Lecture Handout 20: Population structure and drift; gene flow and selection.

Wahlund effect refers to reduction of heterozygosity in a population caused by subpopulation structure. If two or more subpopulations have different allele frequencies, the overall heterozygosity is reduced, even if the subpopulations themselves are in Hardy-Weinberg Equilibrium. The underlying causes of this population subdivision could be geographic barriers to gene flow followed by genetic drift in the subpopulations.

Population structure and genetic drift. For populations of finite size, genetic drift may result in random differences among them, even if there is some gene flow. Use the **continent-island or island model**; and the one-dimensional **stepping-stone model**.

Figure 9.10. Representations of two different population structures with finite population size: (a) the continent–island or island model and (b) the one-dimensional stepping-stone model.
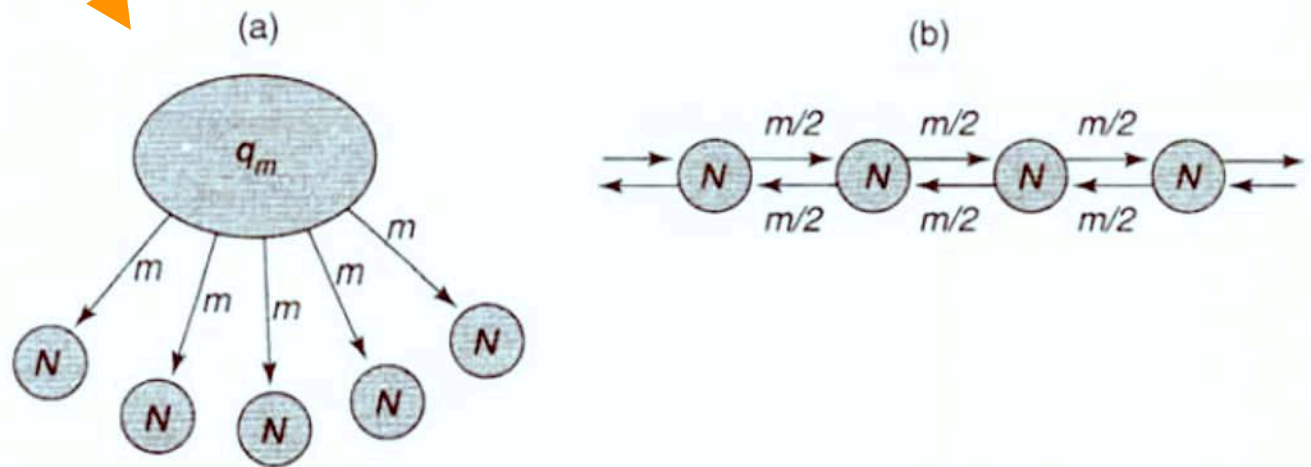
Population structure and genetic drift, **continent-island or island model**: When gene flow and population size on islands are large, allele frequency on islands becomes similar to continent. BUT if gene flow low and/or island populations are small, genetic drift will result in chance differences in allele frequencies on islands, vs continent and vs each other.
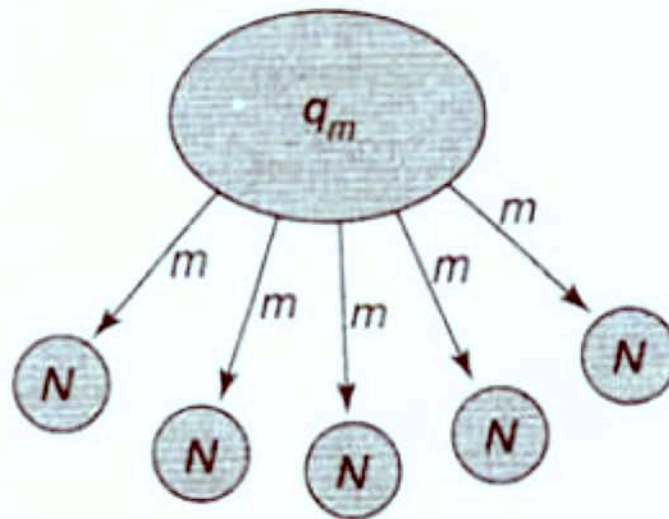
One migrant per generation (N*m* = 1) is generally considered sufficient to prevent the effects of genetic drift among populations. (But there is debate as to whether one migrant per generation is sufficient, eg for the connectivity of wildlife habitats or for management of gene flow in endangered species.)

The number of migrants can be estimated between two populations. But use this formula as an approximation or general guideline

$$Nm = \frac{1 - F_{ST}}{4F_{ST}}$$

Differentiation, and the speed of differentiation, between two populations will depend on both effective population size and on gene flow (or migration), m.
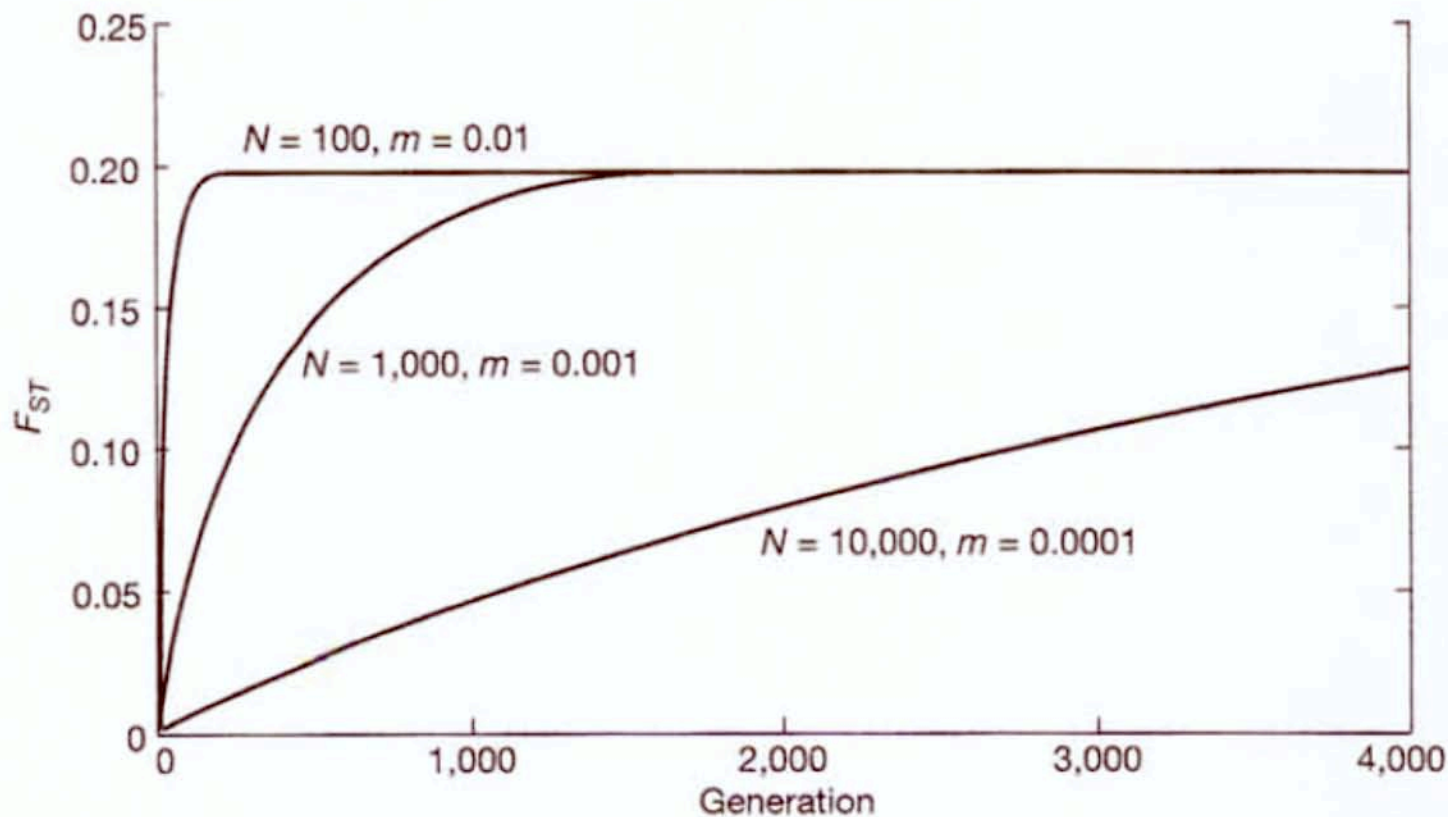

Figure 9.11. The amount of differentiation (F_{ST}) expected over generations for three different combinations of effective population size N and gene flow m.

Wright (1940): Assume A_2 in migrants is constant $q_m = 0.5$. The differentiation across the island populations will be much less when migration is high and/or island population size is high (so N X m is high).

Figure 9.12. The equilibrium distribution of allele frequencies for the island model for different values of Nm where $q_m = 0.5$ (after Wright, 1969).
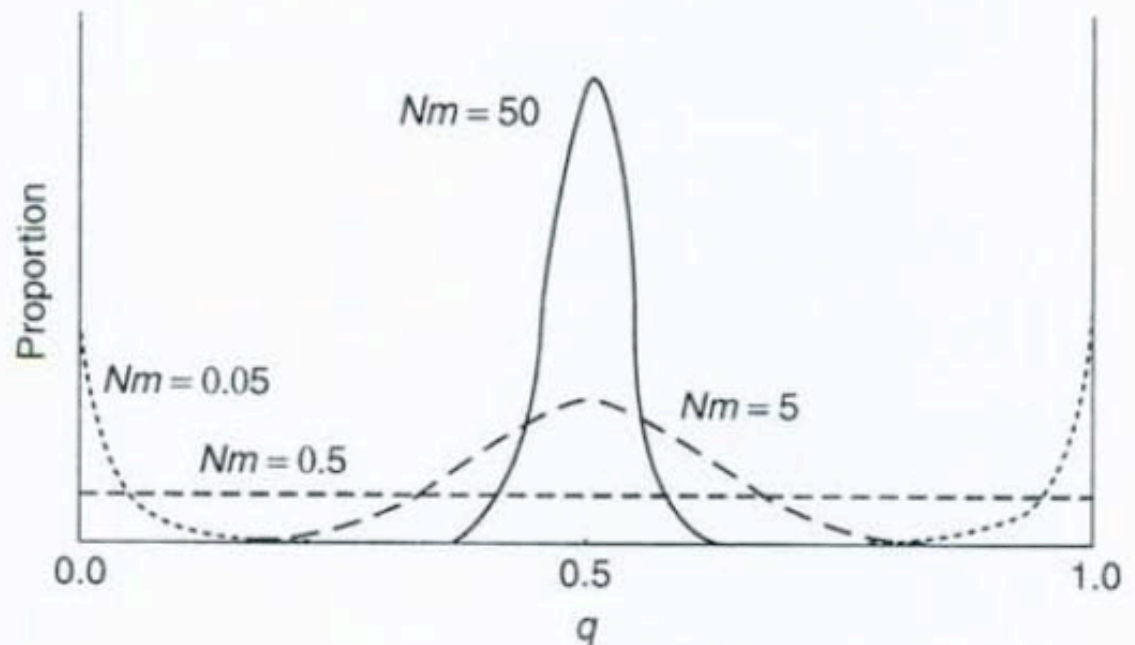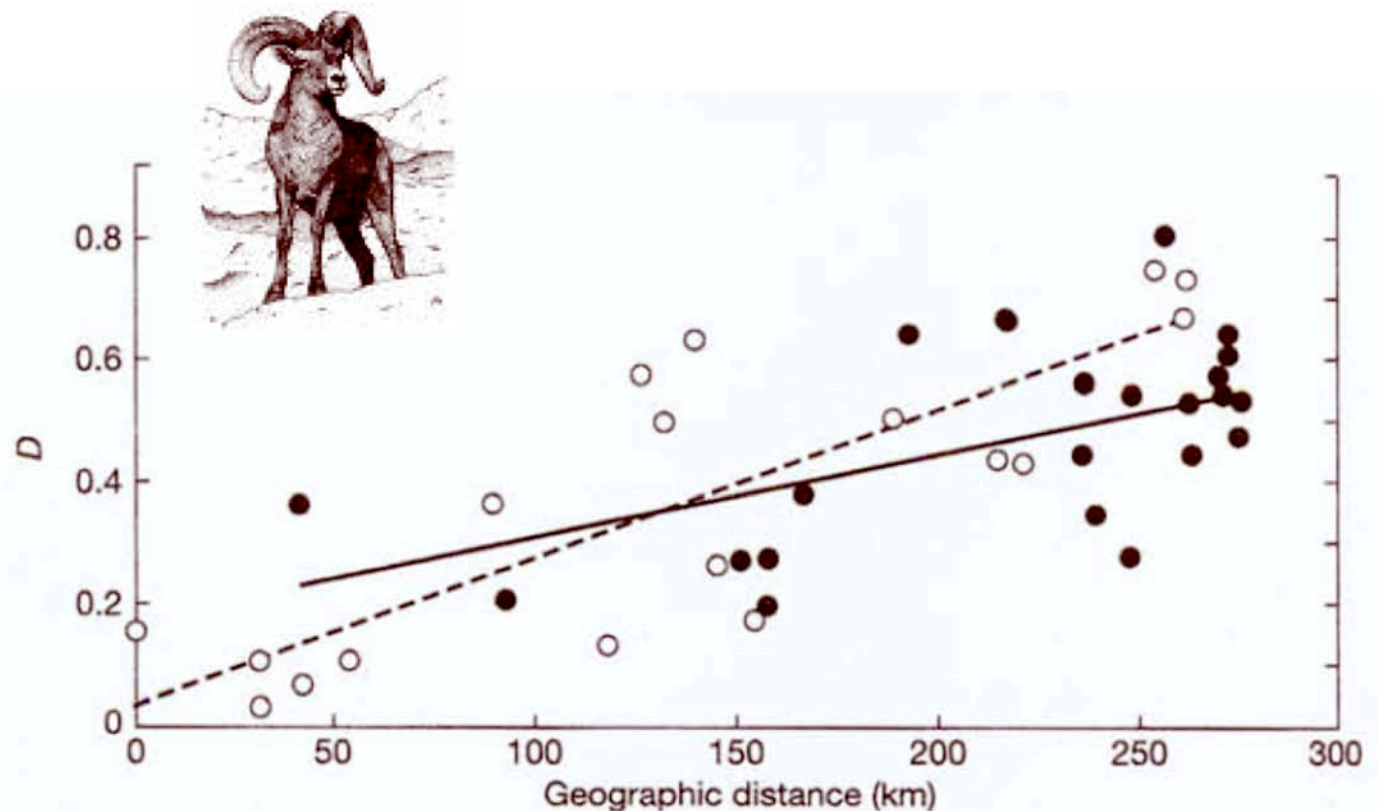
Population structure and genetic drift,
stepping-stone model: populations are
arrayed in a one dimensional spatial pattern
and gene flow is restricted to adjacent
populations (eg, serial oases in a desert; or
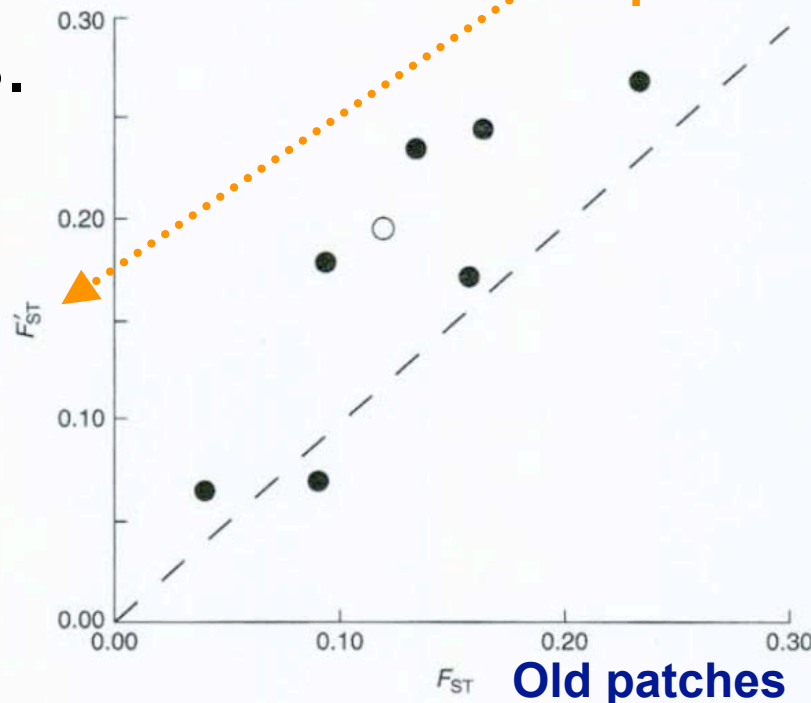serial forest patches in farmland)
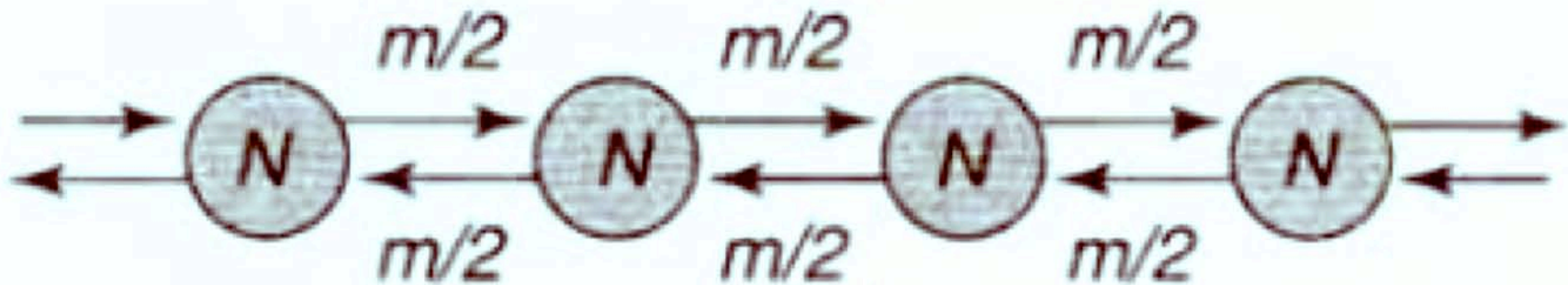
Isolation by distance, like **stepping-stone model** but populations are continuous across the landscape (not island-like) in a pattern related to distribution of suitable habitat. Leads to **distance-dependent gene flow** with genetic divergence increasing with geographic distance.

Figure 9.13. Genetic distance for microsatellite loci between populations of desert bighorn sheep plotted against geographic distance where the open circles (and broken line) are within putative subspecies and the closed circles (and solid line) are between putative subspecies (from Gutiérrez-Espeleta *et al.*, 2000).

Metapopulation: subpopulations exist in discrete habitat patches, and these subpopulations may turnover with extinctions and recolonizations from other patches; eg *Silene alba*, dioecious perennial with high rates of local extinction and recolonization. More differences between new patches due to founder effects.

Figure 9.15. F_{ST} values estimated for 12 recently colonized (F'_{ST}) and 11 established (F_{ST}) populations of *Silene alba* from allele frequencies at seven polymorphic allozyme loci (solid circles), as well as an estimate combined across loci (open circle). Note that F'_{ST} is larger than F_{ST} at six of seven loci (after McCauley *et al.*, 1995).

Gene flow and selection, continent island-model, example: **genetic restoration** of the Florida panther (puma) by releasing 8 outbred Texas mountain lion (puma).

| | No Texas ancestry | Texas ancestry | | | | Total |
		F_1	F_2	BC-Texas	BC-Florida	
Kinked tail	0.88 (48)	0.00 (17)	0.00 (7)	0.00 (3)	0.20 (15)	0.07 (42)
Cowlick	0.93 (46)	0.20 (10)	0.00 (5)	0.00 (1)	0.60 (5)	0.24 (21)
Chryptorchidism	0.68 (22)	0.00 (2)	0.00 (2)	—	0.00 (1)	0.00 (5)

Gene flow and selection: Continent island-model, example, **patch disappearance.** Even a favorable genetic variant may tend to disappear from an "island" due to gene flow from the "continent", eg water snake, *Nerodia sipedon*. Gray unbanded forms have selective advantage on islands, yet are replaced by banded migrants from the mainland. Stable or unstable equilibria are possible (depend on gene flow, selection, and dominance).

Cline or kline: a directional change in allele frequency over space or subpopulations. May be a combination of differential selection in various parts of the population, in combination with population substructure. May be a temporally **stable** or **transient**. The change in allele frequency may be stepped (or steep) over short distances, or a gradual gradient over long distances.

Cline or kline: example, malaria resistance

Figure 9.20. The observed allele frequencies (a) for the sickle-cell allele in some Liberian populations and (b) for the thalassemia allele in Sardinia (from Livingstone, 1969).
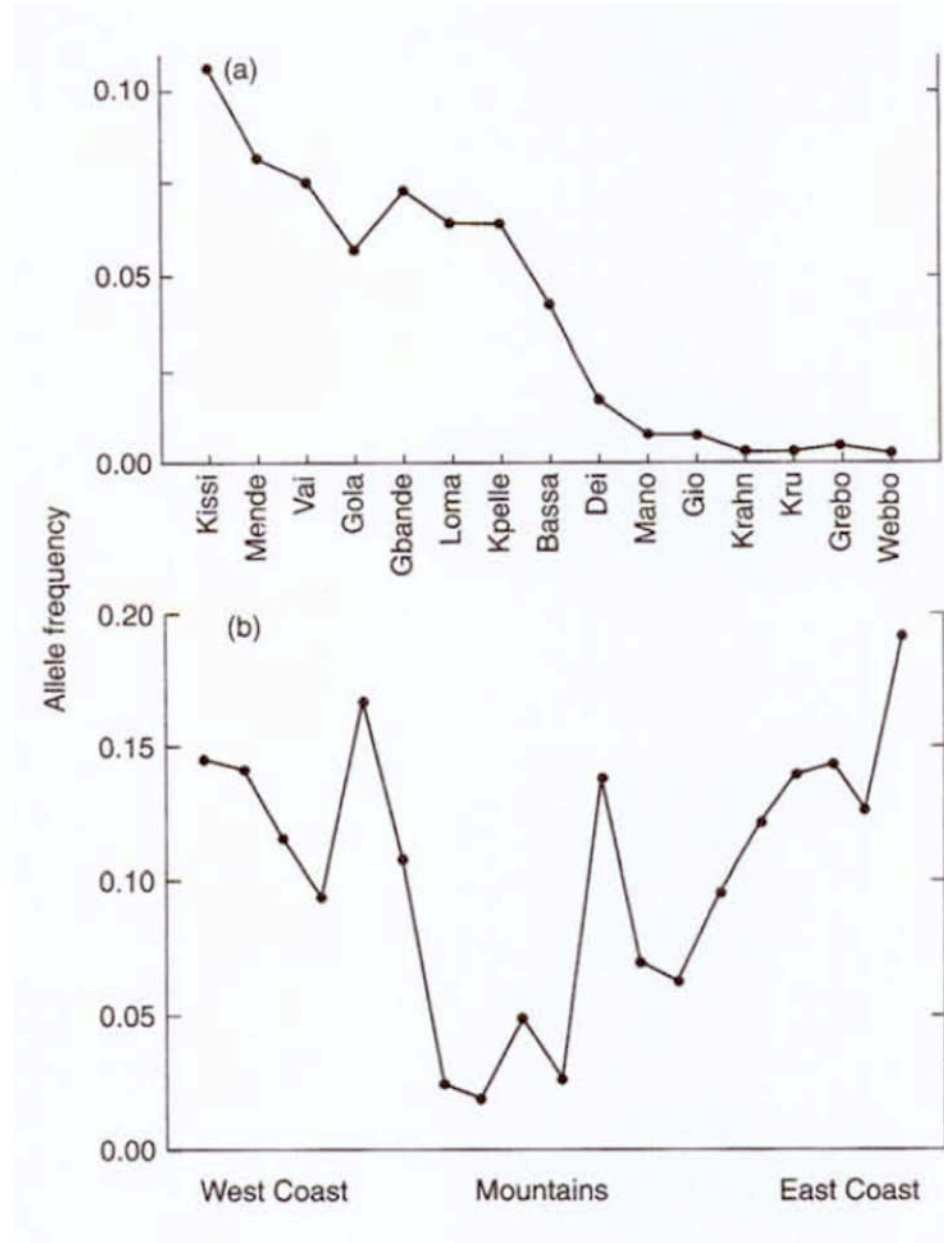
Cline or kline: example, melanic forms in the rock pocket mouse, *Chaetodipus intermedius*

TABLE 9.12 Polymorphism at the five nucleotide sites, each one resulting in an amino acid change, that differentiate melanic and light alleles at the *Mc1r* gene in the samples of *C. intermedius* from the Pinacate population (Nachman *et al.*, 2003). The number (*N*) of each genotype caught in the two different environments is given.

| Phenotype | Background | N | Genotype | Position | | | | |
				52	325	478	633	699
Melanic	Dark	11	DD	T	T	T	C	C
				T	T	T	C	C
Melanic	Dark	5	Dd	T	T	T	C	C
				C	C	C	T	A
Melanic	Light	1	Dd	T	T	T	C	C
				C	C	C	T	A
Light	Dark	2	dd	C	C	C	T	A
				C	C	C	T	A
Light	Light	10	dd	C	C	C	T	A
				C	C	C	T	A