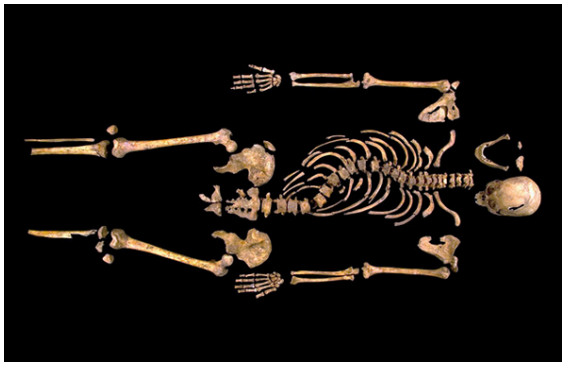
In the news…

- Bones Under Parking Lot Belonged to Richard III http://www.nytimes.com/2013/02/05/world/europe/richard-the-third-bones.html



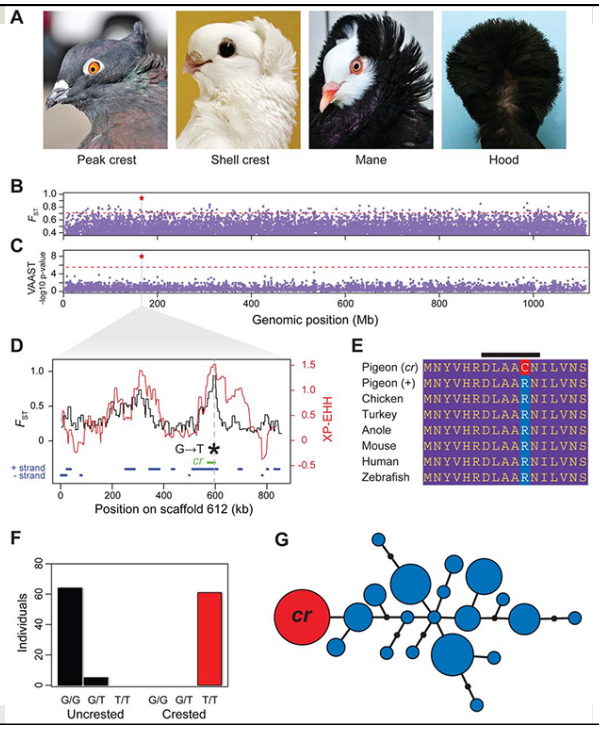
In the news…

- Bones Under Parking Lot Belonged to Richard III
- Michael Ibsen, one of two descendants of Richard III's sister, Anne of York, whose DNA was used to confirm the identity of the skeleton.
- tests at 3 laboratories in England and France found that the descendants' mtDNA matched DNA from the parking lot skeleton. All 3 samples belong to a mtDNA lineage that is carried by only 1 - 2 % of the English population, rare enough to satisfy the project team that a match had been found

In the news…

- Pigeons Get a New Look
  - http://www.nytimes.com/2013/02/05/science/pigeons-a-darwin-favorite-carry-new-clues-to-evolution.html
  - http://www.sciencemag.org/content/early/2013/01/30/science.1230422

Genetic basis of crest



Chapter 3 – Genetic Drift & N_e

Genetic Drift

Effective Population Size

Relationship Between Drift and Inbreeding

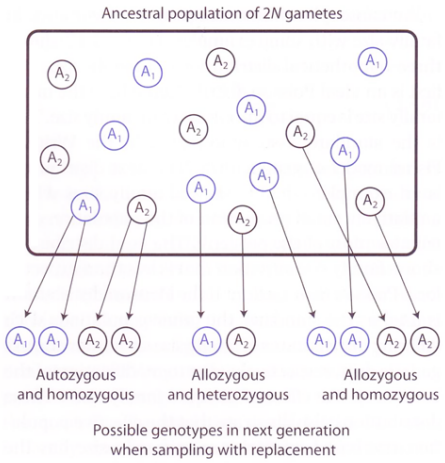
The Coalescent

Relationship between drift and inbreeding

- Both drift and inbreeding increase autozygosity (identical by descent, IBD)
  - in a finite population, inbreeding is inevitable
- Inbreeding coefficient: probability that the two alleles at a locus within an individual are IBD
- Fixation index: "excess" homozygosity in comparison to HW expectations
  - $F = (H_e - H_0)/H_e$, where H is heterozygosity
- Fixation index: probability that the two alleles selected at random from a population are IBD

"Inbreeding" in a finite population

Figure 3.18 Autozygosity and allozygosity in a finite population where identity by descent is related to the size of the population. Finite populations accumulate genotypes containing alleles identical by descent through random sampling in a manner akin to mating among relatives. In this example, alleles in the ancestral gamete pool identical in state are not identical by descent. Sampling of alleles takes place to form the diploid genotypes of the next generation. By chance, the same allele can be sampled twice to form an autozygous genotype with probability $\frac{1}{2N_e}$. The chance of not sampling the same allele twice is the probability of all other outcomes or $1 - \frac{1}{2N_e}$. Autozygous genotypes must be homozygous but allozygous genotypes can be either homozygous or heterozygous.



"Identical by Descent"

- what is the probability that two randomly sampled alleles are identical by descent (i.e., "replicas of a gene present in a previous generation")?
  - Wright's "fixation index" F
- at the start of the process (time 0), "declare" all alleles in the population to be unique or unrelated, $F_t = 0$ at $t = 0$
- in the next generation, the probability of two randomly sampled alleles being copies of the same allele from a single parent = $1/(2N_e)$, so…

"Identical by Descent"

$$F_t = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right) F_{t-1}$$

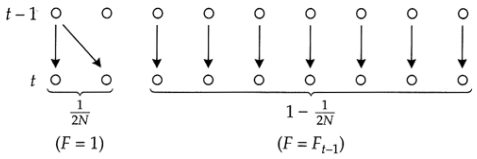


FIGURE 3.10 Diagram illustrating the reasoning behind the recursion for F in a finite population. When the gametes are drawn to make up the population at generation t, there is a chance $1/(2N)$ that any pair of alleles will have been identical in generation $t - 1$. If this happens, the probability of identity is 1. For the allele pairs drawn in generation t from two distinct alleles at generation $t - 1$ [the probability of this happening is $1 - 1/(2N)$], the probability of identity is F_{t-1}. Adding the probabilities of these two events, we get $F_t = 1/(2N) + [1 - 1/(2N)]F_{t-1}$.

Fixation Index

$$F_t = \frac{1}{2N_e} + \left(1 - \frac{1}{2N_e}\right) F_{t-1}$$

= probability that alleles are copies of the same gene from the immediately preceding generation ***plus*** the probability that the alleles are copies of the same gene from an earlier generation

or

$$F_t = 1 - \left(1 - \frac{1}{2N_e}\right)^t$$

assuming $F_0 = 0$

compare to: mean time to fixation for new mutant = ~$4N$

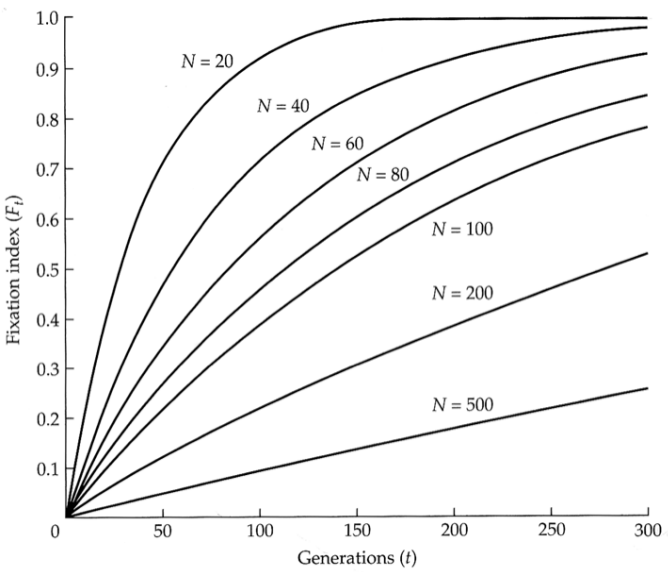


FIGURE 3.11 Increase of F_t in ideal populations as a function of time and effective population size N.

Heterozygosity

$$H_t = \left(1 - \frac{1}{2N_e}\right) H_{t-1}$$

heterozygosity declines by a factor of $(1 - 1/2N_e)$ each generation

or

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

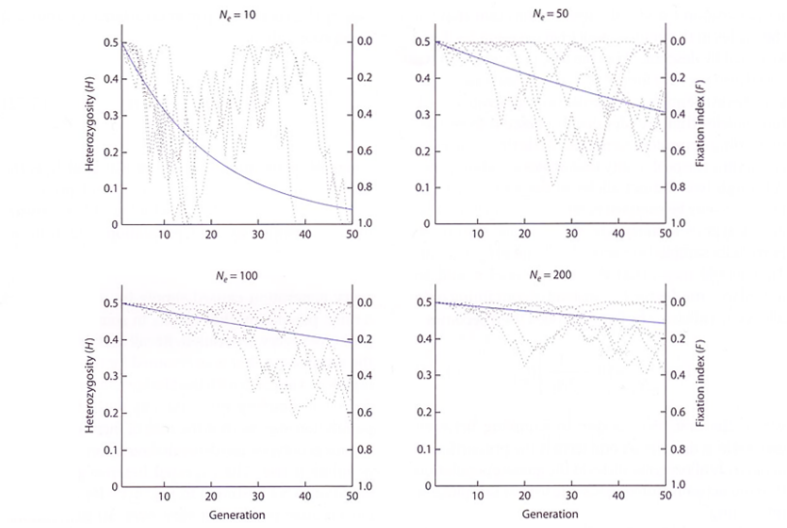
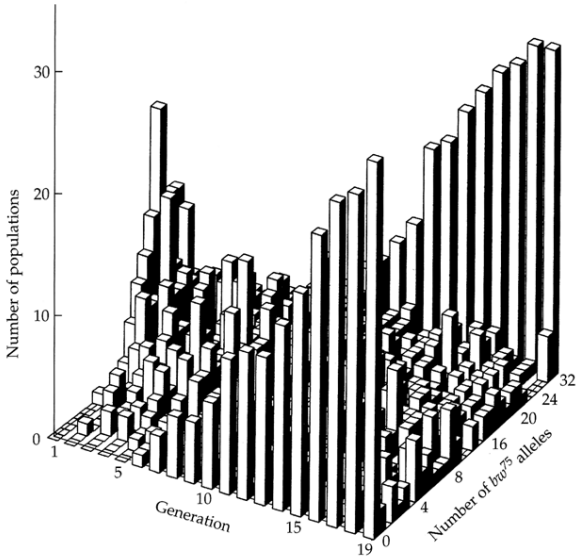
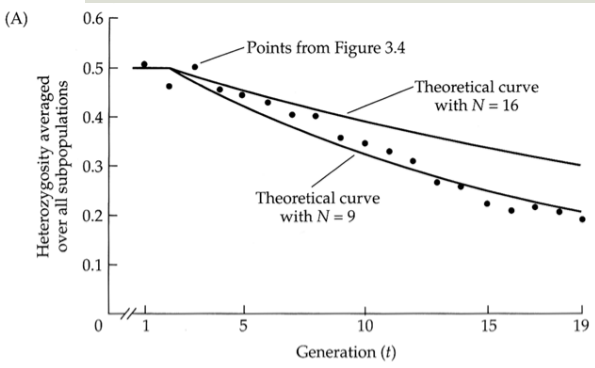


Figure 3.19 The decline in heterozygosity as a consequence of genetic drift in finite populations. The solid lines show expected heterozygosity over time according to $H_t = \left(1 - \frac{1}{2N_e}\right) H_{t-1}$. The decrease in heterozygosity can also be thought of as an increase in autozygosity or the fixation index (F) through time under genetic drift. The dotted lines in each panel are levels of heterozygosity ($2pq$) in six replicate finite populations experiencing genetic drift. There is substantial random fluctuation around the expected value for any individual population.

Random genetic drift in 107 *Drosophila* populations;
8 males, 8 females each generation





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

$$\approx H_0 e^{-t/2N_e}$$

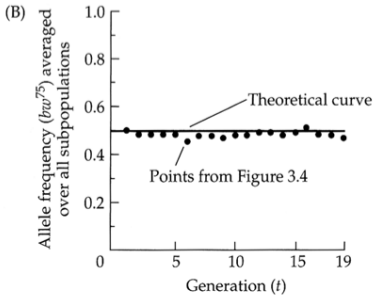


FIGURE 3.12 Theoretical curves for average heterozygosity among subpopulations (A) with $N = 9$ or $N = 16$, along with actual values (plotted as points) from the experiment in Figure 3.4. Part (B) shows the theoretically expected average allele frequency among the 107 subpopulations and the observed average. (Data from Buri 1956.)

More Effective Population Size Concepts

- Inbreeding effective population size
  - the size of an ideal population with the same probability of randomly sampled alleles being IBD as the real population
- Variance effective population size
  - the size of an ideal population with the same sampling variance in allele frequency as the real population