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Assessing the fitness consequences of mitonuclear interactions in natural populations

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ABSTRACT

Metazoans exist only with a continuous and rich supply of chemical energy from oxidative phosphorylation in mitochondria. The oxidative phosphorylation machinery that mediates energy conservation is encoded by both mitochondrial and nuclear genes, and hence the products of these two genomes must interact closely to achieve coordinated function of core respiratory processes. It follows that selection for efficient respiration will lead to selection for compatible combinations of mitochondrial and nuclear genotypes, and this should facilitate coadaptation between mitochondrial and nuclear genomes (mitonuclear coadaptation). Herein, we outline the modes by which mitochondrial and nuclear genomes may coevolve within natural populations, and we discuss the implications of mitonuclear coadaptation for diverse fields of study in the biological sciences. We identify five themes in the study of mitonuclear interactions that provide a roadmap for both ecological and biomedical studies seeking to measure the contribution of intergenomic coadaptation to the evolution of natural populations. We also explore the wider implications of the fitness consequences of mitonuclear interactions, focusing on central debates within the fields of ecology and biomedicine.

Key words: mitochondria, coadaptation, coevolution, epistatic interactions, gene flow, speciation, mitochondrial medicine, fitness.

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I. INTRODUCTION

Life depends on efficient production of useable energy. The substantial energy needs of most metazoans are met by the oxidative phosphorylation (OXPHOS) system embedded within the inner membrane of mitochondria, which produces approximately 90% of the ATP available to cells (Lane & Martin, 2010). The enzyme complexes that mediate OXPHOS are comprised of numerous polypeptide subunits. Most of these subunits are encoded by nuclear genes and are transported into mitochondria. However, multiple proton-translocating subunits (13 in bilaterian animals) are encoded by the mitochondrial DNA (mtDNA) (Bar-Yaacov, Blumberg & Mishmar, 2012). Consequently, energy production in eukaryotes must rely on a critical set of interactions between genes that span two distinct genomes (Rand, Haney & Fry, 2004; Wolff *et al.*, 2014; Hill, 2015).

Because the products of mitochondrial genes play a key role in enabling core respiratory processes, it was long assumed that variants that appeared within the mtDNA sequence would be quickly removed by purifying selection (Avise, 2004). This assumption has been supported by analyses of ratios of nonsynonymous (amino acid-changing) to synonymous (putatively silent) mutations across key mitochondrial genes (mt genes) of metazoans (Rand, 2001; Stewart *et al.*, 2008*a*; Nabholz, Ellegren & Wolf, 2013; Popadin *et al.*, 2013; Zhang & Broughton, 2013). Accordingly, a generation of evolutionary biologists, from the 1980s onwards, worked under the purview that the mitochondrial sequence variation segregating within or among populations was selectively neutral (Ballard & Whitlock, 2004; Dowling, Friberg & Lindell, 2008; Ballard & Pichaud, 2014).

By the mid-1990s, however, several studies had emerged that refuted the strict neutrality of variation in mtDNA sequence (Ballard & Kreitman, 1994; Nachman, Boyer & Aquadro, 1994; Rand, Dorfsman & Kann, 1994; Nachman *et al.*, 1996; Pichaud *et al.*, 2012). In subsequent years, a series of experimental studies highlighted numerous cases in which the genetic variation found within the mitochondrial genome was clearly non-neutral (i.e. functional), with pervasive effects on metabolic function (Willett, 2008; Arnqvist *et al.*, 2010; Pichaud *et al.*, 2012; Barreto & Burton, 2013*a*; Bock, Andrew & Rieseberg, 2014; Wolff *et al.*, 2016) and the expression of life-history traits (James & Ballard, 2003; Rand, Fry & Sheldahl, 2006; Clancy, 2008; Dowling *et al.*, 2009; Dowling, Meerupati & Arnqvist, 2010; Ma *et al.*, 2016; Roux *et al.*, 2016). Furthermore, these non-neutral mitochondrial effects often exhibited evidence of epistatic interactions with nuclear genes (Dobler *et al.*, 2014; Wolff *et al.*, 2014), consistent with the premise that interactions between mitochondrial and nuclear genomes drive the functionality of OXPHOS.

II. EVIDENCE FOR COEVOLUTION OF MITOCHONDRIAL AND NUCLEAR GENOMES

Research efforts have since aimed to dissect the evolutionary mechanisms that generate functional mitochondrial variation, and much emphasis has been placed on the potential for accumulation of mildly deleterious mutations in mtDNA (Lynch & Blanchard, 1998; Neiman & Taylor, 2009). The notion of a high mitochondrial mutation load runs contrary to the expectation that strong purifying selection would effectively prevent the accumulation of non-neutral variants. However, studies in mutant mouse models have suggested that purifying selection may only be fully effective at removing non-synonymous mtDNA mutations from the female germ line when these mutations confer severely pathogenic effects (Fan *et al.*, 2008; Stewart *et al.*, 2008*a*,*b*). Mitochondrial mutations of moderate effect, including those in transfer RNA (tRNA) and ribosomal RNA (rRNA) genes, have been reported to escape selection and be transmitted across generations (Alston *et al.*, 2017; Barreto *et al.*, 2018). When combined with the observation that mitochondrial genes of many eukaryotes mutate at much higher rates than nuclear genes (Brown, George & Wilson, 1979; Lynch, 1997; Smith & Keeling, 2015; Havird & Sloan, 2016), and that these mutations reside in a genome that has traditionally been thought to experience very low rates of recombination (i.e. an efficient mechanism of preventing mutational accumulation) (Hagström *et al.*, 2014), there would appear to be ample opportunity for mutations to accumulate and contribute to functional mitochondrial variation.

If left unchecked, mutational erosion of the mitochondrial genome would quickly lead to degradation of energy production and metabolic homeostasis (Lynch & Blanchard, 1998). It is therefore theorized that mutational erosion should create selection for nuclear genotypes able to offset the negative metabolic effects caused by mtDNA mutations (Rand *et al.*, 2004). Indeed, several studies have now identified signatures of complementary changes in interacting nuclear-encoded genes that have evolved in conjunction with sequence changes in the mitochondrial genome (Osada & Akashi, 2012; Barreto & Burton, 2013*b*; Sloan *et al.*, 2014; Van Der Sluis *et al.*, 2015; Havird *et al.*, 2015*b*, 2017; Barreto *et al.*, 2018; Yan, Ye & Werren, 2018). These tandem changes appear consistent with a model of compensatory mitonuclear coevolution. Under this model, the mitochondrial genome

would provide a mutational pressure that precipitates coadaptation between mitochondrial and nuclear genomes within populations (Ellison & Burton, 2008*b*; Yee, Sutton & Dowling, 2013; Barreto & Burton, 2013*b*; Havird *et al.*, 2015*b*).

The importance of compensatory coevolution between the nuclear and mitochondrial genomes is, however, a topic of current debate (Sloan, Havird & Sharbrough, 2017), and the argument that an asexual and uniparental mode of inheritance makes mtDNA prone to deleterious mutation accumulation has been criticized on both empirical and theoretical grounds (Popadin *et al.*, 2013; Zhang & Broughton, 2013; Cooper *et al.*, 2015; Christie & Beekman, 2016). Long-held views regarding the effective haploidy, low effective population size, and inefficient selection of the mitochondrial genome are being challenged (Ballard & Whitlock, 2004; Cooper *et al.*, 2015). Indeed, the fact that mtDNA molecules exist in hundreds to thousands of copies per cell suggest it might be better viewed as a polyploid genome (Greaves & Taylor, 2006). Across eukaryotes, there are variable rates of biparental inheritance of mtDNA and at least occasional recombination between divergent mtDNA molecules (Greiner, Sobanski & Bock, 2015; Ma & O'Farrell, 2015). In bilaterian animals, there is also a genetic bottleneck in mtDNA copy number through the germ line (Stewart & Larsson, 2014), which could provide an effective means by which selection can effectively purge primordial germ cells carrying mtDNA molecules with pathogenic mutations (Burr, Pezet & Chinnery, 2018). Together, these factors (polyploidy, some degree of biparental inheritance, recombination, and a genetic bottleneck during oogenesis) are providing new insights into the dynamics of selection that shape trajectories of mitochondrial genome evolution.

There is also growing interest in the role of *adaptive* changes in mitochondrial genomes, and recent research suggests that a substantial fraction of non-synonymous substitutions in mitochondrial genes may be driven by positive selection (James, Piganeau & Eyre-Walker, 2016). Because of the intimate functional integration between nuclear and mitochondrial genomes, adaptive changes in mtDNA are likely to have epistatic effects and shift selection pressures on the nuclear genome. Indeed, many examples that have been interpreted as supporting a model of compensatory mitonuclear coevolution (Osada & Akashi, 2012; Barreto & Burton, 2013*b*; Sloan *et al.*, 2014; Van Der Sluis *et al.*, 2015; Havird *et al.*, 2015*b*, 2017; Yan *et al.*, 2018) are also consistent with other forms of mitonuclear coevolution that do not depend on the accumulation of deleterious mitochondrial mutations (Sloan *et al.*, 2017). Regardless of the relative contributions of deleterious, neutral, and beneficial changes in triggering the coevolutionary process, natural selection is expected to favour beneficial combinations of alleles spanning mitochondrial and nuclear genomes and give rise to coadapted mitonuclear genotypes (Rand *et al.*, 2004; Burton, Pereira & Barreto, 2013; Wolff *et al.*, 2014; Hill, 2015).

Herein, we emphasize that further research attention is required to decipher the biological significance of mitonuclear interactions. Despite the ubiquity of co-functioning mitochondrial and nuclear genes, our understanding of the contribution of mitonuclear genetics to metazoan fitness remains incomplete, and most insights are from laboratory-based studies of model organisms. A focus on mitonuclear coadaptation is likely to contribute tangibly to our understanding of basic ecological concepts, such as speciation and the dynamics of sexual conflict (Hill, 2015; Wolff *et al.*, 2016). Furthermore, the implications of such interactions might resonate beyond the evolutionary and ecological sciences, into the realm of biomedicine (Mishmar & Zhidkov, 2010; Wallace, 2010; Dowling, 2014; Gershoni *et al.*, 2014). To inform future research directions, we identify and discuss five themes that have emerged from the study of mitonuclear interactions over the past two decades (Table 1).

III. IMPLICATIONS OF MITONUCLEAR INTERACTIONS SPANNING ECOLOGY AND BIOMEDICINE

It has been proposed that the necessity for mitonuclear coadaptation for cellular respiration may underlie a range of core evolutionary innovations and concepts. These include the evolution of sex and two sexes in eukaryotes (Hadjivasiliou *et al.*, 2013; Havird, Hall & Dowling, 2015*a*), the evolution of a sequestered germ line in bilaterian animals (Radzvilavicius *et al.*, 2016), climate and resource adaptation (Camus *et al.*, 2017; Sunnucks *et al.*, 2017), sexual selection (Hill & Johnson, 2013; Hill, 2018), and speciation (Dowling *et al.*, 2008; Burton & Barreto, 2012; Hill, 2016).

The role of mitonuclear interactions in mediating the process of speciation is currently a major area of scientific research and debate (Hill, 2017; Sloan *et al.*, 2017). It has been proposed that independent coevolution of mt and nuclear genes in isolated populations could lead to uniquely coadapted sets of genes that are not compatible with the coadapted mt and nuclear genes of other populations. If this is the case, gene flow and hybridization events between diverging populations could produce negative phenotypic outcomes due to Dobzhansky–Muller incompatibilities underpinned by mitonuclear interactions (Levin, 2003; Dowling *et al.*, 2008; Gershoni, Templeton & Mishmar, 2009; Burton & Barreto, 2012; Hill, 2017). In theory, therefore, population divergence driven by mitonuclear interactions represents a plausible model underlying the evolution of reproductive isolation between incipient populations, and ultimately speciation. However, the hypothesis that mitonuclear coadapation plays a direct and general role in driving speciation processes remains controversial and requires further investigation (Gershoni *et al.*, 2009; Chou & Leu, 2010; Burton & Barreto, 2012; Bar-Yaacov *et al.*, 2015; Eyre-Walker, 2017; Hill, 2017; Sloan *et al.*, 2017).

The fitness consequences of mitonuclear interactions are also relevant for human medicine. Ongoing research is exploring the significance of diverse mitochondrial haplotypes across human populations (Mishmar *et al.*, 2003; Wallace, 2010). An emerging research focus in biomedicine

Table 1. Five themes in the study of mitonuclear interactions

1. **Relentless selection for mitonuclear compatibility across ontogeny**. Mitonuclear interactions have fitness consequences at multiple stages of development, which may result in compounding effects in filtering out maladapted mitonuclear genotypes.

   Prediction: the frequencies of mitochondrial (mt) and nuclear-encoded mitochondrial (N-mt) genes are predicted to change across life stages via selection for mitonuclear compatibility and functionality.

2. **Mitonuclear coadaptation is manifested in mitochondrial physiology**. The localized role of mt gene products within the mitochondria leads to the expectation that deleterious effects of maladapted mitonuclear genotypes will be mediated by changes in mitochondrial function.

   Prediction: incompatibilities in coadapted sets of mt and N-mt genes will have effects targeted to the physiological and biochemical properties of mitochondria.

3. **Generational delays**. Mitonuclear incompatibilities may be shielded by dominance in the F1 generation and may be affected by sex linkage.

   Prediction: the negative effects of novel combinations of mitochondrial and nuclear genes may not be evident until F2 and later generations.

4. **Mitonuclear incompatibilities need not involve protein–protein interactions or myriad substitutions.** Although most attention has focused on the protein–protein interactions that occur within oxidative phosphorylation (OXPHOS) complexes, there are many other arenas for mitonuclear interactions, including mitochondrial translation, transcription, and DNA replication. Single changes in mt or nuclear genes can also cause severe incompatibilities. Moreover, because many or most of the sequence changes that contribute to divergence in nuclear and mt genes may be neutral, the actual variants responsible for mitonuclear incompatibilities likely represent a small subset of total sequence change.

   Prediction: mitonuclear incompatibilities can be caused by a small number of variants that need not change amino acid sequence and that may not be proportional to overall sequence divergence.

5. **Mitonuclear coadaptation is dependent on complex genotype × genotype × environment interactions**. Mitochondrial function and physiology is highly context dependent, so the signatures of mitonuclear coadaptation are likely to be as well.

   Prediction: the outcomes of genetic interactions between mitochondrial and nuclear genomes will be dependent on the genetic [*via* epistasis involving other mtDNA and nuclear single nucleotide polymorphisms (SNPs)], physiological (e.g. the sex in which the mtDNA is expressed) and abiotic environment.

considers whether human phenotypes are dependent on the nuclear background in which mitochondrial haplotypes are expressed (Levin *et al.*, 2014). Notably, mitonuclear interactions have also been implicated as putative contributors to health outcomes associated with the emerging germline therapy of mitochondrial replacement (Reinhardt, Dowling & Morrow, 2013;Morrow *et al.*, 2015; Dobler *et al.*, 2018) (Fig. 1). Mitochondrial replacement is a modified form of *in vitro* fertilization that could enable prospective mothers that suffer from mtDNA-induced mitochondrial diseases to produce offspring that are free from the mother's mtDNA mutations (Tachibana *et al.*, 2009, 2013; Craven *et al.*, 2010). The technique pairs a patient's nuclear chromosomes, or fertilized pronuclei, with a healthy complement of donor mitochondrial genes inside the donor's oocyte. Concerns have been raised, however, that the approach may create novel combinations of patient nuclear genotype and donor mtDNA haplotype that have not been previously tested by natural selection and that may lead to unanticipated negative outcomes (Morrow *et al.*, 2015; Dobler *et al.*, 2018). The potential negative effects of producing novel mitonuclear combinations in human oocytes remain widely debated (Reinhardt *et al.*, 2013; Chinnery *et al.*, 2014; Morrow *et al.*, 2015; Sloan, Fields & Havird, 2015; Eyre-Walker, 2017; Rishishwar & Jordan, 2017; Zaidi & Makova, 2018), with a recent meta-analysis presenting evidence that suggests mitonuclear interactions are likely to affect health outcomes in humans, and indeed seem to be associated with stronger effect sizes in humans than other metazoans (Dobler *et al.*, 2018).

IV. EMERGING THEMES IN STUDIES OF MITONUCLEAR COADAPTATION

An improved understanding of mitonuclear evolutionary dynamics is required to elucidate the role of mitonuclear interactions in ecological processes such as speciation and biomedical procedures like mitochondrial replacement therapy. Below we detail five themes that we believe should guide future research in this field. These themes have not been synthesized previously into a single framework or readily acknowledged in the current literature. However, we believe each of these themes deserves consideration, particularly when applied to inferences from natural populations and to implications beyond the fields of ecology and evolution.

(1) Theme 1: selection for mitonuclear compatibility should be strong and should exist across all stages of ontogeny

Selection for efficient mitochondrial function, and hence mitonuclear compatibility, is expected to be intense, and it might well begin as early as oogenesis, with massive selection on cells in the germ line (Krakauer & Mira, 1999; Fan *et al.*, 2008; Stewart *et al.*, 2008*a*; Dowling, 2014; Radzvilavicius

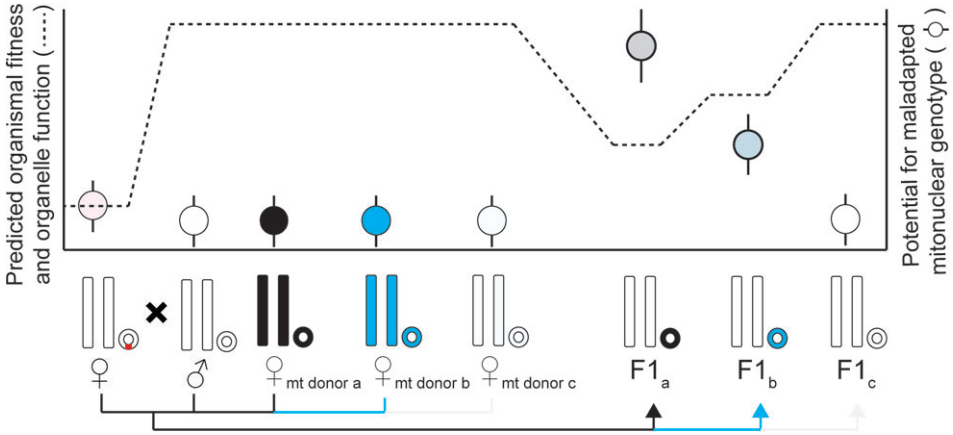

Fig. 1. Predicted organismal fitness, organelle function, and potential for maladapted mitonuclear genotypes during mitochondrial replacement therapy. Three possible mitochondrial donors are shown, yielding variable degrees of conceivable mitonuclear incompatibilities. Importantly, deleterious mtDNA mutations (shown in red) have *known* fitness consequences, while those resulting from mitonuclear incompatibilities are *predicted* and likely complex.

et al., 2016; De Fanti *et al.*, 2017). When there are multiple mitochondrial genotypes per cell, natural selection becomes inefficient in either eliminating deleterious genotypes or promoting highly functional genotypes (Radzvilavicius *et al.*, 2016). In bilaterian animals, germ line selection on mt genotypes is therefore seemingly facilitated by a well-documented bottleneck in the number of mtDNA molecules per primary oocyte (Wai, Teoli & Shoubridge, 2008; Stewart & Larsson, 2014). This mitochondrial genetic bottleneck enables natural selection to screen oocytes based on their metabolic integrity, underpinned by their mtDNA genotype (which should be fairly homogenous due to the bottleneck) and modulated by an effect of the diploid nuclear genomic background (Cree *et al.*, 2008; Wai *et al.*, 2008). During these stages, there is also a massive cull in the population of oocytes *via* a process called atresia. Together, this provides two levels by which selection might screen for best-functioning mitochondria. Emerging evidence supports the contention that the mitochondria are active within primordial germ cells and developing oocytes (Ge *et al.*, 2012; Kasashima, Nagao & Endo, 2014; Hayashi *et al.*, 2017). Thus, we hypothesize that only those oocytes with full capacity for efficient respiratory function, requiring compatible mitonuclear genotypes, reach maturity (Dumollard, Duchen & Carroll, 2007; Stewart & Larsson, 2014). Germ line selection could well represent a core mechanism favouring the transmission of compatible mitonuclear genotypes across generations (Lane, 2005; Morrow *et al.*, 2015; Radzvilavicius *et al.*, 2016), preventing the inter-generational mutational meltdown of the mitochondrial genome predicted by theory (Lynch *et al.*, 1993; Lynch & Blanchard, 1998; Stewart *et al.*, 2008*a*; Cooper *et al.*, 2015), but more data are needed to assess the importance of selection on germ lines. Furthermore, this process can be completed within the developing female foetus during embryogenesis. In humans, this occurs decades before the female is likely to mate and produce her own offspring.

In addition, there may be considerable opportunity for selection to act on mitonuclear interactions during the development of cells from spermatogonia to mature sperm cells, but this topic seems not to have been investigated. In humans, a single ejaculate contains approximately 10^8 sperm, with only one sperm fertilizing an egg. Again, the difference between a successful and unsuccessful sperm is not random, and strong postcopulatory selection will act on the male ejaculate (Simmons, 2001). Swimming speed and endurance, capacity to cope with chemical barriers, and ability to penetrate the egg faster than competitors dictate success (Snook, 2005; Pizzari, 2009), and sperm derive at least part of the energy that underlies these functions from OXPHOS (Ruiz-Pesini *et al.*, 2007). With few exceptions (Barr, Neiman & Taylor, 2005), the mitochondria that power sperm are not transmitted to offspring. By contrast, the paternal nuclear genome, which includes over 1000 nuclear-encoded mitochondrial (N-mt) genes, is transmitted (Calvo & Mootha, 2010). These N-mt genes create the majority of the mitochondrial proteome, and many interact closely with the mitochondrial-encoded gene products, such that strong selection on mitochondrial function will plausibly lead to strong selection on paternal N-mt genotypes in the sperm that enable cofunction with the common mt genotype of that population.

Selection for mitonuclear compatibility should then continue at every developmental stage following fertilization (Chan, 2006; Latorre-Pellicer *et al.*, 2016). For instance, in mammals, not all zygotes will successfully implant in the uterine wall; many developing embryos are spontaneously aborted; many individuals die during early development; and only a portion of the offspring born into the population will survive to reproductive maturity and succeed in procuring a mate and ultimately in producing viable offspring themselves. The chances of surviving through all of these stages of selection are minimal. The haploid gamete that survives pre-zygotic selection, and then as a diploid genome survives

all post-zygotic phases of selection thrown its way, can be considered a one-in-a-million winner in the lottery of life. We propose that at each of these life stages, selection for mitonuclear compatibility could be key. That is, although mitochondrial and nuclear alleles are unlinked and segregate randomly, strong selection through ontogeny could ensure that each adult in the population harbours a fully compatible mitonuclear genotype. The majority of the competition that underlies such selection is, however, difficult to detect unless one makes extremely careful and detailed observations across life stages. Such studies should be a priority for future research.

(2) Theme 2: mitonuclear coadaptation is manifested in mitochondrial physiology

Under a model of mitonuclear coadaptation, mismatching of coevolved mitonuclear genomes should lead to reduced organismal fitness specifically due to compromised mitochondrial function and disturbed bioenergetics (Gershoni *et al.*, 2009). However, given that validation can be operationally very challenging, observed dysfunction in crosses between divergent populations is seldom linked to specific mitonuclear incompatibilities and loss of mitochondrial function. Most experimental designs aimed at disrupting coevolved mitonuclear genotypes, such as crossing individuals from genetically divergent populations, also disrupt coevolved epistatic combinations of nuclear genes, and in such studies nuclear–nuclear rather than mito–nuclear gene interactions might have the largest effect on organismal fitness. While reciprocal crossing designs go some way towards removing the confounding effects of nuclear–nuclear interactions, by shifting the focus onto putative mitonuclear interactions, such designs come with a caveat in species with genetic sex determination because the genotype of offspring of the heterogametic sex will differ across each of the reciprocal crosses. Furthermore, offspring produced by these crosses are prone to effects from other extranuclear sources of variance, such as differences in the microbiome profiles of the mothers or, in some arthropods, cytoplasmic incompatibility caused by *Wolbachia* infection (Werren, Baldo & Clark, 2008; Schaefer, Nadeau & Wray, 2015).

One method for isolating mitonuclear effects is to replace the mtDNA from one lineage with the mtDNA from another lineage thereby creating novel mitonuclear gene combinations. Such genomic rearrangement can be achieved either by backcrossing over multiple generations (taking advantage of the maternal inheritance of mtDNA, but biparental inheritance of nuclear genes) or by using genetic tools that suppress recombination to enable chromosome substitution across generations (Dowling *et al.*, 2008). The outcome of such manipulations is the creation of a genetic strain of organism that possesses a novel mitonuclear genotype, in an otherwise intact diploid nuclear background. This combination of approaches allows the researcher to home in on the role of mitonuclear interactions in maintaining organismal function. Such approaches are, however, only possible in study species that are easily propagated in the laboratory environment and that have short generations.

One key prediction that can be tested in natural populations is that mitonuclear incompatibilities should have disproportionate effects on mitochondrial function. Moreover, mitochondrial physiology should be affected in a predictable manner according to the specific components that are influenced by incompatibilities (Burton *et al.*, 2013). A prime testing ground for assessment of mitonuclear effects distinct from nuclear–nuclear effects is comparison between OXPHOS complexes composed of both mt- and nuclear-encoded subunits, and complexes with only nuclear-encoded subunits. In many eukaryotes, Complex II (succinate dehydrogenase) is made up entirely of nuclear-encoded proteins, while other complexes responsible for OXPHOS function are chimeric assemblies of nuclear- and mitochondrial-encoded proteins (Rand *et al.*, 2004) (Fig. 2). Complex II function should therefore remain stable (or may even increase as a compensatory measure) regardless of altered mitonuclear interactions, while Complex I (nicotinamide adenine dinucleotide dehydrogenase) and Complex IV (cytochrome *c* oxidase) activity are predicted to vary with the mitochondrial genomic background. This prediction was supported in studies with copepods and fruit flies in which mitochondrial and nuclear genotypes from divergent populations were introgressed. In the fruit fly experiment, when hybrids were created that carried nuclear-encoded genes for a tRNA synthetase from *Drosophila melanogaster* and mt-encoded tRNA from *D. simulans*, poor cofunctioning of these non-coadapted mt and N-mt genes caused impairment of translation of mt-encoded OXPHOS subunits with significant effects on Complexes I, III, and IV but no effects on Complex II (Meiklejohn *et al.*, 2013). In the copepod experiment, hybrid crosses between divergent populations of *Tigriopus californicus* reduced activities of OXPHOS Complexes I, III, IV, and V but not Complex II (Ellison & Burton, 2006). These are among the clearest demonstrations of hybrid dysfunction resulting from mitonuclear interactions because they compellingly indicate that breakdown is only manifested for enzymes under dual control of both nuclear and mitochondrial genomes.

In addition to measuring activities of OXPHOS complexes, a range of other approaches can provide insight into mitochondrial physiology. Notably, production of ATP and generation of reactive oxygen species (ROS) have been shown to vary with mitochondrial genotype (Ellison & Burton, 2006, 2008*a*; Estes *et al.*, 2011; Hicks, Denver & Estes, 2013; Barreto & Burton, 2013*a*; Barreto, Pereira & Burton, 2015; Latorre-Pellicer *et al.*, 2016). In tractable systems, detailed examination of respiration profiles from isolated mitochondria could also reveal the mechanistic basis for lower fitness in compromised individuals (Chung, Bryant & Schulte, 2017; Mowry *et al.*, 2017; Zhang *et al.*, 2018). While rarely adopted, whole-organism measurements of basal and maximal metabolic rates may also be useful for assessing the fitness consequences of mitonuclear interactions (Sunnucks *et al.*, 2017).

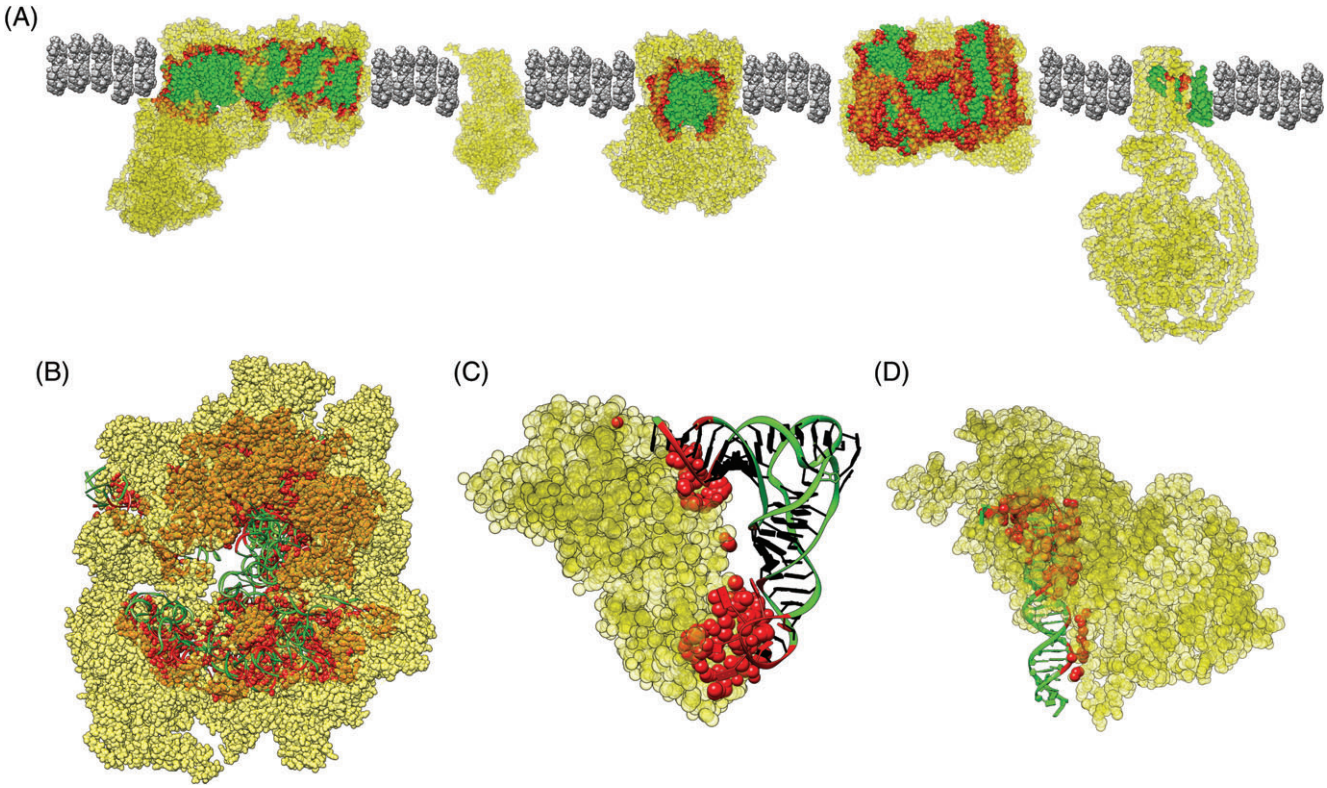

Fig. 2. Examples of mitonuclear interactions.: (A) multisubunit protein complexes of the electron transport chain, (B) mitochondrial ribosomal RNA (rRNA) and nuclear ribosomal proteins of the mitochondrial ribosome, (C) mitochondrial transfer RNA-threonine (tRNA-Thr) and nuclear threonyl-tRNA synthetase, and (D) mitochondrial DNA and nuclear DNA polymerase gamma. Non-interacting mitochondrial-encoded components are shown in green, nuclear-encoded components are in yellow, and interacting residues that physically contact residues encoded by both genomes are in red. All models are from mammals, except C which is from yeast. Interacting residues were identified following Sharbrough *et al.* (2017). PDB accessions used in structural depictions are 5LNK, 1ZOY, 1BGY, 1V54, 5ARA, 3J9M, 4YYE, and 5C51.

(3) Theme 3: generational delays

Research into the capacity for mitonuclear incompatibilities to evolve in natural populations suggests that, when such incompatibilities emerge, they may not be revealed until F2 and subsequent generations (Burton, Ellison & Harrison, 2006) (Fig. 3). The apparent lack of mitonuclear incompatibilities in the F1 generation from some crosses may arise because offspring receive a full haploid copy of each autosomal chromosome from each parent. Under this model, a full haploid maternal complement of nuclear genes would often be sufficient to maintain mitonuclear-mediated organismal function. As we outlined in Theme 1, a reproductively mature female has survived multifaceted phases of selection, from both pre-fertilization to post-fertilization and across the entire ontogeny. As a result of relentless selection throughout ontogeny, a mother's nuclear genotype should be predicted to function well with her mitochondrial genotype. Therefore, even if the father's nuclear genetic contribution to the offspring genotype exhibits incompatibility with the maternal mitochondrial haplotype, effects of mitonuclear incompatibility may not manifest in the F1 generation because the compatible nuclear alleles provided by the female may mask the effects of less-functional variants provided by the male (Burton & Barreto, 2012; Stelkens, Schmid & Seehausen, 2015). If F1 hybrids are crossed to create F2 hybrids, however, the segregation of diploid nuclear genes will generate recombinant genotypes, with some individuals receiving two paternal copies at a given nuclear locus.

The degree to which incompatibilities are masked in the F1 generation will depend on dominance relationships among alleles (Turelli & Orr, 2000; Raj *et al.*, 2010) because it is expected that both sets of alleles will be expressed in F1s. The degree of masking should also depend on whether the relevant nuclear genes are autosomal or sex-linked (Hill & Johnson, 2013; Hill, 2014). Researchers also face a challenge in separating the effects of any deleterious mitonuclear interactions from the potentially offsetting benefits of heterosis ('hybrid vigour') that are often seen in F1s, and which is attributable to the masking of deleterious recessive mutations within the nuclear genome (Edmands, 2007).

The best description of generational delays in the negative effects of mitonuclear incompatibilities in hybrid crosses comes from studies of the copepod, *T. californicus*, which have no sex chromosomes. When individuals from genetically

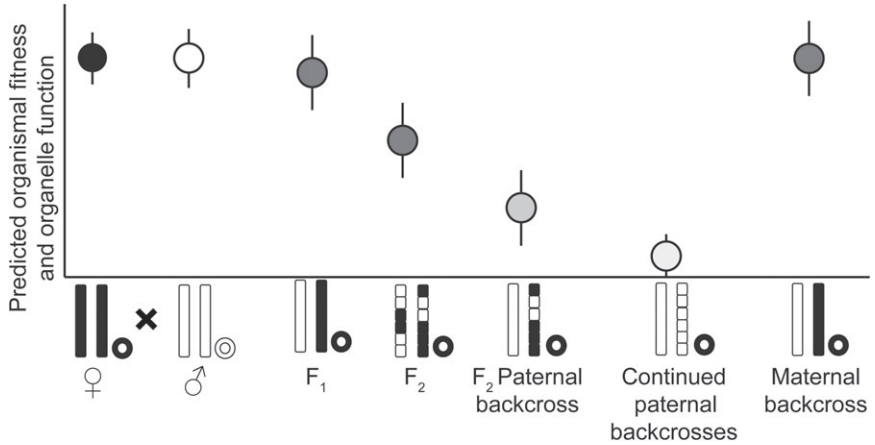

Fig. 3. Predicted organismal fitness and organelle function across generations. In the F1 generation, mitonuclear incompatibilities may generally be masked by retention of a maternal allele. Most mitonuclear incompatibilities are predicted to occur in F2 or later generations. After Burton *et al.* (2013).

divergent populations are crossed, F1 offspring typically exhibit a fitness gain relative to the parental populations. In F2 and later-generation recombinants, however, hybrids suffer a fitness cost. Furthermore, full fitness is restored when F2 hybrid females are backcrossed to males from the maternal lineage (Ellison & Burton, 2008*b*). The fitness advantage in the F1 generation in this example can be ascribed to heterosis associated with the creation of offspring exhibiting genome-wide heterozygosity in the diploid nuclear genome. There appear to be no negative effects of interpopulation hybridization at this F1 stage. Yet, F2 offspring clearly have reduced fitness relative to parental populations, and given that fitness outcomes are only restored upon backcrossing with the maternal population, this implicates mitonuclear incompatibilities as drivers of these effects (Fig. 3).

(4) Theme 4: mitonuclear incompatibilities can be created by single base substitutions and are not limited to protein-encoding genes

The overall genetic divergence of individuals can be a misleading index of mitonuclear compatibility. Many of the changes that distinguish mitochondrial haplotypes are likely to be neutral or nearly so. Only a subset of nuclear gene products are transported to the mitochondrion, and only a small proportion of these nuclear genes whose products function in mitochondria will interact closely with mitochondrial gene products (Burton & Barreto, 2012; Aledo *et al.*, 2014). Thus, if mt and N-mt genes are under strong purifying selection, then there is clearly a potential for substantial divergence in both nuclear and mitochondrial nucleotide sequences with no loss of mitonuclear compatibility. Moreover, given many of the nuclear gene products that function in the mitochondrion also have functions outside of the mitochondrion (Burak *et al.*, 2013; Blumberg *et al.*, 2014; Chatterjee *et al.*, 2016), evolutionary changes to such proteins could be driven by selection that is not related to mitonuclear coadaptation. Conversely, numerous examples now support the contention that mitonuclear incompatibilities leading to loss of fitness could be brought about by a few key changes to either the mitochondrial or nuclear genotype (Aledo *et al.*, 2014; Camus *et al.*, 2015). Indeed, single point mutations in nuclear and mitochondrial genes have been shown to be the basis for mitochondrial dysfunction in heterospecific hybrid crosses (Meiklejohn *et al.*, 2013).

To date, most studies on mitonuclear interactions have focused on protein–protein interactions in OXPHOS complexes co-encoded by nuclear and mitochondrial genomes (e.g. (Kwong *et al.*, 2012; Osada & Akashi, 2012; Zhang & Broughton, 2013; Havird *et al.*, 2015*b*). However, the biochemical machinery that enables translation of mitochondrial genes has both nuclear protein components and mitochondrial RNA components, namely tRNAs and rRNAs (Fig. 2B, C). The mitochondrial-encoded RNA components must co-function with nuclear-encoded proteins (Wallace, 2007; Bar-Yaacov *et al.*, 2012; Burton & Barreto, 2012; Sloan *et al.*, 2014). The replication and transcription of the mitochondrial genome also involves the interaction of nuclear-encoded proteins with the mtDNA itself (Ellison & Burton, 2008*a*, 2010) (Fig. 2D).

Epistasis may occur even when there is no physical interaction of gene products because the coordinated function of mitochondrial and nuclear gene products depends critically on retrograde (mitochondria to nucleus) and anterograde (nucleus to mitochondria) signalling (Moore & Williams, 2005; Woodson & Chory, 2008; Clark, Alani & Aquadro, 2012; Monaghan & Whitmarsh, 2015; Baris *et al.*, 2017). Such signalling requires that both genomes correctly recognize and respond to signals from each other. It should also be noted that new types of mitonuclear interactions are still being discovered; for instance, there is some evidence that mt genomes encode small RNAs (Pozzi *et al.*, 2017) and several small peptides, such as humanin and mitochondrial open reading frame of the 12S rRNA-c (MOTS-c), are encoded by the mt genome (Lee, Yen & Cohen, 2013; Lee

et al., 2015). These newly discovered mitochondrial products could play an important role in retrograde signalling. In sum, mitonuclear incompatibilities can be caused by more than just compromised protein–protein interactions.

(5) Theme 5: mitonuclear coadaptation is dependent on complex genotype × genotype × environment interactions

There is a tendency to catalogue mitonuclear gene combinations as either high or poorly performing in terms of their phenotypic effects. However, the phenotype that results from any given mitochondrial and nuclear genotype combination will also depend critically on the environment. This view is supported by laboratory studies of invertebrate models, which have confirmed that the performance associated with particular mitonuclear genotypes is routinely contingent on the environmental context (Willett & Burton, 2001, 2003; Ellison & Burton, 2006; Dowling, Abiega & Arnqvist, 2007; Arnqvist *et al.*, 2010; Dowling *et al.*, 2010; Hoekstra, Siddiq & Montooth, 2013; Zhu, Ingelmo & Rand, 2014; Mossman *et al.*, 2016). As an example, in crosses between the fruit flies *D. melanogaster* and *D. simulans*, incompatibilities in the products of mt and nuclear genes slow down larval development and reduce survival at 25°C but have no effect on growth or survival at 16°C (Hoekstra *et al.*, 2013).

In addition, studies of spatial variation in mitochondrial haplotype distributions in humans and other metazoans in their natural environments demonstrate that mutational patterns at key protein-coding genes within the mtDNA sequence closely conform to patterns predicted under a scenario of climatic adaptation (Mishmar *et al.*, 2003; Ruiz-Pesini, 2004; Balloux *et al.*, 2009; Cheviron & Brumfield, 2009; Quintela *et al.*, 2014; Silva *et al.*, 2014; Morales *et al.*, 2015; Camus *et al.*, 2017). Indeed, a growing view has emerged that environmental context dependency in mitochondrial disease expression is likely to be common in humans (Mishmar *et al.*, 2003; Wallace, 2005).

For example, emerging evidence supports a role for climatic adaptation in shaping population frequencies of a mtDNA mutation (T3394C) associated with Leber's hereditary optic neuropathy (LHON) in humans, a mitochondrial disease that causes blindness, and which is associated with male biases in penetrance. Ji *et al.* (2012) reported that although T3394C has arisen multiple times across the human mitochondrial phylogeny, it is highly enriched on haplotypes that are common in high-altitude Asian populations (M9 haplotype in Tibet, and the C4a4 haplotype in the Indian Deccan Plateau). Indeed, the T3394C variant is 22 times more likely to be found at altitudes above 1500 m than among low-altitude Han Chinese populations. Furthermore, functional analyses of transmitochondrial cybrid lines have shown that this mutation causes reductions in mitochondrial complex I activity of between 7 and 28% when expressed on the lowland BC4 and F1 Asian haplotypes, but no such reductions on the M9 haplotype (Ji *et al.*, 2012). This result, when coupled with the observations of spatial enrichment of the T3394C variant in high-altitude populations, lends support to the suggestion that the 3394C mutation could well be adaptive at high altitudes, while pathological at low altitudes.

Finally, we note that it is likely that the outcomes of mitonuclear interactions will vary across the sexes, although research into this contention is still in its relative infancy. The two sexes represent very different environments in which mitochondria must function. For example, the female gonads and gamete are metabolically quiescent relative to their male counterparts (Short, 1997; Vaught & Dowling, 2018), with the gametes exhibiting striking differences in both size and mtDNA copy number. Because mitochondria are transmitted through the female lineage, mitochondrial mutations that are male-harming can in theory escape the action of natural selection. Such mutations can therefore increase and linger in populations and be fixed through neutral mechanisms or even spread through positive selection if they confer fitness advantages to females (Frank & Hurst, 1996; Gemmell, Metcalf & Allendorf, 2004; Beekman, Dowling & Aanen, 2014). This 'mother's curse' may be key to explaining why mitochondrial diseases such as LHON exhibit much higher penetrance in males (Yen, Wang & Wei, 2006; Ventura *et al.*, 2007; Milot *et al.*, 2017). Experimental evidence has emerged to indicate that some of the genetic variation that delineates naturally occurring mtDNA haplotypes in fruit flies (*D. melanogaster*) may exhibit male biases in effects on key life-history traits tied to reproduction and survival (Innocenti, Morrow & Dowling, 2011; Camus, Clancy & Dowling, 2012; Camus *et al.*, 2015; Dowling, Tompkins & Gemmell, 2015; Immonen *et al.*, 2016; Camus & Dowling, 2018). Indeed, some of this mitochondrial genetic variation appears to be overtly sexually antagonistic, augmenting female reproductive outcomes, at cost to males (Camus & Dowling, 2018). The studies of sex biases in mitochondrial genetic variation conducted to date, however, have all compared the sex-specific fitness effects of mtDNA haplotypes when placed against highly controlled nuclear backgrounds lacking segregating genetic variation. While providing proof-of-concept, future studies will need to establish whether male biases in levels of mitochondrial genetic variation underpinning key life-history traits are replicable across diverse nuclear backgrounds. Nonetheless, other case studies supporting the mother's curse hypothesis have come to light in flies (Patel *et al.*, 2016), mice (Nakada *et al.*, 2006), rabbits (Smith, Turbill & Suchentrunk, 2010) and humans (Martikainen *et al.*, 2017) of mtDNA polymorphisms exerting negative effects exclusively on male components of fertility (Vaught & Dowling, 2018).

V. IMPLICATIONS AND OUTLOOK

(1) Implications for understanding speciation

We strongly advocate consideration of mitonuclear interactions in future studies that seek to understand species boundaries in natural populations. As discussed below,

rapid advances in fields such as population genomics and molecular modelling increasingly allow inferences to be made about mitonuclear interactions in wild populations of diverse species. However, a deeper understanding of the fitness consequences of these interactions generally demands manipulative experiments, such as quantitative genetic crosses and mitochondrial respiration measurements. The practical constraints of working with many vertebrate species such as wild bird populations, which produce few offspring and will not breed in captivity, make such experiments highly challenging if not impossible. It can therefore be instructive to consider the study of speciation in animals, notably wild populations of invertebrates, for which such constraints have been overcome.

The aforementioned splash pool copepod, *Tigriopus californicus*, may be the model system in which the role of mitonuclear interactions has been most completely studied (Burton *et al.*, 2013; Yang *et al.*, 2017; Barreto *et al.*, 2018). Many aspects of these studies have been detailed in the above sections of this review. Here we point out two aspects of the biology of this organism that set the stage for development of mitonuclear coadaptation. First, rates of mtDNA substitution are high: Willett (2012) estimated that the rate of substitutions at synonymous sites in *T. californicus* mtDNA is 55-fold higher than the rate in nuclear genes. Second, *T. californicus* populations show strong population structure. Restricted gene flow among populations has resulted in not only high levels of mtDNA divergence across populations, but also the opportunity for uniquely coadapted nuclear genotypes among populations in response to the extensive mtDNA divergence (Barreto *et al.*, 2018).

Numerous studies of mitonuclear interactions have taken advantage of the *Tigriopus* system and these have been discussed within each of the themes developed above. The importance of considering fitness variation across life stages (Theme 1) can at least partially be addressed in this system by determining allelic frequencies of candidate genes in a sample of newly hatched larvae to their frequencies in surviving adults from the same cohort. In an analysis of the alleles of the cytochrome *c* gene (*cytC*; a nuclear gene encoding a protein essential to OXPHOS function), Willett & Burton (2001) observed expected Mendelian genotypic ratios in F2 hybrid larvae, but in adult animals from the same cross they observed that the ratios were skewed in favour of combinations that restored the population-specific coevolved mitonuclear genotypes. In addition to suggesting that *cytC* has coevolved with mitotype, this type of experiment isolates the form of selection as larval-to-adult viability selection. In this particular case, *in vitro* biochemical experiments and site-directed mutagenesis further verified the functional coevolution of *cytC* with mitotype, and demonstrated that only a single amino acid substitution was needed to change dramatically the functional interaction between a nuclear gene and a mitochondrially co-encoded OXPHOS complex (Rawson & Burton, 2002; Harrison & Burton, 2006) (Theme 4).

Although there are clear examples of protein–protein interactions underlying mitochondrial dysfunction in *Tigriopus* hybrids, it is also clear that other types of interactions likely contribute to mitonuclear incompatibilities (Theme 4). Ellison & Burton (2010) found that population mismatches between mtDNA and mitochondrial RNA polymerase resulted in reduced mtDNA gene expression, and Barreto & Burton (2013*b*) found evidence for coevolution in nuclear-encoded ribosomal proteins that interact with rRNA encoded in the mtDNA. Recent work suggests that there is a genome-wide pattern of elevated rates of evolution among nuclear genes known to interact with mtDNA or its gene products compared to nuclear genes lacking those interactions.

As discussed earlier, the impact of environmental variation on mitonuclear interactions is often overlooked and can be substantial (Theme 5). Willett & Burton (2003) found that the relative fitness of *cytC* genotypes not only depended on mitotype (see above), but also on the thermal environment. The disruptive effect of population mismatches in mtDNA and mitochondrial RNA polymerase cited above is accentuated under conditions of osmotic stress when the energetic costs of osmoregulation require an upregulation of mitochondrial ATP synthesis (Ellison & Burton, 2008*a*).

These studies with copepods clearly established the negative effects of incompatibilities between mitochondrial and nuclear genes that arise when populations diverge in allopatry, and the potential for such incompatibilities to disrupt gene flow among populations. The implications for speciation are clear. What remains to be established is the relative importance of mitonuclear interactions compared to other potential mechanisms for disruption of gene flow in the process of speciation, and such broader insights will only come with a consideration of mitonuclear interactions in studies of speciation.

(2) Implications for best practices in mitochondrial replacement therapy

It is now well established that the penetrance of numerous disease-conferring mtDNA mutations is affected by a range of modifier alleles that lie within the nuclear genome (Taanman, 2001; Bykhovskaya *et al.*, 2004; Ballana *et al.*, 2007; Davidson *et al.*, 2009; Luo, Hou & Yang, 2013; Wang *et al.*, 2015; Morrow & Camus, 2017). Thus, signatures of mitonuclear epistasis, moderating disease penetrance and outcomes, are known to be common in human populations.

To date, discussion of the capacity for mitochondrial replacement therapy to lead to compromised mitonuclear function has focused on (*i*) the anticipation of problems based on understanding patterns of genetic variation and structure within and among human populations, and (*ii*) an assessment of the outcomes of mitochondrial replacement in animal models and humans. A mitonuclear perspective that draws on insights from studies of natural non-human populations should be helpful in developing best practices for performing mitochondrial replacement techniques in humans. First, following Theme 1, full assessment of the outcome of any combination of mitochondrial and nuclear genes can only come after a complete lifetime because many

of the negative consequences of mitonuclear dysfunction might be late-onset diseases like Alzheimer's or Parkinson's diseases (Hudson *et al.*, 2014).

Moreover, researchers should be skeptical of attempts to draw inferences regarding the potential for mitonuclear incompatibilities in humans from assessments of genome-wide covariation between levels of mtDNA and nuclear divergence in the adult population. This is evident from a recent study that attempted to assess the risk of negative outcomes of mitochondrial replacement therapy in humans based on mitonuclear incompatibilities by observing patterns of mitochondrial haplotype and nuclear introgression in humans (Rishishwar & Jordan, 2017). The researchers used the whole mitochondrial and nuclear genome sequences of 2054 'healthy adult' humans available through the 1KGP project (The 1000 Genomes Project Consortium, 2015), which included 'five major continental population groups,' to assess the possibility that there may be incompatibilities between some mt and N-mt genes between some human populations. The rationale for the analysis was that, if individuals who carry nuclear genes from one population and mitochondrial genes from another population can exist as healthy adults, then admixture of nuclear and mitochondrial genes from divergent populations might not present a substantial risk of mitonuclear incompatibilities in mitochondrial replacement therapy.

There are multiple potential problems associated with such inferences. Firstly, they do not adequately consider the possibility of selection operating against mitonuclear genotypes at earlier life stages (Theme 1). Assessment of healthy adults provides no insights into whether selection had eliminated mitonuclear incompatibilities at earlier life stages in individuals not sampled. Secondly, such inferences are based on genome-wide patterns of mitonuclear association and divergence, and such broad-brushed approaches to assessing mitonuclear genetics overlook the likely scenario that the relevant associations among nuclear genes will be limited to relatively small numbers of key loci that interact with the mt genome (Theme 4). As we have discussed above, mitonuclear incompatibilities might be underpinned by divergence at a small number of sequence sites that are under strong selection for mitochondrial function. Finally, the statement that subjects in the data set were healthy presents an untested assumption because no phenotypic data are presented in the study. Ideally, one would try to link population genomic patterns of mitonuclear genotypes to detailed measures of phenotype (including information on mitochondrial function; Theme 2) (Morales *et al.*, 2015; Baris *et al.*, 2017).

While technically challenging, it is important that biomedical researchers seek formally to test the capacity for mitonuclear interactions to affect the outcomes of mitochondrial replacement therapy in non-human primate models, or in human oocytes themselves. In this regard, a recent study by Hyslop *et al.* (2016) provides potential insights into a role of mitonuclear interactions in shaping health outcomes of zygotes following mitochondrial replacement. They utilized a technique known as pronuclear transfer, to move the pronuclei of fertilized zygotes to eunucleated donor embryos, thus creating the opportunity to place the diploid nuclear zygote contributed by one male and female alongside a mitochondrial haplotype contributed by a different female. The authors used this approach to create two types of zygotes. Autologous zygotes were generated by removing and then returning the same pronuclei back into the same zygotes. Autologous zygotes were therefore procedural controls, carrying identical mitonuclear genotypes prior to and following the procedure. Heterologous zygotes were generated by transferring pronuclei from one zygote to another, using donor and parental oocytes that differed in their mtDNA haplogroups. The authors reported lower rates of blastocyst formation in heterologous zygotes than autologous zygotes, raising the possibility that mitonuclear interactions could be conferring negative effects in the early stages of embryogenesis. That said, the capacity to draw clear inferences from the experiment was somewhat limited by the caveat that creation of heterologous zygotes involved transferring pronuclei from vitrified to fresh oocytes, or *vice versa*, while creation of the autologous zygotes did not.

Humans currently experience substantial gene exchange among most populations around the globe, but this connectivity among human populations is a recent event in the history of *Homo sapiens*. Throughout most of the history of our species, numerous human populations evolved largely in isolation (Akey *et al.*, 2004; Bamshad *et al.*, 2004). A consideration of gene flow among human populations is important because, in a panmictic population, segregation perpetually breaks down genetic associations established by selection (Eyre-Walker, 2017). By contrast, among isolated populations there is a much greater capacity for the evolution of unique genetic associations (Barreto *et al.*, 2018). The isolation of many populations throughout human evolution makes it plausible that mitonuclear incompatibilities might exist in the modern human population.

(3) The future will rely on integration of molecular, biochemical and ecological approaches

Looking to the future, we advocate that integrative approaches are needed to understand the molecular basis and fitness consequences of mitonuclear interactions (Sunnucks *et al.*, 2017). Genotype-to-phenotype links can be developed by combining: (*i*) sequencing of mitochondrial and nuclear genomes to detect sites of selection in populations; (*ii*) molecular modelling and mapping to predict the effects of substitutions on protein structure, function, and interactions; and, where feasible, (*iii*) respirometry and fitness measurements to infer consequences of substitutions at mitochondrial, organismal, and population levels.

Molecular modelling is emerging as a particularly valuable tool to make predictions about the effects of mitonuclear interactions on mitochondrial respiration (Grossman *et al.*, 2004; Scott *et al.*, 2011). Driven by recent advances in structural biology, complete three-dimensional structures are now available of the mammalian OXPHOS complexes

(Tsukihara *et al.*, 1996; Iwata, 1998; Fiedorczuk *et al.*, 2016; Zhu, Vinothkumar & Hirst, 2016) and the mammalian respirasome supercomplex (Gu *et al.*, 2016; Wu *et al.*, 2016; Guo *et al.*, 2017; Davies, Blum & Kühlbrandt, 2018). It is therefore possible to use these structures to analyse direct molecular interactions between nuclear and mitochondrial gene products. Construction of homology models of sequenced variants of OXPHOS subunits facilitates predictions about how substitutions may affect structure, function, and interactions of OXPHOS complexes. Such approaches have inferred climate-driven positive selection in mitochondrial-encoded Complex I components in a range of animal taxa (Finch *et al.*, 2014; Garvin *et al.*, 2014; Caballero *et al.*, 2015). Structural mapping has also recently provided evidence of epistatic interactions between mitochondrial-encoded and nuclear-encoded Complex I variants potentially under climate-driven selection (Garvin *et al.*, 2016; Morales *et al.*, 2018). As we have noted, mitonuclear incompatibilities need not involve direct interactions within multi-subunit complexes (Innocenti *et al.*, 2011; Baris *et al.*, 2017). Nevertheless, the direct molecular interactions between nuclear and mitochondrial gene products remain leading candidates as sites of mitonuclear imcompatibilites. In accordance with Theme 4, homology modelling is also an option to probe protein–DNA and protein–RNA mitonuclear interactions (Bar-Yaacov *et al.*, 2015).

It is important to note, however, that molecular understanding of mitonuclear interactions remains in its infancy. The complete atomic resolution of Complex I and the respirasome were only recently resolved (Fiedorczuk *et al.*, 2016; Gu *et al.*, 2016; Zhu *et al.*, 2016; Guo *et al.*, 2017) and only low-resolution structures of metazoan ATP synthase have been published (Zhou *et al.*, 2015). As a result, there is limited information from only a handful of model species about the structure, function, and interactions of many OXPHOS subunits and their residues. Thus, it is rarely justified to make detailed mechanistic inferences from molecular modelling, and any predictions should be treated with caution until empirically tested (e.g. respirometry measurements). We anticipate that future advances will increase the predictive power of molecular modelling: higher resolution structures of the respirasome and ATP synthase; improved understanding of how OXPHOS complex structure relates to function at a range of levels and in specific environments; and development of molecular dynamics simulations for these complexes that may reveal the sources of environmental interactions. In turn, such approaches may allow screening for compatible mitonuclear interactions in mitochondrial replacement therapy and help consolidate genotype-to-phenotype links in mitonuclear ecology.

VI. CONCLUSIONS

(1) Only in the last couple of decades has the significance of mitochondrial variation, and the interactions of mitochondrial and nuclear genes, been incorporated into a conceptual framework for understanding population structure and speciation.

(2) Only a minority of studies consider the potential effects of mitonuclear interactions when assessing adaptation and the genetic basis for variation in individual performance.

(3) Interacting mitochondrial and nuclear genotypes are likely to play a key role in how populations are structured, with implications for the process of speciation and for medical therapies involving recombining mitochondrial and nuclear genotypes.

(4) The key question is how much of an overall effect will arise from mitonuclear interactions *versus* interactions among nuclear genes, and this question can only be answered with a greater research focus on mitonuclear interactions.

(5) Our growing understanding of the coevolution, coadaptation, and co-function of the products of mitochondrial and nuclear genes in natural populations has established a set of themes that should guide further research.

(6) The future lies in the integration of a mechanistic understanding of the biochemical and biophysical consequences of mitochondrial and nuclear genotypes with population biology and ecology.

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VIII. REFERENCES

Akey, J. M., Eberle, M. A., Rieder, M. J., Carlson, C. S., Shriver, M. D., Nickerson, D. A. & Kruglyak, L. (2004). Population history and natural selection shape patterns of genetic variation in 132 genes. *PLoS Biology* **2**, e286.

Aledo, J. C., Valverde, H., Ruíz-Camacho, M., Morilla, I. & López, F. D. (2014). Protein-protein interfaces from cytochrome c oxidase i evolve faster than nonbinding surfaces, yet negative selection is the driving force. *Genome Biology and Evolution* **6**, 3064–3076.

Alston, C. L., Rocha, M. C., Lax, N. Z., Turnbull, D. M. & Taylor, R. W. (2017). The genetics and pathology of mitochondrial disease. *Journal of Pathology* **241**, 236–250.

Arnqvist, G., Dowling, D. K., Eady, P., Gay, L., Tregenza, T., Tuda, M. & Hosken, D. J. (2010). Genetic architecture of metabolic rate: environment specific epistasis between mitochondrial and nuclear genes in an insect. *Evolution* **64**, 3354–3363.

Avise, J. C. (2004). *Molecular Markers, Natural History, and Evolution*. Sinauer, Sunderland, MA.

Ballana, E., Mercader, J. M., Fischel-Ghodsian, N. & Estivill, X. (2007). MRPS18CP2 alleles and DEFA3 absence as putative chromosome 8p23.1 modifiers of hearing loss due to mtDNA mutation A1555G in the 12S rRNA gene. *BMC Medical Genetics* **8**, 81.

Ballard, J. W. O. & Kreitman, M. (1994). Unraveling selection in the mitochondrial genome of *Drosophila*. *Genetics* **138**, 757–772.

Ballard, J. W. O. & Pichaud, N. (2014). Mitochondrial DNA: more than an evolutionary bystander. *Functional Ecology* **28**, 218–231.
Ballard, J. W. O. & Whitlock, M. C. (2004). The incomplete natural history of mitochondria. *Molecular Ecology* **13**, 729–744.
Balloux, F., Handley, L.-J. L., Jombart, T., Liu, H. & Manica, A. (2009). Climate shaped the worldwide distribution of human mitochondrial DNA sequence variation. *Proceedings of the Royal Society B: Biological Sciences* **276**, 3447–3455.
Bamshad, M., Wooding, S., Salisbury, B. A. & Stephens, J. C. (2004). Deconstructing the relationship between genetics and race. *Nature Reviews Genetics* **5**, 598–609.
Baris, T. Z., Wagner, D. N., Dayan, D. I., Du, X., Blier, P. U., Pichaud, N., Oleksiak, M. F. & Crawford, D. L. (2017). Evolved genetic and phenotypic differences due to mitochondrial-nuclear interactions. *PLoS Genetics* **13**, 1–23.
Barr, C. M., Neiman, M. & Taylor, D. R. (2005). Inheritance and recombination of mitochondrial genomes in plants, fungi and animals. *New Phytologist* **168**, 39–50.
Barreto, F. S. & Burton, R. S. (2013*a*). Elevated oxidative damage is correlated with reduced fitness in interpopulation hybrids of a marine copepod. *Proceedings of the Royal Society B: Biological Sciences* **280**, 20131521.
Barreto, F. S. & Burton, R. S. (2013*b*). Evidence for compensatory evolution of ribosomal proteins in response to rapid divergence of mitochondrial rRNA. *Molecular Biology and Evolution* **30**, 310–314.
Barreto, F. S., Pereira, R. J. & Burton, R. S. (2015). Hybrid dysfunction and physiological compensation in gene expression. *Molecular Biology and Evolution* **32**, 613–622.
Barreto, F. S., Watson, E. T., Lima, T. G., Willett, C. S., Edmands, S., Li, W. & Burton, R. S. (2018). Genomic signatures of mitonuclear coevolution across populations of *Tigriopus californicus*. *Nature Ecology and Evolution* **2**, 1250–1257.
Bar-Yaacov, D., Blumberg, A. & Mishmar, D. (2012). Mitochondrial-nuclear co-evolution and its effects on OXPHOS activity and regulation. *Biochimica et Biophysica Acta - Gene Regulatory Mechanisms* **1819**, 1107–1111.
Bar-Yaacov, D., Hadjivasiliou, Z., Levin, L., Barshad, G., Zarivach, R., Bouskila, A. & Mishmar, D. (2015). Mitochondrial involvement in vertebrate speciation? The case of Mito-nuclear genetic divergence in chameleons. *Genome Biology and Evolution* **7**, 3322–3336.
Beekman, M., Dowling, D. K. & Aanen, D. K. (2014). The costs of being male: are there sex-specific effects of uniparental mitochondrial inheritance? *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences* **369**, 20130440.
Blumberg, A., Sailaja, B. S., Kundaje, A., Levin, L., Dadon, S., Shmorak, S., Shaulian, E., Meshorer, E. & Mishmar, D. (2014). Transcription factors bind negatively selected sites within human mtDNA genes. *Genome Biology and Evolution* **6**, 2634–2646.
Bock, D. G., Andrew, R. L. & Rieseberg, L. H. (2014). On the adaptive value of cytoplasmic genomes in plants. *Molecular Ecology* **23**, 4899–4911.
Brown, W. M., George, M. & Wilson, A. C. (1979). Rapid evolution of animal mitochondrial DNA. *Proceedings of the National Academy of Sciences of the United States of America* **76**, 1967–1971.
Burak, E., Yogev, O., Sheffer, S., Schueler-Furman, O. & Pines, O. (2013). Evolving dual targeting of a prokaryotic protein in yeast. *Molecular Biology and Evolution* **30**, 1563–1573.
Burr, S. P., Pezet, M. & Chinnery, P. F. (2018). Mitochondrial DNA heteroplasmy and purifying selection in the mammalian female germ line. *Development Growth and Differentiation* **60**, 21–32.
Burton, R. S. & Barreto, F. S. (2012). A disproportionate role for mtDNA in Dobzhansky-Muller incompatibilities? *Molecular Ecology* **21**, 4942–4957.
Burton, R. S., Ellison, C. K. & Harrison, J. S. (2006). The sorry state of F-2 hybrids: consequences of rapid mitochondrial DNA evolution in allopatric populations. *American Naturalist* **168**, S14–S24.
Burton, R. S., Pereira, R. J. & Barreto, F. S. (2013). Cytonuclear genomic interactions and hybrid breakdown. *Annual Review of Ecology, Evolution, and Systematics* **44**, 281–302.
Bykhovskaya, Y., Mengesha, E., Wang, D., Yang, H., Estivill, X., Shohat, M. & Fischel-Ghodsian, N. (2004). Human mitochondrial transcription factor B1 as a modifier gene for hearing loss associated with the mitochondrial A1555G mutation. *Molecular Genetics and Metabolism* **82**, 27–32.
Caballero, S., Duchêne, S., Garavito, M. F., Slikas, B. & Baker, C. S. (2015). Initial evidence for adaptive selection on the NADH subunit two of freshwater dolphins by analyses of mitochondrial genomes. *PLoS One* **10**, 1–17.
Calvo, S. E. & Mootha, V. K. (2010). The mitochondrial proteome and human disease. *Annual Review of Genomics and Human Genetics* **11**, 25–44.
Camus, M. F. & Dowling, D. K. (2018). Mitochondrial genetic effects on reproductive success: signatures of positive intrasexual, but negative intersexual pleiotropy. *Proceedings of the Royal Society B: Biological Sciences* **285**, 20180187.
Camus, M. F., Clancy, D. J. & Dowling, D. K. (2012). Mitochondria, maternal inheritance, and male aging. *Current Biology* **22**, 1717–1721.
Camus, M. F., Wolf, J. B. W., Morrow, E. H. & Dowling, D. K. (2015). Single nucleotides in the mtDNA sequence modify mitochondrial molecular function and are associated with sex-specific effects on fertility and aging. *Current Biology* **25**, 2717–2722.
Camus, M. F., Wolff, J. N., Sgrò, C. M. & Dowling, D. K. (2017). Experimental support that natural selection has shaped the latitudinal distribution of mitochondrial haplotypes in Australian *Drosophila melanogaster*. *Molecular Biology and Evolution* **34**, 2600–2612.
Chan, D. C. (2006). Mitochondria: dynamic organelles in disease, aging, and development. *Cell* **125**, 1241–1252.
Chatterjee, A., Seyfferth, J., Lucci, J., Gilsbach, R., Preissl, S., Böttinger, L., Mårtensson, C. U., Panhale, A., Stehle, T., Kretz, O., Sahyoun, A. H., Avilov, S., Eimer, S., Hein, L., Pfanner, N., et al. (2016). MOF acetyl transferase regulates transcription and respiration in mitochondria. *Cell* **167**, 722–738.e23.
Cheviron, Z. A. & Brumfield, R. T. (2009). Migration-selection balance and local adaptation of mitochondrial haplotypes in Rufous-Collared Sparrows (*Zonotrichia capensis*) along an elevational gradient. *Evolution* **63**, 1593–1605.
Chinnery, P. F., Craven, L., Mitalipov, S., Stewart, J. B., Herbert, M. & Turnbull, D. M. (2014). The challenges of mitochondrial replacement. *PLoS Genetics* **10**, 3–4.
Chou, J. Y. & Leu, J. Y. (2010). Speciation through cytonuclear incompatibility: insights from yeast and implications for higher eukaryotes. *BioEssays* **32**, 401–411.
Christie, J. R. & Beekman, M. (2016). Uniparental inheritance promotes adaptive evolution in cytoplasmic genomes. *Molecular Biology and Evolution* **34**, 677–691.
Chung, D. J., Bryant, H. J. & Schulte, P. M. (2017). Thermal acclimation and population-specific effects on heart and brain mitochondrial performance in a eurythermal teleost (*Fundulus heteroclitus*). *Journal of Experimental Biology* **220**, 1459–1471.
Clancy, D. J. (2008). Variation in mitochondrial genotype has substantial lifespan effects which may be modulated by nuclear background. *Aging Cell* **7**, 795–804.
Clark, N. L., Alani, E. & Aquadro, C. F. (2012). Evolutionary rate covariation : a bioinformatic method that reveals co-functionality and co-expression of genes. *Genome Research* **22**, 714–720.
Cooper, B. S., Burrus, C. R., Ji, C., Hahn, M. W. & Montooth, K. L. (2015). Similar efficacies of selection shape mitochondrial and nuclear genes in both *Drosophila melanogaster* and *Homo sapiens*. *G3* **5**, 1–45.
Craven, L., Tuppen, H. A., Greggains, G. D., Harbottle, S. J., Murphy, J. L., Cree, L. M., Murdoch, A. P., Chinnery, P. F., Taylor, R. W., Lightowlers, R. N., Herbert, M. & Turnbull, D. M. (2010). Pronuclear transfer in human embryos to prevent transmission of mitochondrial DNA disease. *Nature* **465**, 82–85.
Cree, L. M., Samuels, D. C., de Sousa Lopes, S. C., Rajasimha, H. K., Wonnapinij, P., Mann, J. R., Dahl, H. H. & Chinnery, P. F. (2008). A reduction of mitochondrial DNA molecules during embryogenesis explains the rapid segregation of genotypes. *Nature Genetics* **40**, 249–254.
Davidson, M. M., Walker, W. F., Hernandez-Rosa, E. & Nesti, C. (2009). Evidence for nuclear modifier gene in mitochondrial cardiomyopathy. *Journal of Molecular and Cellular Cardiology* **46**, 936–942.
Davies, K. M., Blum, T. B. & Kühlbrandt, W. (2018). Conserved in situ arrangement of complex I and III 2 in mitochondrial respiratory chain supercomplexes of mammals, yeast, and plants. *Proceedings of the National Academy of Sciences* **115**, 3024–3029.
De Fanti, S., Vicario, S., Lang, M., Simone, D., Magli, C., Luiselli, D., Gianaroli, L. & Romeo, G. (2017). Intra-individual purifying selection on mitochondrial DNA variants during human oogenesis. *Human Reproduction* **32**, 1100–1107.
Dobler, R., Rogell, B., Budar, F. & Dowling, D. K. (2014). A meta-analysis of the strength and nature of cytoplasmic genetic effects. *Journal of Evolutionary Biology* **27**, 2021–2034.
Dobler, R., Dowling, D. K., Morrow, E. H. & Reinhardt, K. (2018). A systematic review and meta-analysis reveals pervasive effects of the technique of mitochondrial replacement on health. *Human Reproduction Update* **24**, 519–534.
Dowling, D. K. (2014). Evolutionary perspectives on the links between mitochondrial genotype and disease phenotype. *Biochimica et Biophysica Acta - General Subjects* **1840**, 1393–1403.
Dowling, D. K., Abiega, K. C. & Arnqvist, G. (2007). Temperature-specific outcomes of cytoplasmic-nuclear interactions on egg-to-adult development time in seed beetles. *Evolution* **61**, 194–201.
Dowling, D. K., Friberg, U. & Lindell, J. (2008). Evolutionary implications of non-neutral mitochondrial genetic variation. *Trends in Ecology & Evolution* **23**, 546–554.
Dowling, D. K., Maklakov, A. A., Friberg, U. & Hailer, F. (2009). Applying the genetic theories of ageing to the cytoplasm: cytoplasmic genetic covariation for fitness and lifespan. *Journal of Evolutionary Biology* **22**, 818–827.
Dowling, D. K., Meerupati, T. & Arnqvist, G. (2010). Cytonuclear interactions and the economics of mating in seed beetles. *The American Naturalist* **176**, 131–140.
Dowling, D. K., Tompkins, D. M. & Gemmell, N. J. (2015). The Trojan female technique for pest control: a candidate mitochondrial mutation confers low male fertility across diverse nuclear backgrounds in *Drosophila melanogaster*. *Evolutionary Applications* **8**, 871–880.
Dumollard, R., Duchen, M. & Carroll, J. (2007). The role of mitochondrial function in the oocyte and embryo. *Current Topics in Developmental Biology* **77**, 21–49.

Edmands, S. (2007). Between a rock and a hard place: evaluating the relative risks of inbreeding and outbreeding for conservation and management. *Molecular Ecology* **16**, 463–475.

Ellison, C. K. & Burton, R. S. (2006). Disruption of mitochondrial function in interpopulation hybrids of *Tigriopus californicus*. *Evolution* **60**, 1382–1391.

Ellison, C. K. & Burton, R. S. (2008*a*). Genotype-dependent variation of mitochondrial transcriptional profiles in interpopulation hybrids. *Proceedings of the National Academy of Sciences* **105**, 15831–15836.

Ellison, C. K. & Burton, R. S. (2008*b*). Interpopulation hybrid breakdown maps to the mitochondrial genome. *Evolution* **62**, 631–638.

Ellison, C. K. & Burton, R. S. (2010). Cytonuclear conflict in interpopulation hybrids: the role of RNA polymerase in mtDNA transcription and replication. *Journal of Evolutionary Biology* **23**, 528–538.

Estes, S., Coleman-Hulbert, A. L., Hicks, K. a., de Haan, G., Martha, S. R., Knapp, J. B., Smith, S. W., Stein, K. C. & Denver, D. R. (2011). Natural variation in life history and aging phenotypes is associated with mitochondrial DNA deletion frequency in *Caenorhabditis briggsae*. *BMC Evolutionary Biology* **11**, 11.

Eyre-Walker, A. (2017). Mitochondrial replacement therapy: are Mito-nuclear interactions likely to be a problem? *Genetics* **205**, 1365–1372.

Fan, W., Waymire, K. G., Narula, N., Li, P., Rocher, C., Coskun, P. E., Vannan, M. A., Narula, J., MacGregor, G. R. & Wallace, D. C. (2008). A mouse model of mitochondrial disease reveals germline selection against severe mtDNA mutations. *Science* **319**, 958–962.

Fiedorczuk, K., Letts, J. A., Degliesposti, G., Kaszuba, K., Skehel, M. & Sazanov, L. A. (2016). Atomic structure of the entire mammalian mitochondrial complex I. *Nature* **538**, 406–410.

Finch, T. M., Zhao, N., Korkin, D., Frederick, K. H. & Eggert, L. S. (2014). Evidence of positive selection in mitochondrial complexes I and V of the African elephant. *PLoS One* **9**, e92587.

Frank, S. A. & Hurst, L. D. (1996). Mitochondria and male disease. *Nature* **383**, 224.

Garvin, M. R., Bielawski, J. P., Sazanov, L. A. & Gharrett, A. J. (2014). Review and meta-analysis of natural selection in mitochondrial complex I in metazoans. *Journal of Zoological Systematics and Evolutionary Research* **53**, 1–17.

Garvin, M. R., Templin, W. D., Gharrett, A. J., Decovich, N., Kondzela, C. M., Guyon, J. R. & Mcphee, M. V. (2016). Potentially adaptive mitochondrial haplotypes as a tool to identify divergent nuclear loci. *Methods in Ecology and Evolution* **8**, 821–834.

Ge, H., Tollner, T. L., Hu, Z., Dai, M., Li, X., Guan, H., Shan, D., Zhang, X., Lv, J., Huang, C. & Dong, Q. (2012). The importance of mitochondrial metabolic activity and mitochondrial DNA replication during oocyte maturation in vitro on oocyte quality and subsequent embryo developmental competence. *Molecular Reproduction and Development* **79**, 392–401.

Gemmell, N. J., Metcalf, V. J. & Allendorf, F. W. (2004). Mother's curse: the effect of mtDNA on individual fitness and population viability. *Trends in Ecology & Evolution* **19**, 238–244.

Gershoni, M., Templeton, A. R. & Mishmar, D. (2009). Mitochondrial bioenergetics as a major motive force of speciation. *BioEssays* **31**, 642–650.

Gershoni, M., Levin, L., Ovadia, O., Toiw, Y., Shani, N., Dadon, S., Barzilai, N., Bergman, A., Atzmon, G., Wainstein, J., Tsur, A., Nijtmans, L., Glaser, B. & Mishmar, D. (2014). Disrupting mitochondrial-nuclear coevolution affects OXPHOS complex I integrity and impacts human health. *Genome Biology and Evolution* **6**, 2665–2680.

Greaves, L. C. & Taylor, R. W. (2006). Mitochondrial DNA mutations in human disease. *IUBMB Life* **58**, 143–151.

Greiner, S., Sobanski, J. & Bock, R. (2015). Why are most organelle genomes transmitted maternally? *BioEssays* **37**, 80–94.

Grossman, L. I., Wildman, D. E., Schmidt, T. R. & Goodman, M. (2004). Accelerated evolution of the electron transport chain in anthropoid primates. *Trends in Genetics* **20**, 578–585.

Gu, J., Wu, M., Guo, R., Yan, K., Lei, J., Gao, N. & Yang, M. (2016). The architecture of the mammalian respirasome. *Nature* **537**, 639–643.

Guo, R., Zong, S., Wu, M., Gu, J. & Yang, M. (2017). Architecture of human mitochondrial respiratory megacomplex I2III2IV2. *Cell* **170**, 1247–1257.e12.

Hadjivasiliou, Z., Lane, N., Seymour, R. M. & Pomiankowski, A. (2013). Dynamics of mitochondrial inheritance in the evolution of binary mating types and two sexes. *Proceedings of the Royal Society B-Biological Sciences* **280**, 20131920.

Hagström, E., Freyer, C., Battersby, B. J., Stewart, J. B. & Larsson, N. G. (2014). No recombination of mtDNA after heteroplasmy for 50 generations in the mouse maternal germline. *Nucleic Acids Research* **42**, 1111–1116.

Harrison, J. S. & Burton, R. S. (2006). Tracing hybrid incompatibilities to single amino acid substitutions. *Molecular Biology and Evolution* **23**, 559–564.

Havird, J. C. & Sloan, D. B. (2016). The roles of mutation, selection, and expression in determining relative rates of evolution in mitochondrial versus nuclear genomes. *Molecular Biology and Evolution* **33**, 3042–3053.

Havird, J. C., Hall, M. D. & Dowling, D. K. (2015*a*). The evolution of sex: a new hypothesis based on mitochondrial mutational erosion: mitochondrial mutational erosion in ancestral eukaryotes would favor the evolution of sex, harnessing nuclear recombination to optimize compensatory nuclear coadaptation. *BioEssays* **37**, 951–958.

Havird, J. C., Whitehill, N. S., Snow, C. D. & Sloan, D. B. (2015*b*). Conservative and compensatory evolution in oxidative phosphorylation complexes of angiosperms with highly divergent rates of mitochondrial genome evolution. *Evolution* **69**, 3069–3081.

Havird, J. C., Trapp, P., Miller, C., Bazos, I. & Sloan, D. B. (2017). Causes and consequences of rapidly evolving mtDNA in a plant lineage. *Genome Biology and Evolution* **9**, 323.

Hayashi, Y., Otsuka, K., Ebina, M., Igarashi, K., Takehara, A., Matsumoto, M., Kanai, A., Igarashi, K., Soga, T. & Matsui, Y. (2017). Distinct requirements for energy metabolism in mouse primordial germ cells and their reprogramming to embryonic germ cells. *Proceedings of the National Academy of Sciences of the United States of America* **114**, 8289–8294.

Hicks, K. A., Denver, D. R. & Estes, S. (2013). Natural variation in *Caenorhabditis briggsae* mitochondrial form and function suggests a novel model of organelle dynamics. *Mitochondrion* **13**, 44–51.

Hill, G. E. (2014). Sex linkage of nuclear-encoded mitochondrial genes. *Heredity* **112**, 469–470.

Hill, G. E. (2015). Mitonuclear ecology. *Molecular Biology and Evolution* **32**, 1917–1927.

Hill, G. E. (2016). Mitonuclear coevolution as the genesis of speciation and the mitochondrial DNA barcode gap. *Ecology and Evolution* **6**, 5831–5842.

Hill, G. E. (2017). The mitonuclear compatibility species concept. *The Auk* **134**, 393–409.

Hill, G. E. (2018). Mitonuclear mate choice: a missing component of sexual selection theory? *BioEssays* **40**, 1700191.

Hill, G. E. & Johnson, J. D. (2013). The mitonuclear compatibility hypothesis of sexual selection. *Proceedings of the Royal Society B-Biological Sciences* **280**, 20131314.

Hoekstra, L. A., Siddiq, M. A. & Montooth, K. L. (2013). Pleiotropic effects of a mitochondrial-nuclear incompatibility depend upon the accelerating effect of temperature in Drosophila. *Genetics* **195**, 1129–1139.

Hudson, G., Gomez-Duran, A., Wilson, I. J. & Chinnery, P. F. (2014). Recent mitochondrial DNA mutations increase the risk of developing common late-onset human diseases. *PLoS Genetics* **10**, e1004369.

Hyslop, L. A., Blakeley, P., Craven, L., Richardson, J., Fogarty, N. M. E., Fragouli, E., Lamb, M., Wamaitha, S. E., Prathalingam, N., Zhang, Q., O'Keefe, H., Takeda, Y., Arizzi, L., Alfarawati, S., Tuppen, H. A., et al. (2016). Towards clinical application of pronuclear transfer to prevent mitochondrial DNA disease. *Nature* **534**, 383–386.

Immonen, E., Collet, M., Goenaga, J. & Arnqvist, G. (2016). Direct and indirect genetic effects of sex-specific mitonuclear epistasis on reproductive ageing. *Heredity* **116**, 338–347.

Innocenti, P., Morrow, E. H. & Dowling, D. K. (2011). Experimental evidence supports a sex-specific selective sieve in mitochondrial genome evolution. *Science* **332**, 845–848.

Iwata, S. (1998). Complete structure of the 11-subunit bovine mitochondrial cytochrome bc1 complex. *Science* **281**, 64–71.

James, A. C. & Ballard, J. W. O. (2003). Mitochondrial genotype affects fitness in *Drosophila simulans*. *Genetics* **164**, 187–194.

James, J. E., Piganeau, G. & Eyre-Walker, A. (2016). The rate of adaptive evolution in animal mitochondria. *Molecular Ecology* **25**, 67–78.

Ji, F., Sharpley, M. S., Derbeneva, O., Alves, L. S., Qian, P., Wang, Y., Chalkia, D., Lvova, M., Xu, J., Yao, W. & Simon, M. (2012). Mitochondrial DNA variant associated with Leber hereditary optic neuropathy and high-altitude Tibetans. *Proceedings of the National Academy of Sciences of the United States of America* **109**, 7391–7396.

Kasashima, K., Nagao, Y. & Endo, H. (2014). Dynamic regulation of mitochondrial genome maintenance in germ cells. *Reproductive Medicine and Biology* **13**, 11–20.

Krakauer, D. C. & Mira, A. (1999). Mitochondria and germ-cell death. *Nature* **400**, 125–126.

Kwong, S., Srivathsan, A., Vaidya, G. & Meier, R. (2012). Is the COI barcoding gene involved in speciation through intergenomic conflict? *Molecular Phylogenetics and Evolution* **62**, 1009–1012.

Lane, N. (2005). *Power, Sex, Suicide: Mitochondria and the Meaning of Life*. Oxford University Press, New York.

Lane, N. & Martin, W. (2010). The energetics of genome complexity. *Nature* **467**, 929–934.

Latorre-Pellicer, A., Moreno-Loshuertos, R., Lechuga-Vieco, A. V., Sánchez-Cabo, F., Torroja, C., Acín-Pérez, R., Calvo, E., Aix, E., González-Guerra, A., Logan, A., Bernad-Miana, M. L., Romanos, E., Cruz, R., Cogliati, S., Sobrino, B., et al. (2016). Mitochondrial and nuclear DNA matching shapes metabolism and healthy ageing. *Nature* **535**, 561–565.

Lee, C., Yen, K. & Cohen, P. (2013). Humanin: a harbinger of mitochondrial-derived peptides? *Trends in Endocrinology and Metabolism* **24**, 222–228.

Lee, C., Zeng, J., Drew, B. G., Sallam, T., Martin-Montalvo, A., Wan, J., Kim, S. J., Mehta, H., Hevener, A. L., De Cabo, R. & Cohen, P. (2015).

The mitochondrial-derived peptide MOTS-c promotes metabolic homeostasis and reduces obesity and insulin resistance. *Cell Metabolism* **21**, 443–454.

Levin, D. A. (2003). The cytoplasmic factor in plant speciation. *Systematic Botany* **28**, 5–11.

Levin, L., Blumberg, A., Barshad, G. & Mishmar, D. (2014). Mito-nuclear co-evolution: the positive and negative sides of functional ancient mutations. *Frontiers in Genetics* **5**, 448.

Luo, L. F., Hou, C. C. & Yang, W. X. (2013). Nuclear factors: roles related to mitochondrial deafness. *Gene* **520**, 79–89.

Lynch, M. (1997). Mutation accumulation in nuclear, organelle, and prokaryotic transfer RNA genes. *Molecular Biology and Evolution* **14**, 914–925.

Lynch, M. & Blanchard, J. L. (1998). Deleterious mutation accumulation in organelle genomes. *Genetica* **102**, 29–39.

Lynch, M., Butcher, D., Bürger, R. & Gabriel, W. (1993). The mutational meltdown in asexual populations. *Journal of Heredity* **84**, 339–344.

Ma, H. & O'Farrell, P. H. (2015). Selections that isolate recombinant mitochondrial genomes in animals. *eLife* **4**, e07247.

Ma, H., Marti Gutierrez, N., Morey, R., Van Dyken, C., Kang, E., Hayama, T., Lee, Y., Li, Y., Tippner-Hedges, R., Wolf, D. P., Laurent, L. C. & Mitalipov, S. (2016). Incompatibility between nuclear and mitochondrial genomes contributes to an interspecies reproductive barrier. *Cell Metabolism* **24**, 283–294.

Martikainen, M. H., Grady, J. P., Ng, Y. S., Alston, C. L., Gorman, G. S., Taylor, R. W., McFarland, R. & Turnbull, D. M. (2017). Decreased male reproductive success in association with mitochondrial dysfunction. *European Journal of Human Genetics* **25**, 1163–1165.

Meiklejohn, C. D., Holmbeck, M. A., Siddiq, M. A., Abt, D. N., Rand, D. M. & Montooth, K. L. (2013). An incompatibility between a mitochondrial tRNA and its nuclear-encoded tRNA synthetase compromises development and fitness in *Drosophila*. *PLoS Genetics* **9**, e1003238.

Milot, E., Moreau, C., Gagnon, A., Cohen, A. A., Brais, B. & Labuda, D. (2017). Mother's curse neutralizes natural selection against a human genetic disease over three centuries. *Nature Ecology & Evolution* **1**, 1400–1406.

Mishmar, D. & Zhidkov, I. (2010). Evolution and disease converge in the mitochondrion. *Biochimica et Biophysica Acta - Bioenergetics* **1797**, 1099–1104.

Mishmar, D., Ruiz-Pesini, E., Golik, P., Macaulay, V., Clark, A. G., Hosseini, S., Brandon, M., Easley, K., Chen, E., Brown, M. D., Sukernik, R. I., Olckers, A. & Wallace, D. C. (2003). Natural selection shaped regional mtDNA variation in humans. *Proceedings of the National Academy of Sciences of the United States of America* **100**, 171–176.

Monaghan, R. M. & Whitmarsh, A. J. (2015). Mitochondrial proteins moonlighting in the nucleus. *Trends in Biochemical Sciences* **40**, 728–735.

Moore, J. H. & Williams, S. M. (2005). Traversing the conceptual divide between biological and statistical epistasis: systems biology and a more modern synthesis. *BioEssays* **27**, 637–646.

Morales, H. E., Pavlova, A., Joseph, L. & Sunnucks, P. (2015). Positive and purifying selection in mitochondrial genomes of a bird with mitonuclear discordance. *Molecular Ecology* **24**, 2820–2837.

Morales, H. E., Pavlova, A., Amos, N., Major, R., Kilian, A., Greening, C. & Sunnucks, P. (2018). Concordant divergence of mitogenomes and a mitonuclear gene cluster in bird lineages inhabiting different climates. *Nature Ecology & Evolution* **2**, 1258.

Morrow, E. H. & Camus, M. F. (2017). Mitonuclear epistasis and mitochondrial disease. *Mitochondrion* **35**, 119–122.

Morrow, E. H., Reinhardt, K., Wolff, J. N. & Dowling, D. K. (2015). Risks inherent to mitochondrial replacement. *EMBO Reports* **16**, 541–545.

Mossman, J. A., Biancani, L. M., Zhu, C. & Rand, D. M. (2016). Mitonuclear epistasis for development time and its modification by diet in *Drosophila*. *Genetics* **203**, 463–484.

Mowry, A. V., Donoviel, Z. S., Kavazis, A. N. & Hood, W. R. (2017). Mitochondrial function and bioenergetic trade-offs during lactation in the house mouse (*Mus musculus*). *Ecology and Evolution* **7**, 2994–3005.

Nabholz, B., Ellegren, H. & Wolf, J. B. W. (2013). High levels of gene expression explain the strong evolutionary constraint of mitochondrial protein-coding genes. *Molecular Biology and Evolution* **30**, 272–284.

Nachman, M. W., Boyer, S. N. & Aquadro, C. F. (1994). Nonneutral evolution at the mitochondrial NADH dehydrogenase subunit 3 gene in mice. *Proceedings of the National Academy of Sciences of the United States of America* **91**, 6364–6368.

Nachman, M. W., Brown, W. M., Stoneking, M. & Aquadro, C. F. (1996). Nonneutral mitochondrial DNA variation in humans and chimpanzees. *Genetics* **142**, 953–963.

Nakada, K., Sato, A., Yoshida, K., Morita, T., Tanaka, H., Inoue, S., Yonekawa, H. & Hayashi, J. (2006). Mitochondria-related male infertility. *Proceedings of the National Academy of Sciences of the United States of America* **103**, 15148–15153.

Neiman, M. & Taylor, D. R. (2009). The causes of mutation accumulation in mitochondrial genomes. *Proceedings of the Royal Society B: Biological Sciences* **276**, 1201–1209.

Osada, N. & Akashi, H. (2012). Mitochondrial–nuclear interactions and accelerated compensatory evolution: evidence from the primate cytochrome c oxidase complex. *Molecular Biology and Evolution* **29**, 337–346.

Patel, M. R., Miriyala, G. K., Littleton, A. J., Yang, H., Trinh, K., Young, J. M., Kennedy, S. R., Yamashita, Y. M., Pallanck, L. J. & Malik, H. S. (2016). A mitochondrial DNA hypomorph of cytochrome oxidase specifically impairs male fertility in *Drosophila melanogaster*. *eLife* **5**, 1–27.

Pichaud, N., Ballard, J. W. O., Tanguay, R. M. & Blier, P. U. (2012). Naturally occurring mitochondrial DNA haplotypes exhibit metabolic differences: insight into functional properties of mitochondria. *Evolution* **66**, 3189–3197.

Pizzari, T. (2009). Sexual selection: sperm in the fast lane. *Current Biology* **19**, R292–R294.

Popadin, K. Y., Nikolaev, S. I., Junier, T., Baranova, M. & Antonarakis, S. E. (2013). Purifying selection in mammalian mitochondrial protein-coding genes is highly effective and congruent with evolution of nuclear genes. *Molecular Biology and Evolution* **30**, 347–355.

Pozzi, A., Plazzi, F., Milani, L., Ghiselli, F. & Passamonti, M. (2017). SmithRNAs: could mitochondria "bend" nuclear regulation? *Molecular Biology and Evolution* **34**, 1960–1973.

Quintela, M., Johansson, M. P., Kristjánsson, B. K., Barreiro, R. & Laurila, A. (2014). AFLPs and mitochondrial haplotypes reveal local adaptation to extreme thermal environments in a freshwater gastropod. *PLoS One* **9**, e101821.

Radzvilavicius, A. L., Hadjivasiliou, Z., Pomiankowski, A. & Lane, N. (2016). Selection for mitochondrial quality drives evolution of the germline. *PLoS Biology* **14**, e2000410.

Raj, A., Rifkin, S. A., Andersen, E. & Van Oudenaarden, A. (2010). Variability in gene expression underlies incomplete penetrance. *Nature* **463**, 913–918.

Rand, D. M. (2001). The units of selection on mitochondrial DNA. *Annual Review of Ecology and Systematics* **32**, 415–448.

Rand, D. M., Dorfsman, M. & Kann, L. M. (1994). Neutral and non-neutral evolution of *Drosophila* mitochondrial DNA. *Genetics* **138**, 741–756.

Rand, D. M., Haney, R. A. & Fry, A. J. (2004). Cytonuclear coevolution: the genomics of cooperation. *Trends in Ecology & Evolution* **19**, 645–653.

Rand, D. M., Fry, A. & Sheldahl, L. (2006). Nuclear-mitochondrial epistasis and drosophila aging: introgression of *Drosophila simulans* mtDNA modifies longevity in *D. melanogaster* nuclear backgrounds. *Genetics* **172**, 329–341.

Rawson, P. D. & Burton, R. S. (2002). Functional coadaptation between cytochrome c and cytochrome c oxidase within allopatric populations of a marine copepod. *Proceedings of the National Academy of Sciences of the United States of America* **99**, 12955–12958.

Reinhardt, K., Dowling, D. K. & Morrow, E. H. (2013). Mitochondrial replacement, evolution, and the clinic. *Science* **341**, 1345–1346.

Rishishwar, L. & Jordan, I. K. (2017). Implications of human evolution and admixture for mitochondrial replacement therapy. *BMC Genomics* **18**, 140.

Roux, F., Mary-Huard, T., Barillot, E., Wenes, E., Botran, L., Durand, S., Villoutreix, R., Martin-Magniette, M.-L., Camilleri, C. & Budar, F. (2016). Cytonuclear interactions affect adaptive traits of the annual plant *Arabidopsis thaliana* in the field. *Proceedings of the National Academy of Sciences of the United States of America* **113**, 3687–3692.

Ruiz-Pesini, E. (2004). Effects of purifying and adaptive selection on regional variation in human mtDNA. *Science* **303**, 223–226.

Ruiz-Pesini, E., Díez-Sánchez, C., López-Pérez, M. J. & Enríquez, J. A. (2007). The role of the mitochondrion in sperm function: is there a place for oxidative phosphorylation or is this a purely glycolytic process? *Current Topics in Developmental Biology* **77**, 3–19.

Schaefer, S., Nadeau, J. H. & Wray, H. E. G. A. (2015). The genetics of epigenetic inheritance: modes, molecules, and mechanisms. *The Quarterly Review of Biology* **90**, 381–415.

Scott, G. R., Schulte, P. M., Egginton, S., Scott, A. L. M., Richards, J. G. & Milsom, W. K. (2011). Molecular evolution of cytochrome c oxidase underlies high-altitude adaptation in the bar-headed goose. *Molecular Biology and Evolution* **28**, 351–363.

Sharbrough, J., Havird, J. C., Noe, G. R., Warren, J. M. & Sloan, D. B. (2017). The mitonuclear dimension of Neanderthal and Denisovan ancestry in modern human genomes. *Genome Biology and Evolution* **9**, 1567–1581.

Short, R. V. (1997). The testis: the witness of the mating system, the site of mutation and the engine of desire. *Acta Paediatrica* **86**, 3–7.

Silva, G., Lima, F. P., Martel, P. & Castilho, R. (2014). Thermal adaptation and clinal mitochondrial DNA variation of European anchovy. *Proceedings of the Royal Society B: Biological Sciences* **281**, 20141093.

Simmons, L. W. (2001). *Sperm Competition and its Evolutionary Consequences in the Insects*. Princeton University Press, Princeton, N.J.

Sloan, D. B., Triant, D. A., Wu, M. & Taylor, D. R. (2014). Cytonuclear interactions and relaxed selection accelerate sequence evolution in organelle ribosomes. *Molecular Biology and Evolution* **31**, 673–682.

Sloan, D. B., Fields, P. D. & Havird, J. C. (2015). Mitonuclear linkage disequilibrium in human populations. *Proceedings of the Royal Society B: Biological Sciences* **282**, 20151704.

Sloan, D. B., Havird, J. C. & Sharbrough, J. (2017). The on-again, off-again relationship between mitochondrial genomes and species boundaries. *Molecular Ecology* **26**, 2212–2236.
Smith, D. R. & Keeling, P. J. (2015). Mitochondrial and plastid genome architecture: reoccurring themes, but significant differences at the extremes. *Proceedings of the National Academy of Sciences of the United States of America* **112**, 201422049.
Smith, S., Turbill, C. & Suchentrunk, F. (2010). Introducing mother's curse: low male fertility associated with an imported mtDNA haplotype in a captive colony of brown hares. *Molecular Ecology* **19**, 36–43.
Snook, R. R. (2005). Sperm in competition: not playing by the numbers. *Trends in Ecology and Evolution* **20**, 46–53.
Stelkens, R. B., Schmid, C. & Seehausen, O. (2015). Hybrid breakdown in cichlid fish. *PLoS One* **10**, 1–11.
Stewart, J. B. & Larsson, N.-G. (2014). Keeping mtDNA in shape between generations. *PLoS Genetics* **10**, e1004670.
Stewart, J. B., Freyer, C., Elson, J. L. & Larsson, N.-G. (2008*a*). Purifying selection of mtDNA and its implications for understanding evolution and mitochondrial disease. *Nature Reviews. Genetics* **9**, 657–662.
Stewart, J. B., Freyer, C., Elson, J. L., Wredenberg, A., Cansu, Z., Trifunovic, A. & Larsson, N. G. (2008*b*). Strong purifying selection in transmission of mammalian mitochondrial DNA. *PLoS Biology* **6**, 0063–0071.
Sunnucks, P., Morales, H. E., Lamb, A. M., Pavlova, A. & Greening, C. (2017). Integrative approaches for studying mitochondrial and nuclear genome co-evolution in oxidative phosphorylation. *Frontiers in Genetics* **8**, 25.
Taanman, J. W. (2001). A nuclear modifier for a mitochondrial DNA disorder. *Trends in Genetics* **17**, 609–611.
Tachibana, M., Sparman, M., Sritanaudomchai, H., Ma, H., Clepper, L., Woodward, J., Li, Y., Ramsey, C., Kolotushkina, O. & Mitalipov, S. (2009). Mitochondrial gene replacement in primate offspring and embryonic stem cells. *Nature* **461**, 367–372.
Tachibana, M., Amato, P., Sparman, M., Woodward, J., Sanchis, D. M., Ma, H., Gutierrez, N. M., Tippner-Hedges, R., Kang, E., Lee, H. S., Ramsey, C., Masterson, K., Battaglia, D., Lee, D., Wu, D., et al. (2013). Towards germline gene therapy of inherited mitochondrial diseases. *Nature* **493**, 627–631.
The 1000 Genomes Project Consortium (2015). A global reference for human genetic variation. *Nature* **526**, 68–74.
Tsukihara, T., Aoyama, H., Yamashita, E. & Tomizaki, T. (1996). The whole structure of the 13-subunit oxidized cytochrome c oxidase at 2.8 angstrom. *Science* **272**, 1136.
Turelli, M. & Orr, H. A. (2000). Dominance, epistasis and the genetics of postzygotic isolation. *Genetics* **154**, 1663–1679.
Van Der Sluis, E. O., Bauerschmitt, H., Becker, T., Mielke, T., Frauenfeld, J., Berninghausen, O., Neupert, W., Herrmann, J. M. & Beckmann, R. (2015). Parallel structural evolution of mitochondrial ribosomes and OXPHOS complexes. *Genome Biology and Evolution* **7**, 1235–1251.
Vaught, R. C. & Dowling, D. K. (2018). Maternal inheritance of mitochondria: implications for male fertility? *Reproduction* **155**, R159–R168.
Ventura, D. F., Gualtieri, M., Oliveira, A. G. F., Costa, M. F., Quiros, P., Sadun, F., De Negri, A. M., Salomão, S. R., Berezovsky, A., Sherman, J., Sadun, A. A. & Carelli, V. (2007). Male prevalence of acquired color vision defects in asymptomatic carriers of Leber's hereditary optic neuropathy. *Investigative Ophthalmology and Visual Science* **48**, 2362–2370.
Wai, T., Teoli, D. & Shoubridge, E. A. (2008). The mitochondrial DNA genetic bottleneck results from replication of a subpopulation of genomes. *Nature Genetics* **40**, 1484–1488.
Wallace, D. C. (2005). The mitochondrial genome in human adaptive radiation and disease: on the road to therapeutics and performance enhancement. *Gene* **354**, 169–180.
Wallace, D. C. (2007). Why do we still have a maternally inherited mitochondrial DNA? Insights from evolutionary medicine. *Annual Review of Biochemistry* **76**, 781–821.
Wallace, D. C. (2010). Bioenergetics, the origins of complexity, and the ascent of man. *Proceedings of the National Academy of Sciences of the United States of America* **107**, 8947–8953.
Wang, F., Huang, G., Tian, H., Zhong, Y., Shi, H., Li, Z., Zhang, X., Wang, H. & Sun, F. (2015). Point mutations in KAL1 and the mitochondrial gene MT-tRNA cys synergize to produce Kallmann syndrome phenotype. *Scientific Reports* **5**, 13050.
Werren, J. H., Baldo, L. & Clark, M. E. (2008). *Wolbachia*: master manipulators of invertebrate biology. *Nature Reviews Microbiology* **6**, 741–751.
Willett, C. S. (2008). Significant variation for fitness impacts of ETS loci in hybrids between populations of *Tigriopus californicus*. *Journal of Heredity* **99**, 56–65.
Willett, C. S. (2012). Quantifying the elevation of mitochondrial DNA evolutionary substitution rates over nuclear rates in the intertidal copepod *Tigriopus californicus*. *Journal of Molecular Evolution* **74**, 310–318.
Willett, C. S. & Burton, R. S. (2001). Viability of cytochrome c genotypes depends on cytoplasmic backgrounds in *Tigriopus californicus*. *Evolution* **55**, 1592–1599.
Willett, C. S. & Burton, R. S. (2003). Environmental influences on epistatic interactions: viabilities of cytochrome c genotypes in interpopulation crosses. *Evolution* **57**, 2286–2292.
Wolff, J. N., Ladoukakis, E. D., Enríquez, J. A. & Dowling, D. K. (2014). Mitonuclear interactions: evolutionary consequences over multiple biological scales. *Philosophical Transactions of the Royal Society B: Biological Sciences* **369**, 20130443.
Wolff, J. N., Pichaud, N., Camus, M. F., Cote, G., Blier, P. U. & Dowling, D. K. (2016). Evolutionary implications of mitochondrial genetic variation: mitochondrial genetic effects on OXPHOS respiration and mitochondrial quantity change with age and sex in fruit flies. *Journal of Evolutionary Biology* **29**, 736–747.
Woodson, J. D. & Chory, J. (2008). Coordination of gene expression between organellar and nuclear genomes. *Nature Reviews Genetics* **9**, 383–395.
Wu, M., Gu, J., Guo, R., Huang, Y. & Yang, M. (2016). Structure of mammalian respiratory supercomplex I1III2IV1. *Cell* **167**, 1598–1609.e10.
Yan, Z., Ye, G. & Werren, J. (2018). Evolutionary rate coevolution between mitochondria and mitochondria-associated nuclear-encoded proteins in insects. *bioRxiv*, 288456.
Yang, M., He, Z., Shi, S., Wu, C., Hill, C., Diego, S., Jolla, L., Wallis, G. P., Arntzen, J. W., Venditti, C., Meade, A., Pagel, M., Van Doren, B. M., Campagna, L., Helm, B., et al. (2017). Speciation genomics and a role for the Z chromosome in the early stages of divergence between Mexican ducks and mallards. *Evolution* **11**, 1–21.
Yee, W. K. W., Sutton, K. L. & Dowling, D. K. (2013). In vivo male fertility is affected by naturally occurring mitochondrial haplotypes. *Current Biology* **23**, R55–R56.
Yen, M.-Y., Wang, A.-G. & Wei, Y.-H. (2006). Leber's hereditary optic neuropathy: a multifactorial disease. *Progress in Retinal and Eye Research* **25**, 381–396.
Zaidi, A.A. & Makova, K.D. (2018). Mito-nuclear effects uncovered in admixed populations. *bioRxiv*, 349126.
Zhang, F. & Broughton, R. E. (2013). Mitochondrial-nuclear interactions: compensatory evolution or variable functional constraint among vertebrate oxidative phosphorylation genes? *Genome Biology and Evolution* **5**, 1781–1791.
Zhang, Y., Brasher, A. L., Park, N. R., Taylor, H. A., Kavazis, A. N. & Hood, W. R. (2018). High activity before breeding improves reproductive performance by enhancing mitochondrial function and biogenesis. *The Journal of Experimental Biology* **221**, jeb177469.
Zhou, A., Rohou, A., Schep, D. G., Bason, J. V., Montgomery, M. G., Walker, J. E., Grigorieffniko, N. & Rubinstein, J. L. (2015). Structure and conformational states of the bovine mitochondrial ATP synthase by cryo-EM. *eLife* **4**, e10180.
Zhu, C. T., Ingelmo, P. & Rand, D. M. (2014). GxGxE for lifespan in *Drosophila*: mitochondrial, nuclear, and dietary interactions that modify longevity. *PLoS Genetics* **10**, e1004354.
Zhu, J., Vinothkumar, K. R. & Hirst, J. (2016). Structure of mammalian respiratory complex I. *Nature* **536**, 354–358.

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