia and Siberia. *Nature* **449**:902–4.
- Krings, M., A. Stone, R. Schmitz, H. Krainitzki, M. Stoneking, and S. Pääbo. 1997. Neandertal DNA sequences and the origin of modern humans. *Cell* **90**:19–30.
- Kühlwilm, M., I. Gronau, M. J. Hubisz, C. de Filippo, J. Prado-Martinez, M. Kircher, Q. Fu, H. A. Burbano, C. Lalueza-Fox, and M. de la Rasilla. 2016. Ancient gene flow from early modern humans into Eastern Neanderthals. *Nature* **530**:429–433.
- Lahr, M. M., and R. A. Foley. 1998. Towards a theory of modern human origins: geography, demography, and diversity in recent human evolution. *Yearbook of physical anthropology* **41**:137–176.
- Laikre, L., M. K. Schwartz, R. S. Waples, N. Ryman, and G. W. Group. 2010. Compromising genetic diversity in the wild: unmonitored large-scale release of plants and animals. *Trends in Ecology & Evolution* **25**:520–529.

10. Literature Cited

- Lampert, K. P. 2009. Clonal reproduction in freshwater fish: mechanisms, systematic overview, genetic and ecological consequences. *Fundamental and Applied Limnology* **174**:245–260.
- Lande, R. 1988. Genetics and demography in biological conservation. *Science* **241**:1455–1460.
- Lande, R., S. Engen, B.-E. Sæther, and T. Coulson. 2006. Estimating density dependence from time series of population age structure. *The American Naturalist* **168**:76–87.
- Landguth, E. L., and S. A. Cushman. 2010. CDPOP: A spatially explicit cost distance population genetics program. *Molecular Ecology Resources* **10**:156–161.
- Larcombe, M. J., T. Leaman, R. E. Vaillancourt, and B. M. Potts. 2014. Assessing the risk of gene flow from plantation to native eucalypts: A long-term partnership in biodiversity management. *Australasian Plant Conservation: Journal of the Australian Network for Plant Conservation* **23**:19–21.
- Laval, G., and L. Excoffier. 2004. SIMCOAL 2.0: a program to simulate genomic diversity over large recombining regions in a subdivided population with a complex history. *Bioinformatics* **20**:2485–2487.
- Lavrentovich, M. O., K. S. Korolev, and D. R. Nelson. 2013. Radial Domany-Kinzel models with mutation and selection. *Physical Review E* **87**:012103.
- Lecis, R., M. Pierpaoli, Z. Biro, L. Szemethy, B. Ragni, F. Vercillo, and E. Randi. 2006. Bayesian analyses of admixture in wild and domestic cats (*Felis silvestris*) using linked microsatellite loci. *Molecular Ecology* **15**:119–131.
- Leducq, J.-B., L. Nielly-Thibault, G. Charron, C. Eberlein, J.-P. Verta, P. Samani, K. Sylvester, C. T. Hittinger, G. Bell, and C. R. Landry. 2016. Speciation driven by hybridization and chromosomal plasticity in a wild yeast. *Nature Microbiology* **1**:15003.
- Lee, Y., C. D. Marsden, L. C. Norris, T. C. Collier, B. J. Main, A. Fofana, A. J. Cornel, and G. C. Lanzaro. 2013. Spatiotemporal dynamics of gene flow and hybrid fitness between the M and S forms of the malaria mosquito, *Anopheles gambiae*. *Proceedings of the National Academy of Sciences* **110**:19854–19859.
- Leonard, J., J. Echegaray, E. Randi, and C. Vilà. 2013. Impact of hybridization with domestic dogs on the conservation of wild canids. *Free-Ranging Dogs and Wildlife Conservation* page 170.
- Lescureux, N., and J. D. Linnell. 2014. Warring brothers: The complex interactions between

10. Literature Cited

- wolves (*Canis lupus*) and dogs (*Canis familiaris*) in a conservation context. *Biological conservation* **171**:232–245.
- Li, G., B. W. Davis, E. Eizirik, W. J. Murphy, C.-L. Lin, A. J. Taggart, K. H. Lim, K. J. Cygan, L. Ferraris, and R. Creton. 2016. Phylogenomic evidence for ancient hybridization in the genomes of living cats (Felidae). *Genome research* **26**:1–11.
- Li, J., D. Absher, H. Tang, A. Southwick, A. Casto, S. Ramachandran, H. Cann, G. Barsh, M. Feldman, L. Cavalli-Sforza, and R. Myers. 2008. Worldwide Human Relationships Inferred from Genome-Wide Patterns of Variation. *Science* **319**:1100–1104.
- Linder, C., I. Taha, L. Rieseberg, G. Seiler, and A. Snow. 1998. Long-term introgression of crop genes into wild sunflower populations. *Theoretical and Applied Genetics* **96**:339–347.
- Lindley, J. 1835. *Edwards's Botanical Register*. James Ridgway. London.
- Liu, H., F. Prugnolle, A. Manica, and F. Balloux. 2006. A geographically explicit genetic model of worldwide human-settlement history. *The American Journal of Human Genetics* **79**:230–237.
- Liu, H., and P. Stiling. 2006. Testing the enemy release hypothesis: a review and meta-analysis. *Biological Invasions* **8**:1535–1545.
- Liu, S. J. 2010. Distant hybridization leads to different ploidy fishes. *Science China-Life Sciences* **53**:416–425.
- Lizarralde, M. S., G. Bailliet, S. Poljak, M. Fasanella, and C. Giulivi. 2008. Assessing genetic variation and population structure of invasive North American beaver (*Castor canadensis* Kuhl, 1820) in Tierra del Fuego (Argentina). *Biological Invasions* **10**:673–683.
- Loddiges, C. 1828. *The Botanical Cabinet*. John & Arthur Arch. London.
- Lode, T. 2001. Character convergence in advertisement call and mate choice in two genetically distinct water frog hybridogenetic lineages (*Rana kl esculenta*, *Rana kl grafi*). *Journal of Zoological Systematics and Evolutionary Research* **39**:91–96.
- Losey, J. E., L. S. Rayor, and M. E. Carter. 1999. Transgenic pollen harms monarch larvae. *Nature* **399**:214–214.
- Lotka, A. 1932. The Growth of Mixed Populations: Two Species Competing for a Common Food Supply. *Journal of the Washington academy of Sciences* **22**:461–469.
- Luquet, E., C. Vorburger, F. Hervant, P. Joly, B. Kaufmann, D. S. Schmeller, J. P. Lena, O. Grolet, L. Konecny, and S. Plenet. 2011. Invasiveness of an introduced species: the role of hybridization and ecological constraints. *Biological Invasions* **13**:1901–1915.

10. Literature Cited

- Macaulay, V., C. Hill, A. Achilli, C. Rengo, D. Clarke, W. Meehan, J. Blackburn, O. Semino, R. Scozzari, F. Cruciani, A. Taha, N. K. Shaari, J. M. Raja, P. Ismail, Z. Zainuddin, W. Goodwin, D. Bulbeck, H. J. Bandelt, S. Oppenheimer, A. Torroni, and M. Richards. 2005. Single, rapid coastal settlement of Asia revealed by analysis of complete mitochondrial genomes. *Science* **308**:1034–6.
- MaCulloch, R. D., R. W. Murphy, L. A. Kupriyanova, I. S. Darevsky, and F. D. Danielyan. 1995. Clonal variation in the parthenogenetic rock lizard *Lacerta armeniaca*. *Genome* **38**:1057–1060.
- Macdonald, D. W., and C. Sillero-Zubiri. 2004. The biology and conservation of wild canids. OUP Oxford.
- Mack, R. N., D. Simberloff, W. M. Lonsdale, H. Evans, M. Clout, and F. A. Bazzaz. 2000. Biotic invasions: Causes, epidemiology, global consequences, and control. *Ecological Applications* **10**:689–710.
- Maixner, F., B. Krause-Kyora, D. Turaev, A. Herbig, M. R. Hoopmann, J. L. Hallows, U. Kusebauch, E. E. Vigl, P. Malfertheiner, and F. Megraud. 2016. The 5300-year-old Helicobacter pylori genome of the Iceman. *Science* **351**:162–165.
- Mallet, J. 2007. Hybrid speciation. *Nature* **446**:279–283.
- Mallet, J. 2008. Hybridization, ecological races and the nature of species: empirical evidence for the ease of speciation. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* **363**:2971–2986.
- Mank, J. E., J. E. Carlson, and M. C. Brittingham. 2004. A century of hybridization: decreasing genetic distance between American black ducks and mallards. *Conservation Genetics* **5**:395–403.
- Mantovani, B., and V. Scali. 1992. Hybridogenesis and androgenesis in the stick-insect *Bacillus rossius-Grandii benazzii* (Insecta, Phasmatodea). *Evolution* **46**:783–796.
- Marino, J., and C. Sillero-Zubiri. 2013. *Canis simensis*, Ethiopian Wolf. <http://www.iucnredlist.org>.
- Martino, L. A., A. Osella, C. Dorso, and J. L. Lanata. 2007. Fisher equation for anisotropic diffusion: Simulating South American human dispersals. *Physical Review E* **76**:031923.
- Mason, P. H., and R. V. Short. 2011. Neanderthal-human hybrids. *Hypothesis* **9**:1–5.
- Matondo, B. N., M. Ovidio, J. C. Philippart, and P. Poncin. 2011. Reproductive behaviour and

10. Literature Cited

- sexual production in the first-generation hybrids of roach *Rutilus rutilus* L. x common bream *Abramis brama* L. *Journal of Applied Ichthyology* **27**:859–867.
- Mayer, M., O. Hawlitschek, A. Zahn, and F. Glaw. 2013. Composition of twenty Green Frog populations (*Pelophylax*) across Bavaria, Germany. *Salamandra* **49**:31–44.
- Mayr, E. 1942. Systematics and the origin of species, from the viewpoint of a zoologist. Harvard University Press.
- McCracken, K. G., and R. E. Wilson. 2011. Gene Flow and Hybridization between Numerically Imbalanced Populations of Two Duck Species in the Falkland Islands. *Plos One* **6**.
- McDevitt, A. D., S. Mariani, M. Hebblewhite, N. J. Decesare, L. Morgantini, D. Seip, B. V. Weckworth, and M. Musiani. 2009. Survival in the Rockies of an endangered hybrid swarm from diverged caribou (*Rangifer tarandus*) lineages. *Molecular Ecology* **18**:665–679.
- McGuire, B., M. K. Oli, and L. L. Getz. 2009. Effects of conspecific and heterospecific residents on patterns of immigration in two species of voles. *Acta Theriologica* **54**:321–332.
- Mee, J. A., and S. P. Otto. 2010. Variation in the strength of male mate choice allows long-term coexistence of sperm-dependent asexuals and their sexual hosts. *Evolution* **64**:2808–2819.
- Mee, J. A., and E. B. Taylor. 2012. The cybrid invasion: widespread postglacial dispersal by *Phoxinus* (Pisces: Cyprinidae) cytoplasmic hybrids. *Canadian Journal of Zoology-Revue Canadienne De Zoologie* **90**:577–584.
- Meirmans, P. G. 2011. Marlin, software to create, run, and analyse spatially realistic simulations. *Molecular ecology resources* **11**:146–150.
- Mellars, P. 2006. Going east: new genetic and archaeological perspectives on the modern human colonization of Eurasia. *Science* **313**:796–800.
- Mellars, P. 2011. Palaeoanthropology: the earliest modern humans in Europe. *Nature* **479**:483–5.
- Melo-Ferreira, J., P. Boursot, E. Randi, A. Kryukov, F. Suchentrunk, N. Ferrand, and P. Alves. 2007. The rise and fall of the mountain hare (*Lepus timidus*) during Pleistocene glaciations: expansion and retreat with hybridization in the Iberian Peninsula. *Molecular Ecology* **16**:605–618.
- Mendelson, T. C., and K. L. Shaw. 2012. The (mis) concept of species recognition. *Trends in Ecology & Evolution* **27**:421–427.
- Mendez, F. L., G. D. Poznik, S. Castellano, and C. D. Bustamante. 2016. The Divergence of

10. Literature Cited

- Neandertal and Modern Human Y Chromosomes. *The American Journal of Human Genetics* **98**:728–734.
- Meraner, A., A. Venturi, G. Ficetola, S. Rossi, A. Candiotti, and A. Gandolfi. 2013. Massive invasion of exotic *Barbus barbus* and introgressive hybridization with endemic *Barbus plebejus* in Northern Italy: where, how and why? *Molecular ecology* **22**:5295–5312.
- Meyer, A., W. Salzburger, and M. Schartl. 2006. Hybrid origin of a swordtail species (Teleostei: *Xiphophorus clemenciae*) driven by sexual selection. *Molecular Ecology* **15**:721–730.
- Meyer, M., M. Kircher, M. T. Gansauge, H. Li, F. Racimo, S. Mallick, J. G. Schraiber, F. Jay, K. Prufer, C. de Filippo, P. H. Sudmant, C. Alkan, Q. Fu, R. Do, N. Rohland, A. Tandon, M. Siebauer, R. E. Green, K. Bryc, A. W. Briggs, U. Stenzel, J. Dabney, J. Shendure, J. Kitzman, M. F. Hammer, M. V. Shunkov, A. P. Derevianko, N. Patterson, A. M. Andres, E. E. Eichler, M. Slatkin, D. Reich, J. Kelso, and S. Paabo. 2012. A high-coverage genome sequence from an archaic Denisovan individual. *Science* **338**:222–226.
- Montoya-Burgos, J. I. 2011. Patterns of positive selection and neutral evolution in the protein-coding genes of *Tetraodon* and *Takifugu*. *PLoS One* **6**:e24800.
- Moreau, C., C. Bherer, H. Vezina, M. Jomphe, D. Labuda, and L. Excoffier. 2011. Deep Human Genealogies Reveal a Selective Advantage to Be on an Expanding Wave Front. *Science* .
- Morton, N. 1982. Estimation of demographic parameters from isolation by distance. *Hum. Hered.* **32**:37–41.
- Morton, N. E. 1977. Isolation by distance in human populations. *Ann Hum Genet* **40**:361–5.
- Muhlfeld, C. C., S. T. Kalinowski, T. E. McMahon, M. L. Taper, S. Painter, R. F. Leary, and F. W. Allendorf. 2009. Hybridization rapidly reduces fitness of a native trout in the wild. *Biology Letters* **5**:328–331.
- Muller, K. L. 1998. The role of conspecifics in habitat settlement in a territorial grasshopper. *Animal Behaviour* **56**:479–485.
- Myhr, A. I. 2010. A precautionary approach to genetically modified organisms: challenges and implications for policy and science. *Journal of agricultural and environmental ethics* **23**:501–525.
- Neaves, W. B., and P. Baumann. 2011. Unisexual reproduction among vertebrates. *Trends in Genetics* **27**:81–88.
- Neiva, J., G. A. Pearson, M. Valero, and E. A. Serrao. 2010. Surfing the wave on a borrowed

10. Literature Cited

- board: range expansion and spread of introgressed organellar genomes in the seaweed *Fucus ceranoides* L. *Molecular ecology* **19**:4812–4822.
- Neuenschwander, S., F. Guillaume, J. Goudet, et al. 2008. quantiNemo: an individual-based program to simulate quantitative traits with explicit genetic architecture in a dynamic metapopulation. *Bioinformatics* **24**:1552–1553.
- Nordborg, M. 1998. On the probability of Neanderthal ancestry. *Am J Hum Genet* **63**:1237–40.
- Norris, L. C., B. J. Main, Y. Lee, T. C. Collier, A. Fofana, A. J. Cornel, and G. C. Lanzaro. 2015. Adaptive introgression in an African malaria mosquito coincident with the increased usage of insecticide-treated bed nets. *Proceedings of the National Academy of Sciences* **112**:815–820.
- Novembre, J., T. Johnson, K. Bryc, Z. Kutalik, A. R. Boyko, A. Auton, A. Indap, K. S. King, S. Bergmann, M. R. Nelson, et al. 2008. Genes mirror geography within Europe. *Nature* **456**:98–101.
- Nussberger, B., 2013. Assessing Introgression between European Wildcats (*Felis silvestris silvestris*) and Domestic Cats (*Felis silvestris catus*). Thesis, University of Zurich.
- Nussberger, B., M. Currat, C. S. Quilodrán, N. Ponta, and L. F. Keller. in prep. Range expansion as a potential explanation for introgression in European wildcats .
- Nussberger, B., M. P. Greminger, C. Grossen, L. F. Keller, and P. Wandeler. 2013. Development of SNP markers identifying European wildcats, domestic cats, and their admixed progeny. *Molecular Ecology Resources* **13**:447–460.
- Nussberger, B., P. Wandeler, D. Weber, and L. Keller. 2014. Monitoring introgression in European wildcats in the Swiss Jura. *Conservation Genetics* **15**:1219–1230.
- Nussberger, B., D. Weber, B. Hefti-Gautschi, and P. Lüps. 2007. Neuester Stand des Nachweises und der Verbreitung der Waldkatze (*Felis silvestris*) in der Schweiz. *Mitteilungen der Naturforschenden Gesellschaft in Bern* **64**:67–80.
- Oke, K. B., P. A. Westley, D. T. Moreau, and I. A. Fleming. 2013. Hybridization between genetically modified Atlantic salmon and wild brown trout reveals novel ecological interactions. *Proceedings of the Royal Society of London B: Biological Sciences* **280**:20131047.
- Oliveira, R., R. Godinho, E. Randi, and P. C. Alves. 2008a. Hybridization versus conservation: are domestic cats threatening the genetic integrity of wildcats (*Felis silvestris silvestris*) in Iberian Peninsula? *Philosophical Transactions of the Royal Society B: Biological Sciences* **363**:2953–2961.

10. Literature Cited

- Oliveira, R., R. Godinho, E. Randi, N. Ferrand, and P. C. Alves. 2008b. Molecular analysis of hybridisation between wild and domestic cats (*Felis silvestris*) in Portugal: implications for conservation. *Conservation Genetics* **9**:1–11.
- Osborne, C. E., B. L. Swift, and G. Baldassarre. 2010. Fate of captive-reared and released mallards on eastern Long Island, New York. *Human-Wildlife Interactions* **4**:266–274.
- Papadopoulou, A., J. Bergsten, T. Fujisawa, M. T. Monaghan, T. G. Barraclough, and A. P. Vogler. 2008. Speciation and DNA barcodes: testing the effects of dispersal on the formation of discrete sequence clusters. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* **363**:2987–2996.
- Pasachnik, S. A., A. C. Echternacht, and B. M. Fitzpatrick. 2010. Gene trees, species and species trees in the *Ctenosaura palearis* clade. *Conservation genetics* **11**:1767–1781.
- Peischl, S., I. Dupanloup, M. Kirkpatrick, and L. Excoffier. 2013. On the accumulation of deleterious mutations during range expansions. *Mol Ecol*.
- Pennington, R., 2001. Hunter-gatherer demography. Pages 170–204 in C. Panter-Brick, R. Layton, and P. Rowley-Conwy, editors. *Hunter-gatherers: an interdisciplinary perspective*. Cambridge University Press.
- Peters, J. L., S. A. Sonsthagen, P. Lavretsky, M. Rezsutek, W. P. Johnson, and K. G. McCracken. 2014. Interspecific hybridization contributes to high genetic diversity and apparent effective population size in an endemic population of mottled ducks (*Anas fulvigula maculosa*). *Conservation genetics* **15**:509–520.
- Petit, R. J., and L. Excoffier. 2009. Gene flow and species delimitation. *Trends in Ecology & Evolution* **24**:386–393.
- Pinto, P. V., P. Beja, N. Ferrand, and R. Godinho. 2016. Hybridization following population collapse in a critically endangered antelope. *Scientific reports* **6**.
- Pitts, C. S., D. R. Jordan, I. G. Cowx, and N. V. Jones. 1997. Controlled breeding studies to verify the identity of roach and common bream hybrids from a natural population. *Journal of Fish Biology* **51**:686–696.
- Plötner, J. 1998. Genetic diversity in mitochondrial 12S rDNA of western Palearctic water frogs (Anura, Ranidae) and implications for their systematics. *Journal of Zoological Systematics and Evolutionary Research* **36**:191–201.
- Plötner, J., F. Kohler, T. Uzzell, P. Beerli, R. Schreiber, G. D. Guex, and H. Hotz. 2009. Evolution

10. Literature Cited

- of serum albumin intron-1 is shaped by a 5' truncated non-long terminal repeat retrotransposon in western Palearctic water frogs (Neobatrachia). *Molecular Phylogenetics and Evolution* **53**:784–791.
- Plötner, J., and T. Ohst. 2001. New hypothesis on the systematics of the western Palearctic water frog complex (Anura: Ranidae). *Zoosystematics and Evolution* **77**:5–21.
- Plötner, J., T. Uzzell, P. Beerli, C. Akin, C. C. Bilgin, C. Haefeli, T. Ohst, F. Köhler, R. Schreiber, G. D. Guex, A. N. Litvinchuk, R. Westaway, H. U. Reyer, N. Pruvost, and H. Hotz, 2010. Genetic divergence and evolution of reproductive isolation in Eastern Mediterranean water frogs. Pages 373–403 in M. Glaubrecht and H. Schneider, editors. *Evolution in Action: Case studies in Adaptive Radiation, Speciation and the Origin of Biodiversity*. Springer, Heidelberg, Germany.
- Ponchon, A., R. Garnier, D. Grémillet, and T. Boulinier. 2015. Predicting population responses to environmental change: the importance of considering informed dispersal strategies in spatially structured population models. *Diversity and Distributions* **21**:88–100.
- Powell, A., S. Shennan, and M. G. Thomas. 2009. Late Pleistocene Demography and the Appearance of Modern Human Behavior. *Science* **324**:1298–1301.
- Prufer, K., F. Racimo, N. Patterson, F. Jay, S. Sankararaman, S. Sawyer, A. Heinze, G. Renaud, P. H. Sudmant, C. de Filippo, H. Li, S. Mallick, M. Dannemann, Q. Fu, M. Kircher, M. Kuhlwilm, M. Lachmann, M. Meyer, M. Ongyerth, M. Siebauer, C. Theunert, A. Tandon, P. Moorjani, J. Pickrell, J. C. Mullikin, S. H. Vohr, R. E. Green, I. Hellmann, P. L. Johnson, H. Blanche, H. Cann, J. O. Kitzman, J. Shendure, E. E. Eichler, E. S. Lein, T. E. Bakken, L. V. Golovanova, V. B. Doronichev, M. V. Shunkov, A. P. Derevianko, B. Viola, M. Slatkin, D. Reich, J. Kelso, and S. Paabo. 2014. The complete genome sequence of a Neanderthal from the Altai Mountains. *Nature* **505**:43–49.
- Prugnolle, F., A. Manica, and F. Balloux. 2005. Geography predicts neutral genetic diversity of human populations. *Current Biology* **15**:R159–R160.
- Quilodrán, C. S., M. Currat, and J. I. Montoya-Burgos. 2014a. A General Model of Distant Hybridization Reveals the Conditions for Extinction in Atlantic Salmon and Brown Trout. *Plos One* **9**:e101736.
- Quilodrán, C. S., C. F. Estades, and R. A. Vásquez. 2014b. Conspecific effect on habitat selection of a territorial cavity-nesting bird. *The Wilson Journal of Ornithology* **126**:534–543.
- Quilodrán, C. S., J. I. Montoya-Burgos, and M. Currat. 2015. Modelling interspecific hybridiza-

10. Literature Cited

- tion with genome exclusion to identify conservation actions: the case of native and invasive *Pelophylax* waterfrogs. *Evolutionary Applications* **8**:199–210.
- R Development Core Team. 2015. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria.
- Ramachandran, S., O. Deshpande, C. C. Roseman, N. A. Rosenberg, M. W. Feldman, and L. L. Cavalli-Sforza. 2005. Support from the relationship of genetic and geographic distance in human populations for a serial founder effect originating in Africa. *PNAS* **102**:15942–15947.
- Rasmussen, M., X. S. Guo, Y. Wang, K. E. Lohmueller, S. Rasmussen, A. Albrechtsen, L. Skotte, S. Lindgreen, M. Metspalu, T. Jombart, T. Kivisild, W. W. Zhai, A. Eriksson, A. Manica, L. Orlando, F. M. De La Vega, S. Tridico, E. Metspalu, K. Nielsen, M. C. Avila-Arcos, J. V. Moreno-Mayar, C. Muller, J. Dortsch, M. T. P. Gilbert, O. Lund, A. Wesolowska, M. Karmin, L. A. Weinert, B. Wang, J. Li, S. S. Tai, F. Xiao, T. Hanihara, G. van Driem, A. R. Jha, F. X. Ricaut, P. de Knijff, A. B. Migliano, I. G. Romero, K. Kristiansen, D. M. Lambert, S. Brunak, P. Forster, B. Brinkmann, O. Nehlich, M. Bunce, M. Richards, R. Gupta, C. D. Bustamante, A. Krogh, R. A. Foley, M. M. Lahr, F. Balloux, T. Sicheritz-Ponten, R. Villemans, R. Nielsen, J. Wang, and E. Willerslev. 2011. An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. *Science* **333**:94–98.
- Rasteiro, R., P.-A. Boutrier, D. Monier, D. A. Curbelo, V. Sousa, and L. Chikhi. submitted. SINS: forward simulation of individuals through time and space .
- Rasteiro, R., P.-A. Boutrier, V. C. Sousa, and L. Chikhi. 2012. Investigating sex-biased migration during the Neolithic transition in Europe, using an explicit spatial simulation framework. *Proceedings of the Royal Society of London B: Biological Sciences* page rspb20112323.
- Rasteiro, R., and L. Chikhi. 2013. Female and male perspectives on the neolithic transition in Europe: clues from ancient and modern genetic data. *PloS one* **8**:e60944.
- Ray, N., 2003. Modélisation de la démographie des populations humaines préhistoriques à l'aide de données environnementales et génétiques. Ph.D. thesis, University of Geneva.
- Ray, N., and J. Adams. 2001. A GIS-based vegetation map of the world at the last glacial maximum (25,000-15,000 BP). *Internet Archaeology* **11**.
- Ray, N., M. Currat, P. Berthier, and L. Excoffier. 2005. Recovering the geographic origin of early modern humans by realistic and spatially explicit simulations. *Genome Research* **15**:1161–1167.

10. Literature Cited

- Ray, N., M. Currat, and L. Excoffier. 2003. Intra-deme molecular diversity in spatially expanding populations. *Molecular Biology and Evolution* **20**:76–86.
- Ray, N., M. Currat, and L. Excoffier, 2008. Incorporating Environmental Heterogeneity in Spatially-explicit Simulations of Human Genetic Diversity. Pages 103–117 in S. Matsumura, P. Forster, and C. Renfrew, editors. *Simulations, Genetics and Human Prehistory*. McDonald Institute for Archaeological Research, Cambridge.
- Ray, N., M. Currat, M. Foll, and L. Excoffier. 2010. SPLATCHE2: a spatially explicit simulation framework for complex demography, genetic admixture and recombination. *Bioinformatics* **26**:2993–2994.
- Ray, N., and L. Excoffier. 2009. Inferring past demography using spatially explicit population genetic models. *Hum Biol* **81**:141–57.
- Raybould, A., and A. Gray. 1993. Genetically modified crops and hybridization with wild relatives: a UK perspective. *Journal of Applied Ecology* pages 199–219.
- Rebaudo, F., A. Rouzic, S. Dupas, J.-F. Silvain, M. Harry, and O. Dangles. 2013. SimAdapt: an individual-based genetic model for simulating landscape management impacts on populations. *Methods in Ecology and Evolution* **4**:595–600.
- Reich, D., R. E. Green, M. Kircher, J. Krause, N. Patterson, E. Y. Durand, B. Viola, A. W. Briggs, U. Stenzel, P. L. F. Johnson, T. Maricic, J. M. Good, T. Marques-Bonet, C. Alkan, Q. M. Fu, S. Mallick, H. Li, M. Meyer, E. E. Eichler, M. Stoneking, M. Richards, S. Talamo, M. V. Shunkov, A. P. Derevianko, J. J. Hublin, J. Kelso, M. Slatkin, and S. Paabo. 2010. Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature* **468**:1053–1060.
- Reich, D., N. Patterson, M. Kircher, F. Delfin, M. R. Nandineni, I. Pugach, A. M. Ko, Y. C. Ko, T. A. Jinam, M. E. Phipps, N. Saitou, A. Wollstein, M. Kayser, S. Paabo, and M. Stoneking. 2011. Denisova Admixture and the First Modern Human Dispersals into Southeast Asia and Oceania. *Am J Hum Genet* .
- Ren, G. P., R. J. Abbott, Y. F. Zhou, L. R. Zhang, Y. L. Peng, and J. Q. Liu. 2012. Genetic divergence, range expansion and possible homoploid hybrid speciation among pine species in Northeast China. *Heredity* **108**:552–562.
- Rendine, S., A. Piazza, and L. Cavalli-Sforza. 1986. Simulation and separation by principal components of multiple demic expansions in Europe. *Am. Nat.* **128**:681–706.

10. Literature Cited

- Rhymer, J. M. 2006. S33-4 Extinction by hybridization and introgression in anatine ducks. *Acta Zoologica Sinica* **52**:583–585.
- Rhymer, J. M., and D. Simberloff. 1996. Extinction by hybridization and introgression. *Annual Review of Ecology and Systematics* **27**:83–109.
- Rhymer, J. M., M. J. Williams, and R. T. Kingsford. 2004. Implications of phylogeography and population genetics for subspecies taxonomy of Grey (Pacific Black) Duck *Anas superciliosa* and its conservation in New Zealand. *Pacific Conservation Biology* **10**:57–66.
- Rieseberg, L. H. 1995. The role of hybridization in evolution: old wine in new skins. *American Journal of Botany* **82**:944–953.
- Rieseberg, L. H., O. Raymond, D. M. Rosenthal, Z. Lai, K. Livingstone, T. Nakazato, J. L. Durphy, A. E. Schwarzbach, L. A. Donovan, and C. Lexer. 2003. Major ecological transitions in wild sunflowers facilitated by hybridization. *Science* **301**:1211–1216.
- Rist, L., R. D. Semlitsch, H. Hotz, and H. U. Reyer. 1997. Feeding behaviour, food consumption, and growth efficiency of hemiconal and parental tadpoles of the *Rana esculenta* complex. *Functional Ecology* **11**:735–742.
- Robertson, H. A., J. E. Dowding, G. P. Elliott, R. A. Hitchmough, C. M. Miskelly, C. F. O'Donnell, R. G. Powlesland, P. M. Sagar, R. P. Scofield, and G. A. Taylor. 2013. Conservation status of New Zealand birds, 2012. *New Zealand threat classification series* **4**:22.
- Rodriguez, D. J. 1996. A model for the establishment of polyploidy in plants: Viable but infertile hybrids, iteroparity, and demographic stochasticity. *Journal of Theoretical Biology* **180**:189–196.
- Rozhnov, V. V. 1993. Extinction of the European mink: ecological catastrophe or a natural process? *Lutreola* **1**:10–16.
- Rundle, H., F. Breden, C. Griswold, A. Mooers, R. Vos, and J. Whitton. 2001. Hybridization without guilt: gene flow and the biological species concept. *Journal of Evolutionary Biology* **14**:868–869.
- Rushing, C. S., M. R. Dudash, and P. P. Marra. 2015. Habitat features and long-distance dispersal modify the use of social information by a long-distance migratory bird. *Journal of Animal Ecology* **84**:1469–1479.
- Ryan, M. E., J. R. Johnson, and B. M. Fitzpatrick. 2009. Invasive hybrid tiger salamander geno-

10. Literature Cited

- types impact native amphibians. *Proceedings of the National Academy of Sciences of the United States of America* **106**:11166–11171.
- Saari, S., S. Richter, M. Robbins, and S. H. Faeth. 2014. Bottom-up regulates top-down: the effects of hybridization of grass endophytes on an aphid herbivore and its generalist predator. *Oikos* **123**:545–552.
- Sæther, B.-E., M. Lillegård, V. Grøtan, M. C. Drever, S. Engen, T. D. Nudds, and K. M. Podruzny. 2008. Geographical gradients in the population dynamics of North American prairie ducks. *Journal of Animal Ecology* **77**:869–882.
- Sanchez-Mazas, A., J.-F. Lemaître, and M. Currat. 2012. Distinct evolutionary strategies of human leucocyte antigen loci in pathogen-rich environments. *Philosophical Transactions of the Royal Society of London B: Biological Sciences* **367**:830–839.
- Sanchez-Quinto, F., L. R. Botigue, S. Civit, C. Arenas, M. C. Avila-Arcos, C. D. Bustamante, D. Comas, and C. Lalueza-Fox. 2012. North African populations carry the signature of admixture with Neandertals. *PLoS One* **7**:e47765.
- Sankararaman, S., S. Mallick, M. Dannemann, K. Prüfer, J. Kelso, S. Pääbo, N. Patterson, and D. Reich. 2014. The genomic landscape of Neanderthal ancestry in present-day humans. *Nature* **507**:354–357.
- Satake, A., and H. Araki. 2012. Stocking of captive-bred fish can cause long-term population decline and gene pool replacement: predictions from a population dynamics model incorporating density-dependent mortality. *Theoretical Ecology* **5**:283–296.
- Say, L., S. Devillard, F. Léger, D. Pontier, and S. Ruette. 2012. Distribution and spatial genetic structure of European wildcat in France. *Animal Conservation* **15**:18–27.
- Schmeller, D. S., A. Pagano, A. Plenet, and M. Veith. 2007. Introducing water frogs - Is there a risk for indigenous species in France? *Comptes Rendus Biologies* **330**:684–690.
- Schmidt, D. J., N. R. Bond, M. Adams, and J. M. Hughes. 2011. Cytonuclear evidence for hybridogenetic reproduction in natural populations of the Australian carp gudgeon (*Hypseleotris*: Eleotridae). *Molecular Ecology* **20**:3367–3380.
- Schneider, H., U. Sinsch, and T. S. Sofianidou. 1993. The water frogs of Greece: Bioacoustic evidence for a new species. *Journal of Zoological Systematics and Evolutionary Research* **31**:47–63.

10. Literature Cited

- Schumer, M., R. Cui, D. L. Powell, G. G. Rosenthal, and P. Andolfatto. 2016. Ancient hybridization and genomic stabilization in a swordtail fish. *Molecular ecology* .
- Seehausen, O., G. Takimoto, D. Roy, and J. Jokela. 2008. Speciation reversal and biodiversity dynamics with hybridization in changing environments. *Molecular Ecology* **17**:30–44.
- Seehausen, O., J. J. Van Alphen, and F. Witte. 1997. Cichlid fish diversity threatened by eutrophication that curbs sexual selection. *Science* **277**:1808–1811.
- Semlitsch, R. D., and H. U. Reyer. 1992. Performance of tadpoles from the hybridogenetic *Rana esculenta* complex: interactions with pond drying and interspecific competition. *Evolution* **46**:665–676.
- Serre, D., A. Langaney, M. Chech, M. Teschler-Nicola, M. Paunovic, P. Mennecier, M. Hofreiter, G. Possnert, and S. Pääbo. 2004. No evidence of Neandertal mtDNA contribution to early modern humans. *PLoS Biol* **2**:e57.
- Seyoum, S., M. D. Tringali, R. R. Bielefeld, J. C. Feddersen, R. J. Benedict Jr, A. T. Fanning, B. L. Barthel, C. Curtis, C. Puchulutegui, and A. C. Roberts. 2012. Fifty-nine microsatellite markers for hybrid classification studies involving endemic Florida Mottled Duck (*Anas fulvigula fulvigula*) and invasive Mallards (*A. platyrhynchos*). *Conservation Genetics Resources* **4**:681–687.
- Sgaramella-Zonta, L., and L. Cavalli-Sforza, 1973. A methode for the detection of a demic cline. *in* N. E. Morton, editor. Genetic structure of population. Population Genetics Monograph 3, University of Hawaii Press, Honolulu, HI.
- Shigesada, N., and K. Kawasaki. 1997. Biological Invasions: Theory and Practice. Oxford Series in Ecology and Evolution, Oxford University Press, Oxford.
- Shoo, L. P., D. H. Olson, S. K. McMenamin, K. A. Murray, M. Van Sluys, M. A. Donnelly, D. Stratford, J. Terhivuo, A. Merino-Viteri, S. M. Herbert, P. J. Bishop, P. S. Corn, L. Dovey, R. A. Griffiths, K. Lowe, M. Mahony, H. McCallum, J. D. Shuker, C. Simpkins, L. F. Skerratt, S. E. Williams, and J. M. Hero. 2011. Engineering a future for amphibians under climate change. *Journal of Applied Ecology* **48**:487–492.
- Simberloff, D. 2008. Invasion biologists and the biofuels boom: Cassandras or colleagues. *Weed Science* **56**:867–872.
- Simmonds, E. G., and T. Coulson. 2015. Analysis of phenotypic change in relation to climatic drivers in a population of Soay sheep *Ovis aries*. *Oikos* **124**:543–552.

10. Literature Cited

- Simonti, C. N., B. Vernot, L. Bastarache, E. Bottinger, D. S. Carrell, R. L. Chisholm, D. R. Crosslin, S. J. Hebring, G. P. Jarvik, and I. J. Kullo. 2016. The phenotypic legacy of admixture between modern humans and Neandertals. *Science* **351**:737–741.
- Skoglund, P., and M. Jakobsson. 2011. Archaic human ancestry in East Asia. *Proc Natl Acad Sci U S A* **108**:18301–6.
- Skoglund, P., H. Malmström, A. Omrak, M. Raghavan, C. Valdiosera, T. Günther, P. Hall, K. Tamboets, J. Parik, K.-G. Sjögren, et al. 2014. Genomic diversity and admixture differs for Stone-Age Scandinavian foragers and farmers. *Science* **344**:747–750.
- Skoglund, P., H. Malmström, M. Raghavan, J. Storå, P. Hall, E. Willerslev, M. T. P. Gilbert, A. Götherström, and M. Jakobsson. 2012. Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe. *Science* **336**:466–469.
- Söderquist, P., J. Norrström, J. Elmberg, M. Guillemain, and G. Gunnarsson. 2014. Wild Mallards Have More “Goose-Like” Bills Than Their Ancestors: A Case of Anthropogenic Influence? *PloS one* **9**:e115143.
- Sokal, R. R. 1991. Ancient movement patterns determine modern genetic variances in Europe. *Human Biology* **63**:589–606.
- Soltis, D. E., and P. S. Soltis. 1999. Polyploidy: recurrent formation and genome evolution. *Trends in Ecology & Evolution* **14**:348–352.
- Soltis, P. S., and D. E. Soltis. 2009. The role of hybridization in plant speciation. *Annual review of plant biology* **60**:561–588.
- Som, C., B. R. Anholt, and H. U. Reyer. 2000. The effect of assortative mating on the coexistence of a hybridogenetic waterfrog and its sexual host. *American Naturalist* **156**:34–46.
- Som, C., and H. U. Reyer. 2006. Demography and evolution of pure hybridogenetic frog (*Rana esculenta*) populations. *Evolutionary Ecology Research* **8**:1235–1248.
- Sommer, R., and N. Benecke. 2006. Late Pleistocene and Holocene development of the felid fauna (Felidae) of Europe: a review. *Journal of Zoology* **269**:7–19.
- Song, Y., S. Endepols, N. Klemann, D. Richter, F.-R. Matuschka, C.-H. Shih, M. W. Nachman, and M. H. Kohn. 2011. Adaptive introgression of anticoagulant rodent poison resistance by hybridization between old world mice. *Current Biology* **21**:1296–1301.
- Soulé, M. E. 1985. What is conservation biology? *BioScience* **35**:727–734.
- Spiegel, O., S. T. Leu, A. Sih, S. S. Godfrey, and C. M. Bull. 2015. When the going gets tough:

10. Literature Cited

- behavioural type-dependent space use in the sleepy lizard changes as the season dries. Page 20151768 in Proc. R. Soc. B, volume 282. The Royal Society.
- Stahl, P., and M. Artois. 1994. Status and conservation of the wildcat (*Felis silvestris*) in Europe and around the Mediterranean rim. Council of Europe.
- Steele, J. 2009. Human dispersals: mathematical models and the archaeological record. *Human Biology* **81**:121–140.
- Steele, J., J. Adams, and T. Sluckin. 1998. Modelling paleoindian dispersals. *World Archaeology* **30**:286–305.
- Stewart, J. R., and C. B. Stringer. 2012. Human evolution out of Africa: the role of refugia and climate change. *Science* **335**:1317–1321.
- Streicher, J. W., T. J. Devitt, C. S. Goldberg, J. H. Malone, H. Blackmon, and M. K. Fujita. 2014. Diversification and asymmetrical gene flow across time and space: lineage sorting and hybridization in polytypic barking frogs. *Molecular ecology* **23**:3273–3291.
- Stringer, C. 2014. Why we are not all multiregionalists now. *Trends in ecology & evolution* **29**:248–251.
- Sukumaran, J., and M. T. Holder. 2011. Ginkgo: spatially-explicit simulator of complex phylo-geographic histories. *Mol Ecol Resour* **11**:364–9.
- Sunquist, M., and F. Sunquist. 2002. Wild cats of the world. University of Chicago Press.
- Szostek, K. L., M. Schaub, and P. H. Becker. 2014. Immigrants are attracted by local pre-breeding and recruits in a seabird colony. *Journal of Animal Ecology* **83**:1015–1024.
- Tanaka, Y. 2010. Recombination and epistasis facilitate introgressive hybridization across reproductively isolated populations: a gamete-based simulation. *Evolutionary Ecology Research* **12**:523–544.
- Taylor, E., J. Boughman, M. Groenenboom, M. Sniatynski, D. Schluter, and J. Gow. 2006. Speciation in reverse: morphological and genetic evidence of the collapse of a three-spined stickleback (*Gasterosteus aculeatus*) species pair. *Molecular Ecology* **15**:343–355.
- Taylor, S. A., E. L. Larson, and R. G. Harrison. 2015. Hybrid zones: windows on climate change. *Trends in Ecology & Evolution* **30**:398–406.
- Tietje, G. A., and H. U. Reyer. 2004. Larval development and recruitment of juveniles in a natural population of *Rana lessonae* and *Rana esculenta*. *Copeia* **3**:638–646.
- Tinti, F., and V. Scali. 1995. Allozymic and cytological evidence for hemiconal, all-paternal, and

10. Literature Cited

- mosaic offspring of the hybridogenetic stick insect *Bacillus rossius-grandii grandii*. *Journal of Experimental Zoology* **273**:149–159.
- Todesco, M., M. A. Pascual, G. L. Owens, K. L. Ostevik, B. T. Moyers, S. Hübner, S. M. Heredia, M. A. Hahn, C. Caseys, and D. G. Bock. 2016. Hybridization and extinction. *Evolutionary Applications* doi: 10.1111/eva.12367 .
- Toscano, B. J., D. Pulcini, B. Hayden, T. Russo, M. Kelly-Quinn, and S. Mariani. 2010. An ecomorphological framework for the coexistence of two cyprinid fish and their hybrids in a novel environment. *Biological Journal of the Linnean Society* **99**:768–783.
- Tracey, J. P., B. S. Lukins, and C. Haselden. 2008. Hybridisation between mallard (*Anas platyrhynchos*) and grey duck (*A. superciliosa*) on Lord Howe Island and management options. *Notornis* **55**:1–7.
- Travis, J. M., M. Delgado, G. Bocedi, M. Baguette, K. Bartoń, D. Bonte, I. Boulangeat, J. A. Hodgson, A. Kubisch, and V. Penteriani. 2013. Dispersal and species' responses to climate change. *Oikos* **122**:1532–1540.
- Tubaro, P. L., and D. A. Lijtmaer. 2002. Hybridization patterns and the evolution of reproductive isolation in ducks. *Biological Journal of the Linnean Society* **77**:193–200.
- Turner, D. C. 2000. The domestic cat: the biology of its behaviour. Cambridge University Press.
- Urke, H. A., J. Koksvik, J. V. Arnekleiv, K. Hindar, F. Kroglund, and T. Kristensen. 2010. Seawater tolerance in Atlantic salmon, *Salmo salar* L., brown trout, *Salmo trutta* L., and *S. salar* x *S. trutta* hybrids smolt. *Fish Physiology and Biochemistry* **36**:845–853.
- Van Rensburg, B. J., O. L. Weyl, S. J. Davies, N. J. van Wilgen, D. Spear, C. T. Chimimba, and F. Peacock. 2011. Invasive vertebrates of South Africa. *Biological invasions: economic and environmental costs of alien plant, animal, and microbe species* pages 326–378.
- Van Valen, L. 1976. Ecological species, multispecies, and oaks. *Taxon* pages 233–239.
- Veen, T., T. Borge, S. C. Griffith, G.-P. Saetre, S. Bures, L. Gustafsson, and B. C. Sheldon. 2001. Hybridization and adaptive mate choice in flycatchers. *Nature* **411**:45–50.
- Veeramah, K. R., and M. F. Hammer. 2014. The impact of whole-genome sequencing on the reconstruction of human population history. *Nature Reviews Genetics* **15**:149–162.
- Velema, G., J. Rosenfeld, and E. Taylor. 2012. Effects of invasive American signal crayfish (*Pacifastacus leniusculus*) on the reproductive behaviour of threespine stickleback (*Gasterosteus aculeatus*) sympatric species pairs. *Canadian Journal of Zoology* **90**:1328–1338.

10. Literature Cited

- Verhulst, P. F. 1838. Notice sur la loi que la population poursuit dans son accroissement. Correspondance Mathematique et Physique **10**:113–121.
- Vernot, B., and J. M. Akey. 2014. Resurrecting surviving Neandertal lineages from modern human genomes. *Science* **343**:1017–21.
- Volterra, V. 1928. Variations and fluctuations of the number of individuals in animal species living together. *J. Cons. Int. Explor. Mer* **3**:3–51.
- Vonlanthen, P., D. Bittner, A. G. Hudson, K. A. Young, R. Muller, B. Lundsgaard-Hansen, D. Roy, S. Di Piazza, C. R. Largiader, and O. Seehausen. 2012. Eutrophication causes speciation reversal in whitefish adaptive radiations. *Nature* **482**:357–U1500.
- Vorburger, C. 2001a. Fixation of deleterious mutations in clonal lineages: Evidence from hybridogenetic frogs. *Evolution* **55**:2319–2332.
- Vorburger, C. 2001b. Non-hybrid offspring from matings between hemiclonal hybrid waterfrogs suggest occasional recombination between clonal genomes. *Ecology Letters* **4**:628–636.
- Vorburger, C., and H. U. Reyer. 2003. A genetic mechanism of species replacement in European waterfrogs? *Conservation Genetics* **4**:141–155.
- Wakeley, J. 2009. Coalescent Theory: An Introduction. Roberts and Company Publishers, Greenwood Village, Colorado.
- Wall, J. D., M. A. Yang, F. Jay, S. K. Kim, E. Y. Durand, L. S. Stevison, C. Gignoux, A. Woerner, M. F. Hammer, and M. Slatkin. 2013. Higher levels of neanderthal ancestry in East Asians than in Europeans. *Genetics* **194**:199–209.
- Wang, C. 2007. Interpretation of the biological species concept from interspecific hybridization of two *Helicoverpa* species. *Chinese Science Bulletin* **52**:284–286.
- Wegmann, D., M. Currat, and L. Excoffier. 2006. Molecular diversity after a range expansion in heterogeneous environments. *Genetics* **174**:2009–2020.
- Wegmann, D., C. Leuenberger, S. Neuenschwander, and L. Excoffier. 2010. ABCtoolbox: a versatile toolkit for approximate Bayesian computations. *BMC bioinformatics* **11**:116.
- While, G. M., S. Michaelides, R. J. Heathcote, H. E. MacGregor, N. Zajac, J. Beninde, P. Carazo, G. Pérez i de Lanuza, R. Sacchi, and M. A. Zuffi. 2015. Sexual selection drives asymmetric introgression in wall lizards. *Ecology letters* **18**:1366–1375.
- Whitney, K. D., R. A. Randell, and L. H. Rieseberg. 2006. Adaptive introgression of herbivore

10. Literature Cited

- resistance traits in the weedy sunflower *Helianthus annuus*. *The American Naturalist* **167**:794–807.
- Wilbur, H. M. 1976. Density-dependent aspects of metamorphosis in *Ambystoma* and *Rana sylvatica*. *Ecology* **57**:1289–1296.
- Wilbur, H. M., 1996. Multistage life cycles. Pages 75–108 in J. Rhodes, O. E., R. K. Chesser, and M. H. Smith, editors. *Population dynamics in ecological space and time*. Univ. of Chicago Press, Chicago.
- Wiley, E. O. 1978. The evolutionary species concept reconsidered. *Systematic Biology* **27**:17–26.
- Williams, C. L., R. C. Brust, T. T. Fendley, G. R. Tiller Jr, and O. E. Rhodes Jr. 2005. A comparison of hybridization between mottled ducks (*Anas fulvigula*) and mallards (*A. platyrhynchos*) in Florida and South Carolina using microsatellite DNA analysis. *Conservation Genetics* **6**:445–453.
- Williams, M., and B. Basse. 2006. Indigenous gray ducks, *Anas superciliosa*, and introduced mallards, *A. platyrhynchos*. New Zealand: processes and outcome of a deliberate encounter. *Acta Zoologica Sinica* **52**:579–582.
- Wilson, J. R., E. E. Dormontt, P. J. Prentis, A. J. Lowe, and D. M. Richardson. 2009. Something in the way you move: dispersal pathways affect invasion success. *Trends in Ecology & Evolution* **24**:136–144.
- Winkler, K. A., B. Pamminger-Lahnsteiner, J. Wanzenböck, and S. Weiss. 2011. Hybridization and restricted gene flow between native and introduced stocks of Alpine whitefish (*Coregonus* sp.) across multiple environments. *Molecular Ecology* **20**:456–472.
- Wolf, D. E., N. Takebayashi, and L. H. Rieseberg. 2001. Predicting the risk of extinction through hybridization. *Conservation Biology* **15**:1039–1053.
- Wolfe, K. 2003. Evolutionary biology: Speciation reversal. *Nature* **422**:25–26.
- Wood, A. B., and D. R. Jordan. 1987. Fertility of roach x bream hybrids, *Rutilus rutilus* (L) x *Abramis brama* (L), and their identification. *Journal of Fish Biology* **30**:249–261.
- Wright, S. 1943. Isolation by distance. *Genetics* **28**:114–138.
- Yakovlev, V. N., Y. V. Slynn'ko, I. G. Grechanov, and E. Y. Krysanov. 2000. Distant hybridization in fish. *Journal of Ichthyology* **40**:298–311.
- Yamaguchi, N., A. Kitchener, C. Driscoll, and B. Nussberger, 2015. *Felis silvestris*. The IUCN Red List of Threatened Species 2015. <http://www.iucnredlist.org>.

10. Literature Cited

- Youngson, A. F., J. H. Webb, C. E. Thompson, and D. Knox. 1993. Spawning of escaped farmed Atlantic salmon (*Salmo salar*): hybridization of females with brown trout (*Salmo trutta*). Canadian Journal of Fisheries and Aquatic Sciences **50**:1986–1990.
- Zhang, D.-Y. 2014. Demographic model of admixture predicts symmetric introgression when a species expands into the range of another: a comment on Currat et al.(2008). Journal of Systematics and Evolution **52**:35–39.
- Zvelebil, M. 2001. The agricultural transition and the origins of Neolithic society in Europe. Documenta Praehistorica XXVIII **Neolithic studies** **8**:1–26.