

## EEB 2208 LECTURE TOPIC 15

### CONSERVATION GENETICS

#### Reading for this lecture

**Primack:** Chapter 12.

**Discussion reading:** Finkelstein et al. 2012. Lead poisoning and the deceptive recovery of the critically endangered California condor. PNAS 109:11449-11454.

#### 1. Introduction

##### A) GENETIC PROBLEMS ARE MORE LIKELY IN SMALL POPULATIONS

- i) As previously mentioned, small populations are inherently vulnerable for a lot of reasons.
- ii) **Point endemics** (species found in only one place) are especially vulnerable. For instance the Tiburon mariposa lily is found only on one mountain in northern California. The current population is quite large (10,000s), but it is vulnerable to a single catastrophic event that affects the one small site where it occurs.
- iii) Genetic problems also primarily affect small populations – both in the wild and in captivity – and so they exacerbate the effects of demographic and environmental conditions.

##### B) TWO KEY QUESTIONS

- i) What kind of genetic changes occur in small populations?
- ii) Why are they a threat?

#### 2. Genetic variation is lost in small populations, due to drift

##### A) GENETIC DRIFT

- i) **Genetic drift** is a random (neutral) process that leads to changes in the genetic makeup of a population.
- ii) It is different from natural selection, because it results from random variation in birth and death rates. For instance, some individuals may happen (by chance) to produce a lot of young in one year – the genes carried by these individuals will be passed on to the next generation at a high frequency. Other individuals may happen (by chance) to produce few or no young – their genes will be rare or absent in the next generation. By this process, gene frequencies can change.
- iii) Drift happens in all populations, but in moderately large populations the effects of drift are negligible (more on this below). In small populations, however, drift can have large effects on genetic variation.

##### B) THE MATH

- i) The genetic variation (**heterozygosity**) of a population refers to the number and abundance of alleles/genotypes in the population.
- ii) The change in heterozygosity between generations can be determined using this formula:  $H_{t+1} = [1 - (1/2N_e)] * H_t$ .  $H_t$  is the heterozygosity in the current (t) generation and  $H_{t+1}$  is the heterozygosity in the next (t+1) generation.  $N_e$  is a measure of how big the population size is (referred to as the **effective population size**; more on what that means below).
- iii) If you plug some numbers into this equation you can see how heterozygosity changes with different population sizes. Try doing the math with a small population size (e.g.,  $N_e = 5$ ). Then do it again for a larger population size (e.g.,  $N_e = 50$ ), and compare the results.

- iv) Note that the part of the equation  $(1 - 1/2N_e)$  must always be less than one (because  $N_e$  is always positive). This means that heterozygosity will always decline as a result of drift.
- v) If you don't really understand this, go back and work through it again (doing the calculations will help). If you still don't get it, ask for help.
- vi) The rate at which genetic variation is lost from a population will vary depending on the effective population size and on the length of time over which it is measured. See figure in Primack.

C) DOES GENETIC VARIATION ALWAYS DECLINE?

- i) NO!!! The results described above mean that if drift is the only process affecting genetic variation then there will always be a decline. But, other processes also occur.
- ii) Counteracting the loss of variation due to drift is mutation, which increases variation. But, the mutation rate is relatively low and does not change with population size. In large populations, where the loss of variation due to drift is very, very small, the mutation rate can counterbalance the losses. But, in very small populations, the rate of loss (through drift) goes up and the rate of gain (through mutation) stays the same, leading to a net loss.
- iii) If you are considering an endangered population, rather than an entire species, variation can also be increased through immigration. Even relatively low rates of immigration (1 or 2 individuals per generation) can be enough to counter the effects of drift. How would this information influence the way you manage a captive population?

### 3. Effective population size

A) DEFINITIONS

- i) In the equation given above we used a value called  $N_e$ , the **effective population size**. This value is different from the actual population size (sometimes called the **census population size**, because it is the number you would come up with if you did a census and counted every individual in the population). The difference between these two measures is very important.
- ii) The effective population size is a theoretical measure of how many individuals are contributing their genes to the next generation.

B) WHAT INFLUENCES THE EFFECTIVE POPULATION SIZE?

- i)  $N_e$  depends on several different things, including the sex ratio (the more skewed the sex ratio, the smaller  $N_e$  will be relative to  $N$ ), variation among individuals in the number of young produced (a lot of variation reduces  $N_e$ ), and fluctuations in population size.
- ii) Estimating the difference between  $N_e$  and  $N$  can be complex (see Primack). But the key thing to know is that the effective population size is almost always smaller than  $N$ , and often much smaller.
- iii) Since loss of genetic variation depends on  $N_e$ , the rate of loss can be much greater than one would suspect based simply on the number of individuals that you know are in the population. This is why it is really important to consider  $N_e$  rather than  $N$  when assessing the likely genetic effects for a particular population.

#### 4. What are the consequences of losing genetic diversity?

##### A) SHORT TERM EFFECTS

- i) The primary short-term problem is **inbreeding depression**. Inbreeding occurs when close relatives mate, and when populations get small it becomes inevitable that the remaining individuals will be closely related. Consequently, inbreeding is common in very small populations.
- ii) Inbreeding depression arises when individuals are produced that are homozygous for deleterious recessive alleles. The result is reduced survival and reproductive output of the offspring, and these demographic changes can alter the dynamics of the population in a manner that increases the risk of extinction.
- iii) In small populations, genetic diversity is also lost at random, which means that both good and bad alleles can be completely lost from the population. Hence, just through random processes, alleles that have benefits to a species (e.g., those that confer disease resistance) may be lost.

##### B) EXAMPLE: FLORIDA PANTHER

- i) The Florida panther is a subspecies of mountain lion that is clearly isolated from the nearest mountain lion population in Texas. The population has declined considerably and is currently considered an endangered species under the US Endangered Species Act. In the late 1980s there were only 30-50 left and the population had been small for some time.
- ii) At this time, there were signs of inbreeding in the population. For instance, a high proportion of the sperm produced by males was abnormal. A lot of the cats in the population also had kinked tails, which in itself is not necessarily a problem, but is a sign of inbreeding.
- iii) Because immigration was unlikely, conservation managers decided that they needed to do something to reduce the effects of inbreeding. In 1995, mountain lions from Texas were introduced to bring more genetic variation into the population. This move was controversial, because there was concern that mixing individuals from the two populations would be tantamount to destroying the distinct Florida subspecies.
- iv) The offspring of the introduced females proved to have fully functional sperm and to lack kinked tails – a sign that the introductions worked (i.e., they reduced the effects of inbreeding). Populations have also increased since that time (though it is possible this could also be due to other conservation measures); genetic diversity and survival have also increased.
- v) This situation does, however, raise questions about whether the current population is really still a population of Florida panthers. What do you think?

##### C) EXAMPLE: LAKESIDE DAISY

- i) The Lakeside daisy is found around the Great Lakes and is listed as threatened under the Endangered Species Act.
- ii) A remnant population in Illinois was found to produce no seed, and was heading for extinction. The lack of seed-set was because the species is self-incompatible, which means that two individuals with the same genotype cannot produce viable seed, and all individuals in the population had the same genotype.
- iii) The only way for this population to persist was to introduce plants with a different genotype.

##### D) GENERAL EFFECTS OF INBREEDING

- i) A recent study, used simulation models similar to those demonstrated in the PVA lecture to investigate just how serious inbreeding effects could be for a range of species.

- ii) The study looked at about 30 species, all mammals and birds (why do you think this was?).
- iii) The authors created population models that simulated population dynamics and allowed them to estimate the chance of extinction. They also included a component that simulated the effects of inbreeding that would be found in a typical population so that they could compare the model output with and without the genetic effects.
- iv) The result was that the time to extinction was reduced by an average of 37% ... in other words, species went extinct about a third faster when the inbreeding effects were included. If these simulations are accurate, they indicate that predictions that do not account for inbreeding will consistently underestimate the risk of extinction.

#### E) LONG TERM EFFECTS

- i) Loss of genetic variation also has long term consequences for a population because it reduces the potential for that species to adapt to changing conditions. This is because natural selection requires variation in order to act (otherwise there is nothing to select between!).
- ii) An ability to adapt to new conditions might be critical for species in light of fundamental changes in their habitats, e.g., as climate changes, or as chronic pollution arises.

### 5. So how big do populations need to be?

#### A) ESTIMATES BASED ON REAL POPULATIONS

- i) Studies of real populations show that some species can last for a long time with very small populations.
- ii) But, in most cases, at least a few 100 individuals are needed for a population to last >100 years. This suggests that a few 100 is an absolute minimum for fairly long-term (100 yr) viability.
- iii) As noted previously, though, the trouble with real populations is that there are not many data sets that are long enough to say much. So, these estimates may not be very good.

#### B) ESTIMATES BASED ON GENETIC CONSIDERATIONS

- i) Some of the first attempts to estimate MVP in general terms focused on the genetic issues faced by small populations. This work resulted in what was known as the “50/500 rule.”
- ii) The idea was that at least 50 individuals are needed to protect a species from inbreeding effects over the short-term, and at least 500 were needed to avoid serious effects of drift over the long term.
- iii) Lots of people jumped on this and saw it as a nice easy guideline. Unfortunately the rule was misinterpreted in several ways. First, the focus was on the “50” part, whereas the number 500 was more important for long-term conservation. Second, some users of the rule ignored the fact that these numbers refer to the **effective population size** ( $N_e$ ), which is usually much smaller than the real population (see above).
- iv) In fact, it is estimated that  $N_e$  is often 1/5 to 1/10 of  $N$ . Hence, the 50/500 rule basically means that MVP on average should be about 2,500 - 5,000 based on genetic considerations alone. Subsequent research suggests that to avoid losing evolutionary potential within the population, this number should be even higher (up to 10,000 or more).

C) ESTIMATES BASED ON GENERIC POPULATION DYNAMICS

- i) Realistic (but generic) computer simulations suggest that at least 500 individuals are typically needed. And if populations fluctuate a lot, this number could rise to >5,000.
- ii) Like the genetic analyses, this suggests that a few 100 may be too low. But, because both approaches are generic, they are likely to oversimplify things and it is hard to know how they relate to real populations.

D) ESTIMATES BASED ON PVA

- i) Most recently, people have used actual population models for individual species with good data sets to estimate MVP. In one study, 102 vertebrate species were modeled to estimate MVP for 99% persistence over 40 generations. (Why do you think they used generations, instead of years?)
- ii) This study found that the mean MVP was about 7300 adults, while the median was about 5800 adults.
- iii) Similar results were found for different types of animals, but there was a great deal of variation in the individual results.
- iv) The researchers also found that MVP was larger for species that have been studied for a long time. This is probably because long studies do a better job of describing variability in the system. One consequence of this result is that it suggests that MVP estimates based on short-term studies are probably underestimates of the true MVP.

E) CONCORDANCE OF ESTIMATES

- i) Overall, this collection of studies, using a variety of techniques and focusing on different threats, tend to converge on a single result: For a population to be viable over the long term it needs to number at least several 100, and perhaps several 1000 individuals.
- ii) Attempts to come up with a simple rule of thumb like this have been criticized because it is known that there is tremendous variation among specific cases.
- iii) But, if you have absolutely no other information to go on, this rule of thumb might be an OK starting point – as long as you recognize that you could be wrong, and that it would be much better to collect the data needed to investigate the species' individual case.