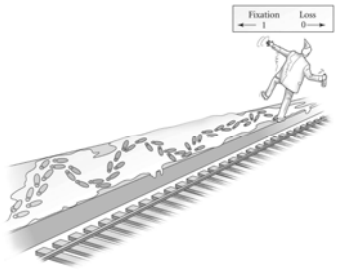
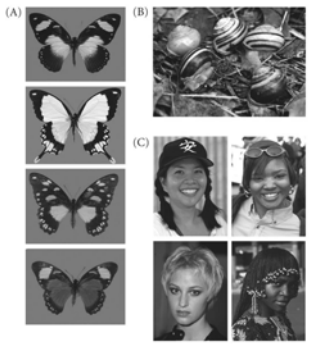
Population Genetics



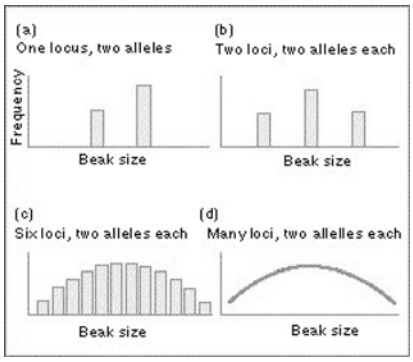
Distinguishing Among Sources of Phenotypic Variation in Populations

- Discrete vs. continuous
- Genotype or environment (nature vs. nurture)

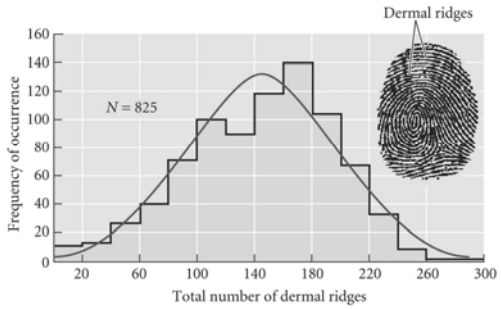
Phenotypic variation - Discrete vs. Continuous



Polygenic Control can create Continuous Variation

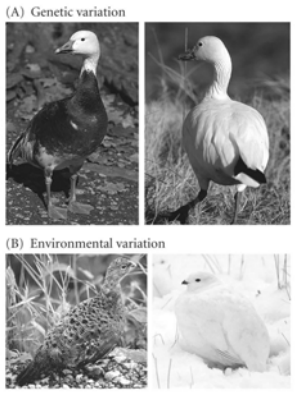


Phenotypic Variation - Discrete vs. Continuous

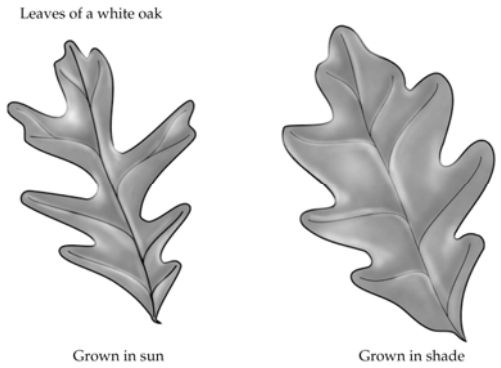


Quantitative or Continuous or Metric Variation, very often Polygenic

Phenotypic variation - genotype or environment?



Phenotypic variation - genotype or environment?



Mechanisms of Evolutionary Change – "Microevolutionary Processes"

- **Mutation:** Ultimate natural resource of evolution, occurs at the molecular level in DNA.
- **Natural Selection:** A difference, on average, between the survival or fecundity of individuals with certain arrays of phenotypes as compared to individuals with alternative phenotypes.
- **Migration:** The movement of alleles from one population to another, typically by the movement of individuals or via long-range dispersal of gametes.
- **Genetic Drift:** Change in the frequencies of alleles in a population resulting from chance variation in the survival and/or reproductive success of individuals; results in nonadaptive evolution (e.g., bottlenecks).

These combined forces affect changes at the level of individuals, populations, and species.

What is Population Genetics?

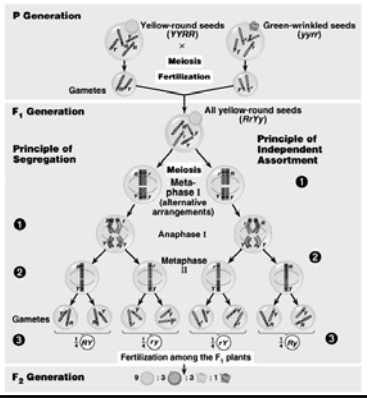
• The study of alleles becoming more or less common over time.

• 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 <u>Absence</u> of Evolution are Determined by the Hardy-Weinberg Equation.

<u>Assumptions:</u>

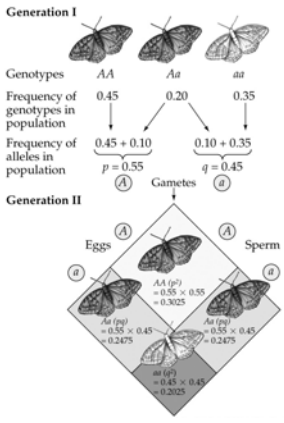
1) No mutation

2) Random mating (panmictic)

3) Infinite population size

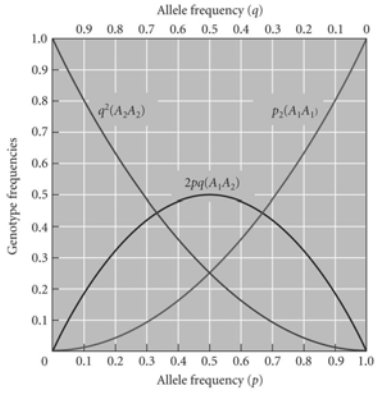
4) No migration or gene flow

5) No selection (= survival & reproduction)



After one generation during which the Hardy-Weinberg assumptions are met, the population will achieve the Hardy-Weinberg equilibrium frequencies:

$$p^2 + 2pq + q^2 = 1$$



Hz most common if allele freqs are b/t 1/3 and 2/3

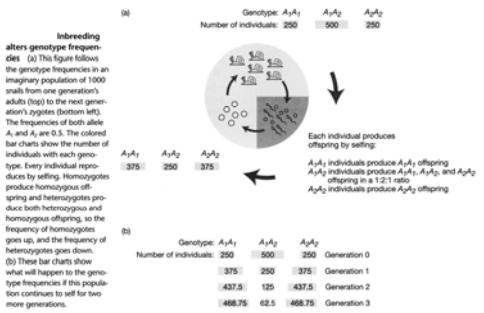
Non-Random Mating

- Also known as Sexual Selection.
- Only causes changes in genotype frequencies, NOT allele frequencies.
- Therefore not a true cause of evolutionary change by itself.

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.

Non-Random Mating: Inbreeding

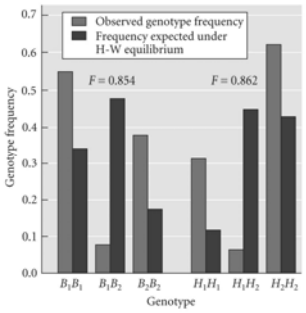


Inbreeding alters genotype frequencies (a) This figure follows the genotype frequencies in an imaginary population of 1000 snails from one generation's adults (top) to the next generation's zygotes (bottom left). The frequencies of both allele A_1 and A_2 are 0.5. The colored bar charts show the number of individuals with each genotype. Every individual reproduces by selfing. Homozygotes produce homozygous offspring and heterozygotes produce both heterozygous and homozygous offspring, so the frequency of homozygotes goes up, and the frequency of heterozygotes goes down. (b) These bar charts show what will happen to the genotype frequencies if this population continues to self for two more generations.

- Fits H.W., but adds twist that gene pool is not thoroughly mixed b/t generations.

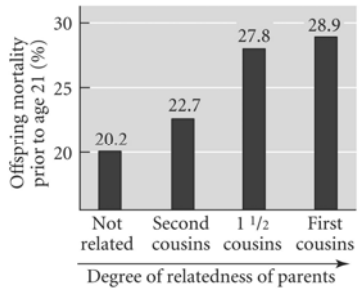
The consequences of inbreeding are similar to positive assortative mating…

Genotype frequencies in a the wild oat.



…but act across the entire genome.

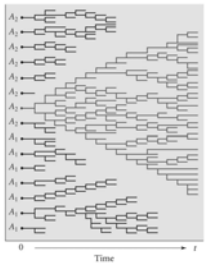
Inbreeding Depression in Humans.



Inbreeding can alter the gene pool because it predisposes **homozygosity**. Potentially harmful recessive alleles - invisible in the parents - become exposed to the forces of natural selection in the children.

Random Genetic Drift

Descent of gene copies
or bacteria or lucky mother.



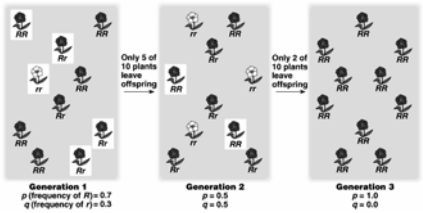
• Populations of finite size where random variation in survival and reproduction yields can cause evolutionary change.
  • **A nonadaptive mechanism!**

• Greater potent in small populations.
  • Founder Effect
  • Population Bottleneck

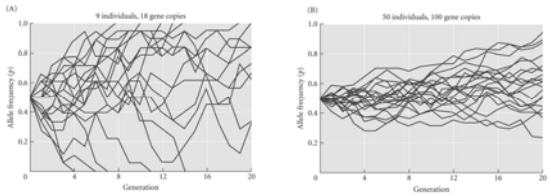
Random Genetic Drift

• Extinction is forever in genes & alleles, as well as with the organisms.

• Leads to the Neutral Theory of Evolution

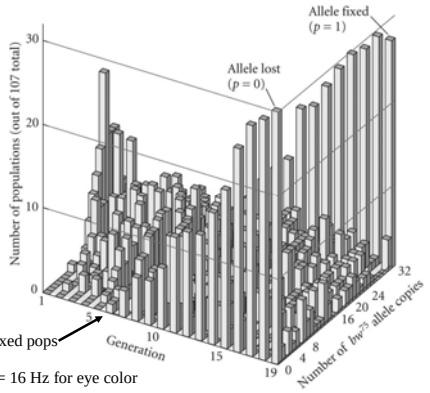


The strength of genetic drift is greater in smaller populations.



The probability that a given allele will become fixed is always equal to the frequency of that allele.

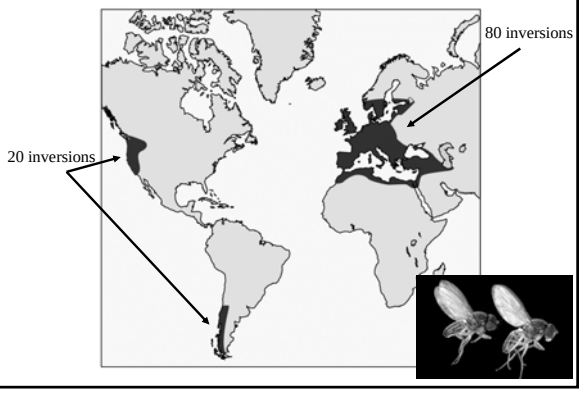
Random genetic drift in 107 experimental populations (Hz) of *D. melanogaster*



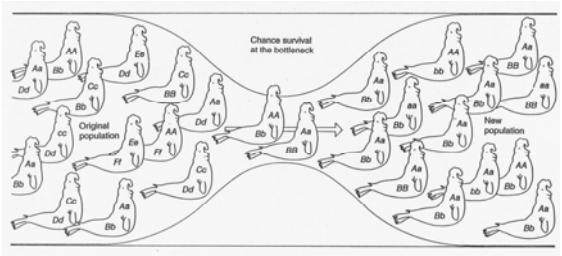
First fixed pops

Each pop = 16 Hz for eye color

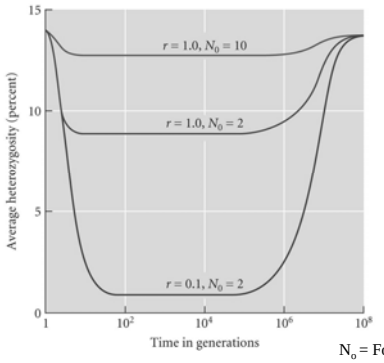
Founder Effect in *Drosophila subobscura*



Population bottlenecks reduce variation and enhance genetic drift



Effects of a bottleneck in population size on genetic variation, as measured by heterozygosity.



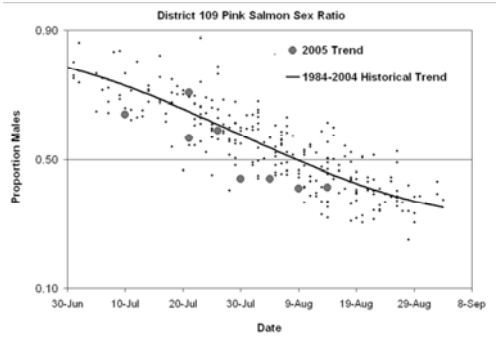
N_o = Founders
r = rate of increase

Population Size (N) vs. Effective Population Size (N_e)

Factors that cause N_e to be less than N

- **Overlap of generations**
- **Variation among individuals in reproductive success**
- **Fluctuations in population size**
- **Unequal sex ratio**

Unequal sex ratio: Pink Salmon



Neutral Theory of Molecular Evolution

- Kimura's Model – Drift dominates molecular evolution and is neutral with respect to fitness. Natural Selection is therefore unimportant regarding molecular evolution. The fallout of this model:
  - Positive Selection is excluded!
  - **The size of the population has no role!**
  - Evolution is a fxn of mutation, chance fixation, and negative selection.
  - **Pseudogenes** become yardstick used to estimate the rate of evolution.

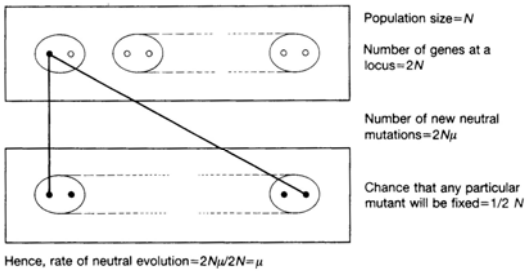


FIG. 8.6. The rate of neutral evolution.

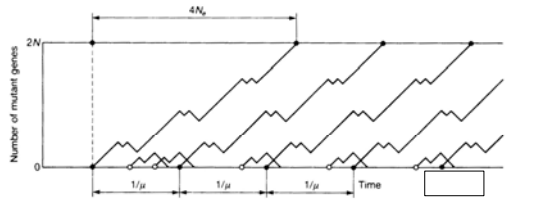


FIG. 8.7. Neutral evolution in a population of constant size. ●, neutral mutations that are fixed; ○, neutral mutations that are lost. For clarity, only a small fraction of the mutations that are lost are shown. The interval between occurrences of mutants that are fixed has been shown as constant, and $=1/\mu$. In fact, the interval has a constant expectation of $1/\mu$, but varies stochastically.

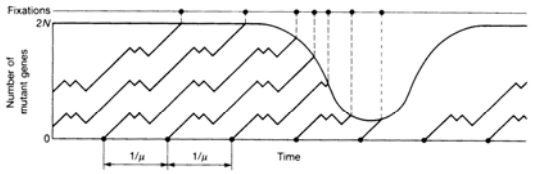


FIG. 8.8. Neutral evolution in a population of varying size. Only mutations that are fixed are shown. The interval between the occurrence of such mutations has a constant expectation $1/\mu$, but fixations are more frequent in a declining population, and less so in an increasing one.

Ultimately, the # of mutations generated is a fxn of pop size, but the chance that a mutation gets fixed is inversely proportional to the pop size due to drift, therefore pop size gets cancelled out!

A small pop fixes mutations quickly through drift, but produces new mutations slowly. A large produces many mutations, but few get fixed.

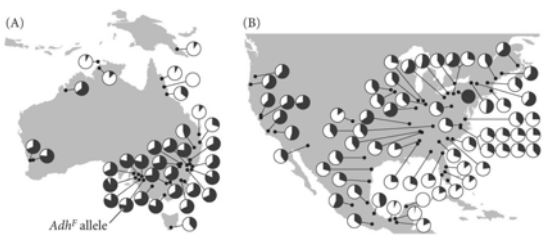
Neutral Theory of Molecular Evolution

• Ultimately, the # of mutations generated is a fxn of pop size, but the chance that a mutation gets fixed is inversely proportional to the pop size due to drift, therefore pop size gets cancelled out!

• A small pop fixes mutations quickly through drift, but produces new mutations slowly. A large produces many mutations, but few get fixed.

• The main concept to get around is that we tend to think of the effects of drift on a relatively short time scale, which emphasizes the decrease in genetic variation with a decreasing pop size (e.g., founder effect). However, evolutionary divergence also has to take into account the generation of genetic variation by mutation not just its fixation!

Clines in the frequency of the *Adh*^{F} allele at alcohol dehydrogenase locus of *D. melanogaster*



Adh Polymorphism

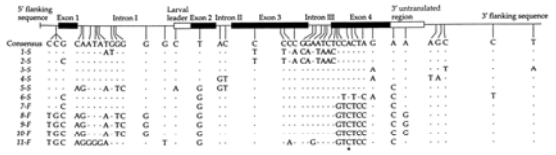


Figure 9.1 Polymorphic nucleotide sites among 11 sequences of the alcohol dehydrogenase gene in *Drosophila melanogaster*. Only differences from the consensus sequence are shown. Dots indicate identity with the consensus sequence. The asterisk in exon 4 indicates the site of the lysine for threonine substitution that is responsible for the fast/slow mobility differences between the two electrophoretic alleles. From Li and Graur (1991), which was modified from Hartl and Clark (1989).

Fast or Slow

TABLE 10.2 *Replacement (nonsynonymous) and synonymous substitutions and polymorphisms within and among three* Drosophila *species*[a]

	Polymorphisms	Substitutions
Replacement	2	7
Synonymous	42	17
Percent replacement	4.5	29.2

Source: Data from McDonald and Kreitman 1991.
[a]*D. melanogaster, D. simulans,* and *D. yakuba.*

NT predicts that the ratio of rates of replacement vs. silent should be constant. Greater replacement/silent ratio among spp. than w/in sp!

TABLE 10.3 *Rates of synonymous and replacement (nonsynonymous) substitutions in some protein-coding genes, calculated from the divergence between humans and several rodent species*

Gene	Number of base pairs compared	Replacement rate[a]	Synonymous rate[a]
Histone 3	135	0.00 ± 0.00	4.52 ± 0.87
Histone 4	102	0.00 ± 0.00	3.94 ± 0.81
Ribosomal protein S17	134	0.06 ± 0.04	2.69 ± 0.53
Actin α	376	0.01 ± 0.04	2.92 ± 0.34
Insulin	51	0.20 ± 0.10	3.03 ± 1.02
Insulin C peptide	31	1.07 ± 0.37	4.78 ± 2.14
α-globin	141	0.56 ± 0.11	4.38 ± 0.77
β-globin	146	0.78 ± 0.14	2.58 ± 0.49
Immunoglobulin κ	106	2.03 ± 0.30	5.56 ± 1.18
Interferon γ	136	3.06 ± 0.37	5.50 ± 1.45
Glyceraldehyde-3-phosphate dehydrogenase	332	0.20 ± 0.04	2.30 ± 0.30
Lactate dehydrogenase A	331	0.19 ± 0.04	4.06 ± 0.49

Source: From Li 1997.
[a]The rate is the number of substitutions per base pair per 10^9 years. A divergence time of 80 million (8×10^7) years between humans and rodents is assumed. Note that replacement rates vary far more than synonymous rates.

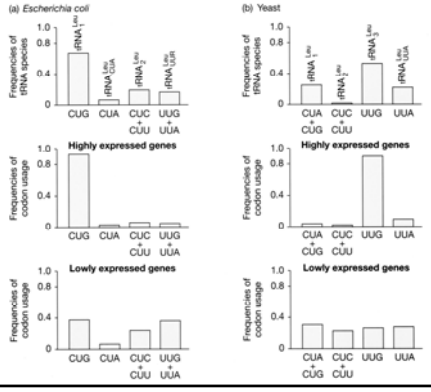
Take Home Message from Table 10.3, etc.

- Mutation rates vary within AND among genes.
- Silent substitutions *almost* always outnumber replacements.
  - Therefore drift dominates over negative selection.
- Pseudogenes are under no selective pressure: ~Measure of mutation.
- Histones and ribosomal RNAs are under strong selective pressure.
- Effects of Natural Selection
  - Positive Selection for advantageous mutations (Rare?)
  - Negative Selection for deleterious mutations (Less Rare?)
  - No Selection for silent mutations or Genetic Drift (Common?)

Positive Selection Affecting Silent Mutation Rates on Single-Copy Genes

- **Codon Bias** – codon usage is not random!
  - Strongest in highly expressed genes like ribosomal proteins.
  - Translation efficiency – speed vs. accuracy.
  - Exposure of silent mutations to natural selection.

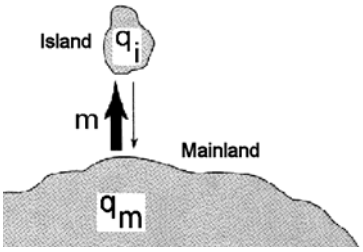
Codon bias correlates with the relative frequencies of tRNA types



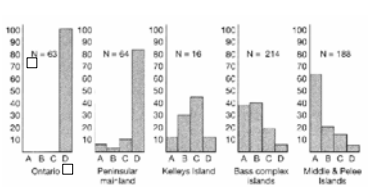
Effects of Migration

- Generally considered a one-way proposition.
- Overall acts to prevent species divergence in populations.
- Example, Lake Erie water snake color patterns.

Island Model of Migration



Where q_i and q_m are the initial allele frequencies on the island and mainland, respectively.

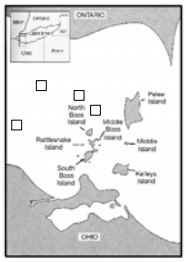


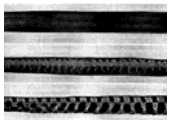
Category A snakes are unbanded, category D are strongly banded, categories B & C are intermediate. Snakes on the Ontario and Peninsular (Ohio) mainland are mostly banded. Snakes on Middle & Pelee Islands, which are furthest from the mainland, are predominantly unbanded.

Banded snakes are non-cryptic on limestone islands and get eaten by gulls.

Recurrent migration can maintain a disadvantageous trait at high frequency in spite of natural selection.

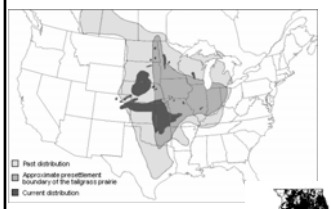
Island distribution of Lake Erie water snakes (*Natrix sipedon*).





Greater Prairie-Chicken: Conservation Genetics

Greater Prairie-Chicken: Historic & Present Range



Habitat reduction:
Islands of prairie in a sea of farmland.

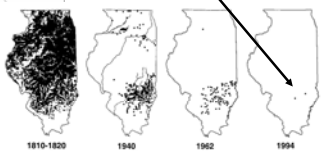


Fig. 1. Illinois prairies during 1810–1820 and distributions of greater prairie chickens in 1940 (25), 1962, and 1994. Prairie distributions for 1810–1820 were derived from R. C. Anderson. [Reprinted from R. C. Anderson, *Transactions of the Illinois State Academy of Science* **63**, 214 (1970), with permission.]

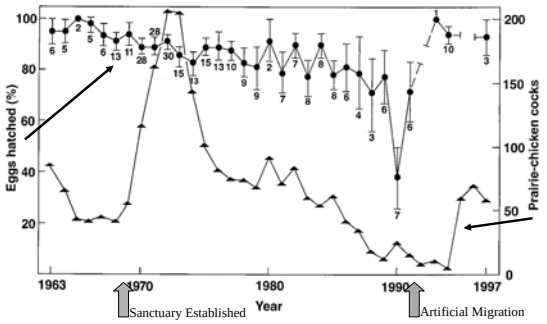


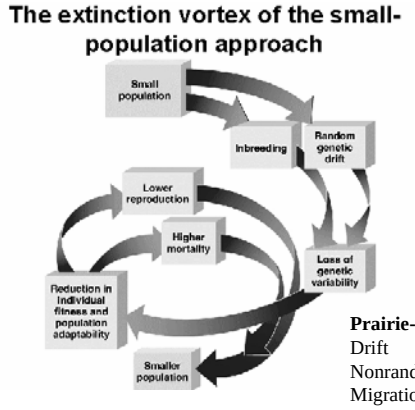
Fig. 2. Annual means for success of greater prairie chicken eggs in 304 fully incubated clutches (circles) and counts of males (triangles) on booming grounds in spring, Jasper County, Illinois, 1963–1997. Translocations of nonresident birds began in August 1992. Test statistics (*24*) for the period 1963–1991 are as follows: egg success rates, $\phi = 4.28$ ($P < 0.001$); male counts, $\phi = 1.88$ ($P = 0.0301$). Bars indicate ± 1 SE and adjacent numbers indicate numbers of nests. For egg fertility rates (not shown), $\phi = 2.18$ ($P = 0.0146$).

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.



Prairie-Chicken Model:
Drift
Nonrandom mating
Migration