Evolutionary Genetics

LV 25600-01 | Lecture with exercises | 4KP



Proportions of admixture in Antioquia (Colombia) - It is well known that Hispanics generally have mixed Indian, African and European ancestry, but the dynamics of admixture at the base of Hispanic populations are heterogeneous.

	auto	X chr	Y chr	mtDNA
First Nation	0.16	0.25	0.01	0.90
European	0.79	0.69	0.94	0.02
African	0.05	0.06	0.05	0.08
Total	1	1	1	1

source: Bedoya et al. (2006)

Genetic **admixture** occurs when previously diverged or isolated genetic lineages mix. Admixture results in the introduction of new genetic lineages into a population.

The Department of **Antioquia** is one of the 32 departments of Colombia, located in the central Northwestern part of Colombia with a narrow section that borders the Caribbean Sea.

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Y-chromosome and mtDNA data suggest little population substructure among the founding Antioquian communities. Interestingly, despite an almost entirely Amerindian mtDNA background, Antioquia has a markedly predominant European ancestry at the autosomal and X-chromosomal level, suggesting that post-foundation continuous admixture with Spanish men (but not native women) increased the European nuclear ancestry of Antioquia. This scenario is consistent with historical information and population genetic theory.

Gene Flow / Migration / Dispersal



Gene flow is defined as the movement of alleles among (sub)populations.

Although gene flow is not synonymous with dispersal, it is certainly true that long-distance dispersal provides the opportunity for long-distance gene flow, and hence for high levels of gene flow among populations.

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Gene flow is any movement of genes (alleles) from one population to another. Gene flow includes lots of different kinds of events, such as pollen being blown to a new destination or people moving to new cities or countries. If genes are carried to a population where those genes previously did not exist, gene flow can be an important source of genetic variation.



The amount of gene flow that goes on between populations varies a lot depending on the type of organism. As you would expect, populations of relatively sedentary organisms are more isolated from one another than populations of very mobile organisms.



Gene flow has several important effects on evolution:

Within a population - It can introduce or reintroduce genes to a population, **increasing genetic variation** of that population.





Across populations - By moving genes around, it can make distant populations genetically similar to one another (**decreasing genetic differentiation**). The more gene flow between two populations, the more likely that two populations will NOT evolve into two species.



The extent of genetic diversity within and between subpopulations can be thought of as a balance between the opposing force of genetic drift, which reduces diversity within populations but increases it between them, and gene flow which brings new genetic diversity into populations but reduces it between them.





1 - m: proportion of non-migrants

 $\Delta p = p_1 - p_0 = [p_0(1 - m) + mp_x] - p_0 = p_0 - mp_0 + mp_x - p_0 = mp_x - mp_0 = m(p_x - p_0)$

A high rate of migration will make subpopulations more similar and reduce (homogenise) genetic variation. Low or no gene flow can lead to genetic differentiation.



PopG Settings		
Population size:	100	
Fitness of genotype AA:	1.0	
Fitness of genotype Aa:	1.0	
Fitness of genotype aa:	1.0	
Mutation from A to a:	0.0	
Mutation from a to A:	0.0	
Migration rate between populations:	0.0	
Initial freqency of allele A:	0.5	
Generations to run:	100	
Populations evolving simultaneously:	10	
Random number seed:	(Autogenerate)	
Defaults	Cancel OK	



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Population size:	100	
Fitness of genotype AA:	1.0	
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Migration rate between populations:	0.5	
Initial freqency of allele A:	0.5	
Generations to run:	100	
Populations evolving simultaneously:	10	
Random number seed:	(Autogenerate)	
Defaults	Cancel OK	

Migration Models

- The **Island-Mainland Model** assumes that offshore islands receive unidirectional migration from the Mainland.
- The **Island Model** assumes that a species is divided into multiple subpopulations, each of which is connected to all of the others (this resembles an island archipelago).
- The alternative **Stepping-Stone Model** assumes that sub-populations are connected only to adjacent sub-populations, in a nearest-neighbor grid.
- A **River** or **Path Model** assumes that each sub-population is connected only to those on either side of it, in linear sequence.

$$p_1 = p_0(1 - m) + mp_x$$

$$p_t = p_x + (p_0 - p_x)(1 - m)^t$$

