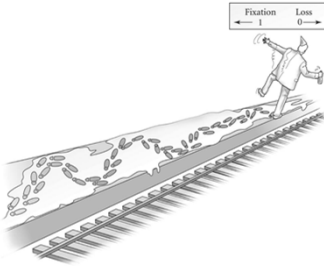


Population Genetics II

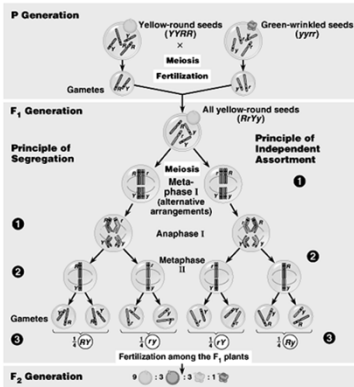


What is Population Genetics?

- The study of alleles becoming more or less common over time.
- Applied Meiosis: Application of Mendel's Law of segregation of alleles.
- Hardy-Weinberg Equilibrium Principle: Acts as a null hypothesis for tracking **allele** and **genotype** frequencies in a population in the absence of evolutionary forces.

Meiosis: Reduction & Division

Meiosis (I) accounts for Segregation of Alleles



Expected Genotype Frequencies in the Absence of Evolution are Determined by the Hardy-Weinberg Equation.

Assumptions:

- 1) No mutation
- 2) Random mating (panmictic)
- 3) Infinite population size (No drift)
- 4) No migration or gene flow
- 5) No selection (= survival & reproduction)

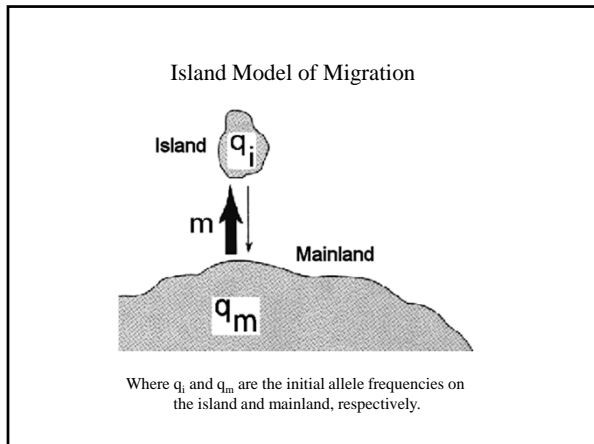


Non-Random Mating

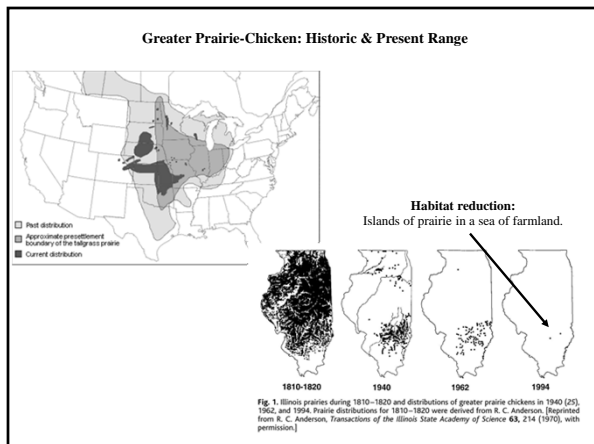
- **Assortative mating**
 - Usually positive with likelihood of mating with similar phenotype.
- **Inbreeding**
 - Special case of assortative mating.
 - The closer the kinship, the more alleles shared and the greater the degree of inbreeding.
 - Inbreeding increases homozygotes, while decreasing heterozygotes.
 - Can expose deleterious recessives to selection.

Effects of Migration

- Generally considered a one-way proposition.
- Overall acts to prevent species divergence in populations.







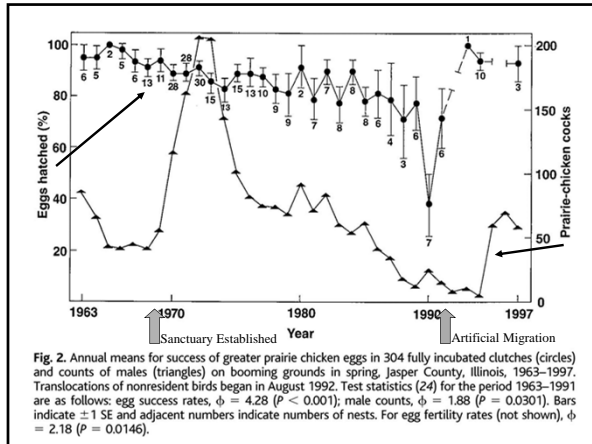


Table 2: Number of alleles per locus found in each of the current populations of Illinois, Kansas, Minnesota, and Nebraska and estimated for the Illinois prebottleneck population

Locus	Illinois	Kansas	Minnesota	Nebraska	Illinois prebottleneck*
ADL42	3	4	4	4	3
ADL23	4	5	4	5	5
ADL44	4	7	8	8	4
ADL146	3	5	4	4	4
ADL162	2	5	4	4	6
ADL230	6	9	8	10	9
Mean	3.67 ^a	5.83 ^b	5.33 ^b	5.83 ^b	5.12 ^b
SE	.56	.75	.84	1.05	.87
Sample size	32	37	38	20	15

Note: SE indicates standard errors of mean number of alleles per locus. Different letters indicate significant differences at $P < .05$ (see "Methods" for statistical analysis).
 * Number of alleles in the Illinois prebottleneck population include both extant alleles that are shared with the other populations and alleles detected in the museum collection.

