BIOB480/BIOE548 notes 11/12/2024

Introduction

- HWs graded—Quiz 3 grades incoming
- Quiz 4 in 1.5 weeks—details soon
- No group project work until you hear from me

Genetic Management of Wild Populations

In practice, conservation genetics allows biologists to tackle the following conservation problems:

1. Resolve taxonomic uncertainties;
2. Delineate management units;
3. Describe and predict levels of inbreeding;
4. Recognize N_e is typically 0.1 of N_c;
5. Recognize loss of V_A hinders response to environmental change;
6. Recognize the relationship between F and δ;
7. Recognize inbreeding can be inferred from H_o/H_e;
8. Recognize that effects of fragmentation can be inferred from allele frequencies

To do so, it is useful to first diagnose genetic issues by asking the following questions:

1. How large (N_e) is the population?
2. Has it experienced bottlenecks in the past?
3. Has it lost genetic diversity?
4. Is it suffering from inbreeding depression?
5. What is its geographic distribution?
6. Is it genetically fragmented?

Declining population size is a pervasive conservation problem. Many of its solutions are non genetic: identifying and removing the cause of the decline, protecting or expanding habitat, reintroducing individuals from captivity or other populations. However, in some cases outcrossing can improve reproductive fitness, a process known as **genetic rescue**.

However, translocating individuals to boost genetic diversity in populations requires careful planning. In order of preference, small populations should be augmented with:

1. Outbred individuals from the same subspecies;
2. Inbred individuals from different populations of the the same subspecies;
3. Captive individuals from the same subspecies;
4. Individuals of different subspecies or species

This order is intended to maximize the benefit of new genetic diversity while minimizing the risk out outbreeding depression or genomic extinction.

More quotidianly, moving indviduals raises practical concerns:

- Which individuals to translocate?
- How many?
- How often?
- From where to where?
- When should translocation begin?
- When should it cease?

Genetics can also be used to inform **reserve design**. The following ecological principles are often used to identify areas that should be protected to preserve biodiversity:

1. Conserve as large an area as possible;
2. Favor large populations and patches of habitat over small ones;
3. Represent the natural geographic and ecological range of a community;
4. Favor sites that contain more than one rare taxon if all else is equal;
5. Minimize edge-to-area ratio and internal fragmentation;
6. Maintain connections among historically contiguous populations

Conservation genetics adds additional considerations:

- Is the reserve large enough to support a genetically viable population?
- Is the species adapted to the habitat in the reserve?
- Should there be one large reserve, or several small reserves?
- Will individuals have connectivity to other populations?
- Does the reserve encompass diverse habitats to facilitate local adaptation?

Lastly, **harvesting** can select for particular traits with a genetic basis (such as tusklessness in elephants) when their phenotypes suffer disproportionate mortality. Quotas can help maintain natural allele frequencies.