BIOB480/BIOE548 notes 11/07/2024

Introduction

- Final HW (#10) posted—due next Thursday, covers 50/500 rule and hybridization. Can be tricky, so bring questions Tuesday.

- Will update final project website with code and instructions over the weekend.

Hybridization

Hybridization is mating between "individuals from two populations, or groups of populations, which are distinguisable on the basis of one or more heritable characters" (Harrison 1990). In conservation genetics, we are often interested in studying hybridization with **diagnostic loci**: alleles that are fixed (i.e., $f(A_1)=1$) in one population and absent in the other.

Hybridization can take two forms, with different evolutionary conservation implications:

- **hybridization without introgression**: individuals from different populations can interbreed, but cannot have fertile offspring, and genetic material does not cross population boundaries.

- **introgressive hybridization**: indviduals from different populations can interbreed and have fertile offspring; genetic material can permeate across population boundaries through *backcrosses*

First-generation hybrids between pure parental taxa are known as **F1s**. Interbreeding among hybrids then produces later generations: **F2s**, **F3s**. **late generation hybrids**. An F1 hybrid has 50% of its genome derived from each parent, with 100% of loci showing interpopulation ancestry. A later generation hybrid will still have roughly 50% of its genome derived from each parent, but will have fewer loci showing interpopulation ancestry, as hybrid x hybrid crosses will end up pairing alleles from the same parental taxon. Backcrosses will end up with greater than 50% of their genome from a single parental taxon, and an intermediate number of loci showing interpopulation ancestry.

In an F2 hybrid, the probability an individual is heterozygous at 5 diagnostic loci is:

$$p(\text{H at 5 loci}) = 0.5^5$$

This is because an F2 individual comes from an F1 x F1 cross. At diagnostic loci, F1 individuals are by definition hetoerozygous. An A_1A_2 x A_1A_2 cross will produce 2 heterozygous genotypes out of four possibilities (A_1A_2 and A_2A_1).

An F1 hybrid backcrossing with one parental taxon will lose 50% of the remainder of its ancestry dervied from the other parent each generation. For example, an F1 hybrid formed by an intial cross between species A and species B followed by 5 generations of backcrossing into species A will end up with <2% of its genome derived from species B ($0.5^6 = 0.015625$).

Hybridization between genetically differentiated populations can cause linkage disequlibirum. Consider the following population formed by 5 individuals each of two parental taxa that differ at two diagnostic loci. Here, treating all individuals as a single population gives us the maximum possible value of D:

- **P**: AB, AB, AB, AB, AB, ab, ab, ab, ab, ab

- $f(A) = 0.5; f(a) = 0.5; f(B) = 0.5; f(b) = 0.5$

- $f(AB) = 0.5; f(ab) = 0.5$

- $D = p(A, B) - p(A)p(B) = 0.25$

F1 hybrids continue to show strong linkage disequilibrium:

- **F1**: AB, ab, Ab, aB, AB, AB, ab, ab, aB, Ab

- $f(A) = 0.5; f(a) = 0.5; f(B) = 0.5; f(b) = 0.5$

- $f(AB) = 0.3; f(ab) = 0.3$

- $D = p(A, B) - p(A)p(B) = 0.1$

However, this decays with time:

- **F2**: aB, Ab, AB, ab, aB, Ab, AB, ab, Ab, aB

- $f(A) = 0.5; f(a) = 0.5; f(B) = 0.5; f(b) = 0.5$

- $f(AB) = 0.2; f(ab) = 0.2$

- $D = p(A, B) - p(A)p(B) = -0.05$

Hybridization can either spread rampantly, creating a **hybrid swarm** where most individuals have some hybrid ancestry, or be restrained by the balance between natural selection and gene flow, creating a **tension zone**, or be restricted to a small region of space where hybrids have superior fitness to either parental taxon, in a **bounded hybrid superiority model**.

Hybridization is of conservation concern for several reasons:

- Hybrids can cause outbreeding depression;

- Sufficient hybridization can reduce population growth as reproductive output is put towards the "dead end" of hybrid individuals (**demographic swamping**);

- Introgressive hybridization can eliminate "pure" parental genomes (**genomic extinction**).

Hybrids also pose problems for conservation policy. Different laws afford hybrids different rights under biodiversity protection policies:

Australia's Biodiversity Conservation Act (2016).

Hybrids are eligible for conservation listing if:

1) they are distinct entities, i.e. the progeny are consistent within the agreed taxonomic limits for that species group;

2) they are capable of self-perpetuating, and are not reliant on parent stock for replacement;

3) they are the product of a natural event

So, hybrid-derived taxa **are eligible**, but hybrid zones are **not**.

US Endangered Species Act

- May 1977: US DOI says that "because it defines 'fish or wildlife' to include any offspring without limitation, the Act's plain meaning dictates coverage of hybrids of listed animal species" (and also applies to plants)
- July 1977: USFWS responds: "...since the Act was clearly passed to benefit endangered species, ...it must have meant the offsrping of two listed species and was not meant to protect a hybrid where that protection would in fact cause jeopardy to the continued existence of a species"
- August 1977: US DOI responds that "hybrids of listed species are not protected under the ESA" (because of potential for hybridization to cause harm)

US Endangered Species Act

- December 1990: USFWS suspends this "Hybrid Policy" as it does not protect taxa derived from hybridization (like the red wolf), or subspecies that interbreed (like Florida panther)
- 1996: USFWS & NOAA propose "Intercross Policy", but not approved

A Shiny app I wrote called HZAM allows for simulations of hybrid zones: https://elinck.shinyapps.io/hzam_shiny/