

LectureHandout 19: Gene flow, migration, population structure.

Gene flow: the transfer of alleles of genes from one population to another

Book definition: movement between groups that results in genetic exchange.

Phylogeography: the joint use of phylogenetic techniques and geographic distributions to understand the spatial relationships and distributions of taxa or genetic markers

Metapopulation: population(s) subdivided into different habitat patches, with extinction occurring in some patches followed by recolonization by other patches.

Continent-island model: represents unidirectional gene flow due to migration (assumes no drift):

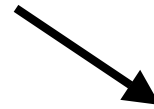
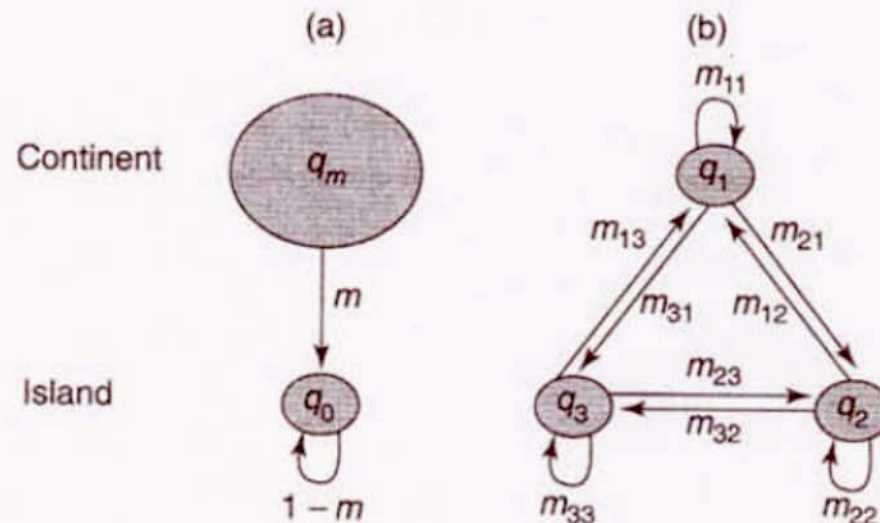
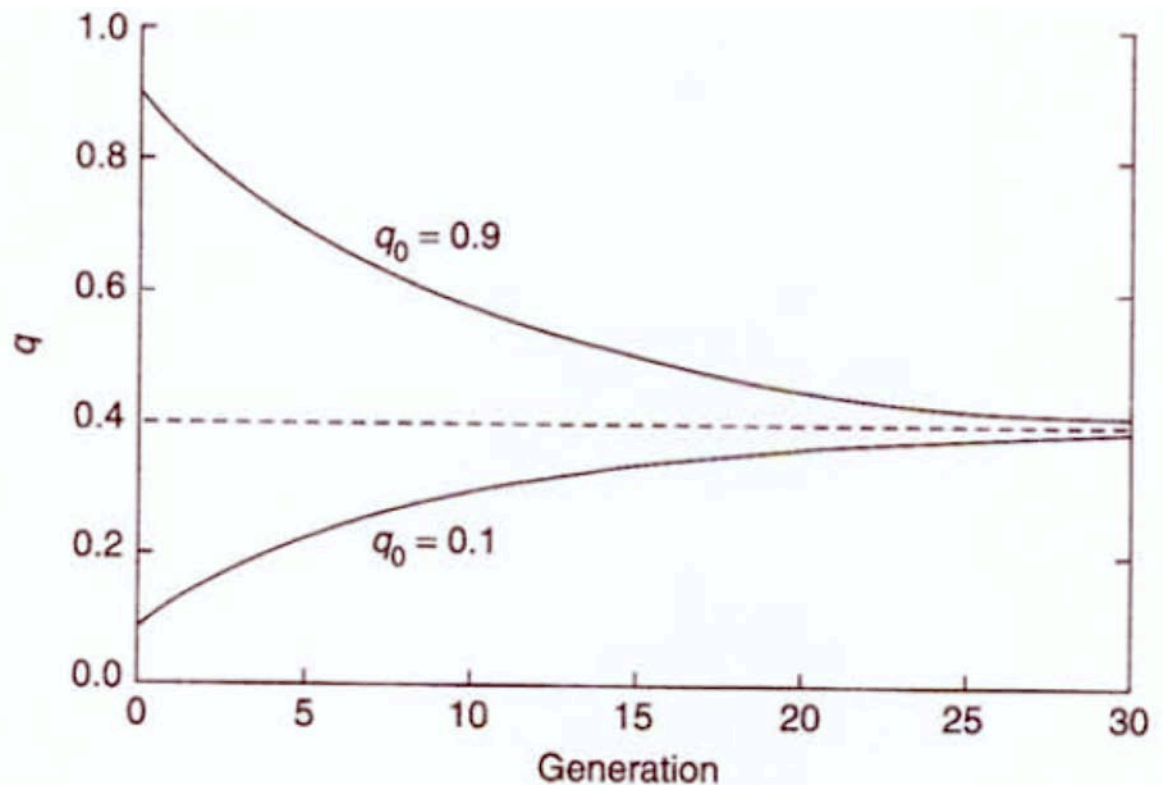


Figure 9.1. Illustration of (a) the continent-island model and (b) population structure with three subpopulations.



Continent-island model: since gene flow is unidirectional, generations of migration will shift allele frequencies on the “island” to match that on the “continent”, eg, when continent and migrant $q_m = 0.4$ and migration (proportion of migrants each generation), $m = 0.1$



Continent-island model, example: the red wolf, *Canis rufus*, subject to introgression of alleles from a much larger coyote population.

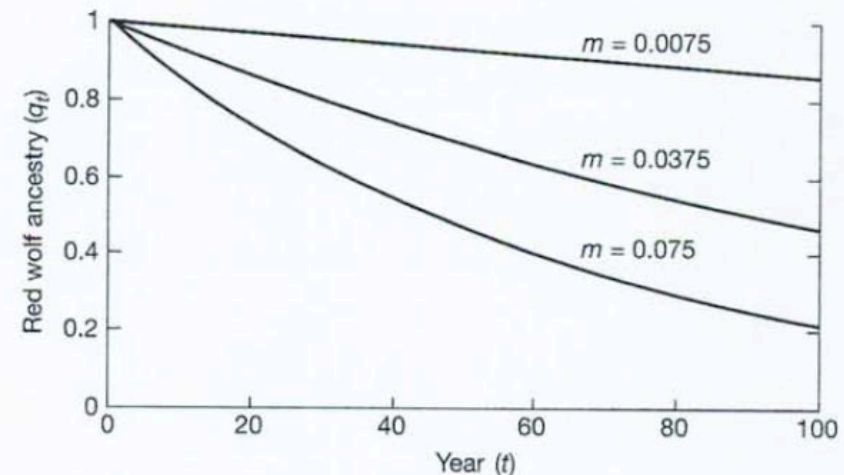
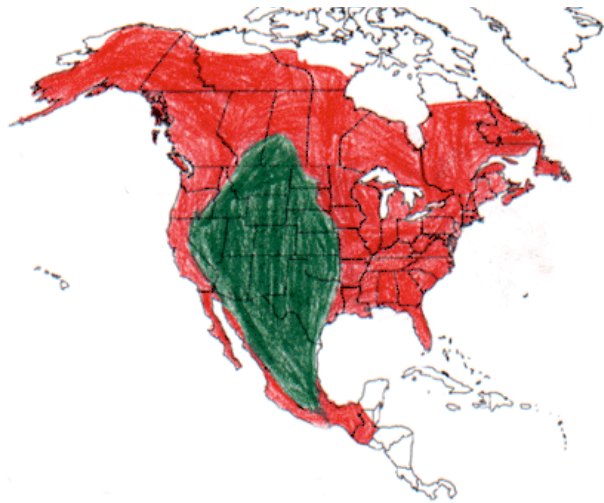


Figure 9.4. The predicted proportion of red wolf ancestry over time when there is gene flow from coyotes as might occur in a continent (coyote)–island (red wolf) model. The proportion of gene flow is assumed to be 0.075 without management intervention and either 0.0375 or 0.0075 if 50% or 90% of the hybrid litters are identified and eliminated.

General model of migration: assumes a population has k subpopulations and gene flow can occur across all parts of the population. Can be modeled using a migration matrix indicating gene flow from each subpopulation to every other subpopulation.

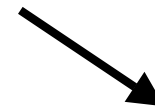
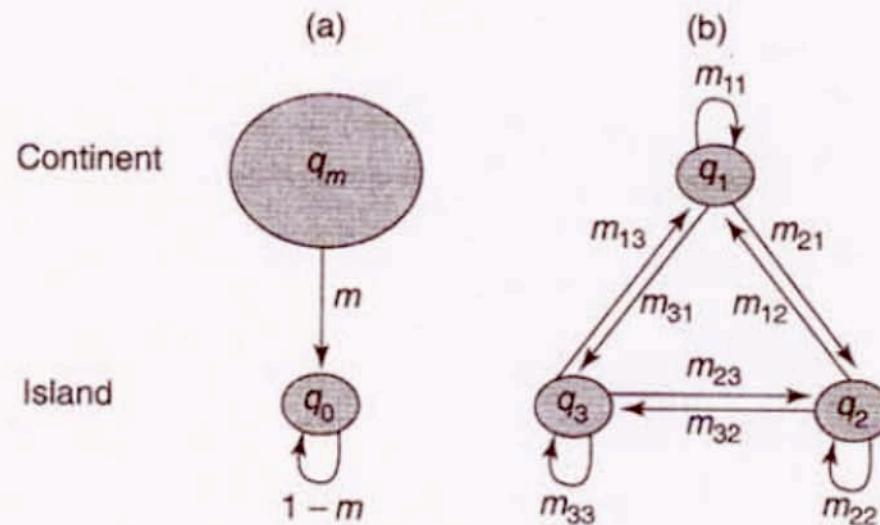


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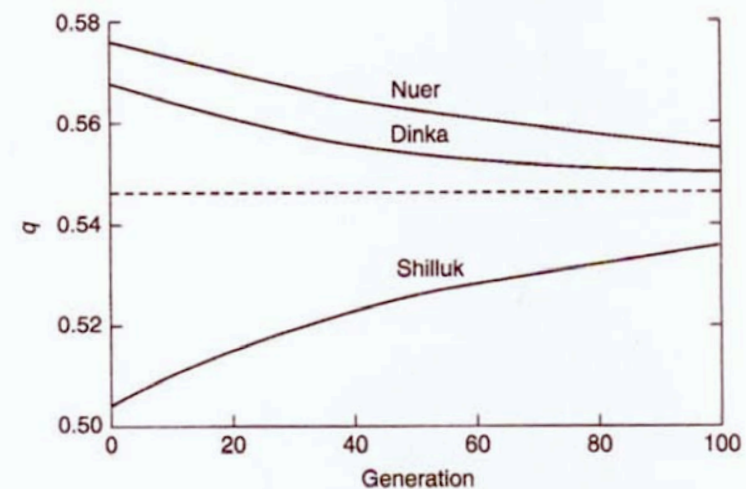
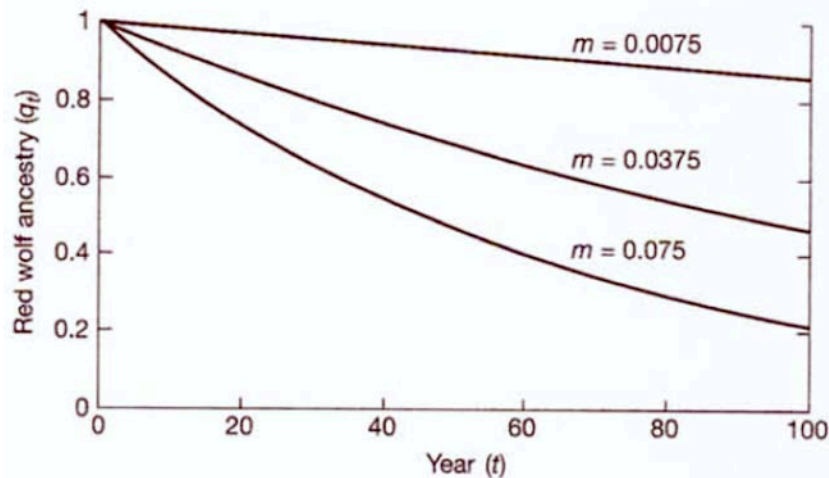


General model of migration: allele frequencies change over time in all subpopulations towards a common frequency.

eg, compare to island-continent model of red wolf

TABLE 9.2 The proportion of gene flow among three Sudanese populations (after Roberts and Hiorns, 1962).

Recipient population	Source population		
	(1) Nuer	(2) Dinka	(3) Shilluk
(1) Nuer	0.9850	0.0125	0.0025
(2) Dinka	0.0138	0.9775	0.0087
(3) Shilluk	0.0000	0.0098	0.9902



Wahlund's principle (Wahlund effect):

When subpopulations between which gene flow is limited (and allele frequencies are different) are grouped together for analysis, there will be a deficiency in heterozygotes and an excess of homozygotes

Compared to a single combined homogeneous population, homozygotes will be more common by V_q (variance), and heterozygotes will be reduced by twice the variance.

Hybrid populations: due to intermating or mixture between two or more parental populations.

Admixture: the proportion of gene flow from an outside population.

$$\begin{aligned}q_1 &= (1 - m)q_0 + mq_m \\ &= q_0 - m(q_0 - q_m)\end{aligned}$$

F coefficients (Sewall Wright): a commonly used approach to partition genetic variation in a subdivided population, which provides a description of differentiation. Allocates genetic variability to the total population level (T), subpopulations (S), and individuals (I).

F_{ST} : Genetic differentiation over subpopulations (fixation index)

F_{IS} : Deviation from Hardy-Weinberg proportions within subpopulations

F_{IT} : Deviation from Hardy-Weinberg proportions in the total population

F_{ST} : Genetic differentiation over subpopulations.
Varies from 0 to 1 (not negative).

F_{IS} : Deviation from Hardy-Weinberg proportions within subpopulations. Positive if excess of homozygotes; negative if deficiency of homozygotes.

F_{IT} : Deviation from Hardy-Weinberg proportions in the total population. Positive if excess of homozygotes; negative if deficiency of homozygotes.

F coefficients: Example

TABLE 9.5 Two hypothetical examples to illustrate the meaning of F coefficients.

<i>Subpopulation</i>	A_1A_1	A_1A_2	A_2A_2	q
1	0.25	0.5	0.25	0.5
2	0.35	0.3	0.35	0.5
	$F_{IS} = 0.2$	$F_{IT} = 0.2$	$F_{ST} = 0.0$	
1	0.25	0.5	0.25	0.5
2	0.49	0.42	0.09	0.3
	$F_{IS} = 0.0$	$F_{IT} = 0.0417$	$F_{ST} = 0.0417$	

GST: (Nei) An estimate of FST:

$$G_{ST} = \frac{H_T - H_S}{H_T}$$

Where H_S is average subpopulation Hardy-Weinberg heterozygosity and

$$H_T = 1 - \sum \bar{p}_i^2$$

Assumes Hardy-Weinberg proportions

Since G_{ST} depends on level of diversity, Nei also proposed a measure of genetic differentiation independent of genetic diversity within populations, called the **minimum genetic distance**:

$$\overline{D}_m = \frac{k}{k-1}(H_T - H_S)$$

Sex differences in gene flow: for many species, level of gene flow is higher in males than females... For humans, sex differences in gene flow may depend on whether societies are matrilineal or patrilineal (which sex moves and which stay in or near their birthplace after marriage)

TABLE 9.8 The mean diversity in mtDNA and Y chromosomes in matrilineal and patrilineal human populations from northern Thailand and the genetic distance in mtDNA and Y chromosomes between matrilineal and between patrilineal human populations (the larger values are given in boldface).

	<i>mtDNA</i>		<i>Y chromosome</i>	
	<i>Matrilineal</i>	<i>Patrilineal</i>	<i>Matrilineal</i>	<i>Patrilineal</i>
Diversity	0.860	0.937	0.965	0.863
Genetic distance	0.290	0.118	0.131	0.451