MIGRATION

- Movement of individuals from one subpopulation to another followed by random mating.
- Movement of gametes from one subpopulation to another followed by fertilization.
- Results in movement of alleles between populations (GENE FLOW).
- Can be a very local or a long-distance phenomenon.





• Change on island from one generation to the next:

$$\Delta p_{l} = p_{l}^{*} - p_{l} = (1 - m)p_{l} + mp_{c} - p_{l}$$

At equilibrium: p_I = p_C











GENETIC DRIFT

- Alteration of gene frequencies due to chance (stochastic) effects.
- Most important in *small* populations.
- Tends to reduce genetic variation as the result of extinction of alleles.
- Generally does not produce a fit between organism and environment; can, in fact, result in nonadaptive or maladaptive changes.









COALESCENCE THEORY

- We can trace the descendents of a gene just like a haploid organism.
- If we look back in time, all of the current gene copies shared a single common ancestor.
- THE GENEALOGY OF THE PRESENT SEQUENCES COALESCES TO A SINGLE COMMON ANCESTOR.
- This process is due to the random extinction of lineages.
- Eventually, in the absence of new mutation, coalescence will result in the fixation of a single allele in the population.













LOSS OF HETEROZYGOSITY IN A RANDOM MATING POPULATION OF N ADULTS

 The rate of loss of heterozygosity per generation is equal to the probability that a newborn contains two alleles at a locus that are identical-by-descent from the previous generation,

= 1/(2N)

- Heterozygosity after 1 generation at size N,

$$H_1 = \left[1 - \frac{1}{2N}\right] * H_0$$

- Heterozygosity after t generations at size N,

$$H_{t} = \left[1 - \frac{1}{2N}\right]^{t} * H_{0} \cong H_{0}e^{-t/(2N)}$$

• Example: After t = 6N generations, $e^{-t/(2N)} = 0.05$, implying that 95% of the original heterozygosity has been lost. This is 60 generations for a population size of 10 breeding adults.





RATE OF GENETIC DRIFT AND FLUCTUATIONS IN POPULATION SIZE

- Effective population size (N_o) : the number of individuals in an ideal population (in which every individual reproduces) in which the rate of genetic drift would be the same as it is in the actual population.
- The rate of genetic drift is highly influenced by the lowest population size in a series of generations.
- The effective population size $({\rm N_o})$ over multiple generations is best represented by the harmonic mean not the arithmetic mean.

$$\frac{1}{N_e} = \frac{1}{t} \left(\frac{1}{N_0} + \frac{1}{N_1} + \dots + \frac{1}{N_{t-1}} \right)$$

RATE OF GENETIC DRIFT AND FLUCTUATIONS IN POPULATION SIZE

Example:

Suppose a population went through a bottleneck as follows:

 What is the effective size (Ne) of this population across all three generations?



GENETIC EFFECTIVE POPULATION SIZE (N_E)

The effective population size is often << than the actual census size</p>

 $N_e \ll N_a$

- Consider a sexual population consisting of N_{m} males and N_{f} females
- The actual size is, $N_a = N_m + N_f$ but,
- The effective size is,

$$N_e = \frac{4N_m N_f}{N_m + N_f}$$











GENETIC DRIFT

How can random genetic drift cause maladaptive evolution?

- Since genetic drift can cause allele frequencies to increase, even deleterious alleles can be advanced and fixed in populations. The result is a decrease in mean population fitness.
- Small populations are especially prone to this effect.

If $s < 1/N_e$

• The effects of drift will dominate the dynamics of allele frequency change from one generation to the next.