

From: [Bill Rooney](#)
To: "scontreras@ag.tamu.edu"
Subject: copying for Agro642
Date: Monday, September 07, 2009 11:43:00 AM
Attachments: [Lecture 2 - Hardy-Weinberg Handouts.pdf](#)
[Agro642 - TAES Sorghum Breeding Program.pdf](#)

Susie:

I need the following files printed and 14 copies produced for my Agro 642 class tomorrow morning (September 8). You can make the copies double sided to save a little paper. Collate and staple each file separately.

I'll pick them up at 9:30 tomorrow morning (class is at 9:35)

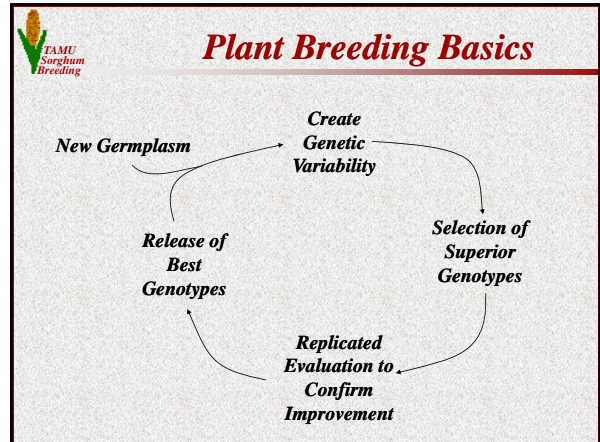
Thanks,

bill

Dr. William L. Rooney
Professor, Sorghum Breeding and Genetics
Chair, Plant Release Committee
Texas A&M University
College Station, Texas 77843-2474
979 845 2151

Texas A&M
Sorghum Breeding Program -
Data Management Procedures

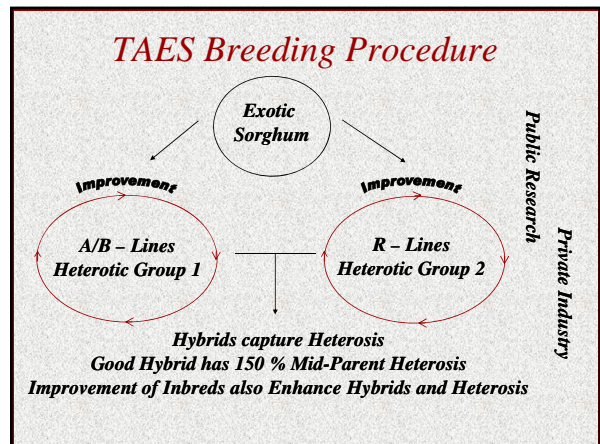
Agro 642

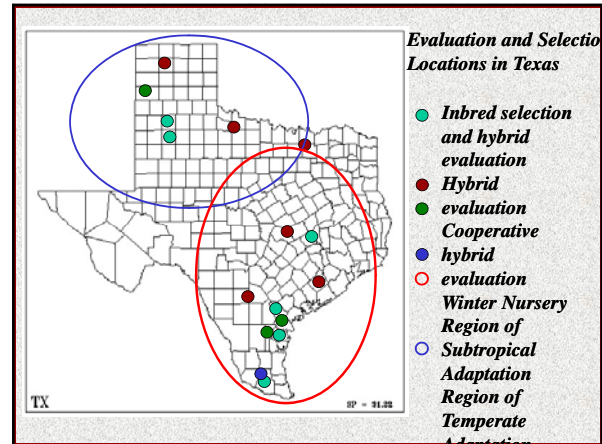
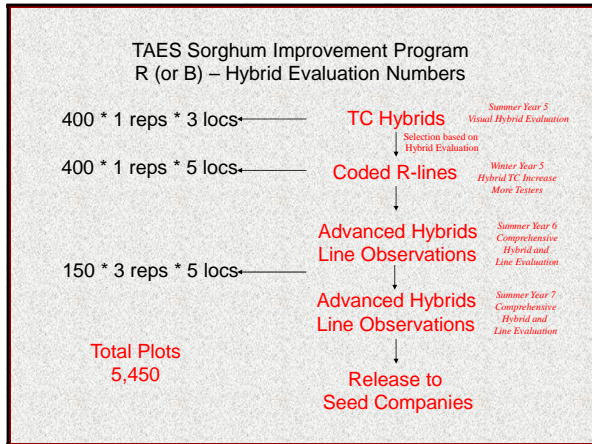
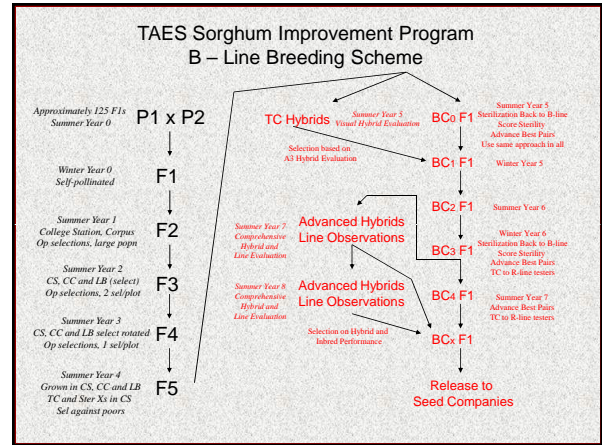
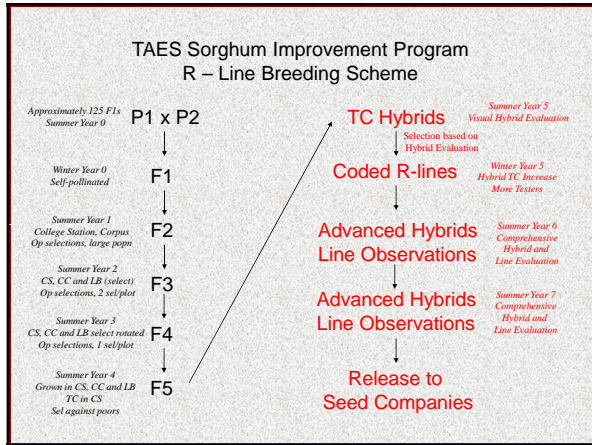
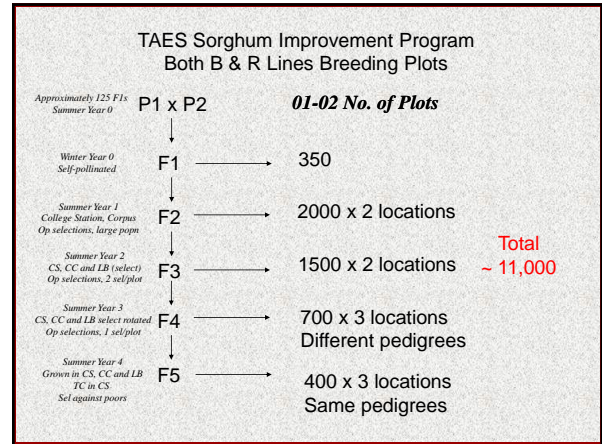
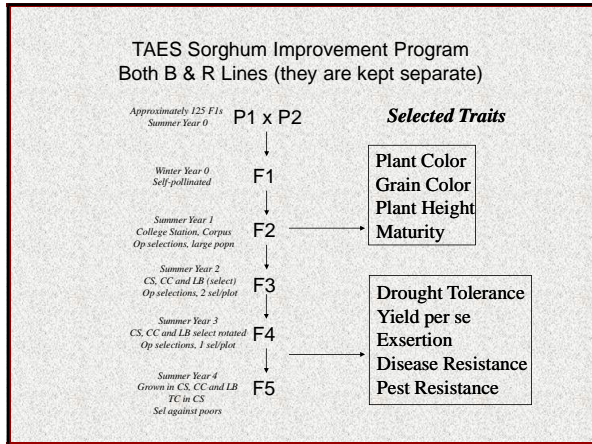


- Sorghum bicolor**
- Cultivar Types
 - Developing Countries: Varieties
 - Developed Countries: Hybrids
 - Breeding Methodology
 - Mostly Pedigree followed by Sterilization and Testcrossing
 - Some Population Breeding using Genetic Male Sterility
 - Hybridization for Hybrid Seed Production
 - Cytoplasmic Male Sterility

- Emphasis - 2009**
- Bioenergy 50%
 - Biomass
 - Sweet
 - Grain 40%
 - Traditional
 - Health Food
 - Forage 10%
 - Grazing
 - Silage
 - Emphasis Defined by Funding
 - Corporate (70%)
 - Ceres
 - Chevron
 - Public (25%)
 - Federal
 - State
 - Commodity (5%)
 - USCP

- TAES Sorghum Breeding Objectives**
- Conduct research on the genetic control of agronomically important traits in sorghum
 - Train undergraduate and graduate students in plant breeding and genetics
 - Release improved germplasm and parental lines to the sorghum breeding industry
- 







Total Numbers - Field

- Breeding Nursery (CC, BE, CS, LB, HW)
 - ~ 11,000 plots (15 acres)
- Advanced Evaluation (all over the place)
 - Line per se (~ 2,000 plots) (3 acres)
 - Hybrids (~ 3,500 plots) (12 acres)
- Research Nursery (WE, CC, BE, CS, LB, HW)
 - ~ 10,000 plots (14 acres)
- Seed Maintenance and Increase (CS, LB)
 - ~ 5,000 plots (8 acres)
- Standard Increases and Border (8 acres)



Total Numbers - Inventory

- Total : 81,468 as of April 1, 2002
 - Hybrids
 - Inbred
 - Research
 - Breeding
- 1992 through 2001 increases
- Must keep accurate weights on standard hybrids and inbred lines as they are used regularly



Data Management - Needs

- Pedigree Updates (must update automatically)
- Inventory Maintenance (keep track seed supply)
- Experimental Design and Randomization
- Labels – packaging, inventory, harvest
- FieldBooks – paper and computer
- Statistical Analysis
- Maps



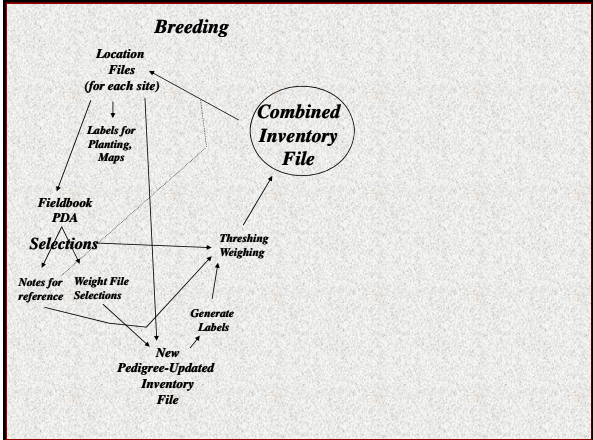
Data Management - Software

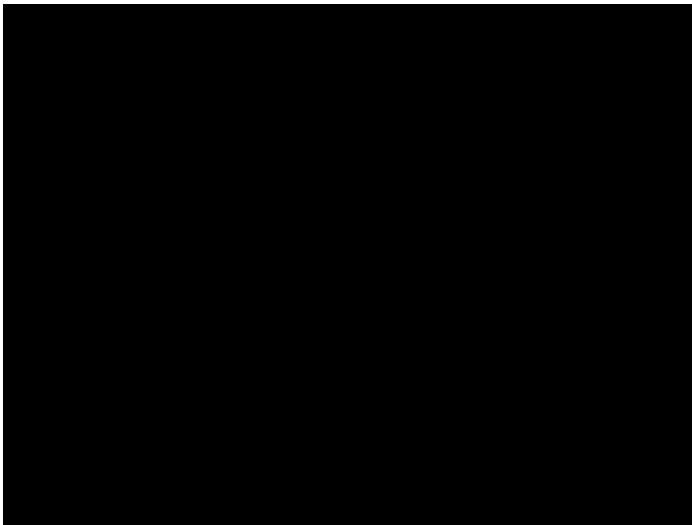
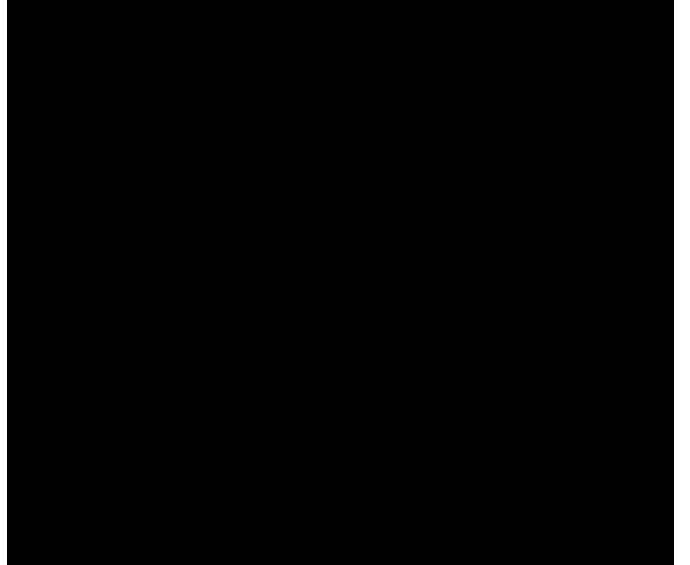
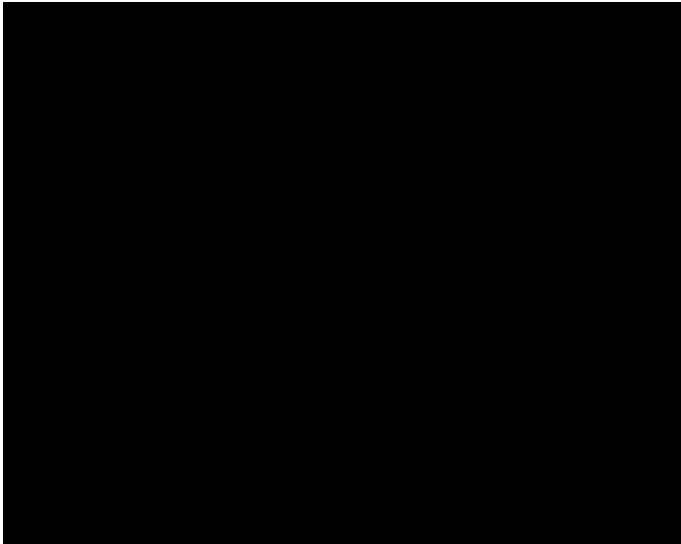
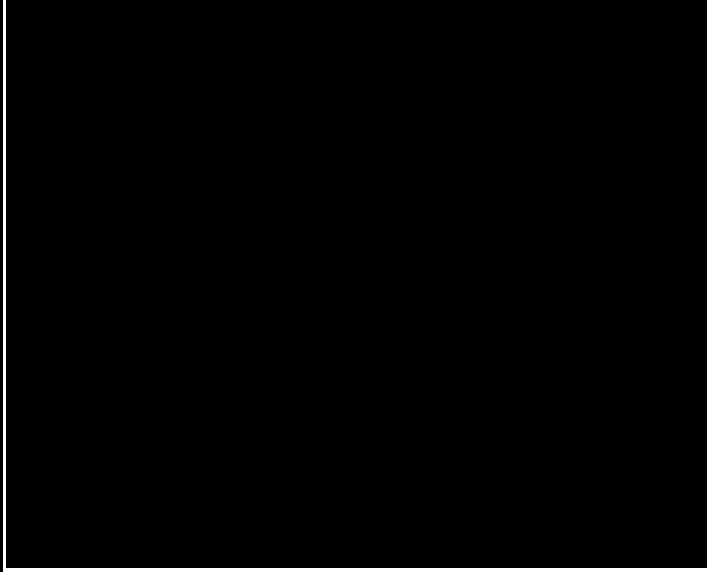
- Microsoft Excel
 - Maps
 - Field Books
 - Data Input
 - Pedigree Updating
 - Inventory Maintenance
 - Experimental Design and Randomization
 - Labels
- SAS
 - Statistical Analysis

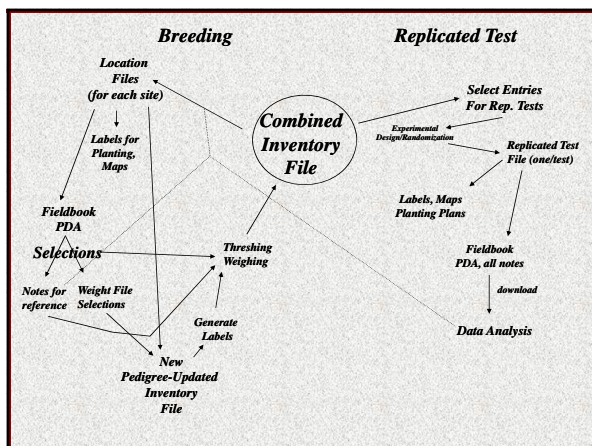
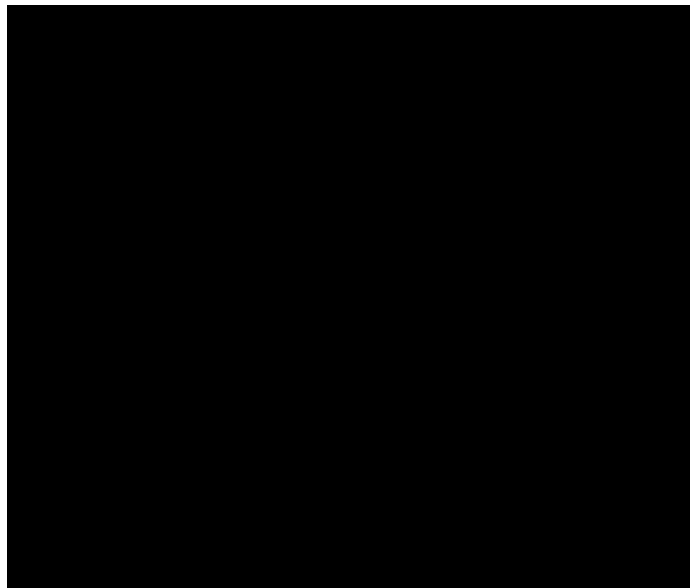
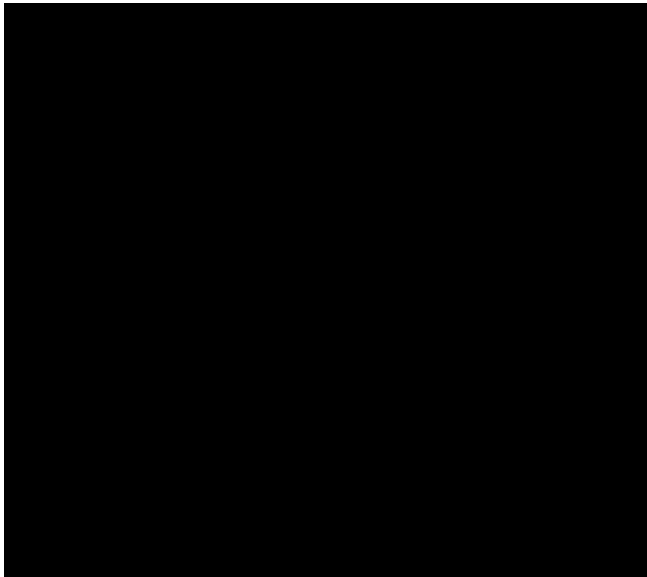
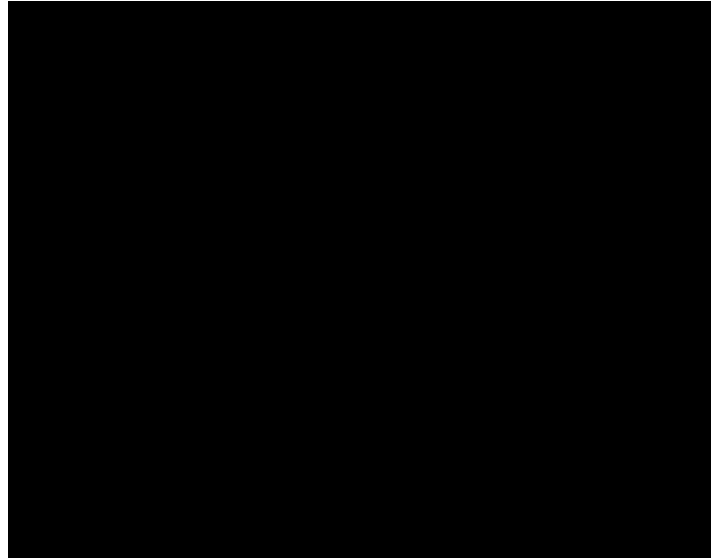
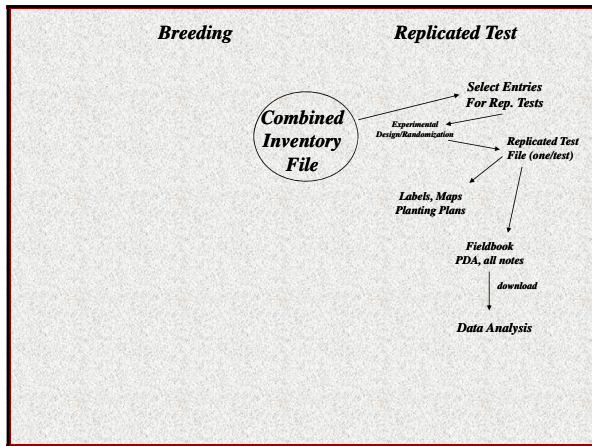


Data Management - Hardware

- Desktop Computer and Printer
- Laptop Computer
- PDA – Compaq iPAQ 3765







***Plant Breeding is a numbers game...
the more you look at, the better your
chance of finding something good.***

***So make sure that your
data management system
allows you to evaluate to
your full potential***

GENOTYPE FREQUENCIES

Genotype	Number	Frequency	Frequency after RM
A ₁ A ₁	240	P ₁₁ = 0.40 (240/600)	p ² = 0.36
A ₁ A ₂	240	P ₁₂ = 0.40 (240/600)	2pq = 0.48
A ₂ A ₂	120	P ₂₂ = 0.20 (120/600)	q ² = 0.16

ALLELE FREQUENCIES

$$p = P_{11} + \frac{1}{2} P_{12} = .40 + \frac{1}{2} (.4) = 0.60$$

$$q = P_{22} + \frac{1}{2} P_{12} = .20 + \frac{1}{2} (.4) = 0.40$$

Potential Cross	Cross Frequency	Genotypes (Frequency) in Next Generation		
		A ₁ A ₁	A ₁ A ₂	A ₂ A ₂
A ₁ A ₁ / A ₁ A ₁	p ² * p ² = p ⁴	p ⁴		
A ₁ A ₁ / A ₁ A ₂	p ² * 2pq = 2p ³ q	1/2 2p ³ q	1/2 2p ³ q	
A ₁ A ₁ / A ₂ A ₂	p ² * q ² = p ² q ²		p ² q ²	
A ₁ A ₂ / A ₁ A ₁	2pq * p ² = 2p ³ q	1/2 2p ³ q	1/2 2p ³ q	
A ₁ A ₂ / A ₁ A ₂	2pq * 2pq = 4p ² q ²	1/4 4p ² q ²	1/2 4p ² q ²	1/4 4p ² q ²
A ₁ A ₂ / A ₂ A ₂	2pq * q ² = 2pq ³		1/2 2pq ³	1/2 2pq ³
A ₂ A ₂ / A ₁ A ₁	p ² * q ² = p ² q ²		p ² q ²	
A ₂ A ₂ / A ₁ A ₂	2pq * q ² = 2pq ³		1/2 2pq ³	1/2 2pq ³
A ₂ A ₂ / A ₂ A ₂	q ² * q ² = q ⁴			q ⁴
	Sum	A ₁ A ₁	A ₁ A ₂	A ₂ A ₂

$$\begin{aligned} \text{Sum for } A_1A_1 &= p^4 + (\frac{1}{2}) 2p^3q + (\frac{1}{2}) 2p^3q + (\frac{1}{4}) 4p^2q^2 \\ &= p^4 + p^3q + p^3q + p^2q^2 \\ &= p^2 (p^2 + 2pq + q^2) \\ &= p^2 \end{aligned}$$

$$\begin{aligned} \text{Sum for } A_1A_2 &= (\frac{1}{2}) 2p^3q + p^2q^2 + (\frac{1}{2}) 2p^3q + (\frac{1}{2}) 4p^2q^2 + (\frac{1}{2}) 2pq^3 + p^2q^2 + (\frac{1}{2}) 2pq^3 \\ &= p^3q + p^2q^2 + p^3q + 2p^2q^2 + pq^3 + p^2q^2 + pq^3 \\ &= pq (p^2 + pq + p^2 + 2pq + q^2 + pq + q^2) \\ &= pq (2p^2 + 4pq + 2q^2) \\ &= 2pq (p^2 + 2pq + q^2) \\ &= 2pq \end{aligned}$$

$$\begin{aligned} \text{Sum for } A_2A_2 &= (\frac{1}{4}) 4p^2q^2 + (\frac{1}{2}) 2pq^3 + (\frac{1}{2}) 2pq^3 + q^4 \\ &= p^2q^2 + pq^3 + pq^3 + q^4 \\ &= q^2 (p^2 + 2pq + q^2) \end{aligned}$$

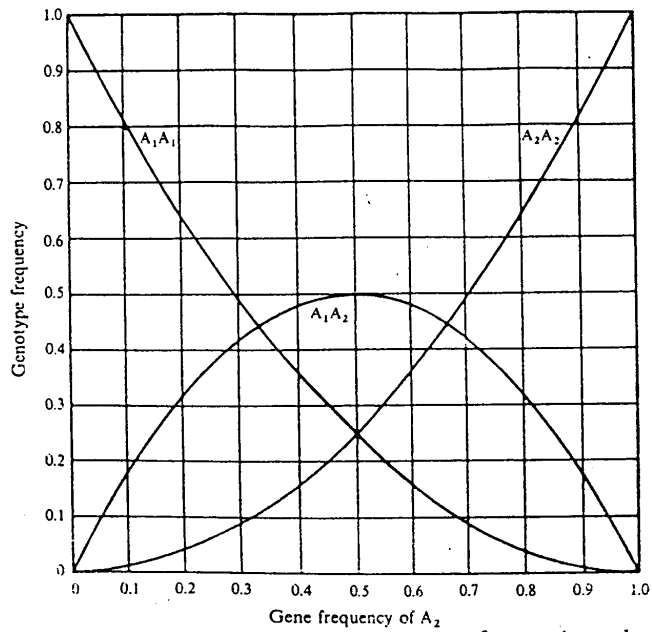


Fig. 1.1. Relationship between genotype frequencies and gene frequency for two alleles in a population in Hardy-Weinberg equilibrium

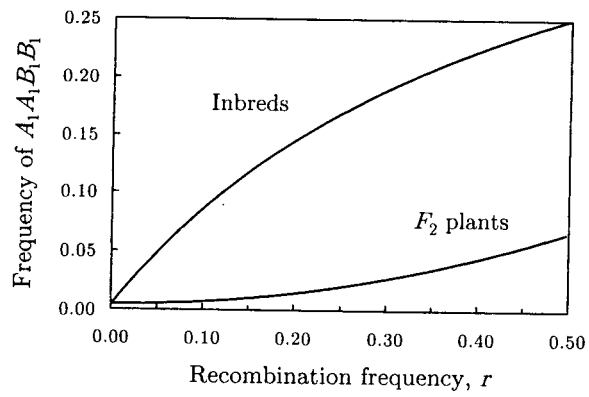


FIGURE 2.3. Effect of linkage on the frequency of $A_1A_1B_1B_1$.

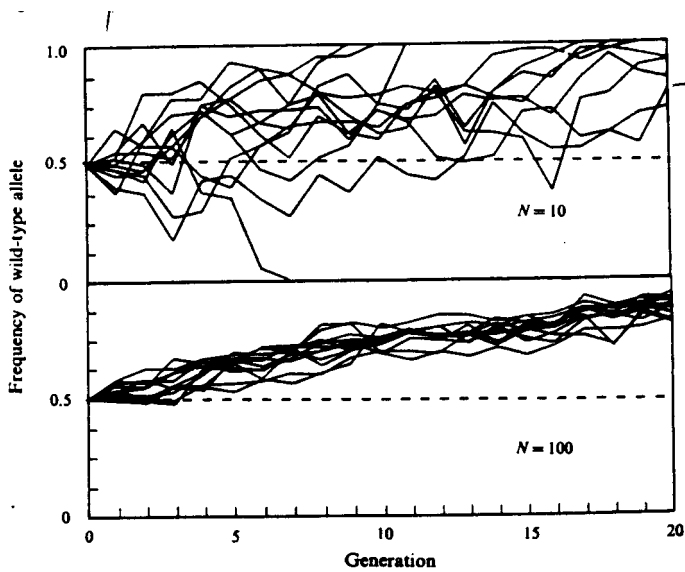
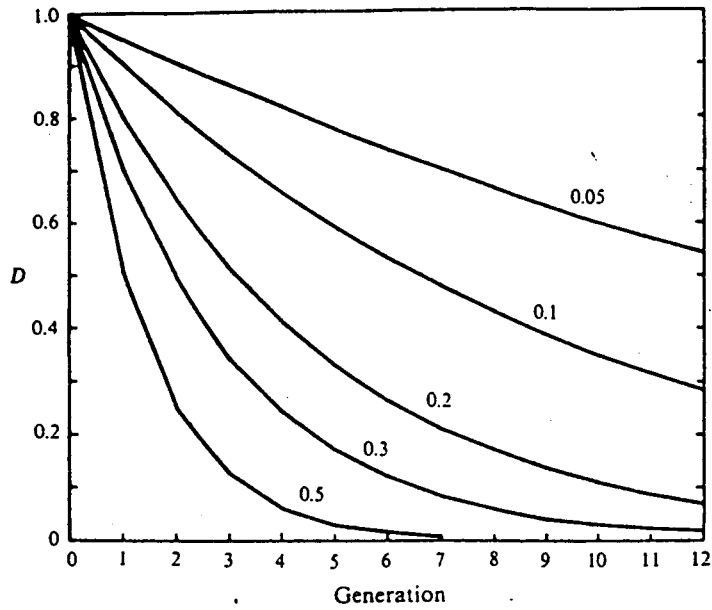


Fig. 3.2. Random drift of a colour gene ('black') in *Tribolium*. Heterozygotes were recognizable, so the gene frequencies were estimated exactly by counting. The figure shows the results with two population sizes, $N = 10$ and $N = 100$. There were 12 lines with each population size. Natural selection favoured the wild-type allele and led to an overall increase in its frequency, random drift causing variation of the lines around the mean, more marked in the small than in the larger populations. (After Rich, Bell, and Wilson, 1979.)

TABLE 2.5. Selection among A_1A_1 , A_1A_2 , and A_2A_2 genotypes.

	A_1A_1	A_1A_2	A_2A_2	Total
Frequency	p^2	$2pq$	q^2	1
Relative fitness	$1 - s_{11}$	$1 - s_{12}$	$1 - s_{22}$	
Contribution	$p^2(1 - s_{11})$	$2pq(1 - s_{12})$	$q^2(1 - s_{22})$	T (see text)
Frequency after selection	$\frac{p^2(1-s_{11})}{T}$	$\frac{2pq(1-s_{12})}{T}$	$\frac{q^2(1-s_{22})}{T}$	1

$$q_1 = \frac{q[1 - (ps_{12} + qs_{22})]}{1 - (p^2s_{11} + 2pqs_{12} + q^2s_{22})}$$

The change in allele frequency due to one generation of selection is

$$\begin{aligned} \Delta q &= q_1 - q \\ &= \frac{pq[p(s_{11} - s_{12}) + q(s_{12} - s_{22})]}{1 - (p^2s_{11} + 2pqs_{12} + q^2s_{22})} \end{aligned}$$

TABLE 2.6. Selection coefficients for specific types of selection.

Type of selection	Selection coefficient against:		
	A_1A_1	A_1A_2	A_2A_2
Against recessive	0	0	1
Partial against recessive	0	0	s_{22}
No dominance	s_{11}	$\frac{1}{2}(s_{11} + s_{22})$	s_{22}
For heterozygotes	s_{11}	0	s_{22}
Against heterozygotes	0	s_{12}	0

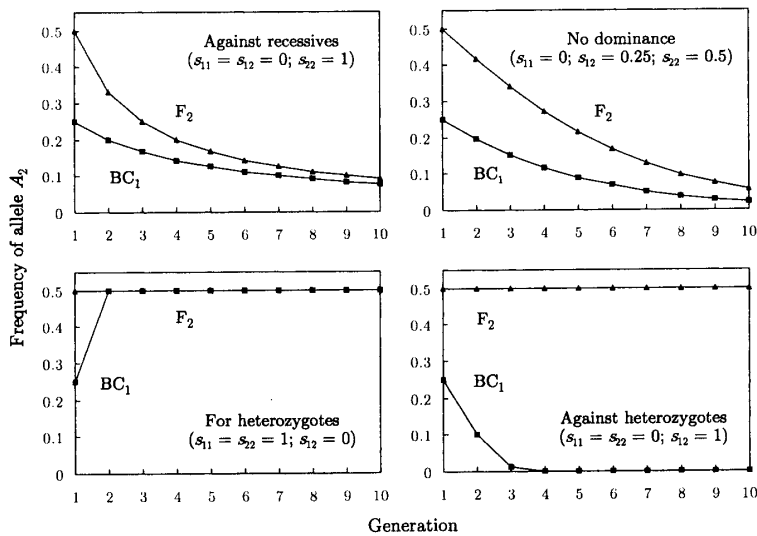


FIGURE 2.5. Changes in q with selection in random-mated populations.

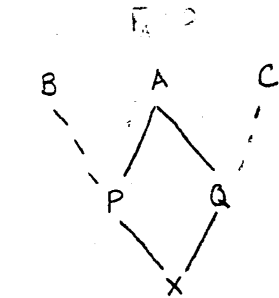
Coefficient of Inbreeding (F) in Pedigreed Populations

F = probability that two alleles in an individual are identical by descent.
 In pedigreed populations, it is possible to definitively calculate an F value on an individual basis.

$$F_x = \sum \frac{1}{2}^n (1 + F_a)$$

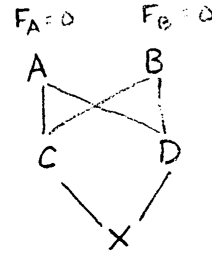
where n = number of parents involved in a loop of relation
 F_a = inbreeding coefficient of the parent providing identical alleles

Examples:



$$F_x = \frac{1}{2}^{(3)} (1 + F_A)$$

$$F_x = \frac{1}{8}$$



$$F_x = \left[\frac{1}{2}^3 (1 + F_A) \right] + \left[\frac{1}{2}^3 (1 + F_B) \right]$$

$$= \frac{1}{8} + \frac{1}{8}$$

$$= \frac{1}{4}$$

1. Determine the number parents with which a loop can be made
2. For each loop count number of parents in loop
3. Sum across all different paths