# **Evolutionary Genetics**

#### LV 25600-01 | Lecture with exercises | 4KP

# **Genetic Drift**





Chapter 3 - Genetic Drift - Page 52-55

**Genetic drift** is a key concept in population genetics. It refers to the **random fluctuations in allele frequencies within a population** that are caused by chance events rather than natural selection. This phenomenon is particularly pronounced in smaller populations, where random events can have a significant impact on the genetic make-up. Over time, **genetic drift can lead to a loss of genetic diversity within a population**. In essence, it's the roll of the genetic dice that can determine the fate of certain traits, demonstrating how randomness can play a crucial role in the evolutionary journey of species.



In each generation, some individuals may, by chance, leave behind a few more offspring (and genes) than other individuals. The genes of the next generation will be the genes of the "lucky" individuals, not necessarily the healthier or "better" individuals. This, in a nutshell, is genetic drift. It happens in ALL populations - there's no escaping the vagaries of chance.

**Genetic drift**, also known as genetic **sampling error** or the **Sewall-Wright** effect, is a change in the gene pool of a population that occurs purely by chance. Genetic drift can cause genetic traits to be lost from a population or to become widespread (fixed) in a population, regardless of the survival or reproductive value of the alleles involved.



Results of computer simulations of changes in allele frequency due to genetic drift for each of three population sizes (N) with an initial allele frequency of 0.5.

Source: Allendorf, Luikart, and Aitken (2013)

#### PopG - Genetic Simulation Program





#### R-package: learnPopGen

Population Genetic Simulations & Numerical Analysis



Genetic drift has several important effects on evolution:

1. **Drift reduces genetic variation in populations**, potentially reducing the ability of a population to evolve in response to new selective pressures.

What is the rate at which genetic variation is lost from populations?



Allele frequencies for 107 *D. melanogaster* populations where 16 individuals (eight of each sex) were randomly chosen to start each new generation. Initially, all 107 populations had equal numbers of the wild-type and  $bw^{75}$  alleles.



adopted from: Buri (1956) Gene frequency in small population of mutant Drosophila.



Heterozygosity after one generation:

$$H_1 = \left(1 - \frac{1}{2N}\right)H_0$$

Heterozygosity after t generations:

$$H_t = \left(1 - \frac{1}{2N}\right)^t H_0$$

► The equation indicates that the heterozygosity declines each generation at a rate inversely dependent on the population size.

Expected heterozygosity (2*pq*) in populations undergoing genetic drift. The line shows the expected change in heterozygosity.



➡ Genetic drift increases homozygosity and decreases heterozygosity.

Genetic drift has several important effects on evolution:

- Drift reduces genetic variation in populations, potentially reducing the ability of a population to evolve in response to new selective pressures.
- 2. Genetic drift acts faster and has **more drastic results in smaller populations**. This effect is particularly important in rare and endangered species.





Population size: **5** Generation time: 20 Number of populations: 10 Initial allele freq.: q=p=0.5 Population size: **20** Generation time: 20 Number of populations: 10 Initial allele freq.: q=p=0.5

	fixed (p=1)	lost (p=0)			fixed (p=1)	lost (p=0)
1	6	4	-	1	0	1
2	5	4		2	0	0
3	6	3		3	0	1
4	3	6		4	1	0
5	3	5		5	2	0
6	4	2		6	0	0
7	2	6		7	1	0
8	4	4		8	2	0
9	3	6		9	3	0
10	3	5		10	0	2
mean	3.9	4.5	>	mean	0.9	0.4



$$H_1 = \left(1 - \frac{1}{2N}\right)H_0$$

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Large changes in allele frequency from one generation to the next are likely in small populations due to chance. This effect may cause an **increase in frequency of alleles that have harmful effects (e.g. inbreeding depression)**. Such deleterious alleles are continually introduced by mutation but are kept at low frequencies by natural selection. Moreover, most of these harmful alleles are recessive, so their harmful effects on the phenotype are only expressed in homozygotes. It is estimated that every individual in a population harbours several of these **harmful recessive alleles** in a heterozygous condition without any phenotypic effects.

(Cruz et al. 2008, vonHoldt et al. 2010)

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- Drift reduces genetic variation in populations, potentially reducing the ability of a population to evolve in response to new selective pressures.
- 2. Genetic drift acts faster and has **more drastic results in smaller populations**. This effect is particularly important in rare and endangered species.
- 3. Genetic drift tends to make different populations different from each other. It can **contribute to speciation**.

#### Genetic drift tend to make different populations different from each other.





**Genetic drift** is an important factor in the process of speciation, particularly in the context of **allopatric speciation**, where populations are physically separated. A classic example of genetic drift, coupled with natural selection and geographic isolation, **contributing to speciation** is the case of the **Galápagos finches**, made famous by Charles Darwin's observations.

In the Galápagos Islands, a group of finch species known collectively as 'Darwin's finches' show remarkable **diversity in beak shape and size**. These variations in beak morphology have evolved to help these finches exploit different food sources, such as seeds, insects or cactus flowers.

A **population bottleneck** is a significant reduction in the size of a population that causes the extinction of many genetic lineages within that population, thereby reducing genetic diversity. Population bottlenecks have occurred in the evolutionary history of many species, including humans.



The probability of an allele being lost after a bottleneck is:

$$(1-p)^{2N}$$



The probability of an **allele** being lost after a bottleneck in a homozygot (clonal) population.

$$(1-p)^{2N} \xrightarrow{p=1}{\longrightarrow} = 0^{2N} = 0$$



The probability of an allele being lost depends on population size and the initial allele frequency.

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If a population is reduced to N individuals for one generation then the expected total number of alleles (A') remaining is:

$$E(A') = A - \sum_{j=1}^{A} (1 - p_j)^{2N}$$

probability of getting lost

A : initial number of alleles pj :the frequency of the jth allele

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Allele Frequency

$$p_1 = 0.9996 \rightarrow \sim 0$$

$$p_2 = 0.0001 \rightarrow \sim 1$$

$$p_3 = 0.0001 \rightarrow ~1$$

$$p_4 = 0.0001 \rightarrow \sim 1$$

$$p_5 = 0.0001 \rightarrow \sim 1$$

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Sum

Expected number of alleles remaining in the population after the bottleneck:

E(A') = 5 - 4 = 1



Source: Allendorf, Luikart, and Aitken (2013) Conservation and the Genetics of Populations. Blackwell Publishing.





The **founder effect** is a particular example of the influence of random sampling. It has been defined by Ernst Mayr: "The establishment of a new population by a few original founders (in an extreme case, by a single fertilised female) who carry only a small fraction of the total genetic variation of the parental population".



The founding of a new population by a small number of individuals could lead to abrupt **changes in allele frequencies and loss of genetic variation**.



Species with lower population **growth rates** may remain at small population sizes for many generations, during which time heterozygosity is further eroded. Therefore, bottlenecks and founder events have a longer lasting effect on the loss of genetic variation in species with lower growth rates.



Simulated loss of heterozygosity and allelic diversity at eight microsatellite loci during a bottleneck of two individuals over five generations. Initial allele frequencies are from a population of brown bears from the Western Brooks Range, Alaska. Adapted from Luikart and Cornuet (1998).

Bottlenecks and founder events have a greater effect on the allelic diversity (number of alleles) in a population than on heterozygosity.



