Falconer & Mackay (1996)
Chapter 01

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Chapter 1: Short summary

Introducing the descriptive tools in Population Genetics

Introducing a very fundamental model in Population and Quantitative Genetics (Hardy-Weinberg Model)

Chapter 1: Extra emphasis

How to measure PG variation

Demonstration of variation by examples

Hardy-Weinberg model

Patterns and processes

1-Locus theory versus 2-Locus theory

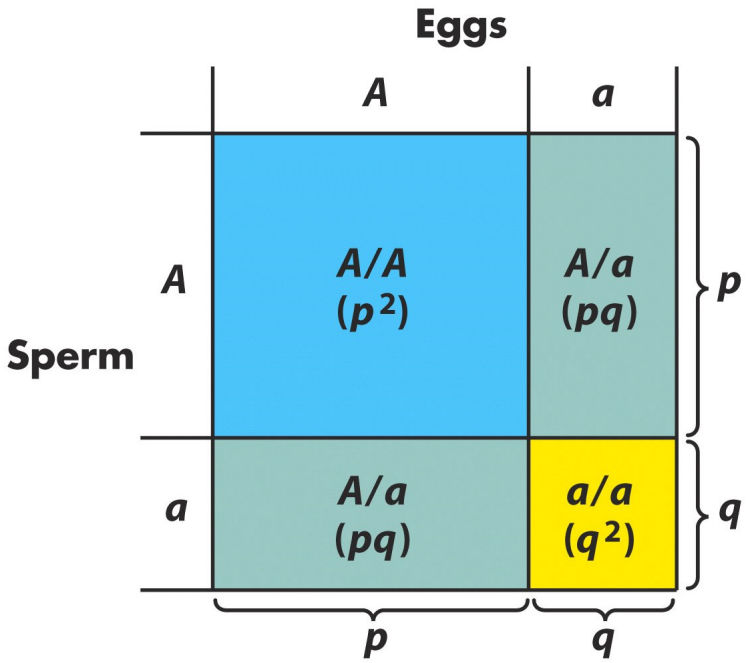
Notation: One locus, two alleles, three genotypes

	Genes		*Genotypes*		
	A_1	A_2	A_1A_1	A_1A_2	A_2A_2
Frequencies	p	q	P	H	Q

$$f_{A/A},\ f_{A/a},\ f_{a/a}$$

$p = f_{A/A} + \frac{1}{2} f_{A/a} = frequency\ of\ A$ $\qquad p = P + \frac{1}{2}H$

$q = f_{a/a} + \frac{1}{2} f_{A/a} = frequency\ of\ a$ $\qquad q = Q + \frac{1}{2}H$



Variation at all levels of the biological systems

Variation of the DNA & RNA (sequence) level

Variation at the chromosomal level

Variation at the AA level

Variation at the protein level

Variation at the physiological level

Variation at the anatomical level

Variation at the …

Variation at the …

Variation at the blood group level

$$p = f_{M/M} + \tfrac{1}{2} f_{M/N}$$

P = 0.835 + ½ 0.156 = 0.913

q = 1-p = 1.000-0.913 = 0.087

P= 0.301 + ½ 0.495 = 0.548

q = 1-p = 1.000-0.548 = 0.452

TABLE 19-1 Frequencies of Genotypes for Alleles at MN Blood Group Locus in Various Human Populations

	Genotype			*Allele frequencies*	
Population	*M/M*	*M/N*	*N/N*	*p*(*M*)	*q*(*N*)
Eskimo	0.835	0.156	0.009	0.913	0.087
Australian Aborigine	0.024	0.304	0.672	0.176	0.824
Egyptian	0.278	0.489	0.233	0.523	0.477
German	0.297	0.507	0.196	0.550	0.450
Chinese	0.332	0.486	0.182	0.575	0.425
Nigerian	0.301	0.495	0.204	0.548	0.452

Source: W. C. Boyd, *Genetics and the Races of Man.* D. C. Heath, 1950.

Hardy-Weinberg Model

Assumptions:

- Diploid organism
- Sexual reproduction
- Normal segregation
- *Genotypes can be distinguished unequivocally*
- Reciprocal equality of mating gametes (i.e. $A_1A_2 = A_1A_2$)
- Equal allele frequency in males and females
- Locus is not sex-linked
- Large population (negligible sampling variance)
- Random mating
- No selection (equal fertility, equal viability)
- No migration
- No mutation
- *Discrete generations*

A hard look at H-W equilibrium

Step	Deduction from: to	Conditions
	Gene frequency in parents	
1a		Normal gene segregation Equal fertility of parents
	Gene frequency in all gametes	
1b		Equal fertilizing capacity of all gametes Large population
	Gene frequency in gametes forming zygotes	
2		Random mating Equal gene frequencies in ♂ and ♀ parents
	Genotype frequencies in zygotes	
3		Equal viability
	Genotype frequencies in progeny	
4	Gene frequency in progeny	

Actually allele frequency

Falconer, D.S., Mackay, T.F.C. (1996)

Formal description

Parent generation
Allele frequencies

$$p^2 : 2pq : q^2 \qquad f_A = p, \quad f_a = q \qquad p+q=1, \quad q=1-p$$

First generation
Genotype frequencies

$$p \times p = p^2 \qquad (p \times q)+(p \times q) = 2pq \qquad q \times q = q^2$$

First generation
Allele frequencies

$$p^2 + pq = p(p+q) = p$$

Second generation
Genotype frequencies

$$p^2 : 2pq : q^2$$

χ^2 (Chi-square) test

	Genotypes				Allele frequencies	
	MM	MN	NN	Total	M	N
# observed	233	385	129	747	0.5696	0.4304
# expected	242.36	366.26	138.38	747		

χ^2 (Chi-square) test

O = Observed number
E = Expected number

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

	Genotypes		
	MM	MN	NN
Number observed	233.00	385.00	129.00
Number expected	242.3	366.26	138.38

$f_M = 0.5696$
$f_N = 0.4304$

$$\chi_1^2 = \frac{(233.00-242.36)^2}{242.36} + \frac{(385.00-366.26)^2}{366.26} + \frac{(129.00-138.38)^2}{138.38} = 1.96$$

Patterns & Processes

Patterns	Processes
Diploid organism	Sexual reproduction
Genotypes can be distinguished unequivocally	Normal segregation
Reciprocal equality of mating gametes	Negligible sampling variance
Equal allele frequency in males and females	Random mating
Locus is not sex-linked	Selection
Large population	Migration
Random mating	Mutation
Equal fertility, equal viability	
Discrete generations	

Extensions of H-W equilibrium

To more than two alleles

To sex linked genes

To more than one locus

Extension to >2 alleles

TABLE 19-3 Frequencies of Various Alleles at Three Enzyme-Encoding Loci in Four Populations of *Drosophila pseudoobscura*

		Population			
Locus (enzyme-encoding)	Allele	Berkeley	Mesa Verde	Austin	Bogotá
Malic dehydrogenase	*A*	0.969	0.948	0.957	1.00
	B	0.031	0.052	0.043	0.00
α-Amylase	*A*	0.030	0.000	0.000	0.00
	B	0.290	0.211	0.125	1.00
	C	0.680	0.789	0.875	0.00
Xanthine dehydrogenase	*A*	0.053	0.016	0.018	0.00
	B	0.074	0.073	0.036	0.00
	C	0.263	0.300	0.232	0.00
	D	0.600	0.581	0.661	1.00
	E	0.010	0.030	0.053	0.00

Source: R. C. Lewontin, *The Genetic Basis of Evolutionary Change.* Columbia University Press, 1974.

Extension to >2 alleles

Use the example of α-amylase from Table 19.3

Allele frequencies

$p = f_A$; $q = f_B$; $r = f_C$; $p + q + r = 0.030 + 0.290 + 0.680 = 1.0$

Genotype frequencies

$p^2 = 0.030 * 0.030 = 0.0009$

$q^2 = 0.290 * 0.290 = 0.0841$

$r^2 = 0.680 * 0.680 = 0.4624$

$2pq = 2 * 0.030 * 0.290 = 0.0174$

$2pr = 2 * 0.030 * 0.680 = 0.0408$

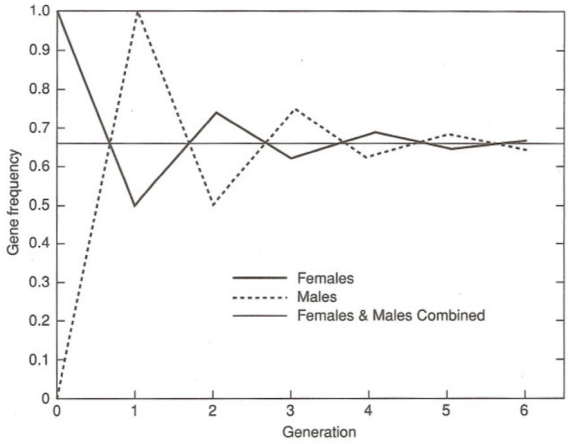
$2qr = 2 * 0.290 * 0.680 = 0.3944$

$p^2 + q^2 + r^2 + 2pq + 2pr + 2qr = 1.0000$

Extension of HWM to sex linked genes

$$p'_m = p_f$$
$$p'_f = \tfrac{1}{2}(p_m + p_f)$$

$$p'_f - p'_m = \tfrac{1}{2}(p_m + p_f) - p_f$$
$$= -\tfrac{1}{2}(p_f - p_m)$$



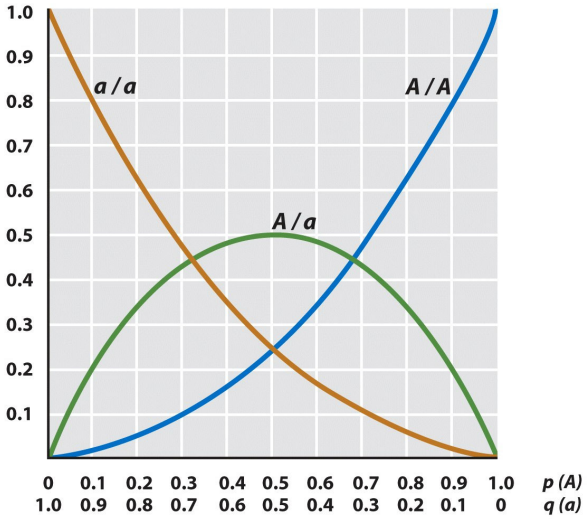
Consequences of H-W equilibrium

Rare alleles are almost never found as homozygous

$f_{PKU/PKU} = q^2$	= 5/55715	= 0.000090	≈ 0.01%
f_{PKU}	= q	= $\sqrt{0.00009}$ = 0.009473 ≈ 0.01	≈ 1%
$f_{PKU/+}$	= 2pq	= 0.018767	≈ 2%

$2pq/q^2 = 0.018767 / 0.000090 = 208.52$

Frequency of recessive alleles



Frequency of the heterozygotes

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Source: W. C. Boyd, *Genetics and the Races of Man*. D. C. Heath, 1950.

$2pq/q^2 = 0.156/0.009 = 17.33$

Extension of HWM to more than 1 locus

Parental genotypes	$A_1A_1B_1B_1$		$A_2A_2B_2B_2$
Parental gametes	A_1B_1		A_2B_2
First generation genotypes		$A_1A_2B_1B_2$	
First generation gametes		$A_1B_1, A_1B_2, A_2B_2, A_2B_1$	

Gametic phase (linkage) disequilibrium

Genes	A_1	A_2	B_1	B_2
Gene frequencies	p_A	q_A	p_B	q_B
Gametic types	A_1B_1	A_1B_2	A_2B_1	A_2B_2
Frequencies, equilibrium	p_Ap_B	p_Aq_B	q_Ap_B	q_Aq_B
Frequencies, actual	r	s	t	u
Difference from equilibrium	$+D$	$-D$	$-D$	$+D$

$$D = ru - st$$

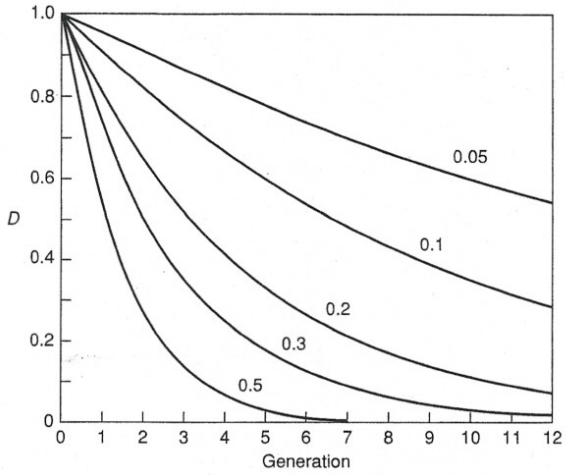
Development of disequilibrium

$$r' = r(1 - c) + p_A p_B c$$

$$\begin{aligned} D' &= r' - p_A p_B \\ &= r(1 - c) - p_A p_B(1 - c) \\ &= (r - p_A p_B)(1 - c) \\ &= D(1 - c) \end{aligned}$$

$$D_t = D_0(1 - c)^t$$

Development of disequilibrium



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Chapter 02

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Nothing in genetics is constant

`Well, in *our* country,' said Alice, still panting a little, `you'd generally get to somewhere else -- if you ran very fast for a long time, as we've been doing.'

`A slow sort of country!' said the Queen. `Now, *here*, you see, it takes all the running *you* can do, to keep in the same place.

"Through the Looking Glass" by Lewis Carroll

Chapter 2: Short summary

Systematic evolutionary forces

- Mating pattern
- Mutation
- (Recombination)
- Migration
- Selection

Chapter 2: Long summary (1)

We have seen that a large random-mating population is stable with respect to gene frequencies and genotype frequencies, in the absence of agencies tending to change its genetic properties.

Chapter 2: Long summary (2)

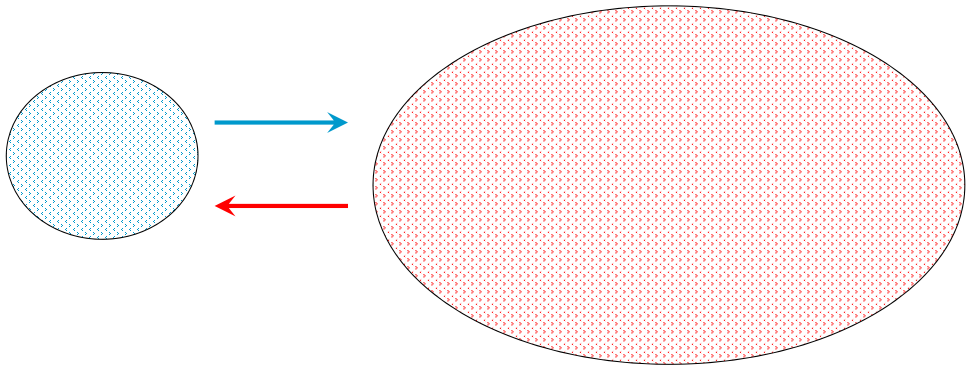
We can now proceed to a study of the agencies through which changes of gene frequency, and consequently of genotype frequencies, are brought about.

There are two sorts of process: systematic processes, which tend to change the gene frequency in a manner predictable both in amount and in direction; and the dispersive process, which arises in small populations from the effects of sampling, and is predictable in amount but not in direction.

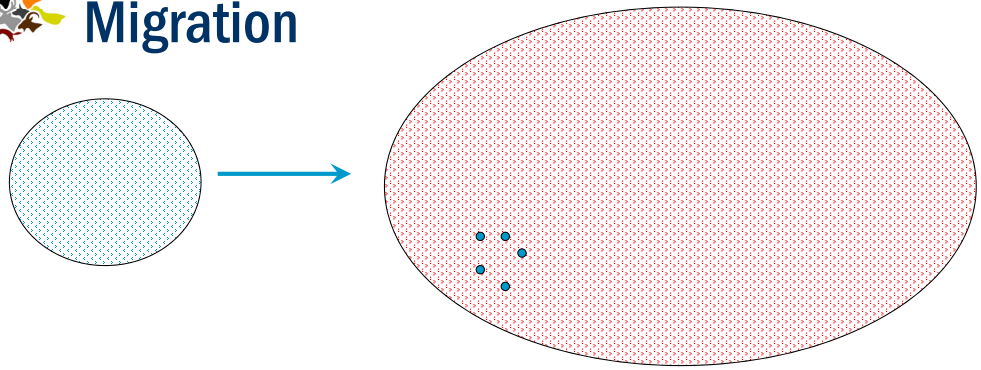
Chapter 2: Long summary (3)

In this chapter we are concerned only with the systematic processes, and we shall consider only large random-mating populations in order to exclude the dispersive process from the picture. There are three systematic processes: migration, mutation, and selection. We shall study these separately at first, assuming that only one process is operating at a time, and then we shall see how the different processes interact.

Migration



Migration



$f_A = P$

$f_{A(t)} = p_t$

Proportion in immigrants = m

Migration

$$q_1 = mq_m + (1 - m)q_0$$
$$= m(q_m - q_0) + q_0$$

$$\Delta q = q_1 - q_0$$
$$= m(q_m - q_0)$$

Mutation

Random mistake in the DNA duplication process

Effective repair mechanisms

Mutation

Mutation rate	A_1	$\underset{v}{\overset{u}{\rightleftharpoons}}$	A_2
Initial gene frequencies	p_0		q_0

After one generation

$$\Delta q = up_0 - vq_0$$

At equilibrium

$$pu = qv$$

$$\frac{p}{q} = \frac{v}{u}$$

$$q = \frac{u}{u+v}$$

Mutation

Let μ be the mutation rate from A to a

Let p_t be the frequency of A in generation t

$$\Delta p = p_t - p_{t-1} = (p_{t-1} - \mu p_{t-1}) - p_{t-1} = -\mu p_{t-1}$$

$$p_n = p_0 e^{-n\mu}$$ (Approximately)

How prevalent are mutations?

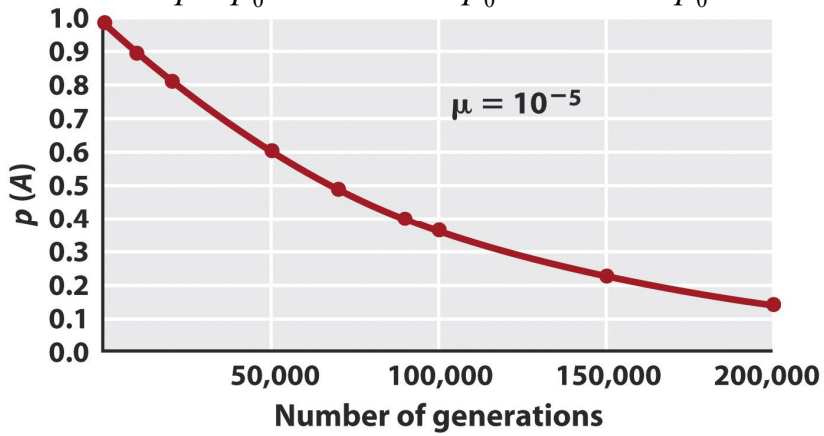
Table 19-8 Point-Mutation Rates in Different Organisms

Organism	Gene	Mutation rate per generation
Bacteriophage	Host range	2.5×10^{-9}
Escherichia coli	Phage resistance	2×10^{-8}
Zea mays (corn)	*R* (color factor)	2.9×10^{-4}
	Y (yellow seeds)	2×10^{-6}
Drosophila melanogaster	Average lethal	2.6×10^{-5}

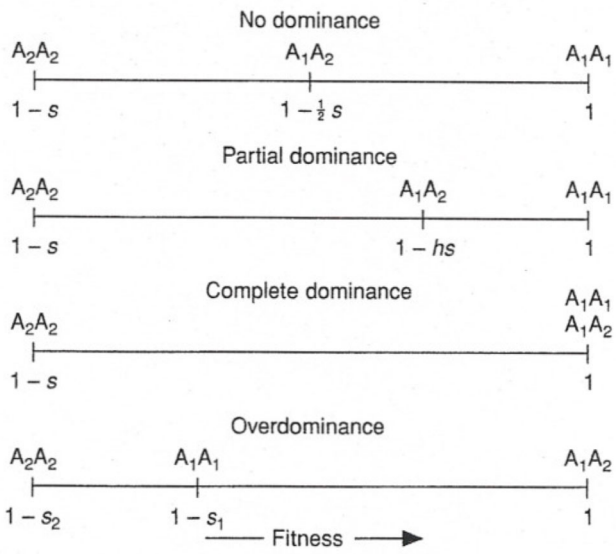
Source: T. Dobzhansky, *Genetics and the Origin of Species*, 3d ed., rev. Columbia University Press, 1951.

Long-term effects of mutation

$$p = p_0\, e^{-(10^4)\times(10^{-5})} = p_0 e^{-0.1} = 0.904\, p_0$$



Selection



Selection

	Genotypes			
	A_1A_1	A_1A_2	A_2A_2	*Total*
Initial frequencies	p^2	$2pq$	q^2	1
Coefficient of selection	0	0	s	
Fitness	1	1	$1 - s$	
Gametic contribution	p^2	$2pq$	$q^2(1 - s)$	$1 - sq^2$

$$q_1 = \frac{q^2(1-s)+pq}{1-sq^2} \qquad q_1 = \frac{q - sq^2}{1-sq^2}$$

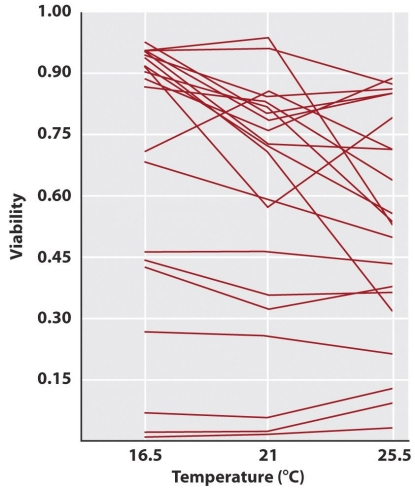
$$\Delta q = q_1 - q \qquad \Delta q = -\frac{sq^2(1-q)}{1-sq^2}$$

Selection

Initial frequencies and fitness of genotypes			New gene frequency	Change of gene frequency
A_1A_1 p^2	A_1A_2 $2pq$	A_2A_2 q^2	q_1	$\Delta q = q_1 - q$
(1) 1	$1-\frac{1}{2}s$	$1-s$	$\frac{q-\frac{1}{2}sq-\frac{1}{2}sq^2}{1-sq}$	$-\frac{\frac{1}{2}sq(1-q)}{1-sq}$
(2) 1	$1-hs$	$1-s$	$\frac{q-hspq-sq^2}{1-2hspq-sq^2}$	$-\frac{spq[q+h(p-q)]}{1-2hspq-sq^2}$
(3) 1	1	$1-s$	$\frac{q-sq^2}{1-sq^2}$	$-\frac{sq^2(1-q)}{1-sq^2}$
(4) $1-s$	$1-s$	1	$\frac{q-sq+sq^2}{1-s(1-q^2)}$	$+\frac{sq^2(1-q)}{1-s(1-q^2)}$
(5) $1-s_1$	1	$1-s_2$	$\frac{q-s_2q^2}{1-s_1p^2-s_2q^2}$	$+\frac{pq(s_1p-s_2q)}{1-s_1p^2-s_2q^2}$

Fitness

Viability, e.g. survival from egg to adult at three different temperatures.



Formal description (1)

Genotype	*A/A*	*A/a*	*a/a*
Frequency (newborns)	p^2	$2pq$	q^2

$$p^2+2pq+q^2=(p+q)^2=1.0$$

Genotype	*A/A*	*A/a*	*a/a*
Frequency (adults)	$p^2 W_{A/A}$	$2pq\,W_{A/a}$	$q^2 W_{a/a}$

Population's mean fitness $\overline{W} = p^2W_{A/A} + 2pqW_{A/a} + q^2W_{a/a}$

Formal description (2)

Genotype	*A/A*	*A/a*	*a/a*
Frequency (adults)	$p^2\frac{W_{A/A}}{\overline{W}}$	$2pq\frac{W_{A/a}}{\overline{W}}$	$q^2\frac{W_{a/a}}{\overline{W}}$

$$p' = A/A + \tfrac{1}{2}A/a = p^2\frac{W_{A/A}}{\overline{W}} + pq\frac{W_{A/a}}{\overline{W}} = p\frac{pW_{A/A}+qW_{A/a}}{\overline{W}}$$

Mean fitness of all individuals carrying the A-allele $\longrightarrow \overline{W}_A$

$$p' = p\frac{\overline{W}_A}{\overline{W}}$$

Formal description (3)

Change in frequency

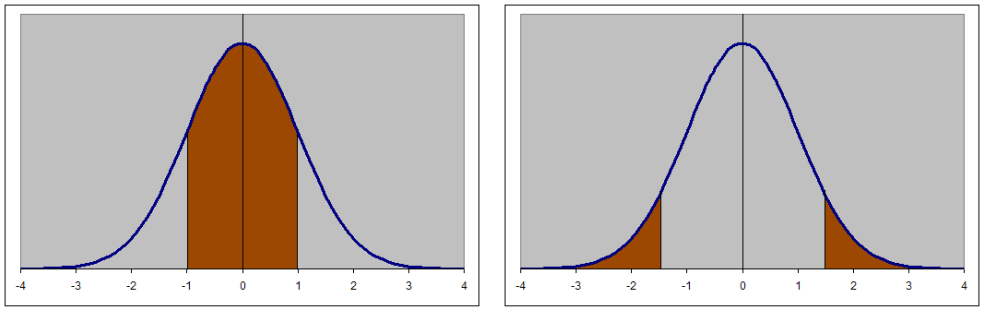
$$\Delta p = p' - p = p\frac{\overline{W}_A}{\overline{W}} - p = \frac{p(\overline{W}_A - \overline{W})}{\overline{W}}$$

$$\overline{W} = p\overline{W}_A + q\overline{W}_a$$

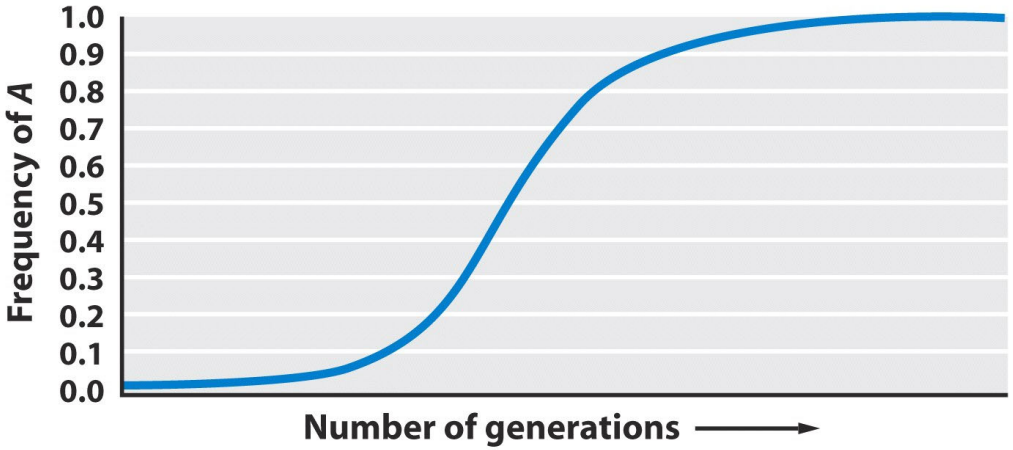
$$\Delta p = \frac{pq(\overline{W}_A - \overline{W}_a)}{\overline{W}}$$

No selection means no selection

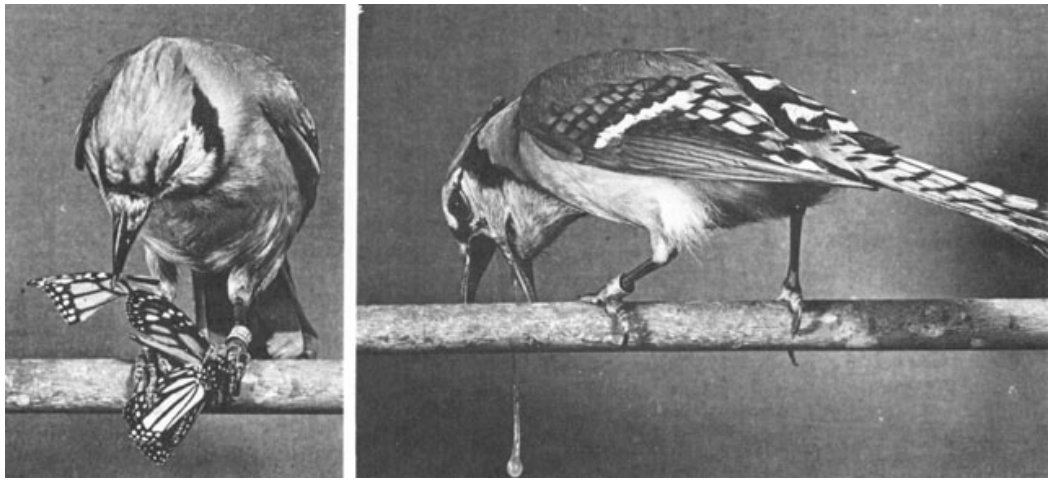
Stabilizing selection Disrupting selection



Rate of change in allele frequency

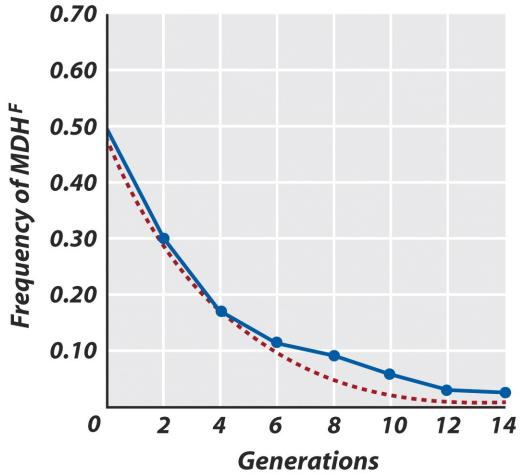


Frequency-dependent fitness



Rapid change of allele frequency

$W_{A/A} = 1.00$
$W_{A/a} = 0.75$
$W_{a/a} = 0.40$



MDH = malic dehydrogenase

Number of generation required

New allele frequency

$$q_1 = \frac{q_0}{1+q_0}$$

$$q_2 = \frac{q_1}{1+q_1} = \frac{q_0}{1+2q_0}$$

$$q_t = \frac{q_0}{1+tq_0}$$

Number of generations

$$t = \frac{q_0 - q_t}{q_0 q_t} = \frac{1}{q_t} - \frac{1}{q_0}$$

Naïve understanding of selection?

Selection against rare recessives

Freq. of albinism genotype = 1/20,000
Freq. of albinism allele, q_0 = 1/141

How many generations are needed to reduce albinism to half of its present value, i.e. 1/40,000 (q_t = 1/200)?

$$t = \frac{1}{q_t} - \frac{1}{q_0}$$ t = 1/200 – 1/141 = 59 Gen. ≈ 1500 years

Balance between mutation and selection

$$\Delta q = up_0 - vq_0$$

(2) 1 $1 - hs$ $1 - s$ $\frac{q - hspq - sq^2}{1 - 2hspq - sq^2}$ $-\frac{spq[q + h(p-q)]}{1 - 2hspq - sq^2}$

$$up - vq = \frac{spq[q + h(p-q)]}{1 - 2hspq - sq^2}$$

Load

Genetic load caused by a recessive allele in one locus

	Genotypes			
	A_1A_1	A_1A_2	A_2A_2	*Total*
Initial frequencies	p^2	$2pq$	q^2	1
Coefficient of selection	0	0	s	
Fitness	1	1	$1 - s$	
Gametic contribution	p^2	$2pq$	$q^2(1 - s)$	$1 - sq^2$

Genetic death: $1 - L$

At equilibrium: L=u (recessive), L=2u (dominant)

Polymorphism

Heterozygote advantage

Frequency-dependent selection

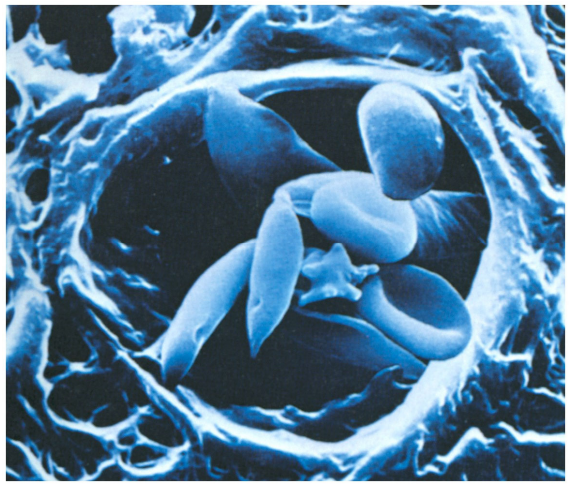
Heterogeneous environment

Transition

Neutral mutation

Heterozygote advantage

Sickle-cell anemia



Lewontin & Hubby, Hubby & Lewontin

According to Lewontin and Hubby (1966):

Average per locus heterozygosity = 12%

Proportion of polymorphic loci = 30%

?

Heterozygote advantage

Hetrozygote advantage

$$\Delta q = \frac{pq(s_1 p - s_2 q)}{1 - s_1 p^2 - s_2 q^2}$$

$$\frac{p}{q} = \frac{s_2}{s_1}$$

$$q = \frac{s_1}{s_1 + s_2}$$

Load $L = \frac{s_1 s_2}{s_1 + s_2}$ $L = s_1 p = s_2 q$

Chapter 2: Extra emphasis

Selection

Neutral mutation theory

Selection? Of what? On what?

In population genetics

"selection" = "natural selection"

"selected" = "differential fitness is observed"

"fitness" = "contribution to the next generation's gene pool"

Selection? Of what?

Selection at the

Gene level?

Individual level?

Group level?

Selection? Of what?

Selection at the

Gene level?

Individual level? Individuals assumed to have the same genotype?

Group level?

Selection? On what?

Selection on

Body size? Weight? Height?

Beauty? Colorfulness?

Life expectancy?

Selection on Fitness

Fitness in the Darwinian sense of the word is a combination of fertility and viability, i.e.

Fitness = fertility x viability

Often expressed as relative to the population's mean

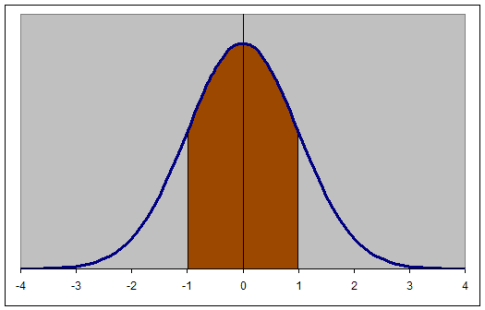
A small example

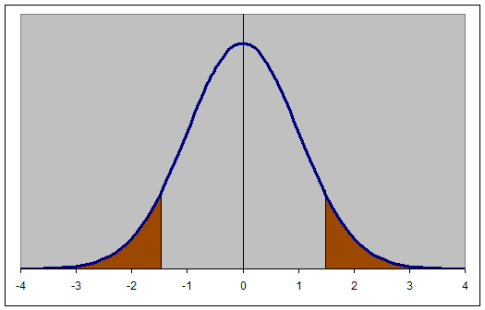
Think of an individual (or genotype)

	Individual		
	1 (AA)	2 (Aa)	3 (aa)
# of offspring	100	90	80
% survival of offspring	80%	90%	100%
# of offspring reaching maturity	80	81	80

No selection means no selection

Stabilizing selection Disrupting selection





Kimura's argument

If $s_1 = s_2 = s$; then $L = s/2$

If $s = 0.01$, then $L = 0.005$

$$L = \frac{s_1 s_2}{s_1 + s_2}$$

In there are *n* overdominant loci with multiplicative effect on fitness, then selective elimination per individual = $1 - e^{-sn/2}$

Let $s = 0.01$ and $n = 2000$, then $1 - e^{-sn/2} \approx 0.9999546$

1.0/0.0000454 = 22026 offspring / individual

is needed to maintain the population size

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Falconer & Mackay (1996)
Chapter 3

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Chapter 3: Long summary (1)

We have now to consider the last of the agencies through which gene frequencies can be changed. This is the dispersive process, which differs from the systematic processes in being random in direction, and predictable only in amount.

Chapter 3: Long summary (2)

In order to exclude this process from the previous discussions we have postulated always a 'large' population, and we have seen that in a large population the gene frequencies are inherently stable. That is to say, [in a large population, and] in the absence of migration, mutation, or selection, the gene and genotype frequencies remain unaltered from generation to generation.

Chapter 3: Long summary (3)

This property of stability does not hold in a small population, and the gene frequencies are subject to random fluctuations arising from the sampling of gametes. The gametes that transmit genes to the next generation carry a sample of the genes in the parent generation, and if the sample is not large the gene frequencies are liable to change between one generation and the next. This random change of gene frequency is the dispersive process.

Chapter 3: Long summary (4)

In this chapter and the next we shall be concerned with the effects of the dispersive process on gene frequencies. If the deductions to be made about gene frequencies seem to be rather remote from reality, it should be remembered that the properties of a population with respect to any genetically determined character depend on gene frequencies. The conclusions are therefore fully relevant to quantitative characters to be dealt with in later chapters.

Chapter 3: Long summary (5)

There are, broadly speaking, four consequences of the dispersive process, which are to be explained and quantified in this chapter. These are not really different consequences, but rather different ways in which the consequences [i.e. patterns] may be seen. They are:

1. Random drift
2. Differentiation between sub-populations
3. Uniformity within sub-populations
4. Increased homozygosity

Chapter 3: Long summary (6)

There are two different ways of looking at the dispersive process and of deducing its consequences.

One is to regard it as a sampling process and to describe it in terms of sampling variance.

The other is to regard it as an inbreeding process and describe it in terms of the genotypic changes resulting from matings between related individuals.

Chapter 3: Extra emphasis

Consequences of small population size

As processes and patterns

Inbreeding and its interpretation

HWM: Summary

In the absence of a number of processes, the pattern of allele and genotype frequencies is constant from generation to generation.

Sampling variance
Random mating
Selection
Migration
Mutation

Two sides of the same coin

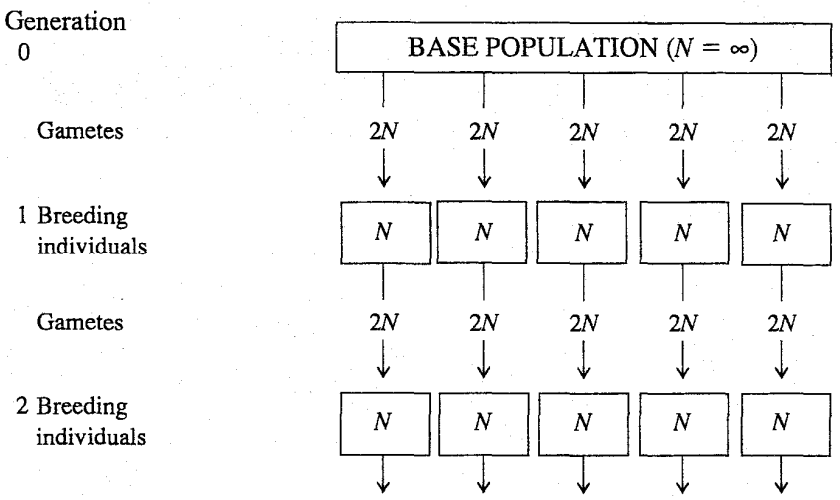
Sampling variance
Random mating

} Process

Random drift
Differentiation between sub-populations
Uniformity within sub-population
Increased homozygosity

} Pattern

The idealized population



Inbreeding as a process

"Inbreeding" is defined as
the process of
two identical copies of one ancestral allele
uniting with each other
in a gamete of a descendant.

Inbreeding as a pattern

"Inbreeding" is defined as
the presence of
two identical copies of the same ancestral allele
at one locus of a descendant
(i.e. identity [identical] by descent, IBD).

Inbreeding as a measurement

"inbreeding coefficient":

The probability of two alleles at one locus being IBD.

The average probability of IDB at all loci of one individual;

OR

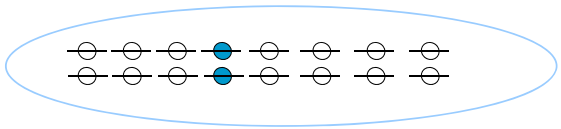
The average probability of IDB in one locus in all individuals.

What does F=1/8 mean?

If we look at many loci in one individual:

- Proportion of loci that are identical by descent in this individual

One individual – many loci

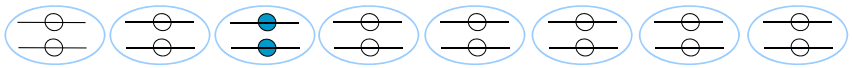


What does F=1/8 mean?

If we look at one locus over many individuals:

- Proportion individuals that are identical by descent for this locus

One locus – many individuals



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Falconer & Mackay (1996)
Chapter 4

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Chapter 4; Long summary (1)

In order to simplify the description of the dispersive process we confined our attention in the last chapter to an idealized population, and to do this we had to specify a number of restrictive conditions, which could seldom be fulfilled in real populations. The purpose of this chapter is to adapt the conclusions of the last chapter to situations in which the conditions imposed do not hold; in other words, to remove the more serious restrictions and bring the conclusions closer to reality.

Chapter 4; Long summary (2)

The restrictive conditions were of two sorts, one sort being concerned with the breeding structure of the population and the other excluding mutation, migration, and selection from consideration. We shall first describe the effects of deviations from the idealized breeding structure, and then consider the outcome of the dispersive process when mutation, migration, or selection are operating at the same time.

Chapter 4: Extra emphasis

Effective population size

Lack of a general formula for calculating N_e

Inbreeding increase, $\Delta F=1/(2N)$

N for an ideal population is called effective population size, N_e

N_e for a population is the size of an ideal population that gives the same inbreeding increase as the population under study (with actual size N)

Effective population size

There is no general equation for all situation, however,

$$\frac{1}{N_e}=\frac{1}{16M}\left[2+\sigma^2_{mm}+\frac{2M}{F}\sigma_{mm,mf}+(\frac{M}{F})^2\sigma^2_{mf}\right]$$
$$+\frac{1}{16F}\left[2+(\frac{M}{F})^2\sigma^2_{fm}+\frac{2F}{M}\sigma_{fm,ff}+\sigma^2_{ff}\right]$$

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Chapter 5

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Chapter 5: Long summary (1)

In the two preceding chapters the genetic properties of small populations were described by reference to the effective number of breeding individuals; and expressions were derived, in terms of the effective number, by means of which the state of dispersion of the gene frequencies could be expressed as the coefficient of inbreeding.

The coefficient of inbreeding, which is the probability of any individual being an identical homozygote, was deduced from the population size and the specified breeding structure. It expressed, therefore, the average inbreeding coefficient of all individuals of a generation.

Chapter 5: Long summary (2)

When pedigrees of the individuals are known, however, the coefficient of inbreeding can be more conveniently deduced directly from the pedigrees, instead of indirectly from the population size. This method has several advantages in practice. Knowledge is often required of the inbreeding coefficient of individuals, rather than of the generation as a whole, and this is what the calculation from pedigrees yields In domestic animals, some individuals often appear as parents in two or more generations, and this overlapping of generations causes no trouble when the pedigrees are known.

Chapter 5: Long summary (3)

The first topic for consideration in this chapter is therefore the computation of inbreeding coefficients from pedigrees. The second topic concerns regular systems of close inbreeding. When self-fertilization is excluded, the rate of inbreeding expressed in terms of the population size is only an approximation, and the approximation is not close enough if the population size is very small. Under systems of close inbreeding, therefore, the rate of inbreeding must be deduced differently, and this is best done also by consideration of the pedigrees.

Chapter 5: Long summary (4)

When the coefficient of inbreeding is deduced from the pedigrees of real populations, it does not necessarily describe the state of dispersion of the gene frequencies. It is essentially a statement about the pedigree relationships, and its correspondence with the state of dispersion is dependent on the absence of the processes that counteract dispersion, in particular on selection being negligible. We were able to use the coefficient of inbreeding as a measure of dispersion in the preceding chapters because the necessary conditions for its relationship with the variance of gene frequencies were specified.

Chapter 5: Extra emphasis

Similar concepts

Different measurement methods

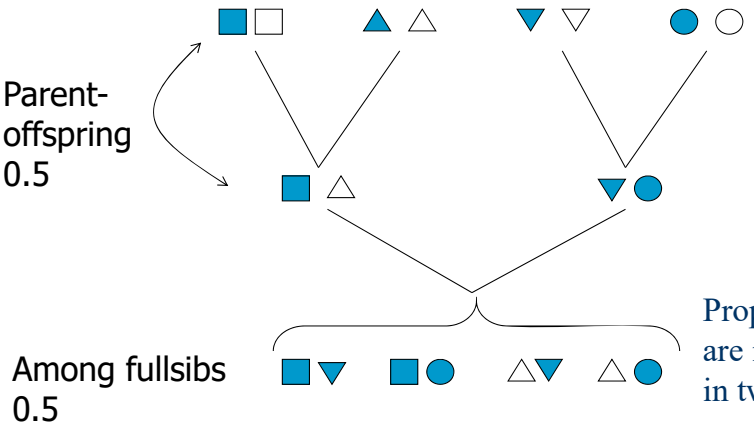
Kärt barn har tusen namn

Coancestry = Coefficient of kinship = consanguinity

The coancestry of any two individuals is identical with the inbreeding coefficient of their progeny if they were mated.

The coancestry of two individuals is the probability that two gametes taken at random, one from each, carry alleles that are identical by descent.

Additive genetic relationship



Measuring the inbreeding coefficient

There are two methods of calculating "inbreeding coefficient":

An approximate method from effective population size;

AND

An exact method from the pedigree information.

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Chapter 6

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Chapter 6: Long summary (1)

It will be obvious, to biologists and laymen alike, that the sort of variation discussed in the foregoing chapters embraces but a small part of the naturally occurring variation.

Chapter 6: Long summary (2)

One has only to consider one's fellow men and women to realize that they all differ in countless ways, but that these differences are nearly all matters of degree and seldom present clear-cut distinctions attributable to the segregation of single genes.

If, for example, we were to classify individuals according to their height, we could not put them into groups labeled 'tall' and 'short', because there are all degrees of height and a division into classes would be purely arbitrary.

Chapter 6: Long summary (3)

Variation of this sort, without natural discontinuities, is called continuous variation, and characters that exhibit it are called quantitative characters or metric characters, because their study depends on measurement instead of on counting.

The genetic principles underlying the inheritance of metric characters are basically those of population genetics outlined in the previous chapters. But since the segregation of the genes concerned cannot be followed individually, new methods of study are needed and new concepts have to be introduced.

Chapter 6: Long summary (4)

The branch of genetics concerned with metric characters is called quantitative genetics or biometrical genetics.

The importance of this branch of genetics need hardly be stressed; most of the characters of economic value to plant and animal breeders are metric characters, and most of the changes concerned in micro-evolution are changes of metric characters.

It is therefore in this branch that genetics has its most important application to practical problems and also its most direct bearing on evolutionary theory.

Chapter 6: Long summary (5)

How does it come about that the intrinsically discontinuous variation caused by genetic segregation is translated into the continuous variation of metric characters?

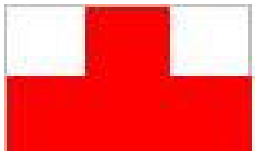
There are two reasons one is the simultaneous segregation of many genes affecting the character, and the other is the superimposition of truly continuous variation arising from non-genetic causes.

Chapter 6: Extra emphasis

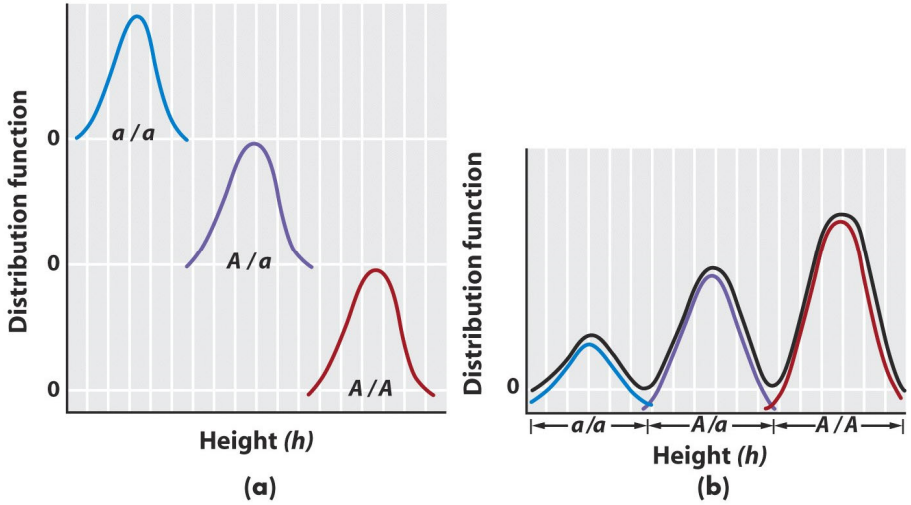
Historical Background

Fisher (1918)	Population Genetics
Wright (1921)	
Haldane (1924)	Quantitative Genetics
Lush (1935) Iowa	Quantitative Genetics
Ivar Johansson (1940's)	
Falconer (1952) Edinburgh	
Henderson (1953) Cornell	Animal Breeding

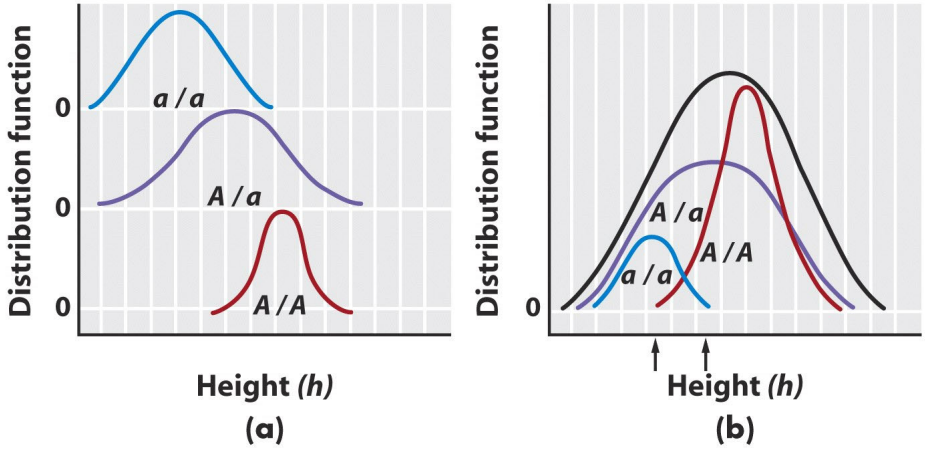
Nature of qualitative variance

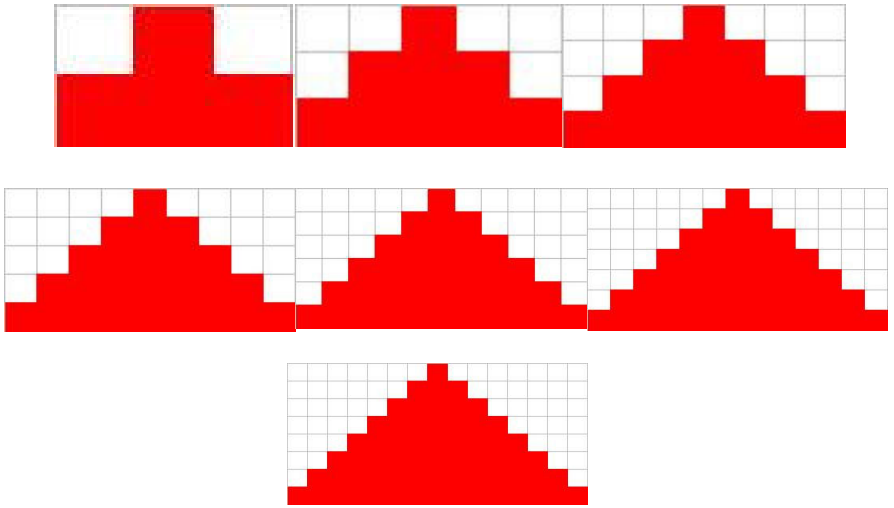


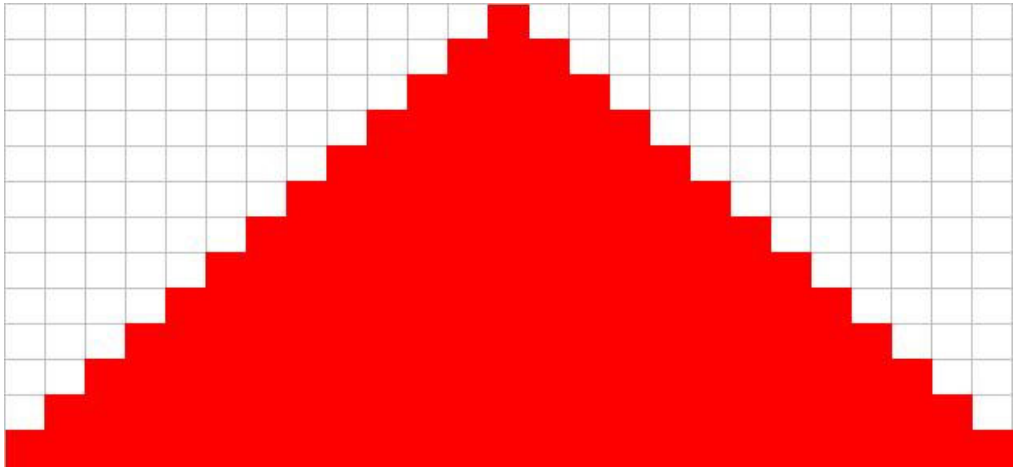
Nature of quantitative variation



Nature of quantitative variation







How many genes? One example!

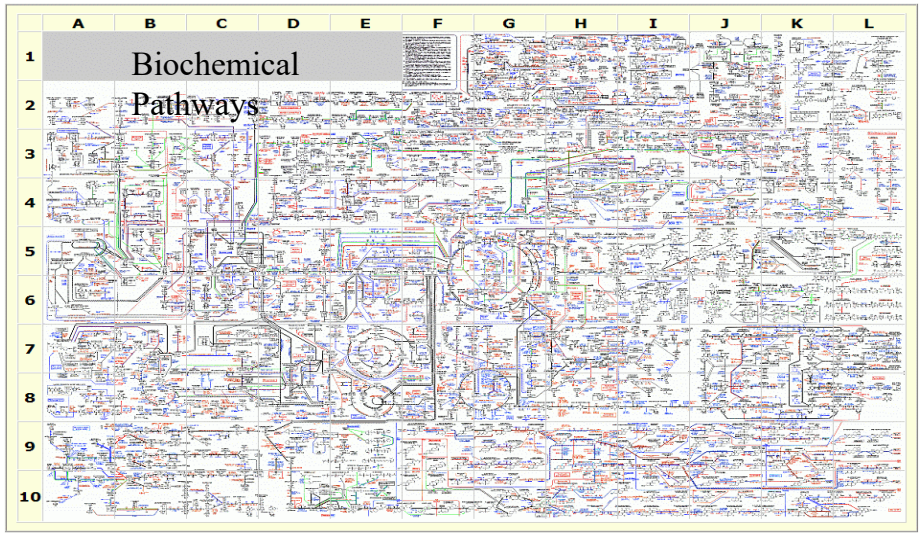
Two pig lines (growth, meat quality)
Phosphorus levels in diet (adequate, deficient, repletion)
RNA samples, oligonucleotide arrays, (over 13000 unique genes)

	Liver	Muscle
Differential expression		
between sire lines	103	339
Dietary treatment	122	18
Interaction	88	31

Grapes et al. (2005)

J

How many genes?



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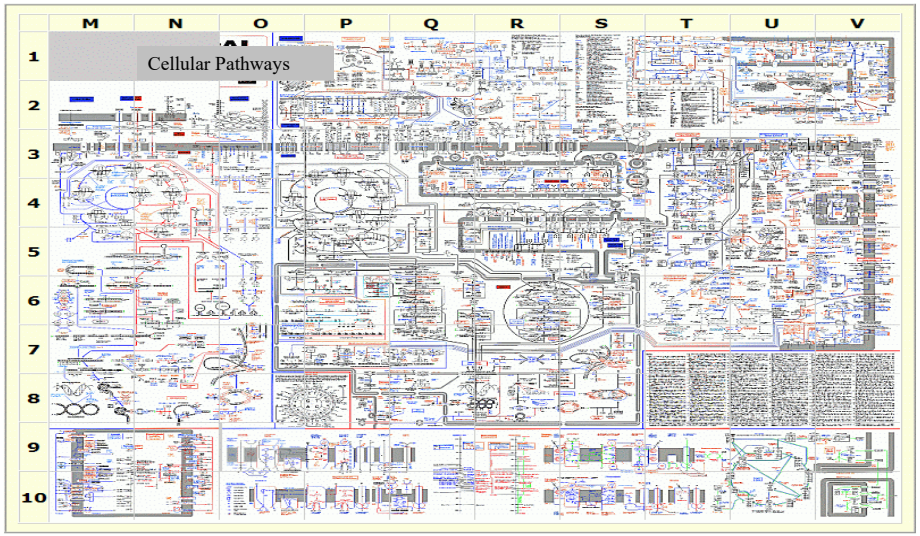
How many genes?

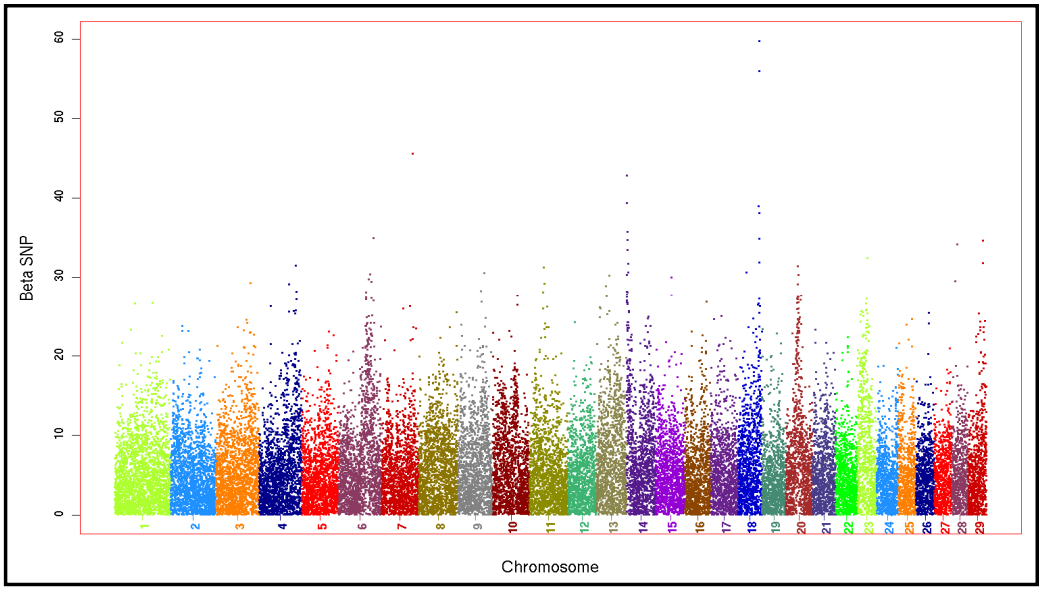


The Infinitesimal Model

Assumptions

- Large number of loci;
- Each locus is unique;
- Two alleles in each locus;
- Additive mode of gene action;
- Equal average effect for all loci within generations;
- No linkage; and
- Equal external effect on all loci within and between generations.
- …

SNP effects



Basic QG model

Additive value

Genotypic value

Dominance deviation

$G = A + D + I$

Interaction deviation

G = A + D + I

What is D?

Interaction of 2 alleles within one locus

What is I?

Interaction of ≥2 alleles across ≥ 2 loci

Interaction deviation

Extension to 2 loci

$$G = G_X + G_Y + I_{XY}$$

$$G_X = A_X + D_X \qquad G_Y = A_Y + D_Y$$

$$I_{XY} = A_XA_Y + A_XD_Y + D_XA_Y + D_XD_Y$$

Basic QG model

$$G = A + D$$

$$V_G = V_A + V_D$$

Let's extend this to more than one locus

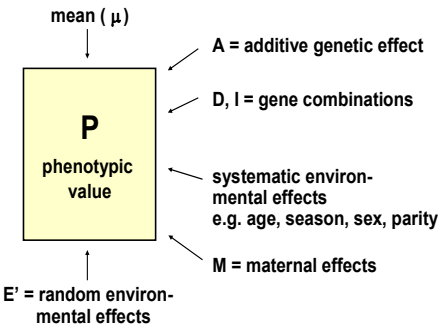
$$\Sigma G_i = \Sigma A_i + \Sigma D_i + ???$$

$$V_G = V_A + V_D + V_{AA} + V_{AD} + V_{DD} + V_{AAA} + \ldots$$

J

"Central Dogma" of AB & QG

$P = G + E$
$G = A + D + I$
$E = \ldots$



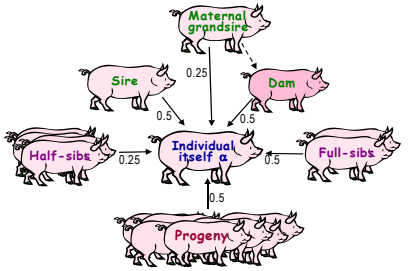
Picture: Strandberg & Malmfors (2003)

$V_P = V_G + V_E$
$V_G = V_A + V_D + V_I$
$V_E = \ldots$

(Ignored: Corvariances between G1 & G2, between G & E, ..., interactions between G & E, between ...)

Common genes

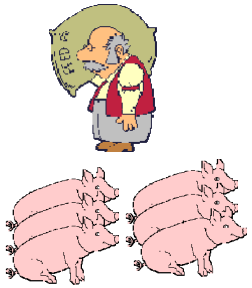
Individuals sharing "genes" resemble each other.



Picture: Strandberg & Malmfors (2003)

Common environment

Individuals sharing environment resemble each other.



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Falconer & Mackay (1996)
Chapter 7

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Chapter 7: Long summary (1)

We have seen in the early chapters that the genetic properties of a population are expressible in terms of the allele frequencies and genotype frequencies.

In order to deduce the connection between these on the one hand and the quantitative differences exhibited in a metric character on the other, we must introduce a new concept, the concept of value, expressible in the metric units by which the character is measured.

Chapter 7: Long summary (2)

The value observed when the character is measured on an individual is the phenotypic value of that individual. All observations, whether of means, variances, or covariances, must clearly be based on measurements of phenotypic values.

Chapter 7: Long summary (3)

In order to analyse the genetic properties of the populations we have to divide the phenotypic value into component parts attributable to different causes.

Explanation of the meanings of these components is our chief concern in this chapter, though we shall also be able to find out how the population mean is influenced by the array of gene frequencies.

Chapter 7: Long summary (4)

The first division of phenotypic value is into components attributable to the influence of genotype and environment. The genotype is the particular assemblage of genes possessed by the individual, and the environment is all the non-genetic circumstances that influence the phenotypic value.

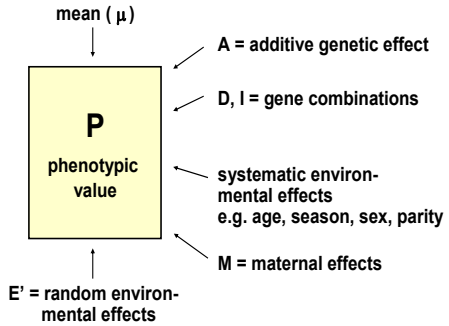
Inclusion of all non-genetic circumstances under the term 'environment' means that the genotype and the environment are by definition the only determinants of phenotypic value.

"Central Dogma" of AB & QG

$P = G + E$

$G = A + D + I$

$E = \ldots$



$V_P = V_G + V_E$

$V_G = V_A + V_D + V_I$

$V_E = \ldots$

Picture: Strandberg & Malmfors (2003)

(Ignored: Corvariances between G1 & G2, between G & E, ..., interactions between G & E, between ...)

Chapter 7: Long summary (5)

The two components of value associated with genotype and environment are the genotypic value and the environmental deviation.

We may think of the genotype conferring a certain value on the individual and the environment causing a deviation from this, in one direction or the other.

Chapter 7: Extra emphasis

Basic QG model

Genotype	A_2A_2		A_2A_1	A_1A_1
Phenotypic value	6	10	12	14
Genotype frequency	q^2		2pq	p^2
Genotypic value	-a	0	d	+a
Genotypic value	-4		2	+4

Population mean (one locus)

Genotype			
A_1A_1	p^2	+a	P^2a
A_1A_2	2pq	d	2pqd
A_2A_2	q^2	-a	$-q^2a$
		Mean* =	a (p-q) + 2dpq

* Expressed as deviation from the phenotypic mean of the two homozygotes

Population mean (one locus)

Genotype			
A_1A_1	p^2 0.9*0.9=0.81	+a 4	P^2a 0.81*4=3.24
A_1A_2	2pq 2*0.9*0.1=0.18	d 2	2pqd 0.18*2=0.36
A_2A_2	q^2 0.1*0.1=0.01	-a -4	$-q^2a$ 0.01*(-4)=-0.04
		Mean* =	a (p-q) + 2dpq 3.24+0.36-0.04=3.56

* Expressed as deviation from the phenotypic mean of the two homozygotes, e.g. 10

Population mean (one locus)

Genotype			
A_1A_1	p^2 0.6*0.6=0.36	+a 4	P^2a 0.36*4=1.44
A_1A_2	2pq 2*0.6*0.4=0.48	d 2	2pqd 0.48*2=0.96
A_2A_2	q^2 0.4*0.4=0.16	-a -4	$-q^2a$ 0.16*(-4)=-0.64
		Mean* =	a (p-q) + 2dpq 1.44+0.96-0.64=1.76

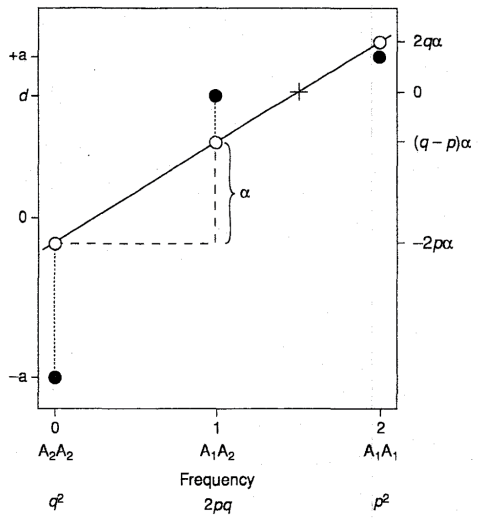
* Expressed as deviation from the phenotypic mean of the two homozygotes, e.g. 10

Average effect of alleles

Type of gamete	Values and frequencies of genotypes produced			Mean value of genotypes produced	Population mean to be deducted	Average effect of alleles
	A_1A_1	A_1A_2	A_2A_2			
	a	d	-a			
A_1	p	q		Pa + qd	-[a (p-q) + 2dpq]	q [a + d (q-p)]
A_2		q	p	-qa + pd	-[a (p-q) + 2dpq]	-p [a + d (q-p)]

Dominance deviation

	Genotypes		
	A_1A_1	A_1A_2	A_2A_2
Frequency	p^2	2pq	q^2
Assigned values	a	d	-a
Deviation from population mean			
Genotypic mean	2q (a – pd)	a (q-p) + d (1-2pq)	-2p (a + qd)
	2q (α – qd)	(q-p) α – 2pqd	-2q (α – pd)
Breeding value	2q α	(q-p)α	-2pα
Dominance deviation	$-2q^2d$	2pqd	$-2p^2d$



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Falconer & Mackay (1996)
Chapter 8

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Book's summary

The genetics of a metric character centres round the study of its variation, for it is in terms of variation that the primary genetic questions are formulated.

The basic idea in the study of variation is its partitioning into components attributable to different causes. The relative magnitude of these components determines the genetic properties of the population.

In this chapter we shall consider the nature of these components and how the genetic components depend on the allele frequency.

The amount of variation is measured and expressed as the variance: when values are expressed as deviations from the population mean the variance is simply the mean of the squared values.

The phenotypic variance can be partitioned into components attributable to different causes. These components we shall call *causal components* of variance, and denote them as before by the symbol *V*.

This chapter has shown how the phenotypic variance of a genetically variable population can be partitioned into four components, two genetic and two environmental. The data needed to do this are of three different kinds, each making a partition into two parts, but in different ways.

Data needed	*Partition made*	*Ratio estimated*
Resemblance between relatives	$(V_A):(V_{NA} + V_{Eg} + V_{Es})$	heritability, V_A/V_P
Genetically uniform group	$(V_A + V_{NA}):(V_{Eg} + V_{Es}) = (V_G):(V_E)$	degree of genetic determination, V_G/V_P
Multiple measurements	$(V_G + V_{Eg}):V_{Es}$	repeatability $(V_G + V_{Eg})/V_P$
All three	$V_A:V_{NA}:V_{Eg}:V_{Es}$	

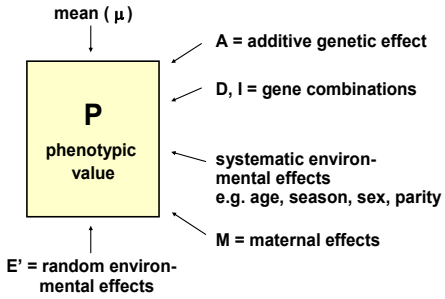
J

"Central Dogma" of AB & QG

P = G + E

G = A + D + I

E = . . .



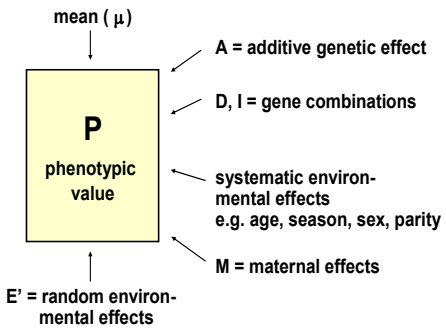
Picture: Strandberg & Malmfors (2003)

"Central Dogma" of AB & QG

$P = G + E$

$G = A + D + I$

$E = \ldots$



$V_P = V_G + V_E$

$V_G = V_A + V_D + V_I$

$V_E = \ldots$

(Ignored: Corvariances between G1 & G2, between G & E, ..., interactions between G & E, between ...)

Picture: Strandberg & Malmfors (2003)

Dominance deviation

	Genotypes		
	A_1A_1	A_1A_2	A_2A_2
Frequency	p^2	2pq	q^2
Assigned values	a	d	-a
Deviation from population mean			
Genotypic mean	2q (a – pd)	a (q-p) + d (1-2pq)	-2p (a + qd)
	2q (α – qd)	(q-p) α – 2pqd	-2q (α – pd)
Breeding value	2q α	(q-p)α	-2pα
Dominance deviation	$-2q^2d$	2pqd	$-2p^2d$

Variance and covariance

Variance = Mean squared deviation

Covariance = Mean cross-product deviation

Additive variance

	Genotypes		
	A_1A_1	A_1A_2	A_2A_2
Frequencies	p^2	$2pq$	q^2
Assigned values	a	d	$-a$
Deviations from population mean:			
Genotypic value	$2q(a - pd)$	$a(q - p) + d(1 - 2pq)$	$-2p(a + qd)$
	$2q(\alpha - qd)$	$(q - p)\alpha + 2pqd$	$-2p(\alpha + pd)$
Breeding value	$2q\alpha$	$(q - p)\alpha$	$-2p\alpha$
Dominance deviation	$-2q^2d$	$2pqd$	$-2p^2d$

$$V_A = (2p\,\alpha)^2\, q^2 + ((q\text{-}p)\,\alpha\,)^2\, 2pq + (-2p\,\alpha)^2\, q^2$$

Dominance variance

	Genotypes		
	A_1A_1	A_1A_2	A_2A_2
Frequencies	p^2	$2pq$	q^2
Assigned values	a	d	$-a$
Deviations from population mean:			
Genotypic value	$2q(a - pd)$	$a(q - p) + d(1 - 2pq)$	$-2p(a + qd)$
	$2q(\alpha - qd)$	$(q - p)\alpha + 2pqd$	$-2p(\alpha + pd)$
Breeding value	$2q\alpha$	$(q - p)\alpha$	$-2p\alpha$
Dominance deviation	$-2q^2d$	$2pqd$	$-2p^2d$

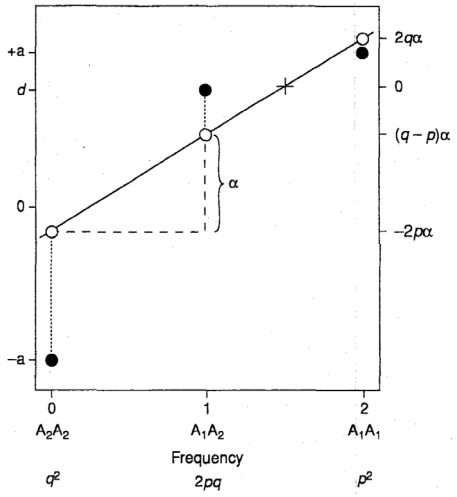
$$V_D = (-2q^2d)^2\, p^2 + (2pqd)^2\, 2pq + (2p^2d)^2\, q^2$$

Additive-dominance covariance

	Genotypes		
	A_1A_1	A_1A_2	A_2A_2
Frequencies	p^2	$2pq$	q^2
Assigned values	a	d	$-a$
Deviations from population mean:			
Genotypic value	$2q(a - pd)$	$a(q - p) + d(1 - 2pq)$	$-2p(a + qd)$
	$2q(\alpha - qd)$	$(q - p)\alpha + 2pqd$	$-2p(\alpha + pd)$
Breeding value	$2q\alpha$	$(q - p)\alpha$	$-2p\alpha$
Dominance deviation	$-2q^2d$	$2pqd$	$-2p^2d$

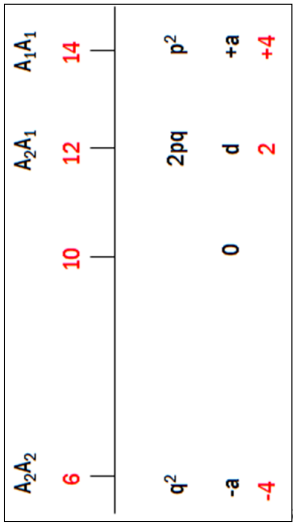
$$COV_{A,D} = -4p^2q^3\alpha d + 4p^2q^2(q-p)\alpha d + 4\, p^3q^2\alpha d = 0$$

Genotypic value, additive value, dominance deviation

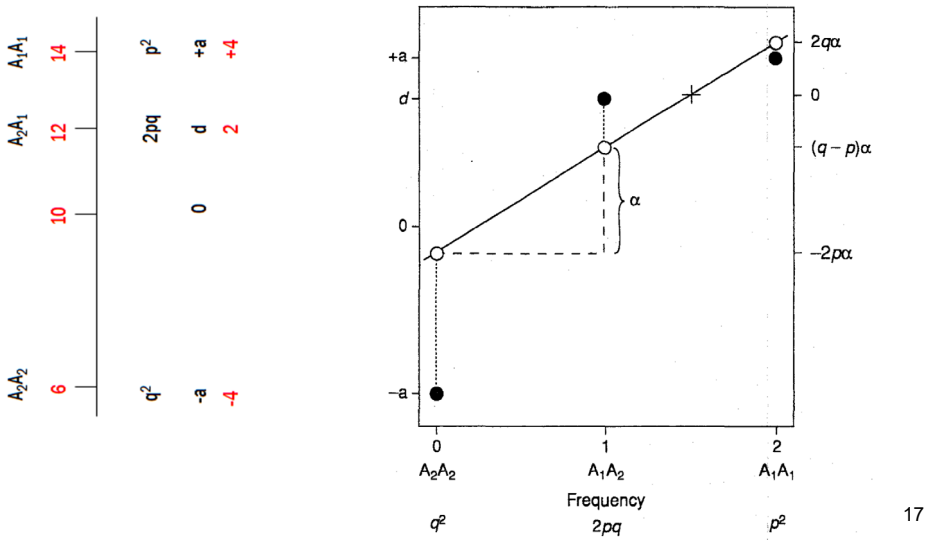


From Chapter 7

Genotype	A_2A_2		A_2A_1	A_1A_1
Phenotypic value	6	10	12	14
Genotype frequency	q^2		$2pq$	p^2
Genotypic value	-a	0	d	+a
Genotypic value	-4		2	+4



Genotypic value, additive value, dominance deviation



Additive variance

$V_A = (2q\ \alpha)^2\ p^2 + ((q\text{-}p)\ \alpha\ )^2\ 2pq + (-2p\ \alpha)^2\ q^2$

$V_A = 4p^2q^2\alpha^2 + 2pq(q\text{-}p)^2\alpha^2 + 4p^2q^2\alpha^2$

$V_A = 2pq\alpha^2(2pq + q^2 - 2pq + p^2 + 2pq)$

$V_A = 2pq\alpha^2(p^2 + 2pq + q^2)$

$V_A = 2pq\alpha^2$

$V_A = 2pq\ ([a + d\ (q\text{-}p)]^2$

Dominance variance

$V_D = (-2q^2d)^2\ p^2 + (2pqd)^2\ 2pq + (2p^2d)^2\ q^2$

$V_D = 4p^2q^4d^2 + 8p^3q^3d^2 + 4p^4q^2d^2$

$V_D = 4p^2q^2d^2\ (p^2 + 2pq + q^2)$

$V_D = (2pqd)^2$

Additive and dominance variance

$$V_A = 2pq\alpha^2 = 2pq\ ([a + d\ (q\text{-}p)]^2$$

$$V_D = (2pqd)^2$$

$$V_G = 2pq\ [a + d\ (q\text{-}p)]^2 + (2pqd)^2$$

Additive genetic variance

From Chapter 8: (EQ. 8.3a,8.3b)

One locus: $V_A = 2pq\,([a + d\,(q-p)]^2 = 2pq\alpha^2$

Many loci: $V_A = \Sigma\, 2p_iq_i\,([a_i + d_i\,(q_i-p_i)]^2 = \Sigma\, 2p_iq_i\alpha_i^2$

Additive genetic variance: consequences

Many loci: $V_A = \Sigma\, 2p_iq_i\,([a_i + d_i\,(q_i-p_i)]^2 = \Sigma\, 2p_iq_i\alpha_i^2$

How many loci?

The value of p, q, a, d for every loci?

Additive genetic variance: Assumptions

Many loci: $V_A = \Sigma\, 2p_iq_i\,([a_i + d_i\,(q_i-p_i)]^2 = \Sigma\, 2p_iq_i\alpha_i^2$

Random distribution of additive effects in all environments (e.g. No GxE)?

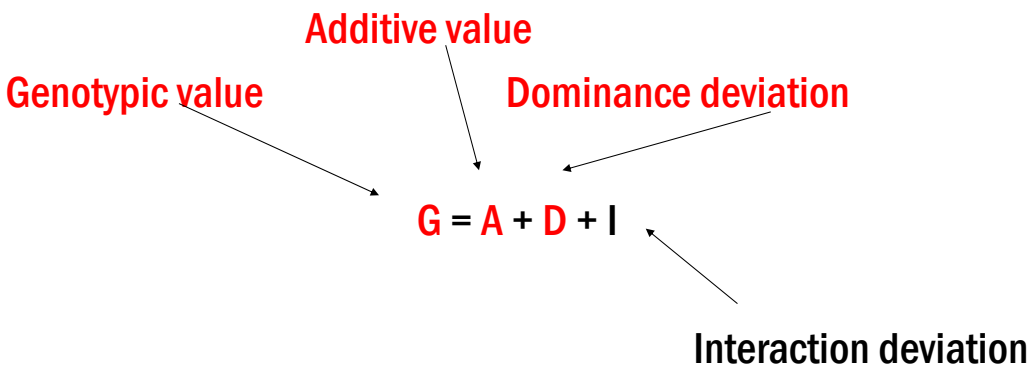
Additive genetic variance: How did we estimate V_A?

Many loci: $V_A = \Sigma\, 2p_iq_i\,([a_i + d_i\,(q_i-p_i)]^2 = \Sigma\, 2p_iq_i\alpha_i^2$

Did we account for non-nucleus genome (e.g. mitochondrial DNA)?

Did we account for non-DNA control mechanisms (e.g. epigenetic effects)?

Basic QG model



G = A + D + I

What is D?

Interaction of 2 alleles within one locus

What is I?

Interaction of ≥2 alleles across ≥ 2 loci

Interaction deviation

Extension to 2 loci

$$G = G_X + G_Y + I_{XY}$$

$$G_X = A_X + D_X \qquad G_Y = A_Y + D_Y$$

$$I_{XY} = A_XA_Y + A_XD_Y + D_XA_Y + D_XD_Y$$

Basic QG model

$$G = A + D$$

$$VG = VA + VD$$

Let's extend this to more than one locus

$$\Sigma G_i = \Sigma Ai + \Sigma Di + ???$$

$$V_G = V_A + V_D + V_{AA} + V_{AD} + V_{DD} + V_{AAA} + \ldots$$

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Falconer & Mackay (1996)
Chapter 9

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The resemblance between relatives is one of the basic genetic phenomena displayed by metric characters, and the degree of resemblance is a property of the character that can be determined by relatively simple measurements made on the population without special experimental techniques.

The degree of resemblance provides the means of estimating the amount of additive genetic variance, and it is the proportionate amount of additive variance (i.e., the heritability) that chiefly determines the best breeding method to be used for improvement.

An understanding of the causes of resemblance between relatives is therefore fundamental to the practical study of metric characters and to its application in animal and plant improvement.

In this chapter, therefore, we shall examine the causes of resemblance between relatives, and show in principle how the amount of additive variance can be estimated from the observed degree of resemblance.

The measurement of the degree of resemblance between relatives rests on the partitioning of the phenotypic variance in a different way, into components corresponding to the grouping of the individuals into families. These components can be estimated directly from the phenotypic values and for this reason we shall call them ***observational components*** of phenotypic variance, and denote them by the symbol σ^2 in order to keep the distinction clear.

Consider, for example, the grouping of individuals into families of full sibs. By the analysis of variance we can partition the total observed variance into two components, between (or among) groups and within groups. The between-group component is the variance of the 'true' means of the groups about the population mean, and the within-group component is the variance of individuals about the true mean of their group.

The true mean of a group is the mean that would be found if it were estimated without error from a very large number of individuals. Now, the resemblance between related individuals, i.e., between full sibs in the case under discussion, can be looked at either as similarity of individuals in the same group, or as difference between individuals in different groups.

The greater the similarity within the groups, the greater will be the difference between the groups. The degree of resemblance can therefore be expressed as the between-group component as a proportion of the total variance.

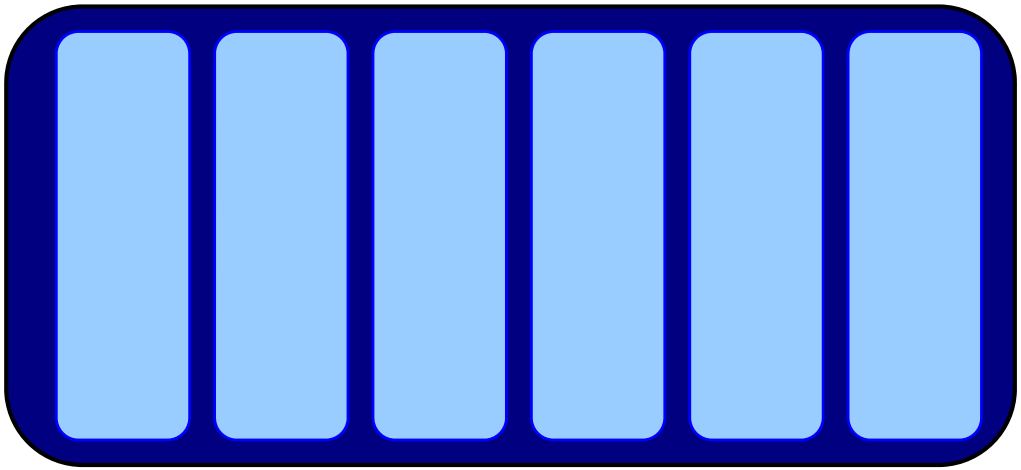
What goes on in Chapter 9

Two concepts

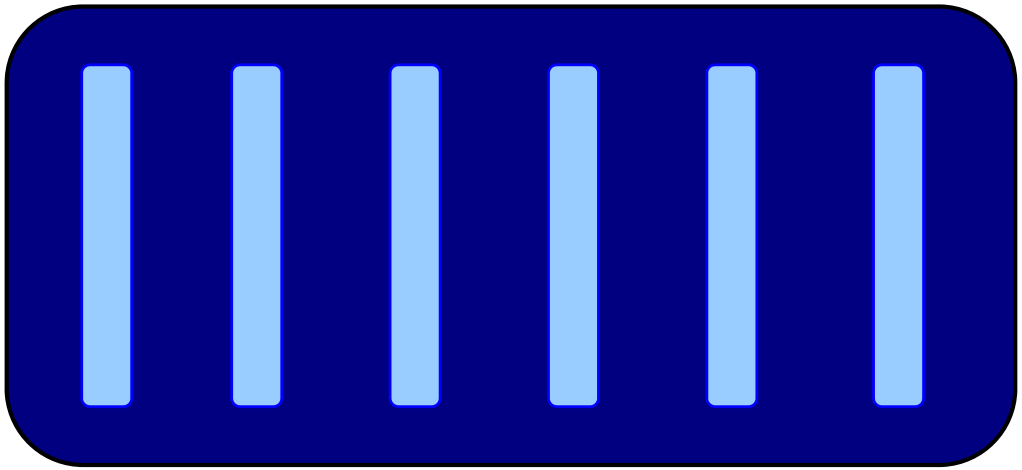
Within group / between group components of (co)variance

(Co)variance between P in one group and P in another group

Within & Between group (co)variance

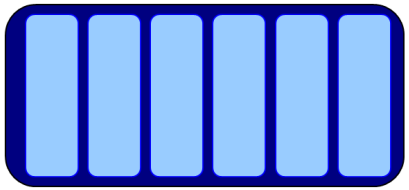


Within & Between group (co)variance



Within & Between group (co)variance

Within group variance:	Large	=	Within group covariance:	Small
Between group variance:	Small	=	Between group covariance:	Large



"Resemblance between related individuals … can be looked at either as similarity of individuals in the same group [within group covariance], or as difference between individuals in different groups[Between group variance]."

Within group covariance = Between group variance

Properties of variance

For non-independent X and Y

e.g. P = G + E

$$V_{(X+Y)} = V_X + V_Y + 2COV_{X,Y}$$

For independent X and Y with departure from linearity

e.g. P = G + E + I

$$V_{(X+Y)} = V_X + V_Y + V_{X,Y}$$

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Chapter 10

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The heritability of a metric character is one of its most important properties. It expresses, as we have seen, the proportion of the total variance that is attributable to differences of breeding values, and this is what determines the degree of resemblance between relatives.

A breeder's point of view?

But the most important function of the heritability in the genetic study of metric characters is its predictive role, expressing the reliability of the phenotypic value as a guide to the breeding value.

A breeder's point of view?

Only the phenotypic values of individuals can be directly measured, but it is the breeding value that determines their influence on the next generation.

A breeder's point of view?

Therefore if the breeder or experimenter chooses individuals to be parents according to their phenotypic values, his success in changing the characteristics of the population can be predicted only from a knowledge of the degree of correspondence between phenotypic values and breeding values.

This degree of correspondence is measured by the heritability.

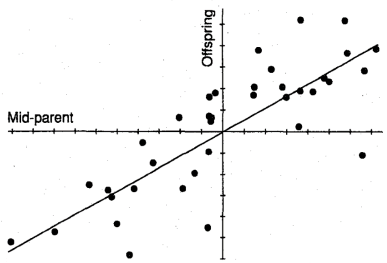
Heritability:

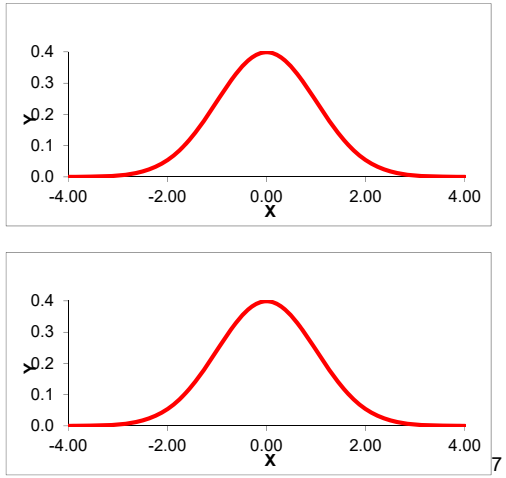
One word,

several meanings,

and numerous misunderstandings

Where does the word heritability come from?





Where does the word heritability come from?

$$h^2 + d^2 + e^2 = 1$$

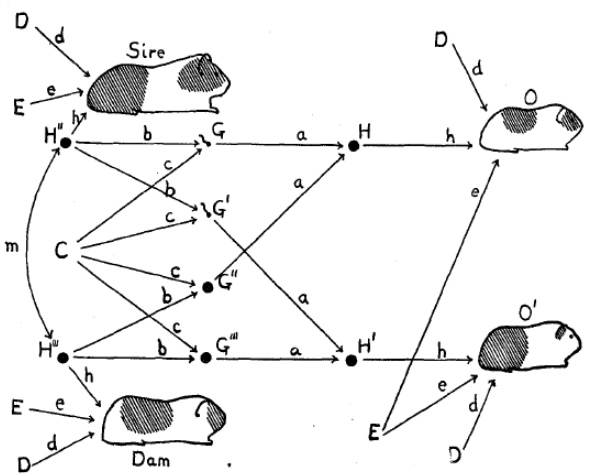


FIGURE 2.—A diagram illustrating the relations between two mated individuals and their progeny. H, H', H'' and H''' are the genetic constitutions of the four individuals. G, G', G'' and G''' are four germ-cells. E and D represent tangible external conditions and chance irregularities as factors in development. C represents chance at segregation as a factor in determining the composition of the germ-cells. Path coefficients are represented by small letters.

An equivalent (TRUE) meaning of the heritability is the regression of breeding value on phenotypic value:

$$h^2 = b_{AP}$$

h^2: Most common definition

Ratio of two variances

$$h^2 = \frac{V_A}{V_P}$$

J

h^2: Realized definition (breeders' formula)

$R = h^2 S$

$R = \sigma^2_A/\sigma^2_P S$

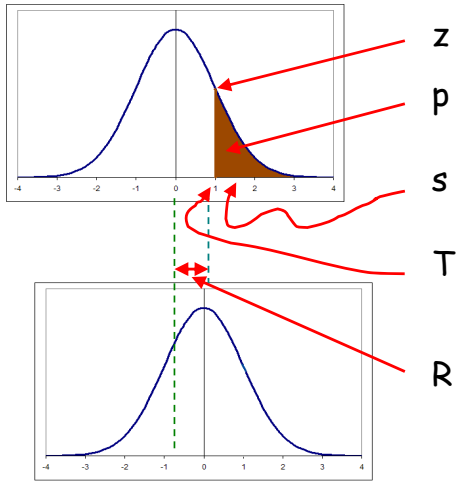
$R = h z/p \sigma_A$

$R = h^2 i \sigma_P$

$R = h i \sigma_A$

$S/\sigma_P = i = z/p$

$h^2 = \sigma^2_A/\sigma^2_P$



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Chapter 11

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Chapter 11: Book's summary (1)

Up to this point the treatment of metric characters has been mainly concerned with the description of the genetic properties of a population as it exists under random mating, with no influences tending to change its properties; now we have to consider the changes brought about by the action of a breeder or experimenter.

Chapter 11: Book's summary (2)

There are two ways in which the action of the breeder can change the genetic properties of the population; the first by the choice of individuals to be used as parents, which constitutes selection, and the second by control of the way in which the parents are mated, which embraces inbreeding and crossbreeding.

Chapter 11: Book's summary (3)

Selection in one form or another is the means whereby all improvement of domesticated animals and plants has been made. In this chapter, therefore, we start consideration of the most important application of quantitative genetics.

Chapter 11: Book's summary (4)

Selection means:
breeding from the 'best' individuals,
whatever 'best' may be.

Chapter 11: Book's summary (5)

The ways in which the theory of quantitative genetics can help in this are, first, by showing how to choose individuals with the best breeding values and, second, by predicting the outcome so that different breeding schemes can be compared.

Chapter 11: Book's summary (6)

The simplest form of selection is to choose individuals on the basis of their own phenotypic values. This is the form of selection to be considered in this chapter.

Chapter 11: Book's summary (7)

In any practical selection programme the number of parents used is more or less restricted, with the result that some inbreeding inevitably takes place, and its effects are superimposed on those of the selection. Any inbreeding effects that there may be will at first be ignored, but they will have to be taken into consideration later. [Where?]

Chapter 11: Book's summary (8)

The basic effect of selection is to change the array of gene frequencies in the manner described in Chapter 2. The changes of gene frequency themselves, however, are now almost completely hidden from us because we cannot deal with the individual loci concerned with a metric character.

Chapter 11: Book's summary (9)

The effects of selection that can be observed are therefore restricted mainly to changes of the population mean. Let us, however, consider the underlying changes of gene frequencies a little further in general terms.

Chapter 11: Book's summary (10)

To describe the change of the genetic properties from one generation to the next we have to compare successive generations at the same point in the life-cycle of the individuals, and this point is fixed by the age at which the character under study is measured. Most often the character is measured at about the age of sexual maturity or on the young adult individuals.

Chapter 11: Book's summary (11)

The selection of parents is made after the measurements, and the gene frequencies among these selected individuals are different from what they were in the whole population before selection.

Chapter 11: Book's summary (12)

If there are no differences of fertility among the selected individuals or of viability among their progeny, then the gene frequencies are the same in the offspring generation as in the selected parents.

Chapter 11: Book's summary (13)

Thus artificial selection - that is, selection resulting from the action of the breeder in the choice of parents - produces its change of gene frequency by separating the adult individuals of the parent generation into two groups, the selected and the discarded, that differ in gene frequencies.

Chapter 11: Book's summary (14)

Natural selection, operating through differences of fertility among the parent individuals, or of viability among their progeny, may cause further changes of gene frequency between the parent individuals and the individuals on which measurements are made in the offspring generation.

Chapter 11: Book's summary (15)

Thus there are three stages at which a change of gene frequency may result from selection: the first through artificial selection among the adults of the parent generation; the second through natural differences of fertility, also among the adults of the parent generation; and the third through natural differences of viability among the individuals of the offspring generation.

Chapter 11: Book's summary (16)

Though natural differences of fertility and viability are always present, they are not necessarily always relevant, because they are not necessarily connected with the genes concerned with the metric character.

Chapter 11: My summary

?

Consequences of selection

Number of parents used is restricted → Inbreeding

Change of allele frequencies → Change of population mean

Two levels of assortative mating → Change of mean and variance

What is selection?

In population genetics:

Selection = Natural selection

Selection on fitness

In quantitative genetics:

Selection = Artificial selection

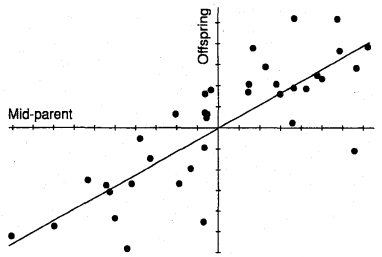
Selection on any trait

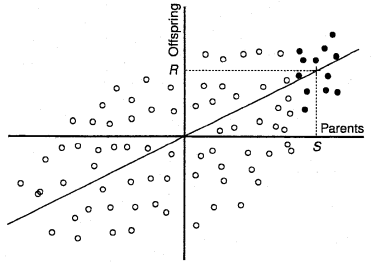
Compare successive generations at the same point in the life-cycle of the individuals (usually about the age of sexual maturity or on the young adult individuals).

The selection of parents is made after the measurements!??

Selection in practice

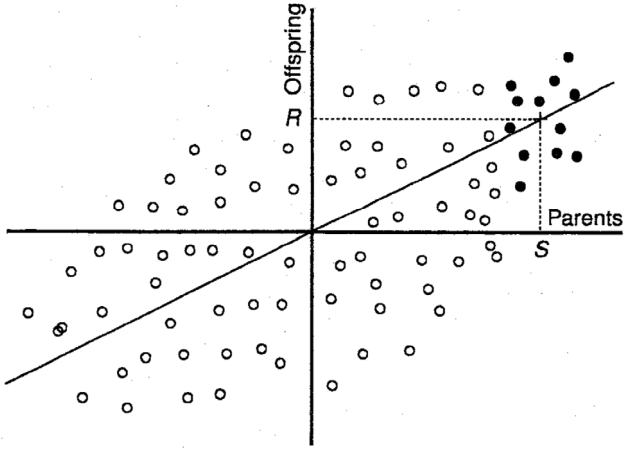
The selection of parents is made after the measurements [*of parents and before measurement of offspring! AND not like the following graphs after measurement of both parents and offspring*]

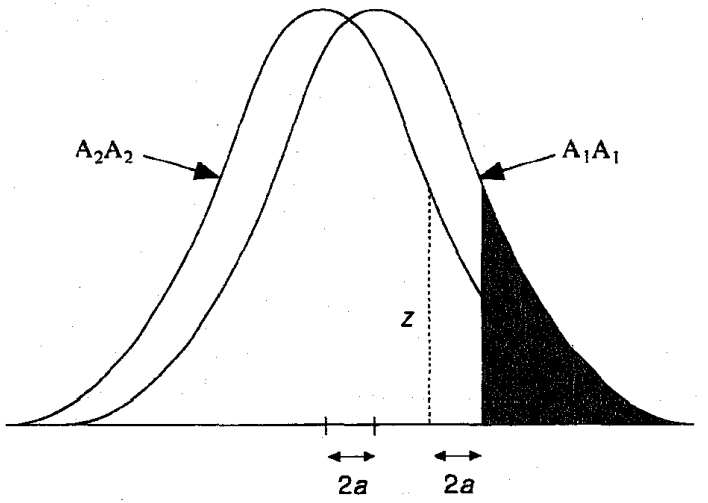




Conceptual definition

$$R = b_{O\bar{P}}S$$

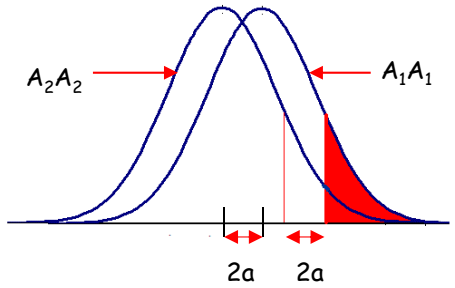




Selection

$$1 - s = \frac{fitness\ of\ \ A_2A_2}{fitness\ of\ \ A_1A_1} = \frac{p(1 - 2ai/\sigma_P)}{p}$$

$$s = i\frac{2a}{\sigma_P}$$



	N	s
Farm animals	~ 10^2	~ 10^{-1}
Natural populations	~ 10^6	~ 10^{-5}

Pattern of change per 1 generation in farm animals =
Pattern of change per 10000 generation in natural populations

Hill & Keightley (1988)

Breeders' formula

$R = h^2 S$

$R = \sigma^2_A/\sigma^2_P S$

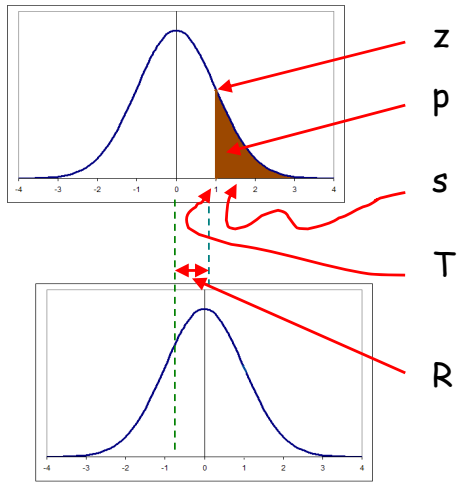
$R = h\ z/p\ \sigma_A$

$R = h^2\ i\ \sigma_P$

$R = h\ i\ \sigma_A$

$S/\sigma_P = i = z/p$

$h^2 = \sigma^2_A/\sigma^2_P$



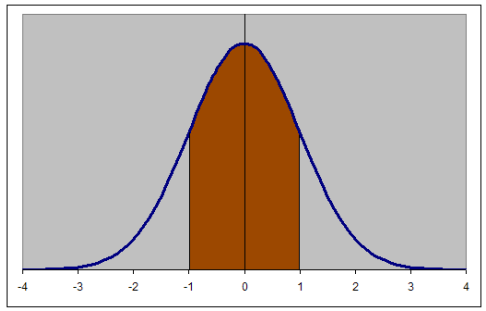
What is selection?

Selection:

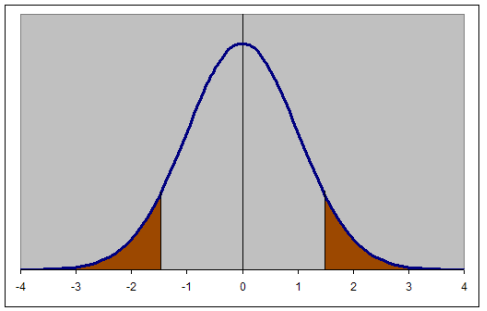
Any differential breeding that would lead to the change of mean and/or variance

selection means no selection

Stabilizing selection



Disrupting selection



$$j = (V_P^* - V_P)/V_P \qquad \ldots [20.7]$$

Extra emphasis

Change of variance

Table 11.1 Variance components in selected parents and their progeny. V_P and V_A are the variances and h^2 the heritability in the parental generation before selection; $k = i(i - x)$, equation [11.9]. Families are full sibs.

Component	*Parents after selection*	*Progeny (Generation 1)*	
Phenotypic	$(1 - k)V_P$		$(1 - \frac{1}{2}h^4k)V_P$
Additive	$(1 - h^2k)V_A$	Between families	$\frac{1}{2}(1 - h^2k)V_A$
		Within families	$\frac{1}{2}V_A$
		Total	$(1 - \frac{1}{2}h^2k)V_A$
Disequilibrium	$-h^2kV_A$		$-\frac{1}{2}h^2kV_A$

Change of variance

$$V_P^* = (1 - k)V_P$$

$$k = i(i - x)$$

$$V_A^* = (1 - h^2k)V_A$$

Bulmer effect

$$V_{A(t+1)} = \tfrac{1}{2}[1 - h^2_{(t)}k]V_{A(t)} + \tfrac{1}{2}V_A$$

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Chapter 12

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Chapter 12: Book's summary (1)

In the last chapter we saw that the theoretical deductions about the effects of artificial selection are limited to the change of the population mean, and strictly speaking over only one generation.

Chapter 12: Book's summary (2)

By changing the gene frequencies, selection changes the genetic properties of the population upon which the effects of further selection depend. And, because the effects of the individual loci are unknown, the changes of gene frequency cannot be predicted, and so the response to selection can be predicted only for as long as the genetic properties remain substantially unchanged.

You cannot eat your cake and have it too. A. Robertson

Chapter 12: Book's summary (3)

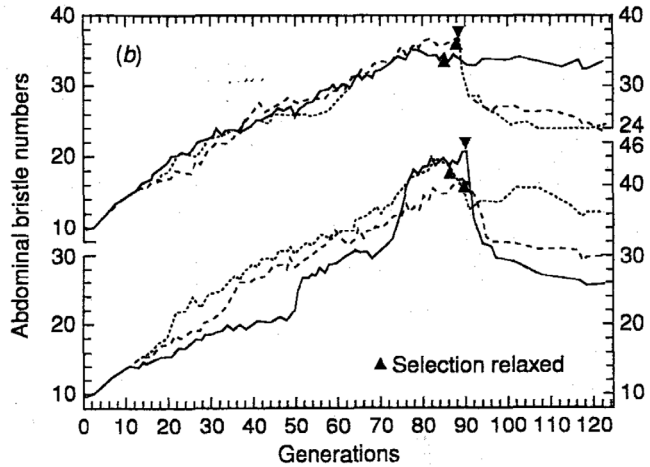
Thus there are many consequences of selection that can be discovered only by experiment. The object of this chapter is to describe briefly what seem to be the most general conclusions about these consequences that have emerged from experimental studies of selection.

Chapter 12: Book's summary (4)

The most important questions to be answered by experiment concern the long-term effects of selection. For how long does the response continue? By how much can the population mean ultimately be changed? What is the genetic nature of the limit to further progress?

Chapter 12: Book's summary (5)

Before dealing with the long-term effects, however, there are two questions to be considered concerning the earlier generations, during which the rate of response remains more or less constant. These are the repeatability of responses and asymmetry of responses to selection in opposite directions.



Theory of limits

The apocalyptic view (Robertson, 1960)

$$R_{(\max)} = 2N_e i h^2 \sigma_P$$

The resurrective view (Hill, 1982)

$$R = 2N_e i V_M / \sigma_P$$

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Chapter 13

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Chapter 13: Book's summary (1)

In our consideration of selection we have up to now supposed that individuals are measured for the character to be selected and that the best are chosen to be parents in accordance with the individual phenotypic values.

Chapter 13: Book's summary (2)

An individual's own phenotypic value, however, is not the only source of information about its breeding value; additional information is provided by the phenotypic values of relatives, particularly by those of full or half sibs. With some characters, indeed, the values of relatives provide the only available information. Milk-yield, to take an obvious example, cannot be measured in males, so the breeding value of a male can only be judged from the phenotypic values of its female relatives.

Chapter 13: Book's summary (3)

The use of information from relatives is of great importance in the application of selection to animal breeding, for two reasons.

Chapter 13: Book's summary (4)

First, the characters to be selected are often ones of low heritability, and with these the mean value of a number of relatives often provides a more reliable guide to breeding value than the individual's own phenotypic value.

Chapter 13: Book's summary (5)

And, second, when the outcome of selection is a matter of economic gain, even quite a small improvement of the response will repay the extra effort of applying the best technique.

Chapter 13: Book's summary (6)

In this chapter we shall outline the principles underlying the use of information from relatives and the choice of the best method of selection.

One example

Table 13.1 Examples of individual values and family means for selection, as explained in the text.

	Family			
Individual	A	B	C	D
1	13	11	7	9
2	10	9	7	5
3	8	6	6	3
4	5	6	4	3
Family mean	9	8	6	5
Overall mean		7		

Information sources

$$P = P_f + P_w$$

Partitioning the variance

Observational component	*Additive variance*	*Phenotypic variance*
Between families, σ^2_B	rV_A	tV_P
Within families, σ^2_W	$(1-r)V_A$	$(1-t)V_P$

Selection methods: 1 trait

Individual (mass, truncation) selection

Family selection

Sib selection, Progeny testing

Within family selection

Combined selection

Index selection

Comparison of selection methods

Table 13.4 Heritability and expected response under different methods of selection.

Method of selection	*Heritability*	*Expected response*
Individual	h^2	$R = i\sigma_P h^2$
Family	$h^2_f = h^2 \frac{1+(n-1)r}{1+(n-1)t}$	$R_f = i\sigma_P h^2 \frac{1+(n-1)r}{\sqrt{n\{1+(n-1)t\}}}$
Sib	$h^2_s = h^2 \frac{nr}{1+(n-1)t}$	$R_s = i\sigma_P h^2 \frac{nr}{\sqrt{n\{1+(n-1)t\}}}$
Within-family	$h^2_w = h^2 \frac{(1-r)}{(1-t)}$	$R_w = i\sigma_P h^2 (1-r)\sqrt{\left[\frac{n-1}{n(1-t)}\right]}$
Combined	—	$R_c = i\sigma_P h^2 \sqrt{\left[1+\frac{(r-t)^2}{(1-t)} \times \frac{(n-1)}{1+(n-1)t}\right]}$

Index selection: 1 trait

Information from relatives

$$I = b_1P_1 + b_2P_2 + b_3P_3 + \ldots \qquad \ldots [13.9]$$

Changes achieved in practice

Species	Trait	Annual response (% of mean)
Poultry	7-8 wk weight	5.6 - 6.5
Beef cattle	Yearling weight	0.3
Poultry	Egg Number	0.9 – 1.7
Pigs	Litter size	1.5
Sheep	Litter size	2.9
Dairy cattle	Milk yield	1.0
Dairy cattle	Fat yield	0.7

Smith (1984)

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Chapter 14

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Selection, and now Inbreeding

We turn our attention now to inbreeding, the second of the two ways open to the breeder for changing the genetic constitution of a population.

Pros and Cons

The harmful effects of inbreeding on reproductive rate and general vigour are well known to breeders and biologists, and were mentioned in Chapter 6 as one of the two basic genetic phenomena displayed by metric characters.

The opposite, or complementary, phenomenon of hybrid vigour resulting from crosses between inbred lines or between different races or varieties is equally well known, and forms an important means of animal and plant improvement.

Two application areas

The production of lines for subsequent crossing in the utilization of hybrid vigour is one of two main purposes for which inbreeding may be carried out.

The other is the production of genetically uniform strains, particularly of laboratory animals, for use in bioassay and in research in a variety of fields.

Bad, worse, worst

Inbreeding in itself, however, is almost universally harmful and the breeder or experimenter normally seeks to avoid it as far as possible, unless for some specific purpose.

Change of mean

In the treatment of inbreeding given in Chapter 3, the consequences were described in terms of the changes of allele frequencies and of genotype frequencies.

Here we have to show how these changes of allele and genotypic frequencies affect metric characters, and how they can account for the observed effects of inbreeding and crossing.

Exception to the rule

The effects of inbreeding to be described do not apply to naturally self-fertilizing plants. Since inbreeding is their normal mating system they cannot be further inbred. They can, however, be crossed and they do then often show hybrid vigour, though less than when inbred lines of outbreeding species are crossed.

Extra emphasis

Myth: Inbreeding depression is the results of …

Myth: Heterosis leads to …

What is inbreeding depression?

?

Calculating population mean (no inbreeding)

Table 7.1

Genotype	*Frequency*	*Value*	*Freq. × Val.*
A_1A_1	p^2	$+a$	p^2a
A_1A_2	$2pq$	d	$2pqd$
A_2A_2	q^2	$-a$	$-q^2a$
		Sum =	$a(p-q)+2dpq$

Genotype frequencies (after inbreeding)

Table 3.1

	Original frequencies	*Change due to inbreeding*	*Origin:*	
			Independent	*Identical*
A_1A_1	p_0^2	$+ p_0q_0F$	$= p_0^2(1-F)$	$+ p_0F$
A_1A_2	$2p_0q_0$	$- 2p_0q_0F$	$= 2p_0q_0(1-F)$	
A_2A_2	q_0^2	$+ p_0q_0F$	$= q_0^2(1-F)$	$+ q_0F$

$$p_0^2 + p_0q_0F \rightarrow p_0^2 + p_0(1-p_0)F \rightarrow p_0^2 + p_0F - p_0^2F \rightarrow P_0^2(1-F) + p_0F$$

Calculating population mean (after inbreeding)

Table 14.2

Genotype	*Frequency*	*Value*	*Frequency × Value*
A_1A_1	$\bar{p}^2 + \bar{p}\bar{q}F$	$+ a$	$\bar{p}^2a + \bar{p}\bar{q}aF$
A_1A_2	$2\bar{p}\bar{q} - 2\bar{p}\bar{q}F$	d	$2\bar{p}\bar{q}d - 2\bar{p}\bar{q}dF$
A_2A_2	$\bar{q}^2 + \bar{p}\bar{q}F$	$- a$	$- \bar{q}^2a - \bar{p}\bar{q}aF$
		Sum	$= a(\bar{p}-\bar{q}) + 2d\bar{p}\bar{q} - 2d\bar{p}\bar{q}F$
			$= a(\bar{p}-\bar{q}) + 2d\bar{p}\bar{q}(1-F)$

Inbreeding depression

Population mean before inbreeding: $M = a(p - q) + 2dpq$

Population mean after inbreeding: $M_F = a(\bar{p} - \bar{q}) + 2d\bar{p}\bar{q}(1 - F)$

Reduction in population mean, or inbreeding depression: $- 2d\bar{p}\bar{q}F$

Inbreeding depression

Single locus

$$M_F = a(\bar{p} - \bar{q}) + 2d\bar{p}\bar{q}(1 - F) \quad \ldots [14.1]$$
$$= M_0 - 2d\bar{p}\bar{q}F \quad \ldots [14.2]$$

Many loci

$$M_F = \Sigma a(\bar{p} - \bar{q}) + 2(\Sigma d\bar{p}\bar{q})(1 - F) \quad \ldots [14.3]$$
$$= M_0 - 2F\Sigma d\bar{p}\bar{q} \quad \ldots [14.4]$$

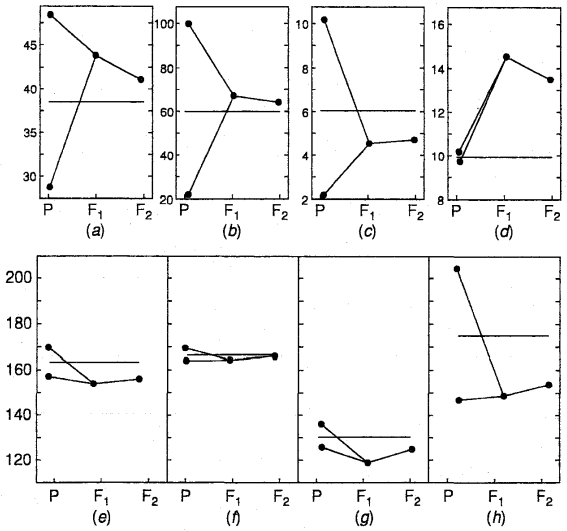
Heterosis

Difference between parental populations and crossed offspring

$$= dy^2$$

$$y = p - p' = q' - q$$

Heterosis?



Properties of …

Allele frequency dependent,
i.e. population specific

$$-2d\bar{p}\bar{q}F$$

Average sub-population dependent
i.e. cross specific

$$dy^2$$

Directional dominance dependent,
i.e. …?

$$y = p - p' = q' - q$$

Directional dominance?

		(1) *Units*	(2) % of *M*	(3) % of σ_P
Man				
Height (cm) at age 10; [Schull, 1962]		2.0	1.6	37
IQ score (percentage points); [Morton, 1978]		4.4	4.4	29
Cattle				
Milk-yield (kg): [Robertson, 1954]		135	3.2	17
Sheep [Morley, 1954]				
Fleece weight (kg)		0.29	5.5	51
Body weight at 1 yr (kg)		1.32	3.7	36
Pigs [Bereskin *et al.*, 1968]				
Litter size (no. born alive)	(*a*)	0.24	3.1	9
Body weight at 154 days (kg)		2.6	4.3	15
Mice				
Litter size: [Bowman and Falconer, 1960]	(*b*)	0.56	7.2	23
Body weight at 6 wks (g): [White, 1972]		0.19	0.6	7
Maize [Cornelius and Dudley, 1974]	(*c*)			
Plant height (cm)	(FS)	5.20	2.1	4
	(S)	5.65	2.3	5
Yield of seed (g/plant)	(FS)	7.92	5.6	25
	(S)	9.65	6.8	30

Other interpretations?

P_1	P_2	F_1
++	--	+-
++	--	+-
--	++	-+
--	++	-+
++	--	+-
--	++	-+

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Chapter 15

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Book's summary (1)

The effect of inbreeding on the genetic variance of a metric character is apparent, in its general nature, from the description of the changes of allele frequency given in Chapter 3

Notice one point:

Throughout discussion in this chapter:

Complete division of a population into separate lines is the extreme case of a process: mating of related individuals

Book's summary (2): Mean

Imagine the whole population, consisting of many lines. Under inbreeding the allele frequencies in the separate lines tend toward the extreme values of 0 or 1, and the lines become differentiated in allele frequency. Since the mean genotypic value of a metric character depends on the allele frequencies at the loci affecting it, the lines become differentiated, or drift apart, in mean genotypic value.

Book's summary (3): Variance

And, since the genetic components of variance diminish as the allele frequencies tend toward extreme values (see Fig. 8.1), the genetic variance within the lines decreases.

The general consequence of inbreeding, therefore, is a redistribution of the genetic variance; the component appearing between the means of lines increases, while the component appearing within the lines decreases.

Book's summary (4)

Inbreeding leads to genetic differentiation between lines and genetic uniformity within lines.

Book's summary (5)

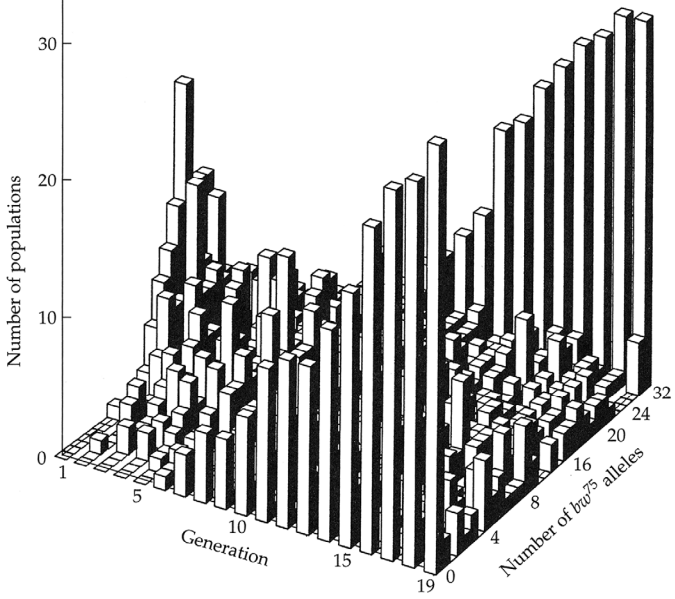
The subdivision of an inbred population into lines introduces an additional observational component of variance, the between-line component, and it is not surprising that this adds a considerable complication to the theoretical description of the components of genetic variance.

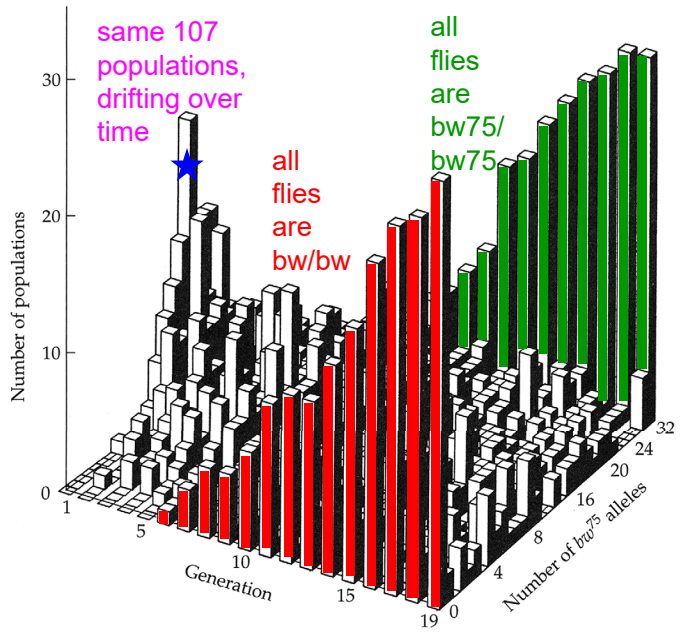
Book's summary (6)

The redistribution of genetic variance is not the only effect of inbreeding; experiments have shown that the environmental variance is sometimes also affected.

Book's summary (7)

Another matter concerning inbreeding to be considered is the genetic stability of highly inbred lines, which is important in connection with the use of 'standard' inbred strains for experimental purposes.





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Chapter 16

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Book's summary (1)

The crossing of inbred lines to produce hybrids plays a major role in the improvement of some plants, most notably maize.

Crossing is also widely used in animal breeding, though highly inbred lines of farm animals are not available because of the severe loss of fertility from inbreeding depression.

Book's summary (2)

Animal crosses are therefore made between mildly inbred lines or between different breeds.

Keywords: Specialized selection lines

Book's summary (3)

We shall be concerned mainly with outbreeding plants, but animals and naturally self-fertilizing plants will be considered briefly in separate sections.

Book's summary (4)

Two simplifications will be made.

First, it will be assumed that the only criterion of merit in plant breeding is yield, though in practice other characters have to be taken into consideration as well as yield.

Book's summary (5)

Two simplifications will be made.

Second, the complications arising from genotype X environment interactions will not be discussed.

Book's summary (6)

A cautionary word:

Technical details will not be given; for these the reader should consult a textbook of plant breeding, e.g., Simmonds (1979).

These analyses of crosses and the later generations derived from them are fully described by Mather and Jinks (1977, 1982) and will not be dealt with here.

Commercial applications

Pure line breeding vs cross-line breeding (crossbreeding)

End-product animals/plants

Breeding animals/plants

End-product animals/plants

Slaughter/meat-type animals

Heavy production systems

Multi-layer production systems

End-product animals/plants

Example: Four-way cross

AxA x BxB → AB ♂

CxC x DxD → CD ♀

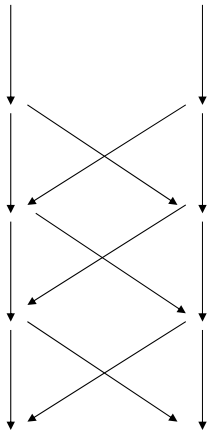
AB ♂ x CD ♀ → ABCD

♂ ♀

Reciprocal recurrent selection

Within line breeding for

Crossbred performance



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Chapter 17

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Book's Summary (1)

The data from any experimental or practical study are obtained in the form most convenient for the measurement of the character. That is to say, the phenotypic values are recorded in grams, centimetres, days, numbers, or whatever unit of measurement is most convenient.

It is tempting to suppose that each character has its 'natural' scale, the scale on which the biological process expressed in the character works.

Book's Summary (2)

Growth is a geometrical rather than an arithmetical process, and a geometric scale would appear to be the most 'natural'.

For example, an increase of 1 g in a mouse weighing 20 g has not the same biological significance as an increase of 1 g in a mouse weighing 2 g; but an increase of 10% has approximately the same significance in both.

For this reason a transformation to logarithms would seem appropriate for measurements of weight.

Book's Summary (3)

This, however, is largely a **subjective** judgement, and some **objective** criterion for the choice of a scale is needed.

Different criteria, however, **are often inconsistent in the scale they indicate** and, moreover, **the same criterion applied to the same character may indicate different scales** in different populations.

Therefore the idea that every character must have its 'natural' and correct scale is largely illusory.

Book's Summary (4)

There are, broadly speaking, three main reasons for making a scale transformation:

(1) to make the distribution normal;

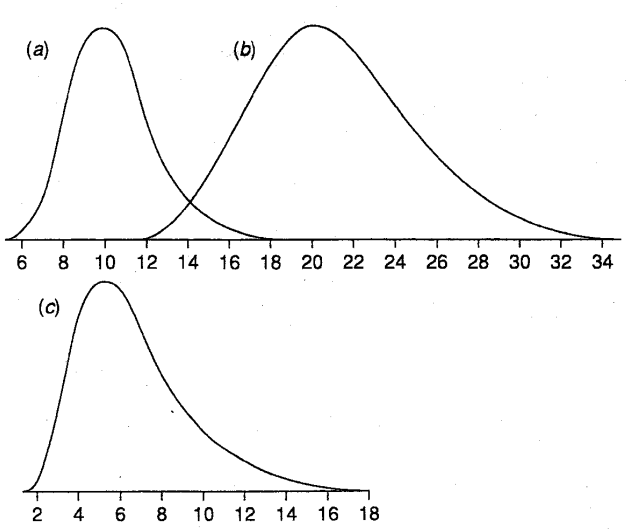
(2) to make the variance independent of the mean; and

(3) to remove or reduce non-additive interactions.

The criterion for the choice of a scale is in each case the empirical one of achieving the particular objective.

Book's Summary (5)

When a scale transformation is called for but is not made, certain phenomena arise, called scale effects, **which disappear when the appropriate transformation is made.** The objectives noted above might equally well be stated as being the removal of these scale effects.

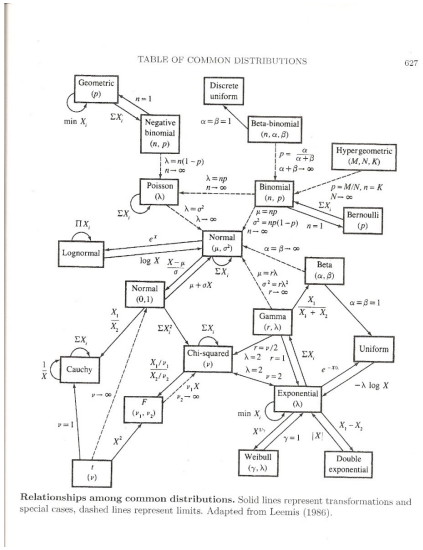


In other words ...

Every statistical model has some underlying assumptions, e.g. the variable under study (data) must follow certain probability distribution.

If departures from the assumed distribution is large, the data must be transformed to conform to the assumed distribution.

Distributions, Distributions, Distributions, Distributions, Distributions, ...



Relationships among common distributions. Solid lines represent transformations and special cases, dashed lines represent limits. Adapted from Leemis (1986).

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Chapter 18

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Book's Summary (1)

There are many characters of biological interest or economic importance which vary in a discontinuous manner but are not inherited in a simple Mendelian manner.

Familiar examples are susceptibility to disease, where there are two phenotypic classes - affected or not-affected - and litter size of the larger mammals that usually bear one young at a time but sometimes two or three.

Book's Summary (2)

There are also discontinuous anatomical differences, such as the number of vertebrae of mice, whose genetics has been extensively studied.

Characters of this sort appear at first sight to be outside the realm of quantitative genetics; yet when they are subjected to genetic analysis they are found to be inherited in the same way as continuously varying characters.

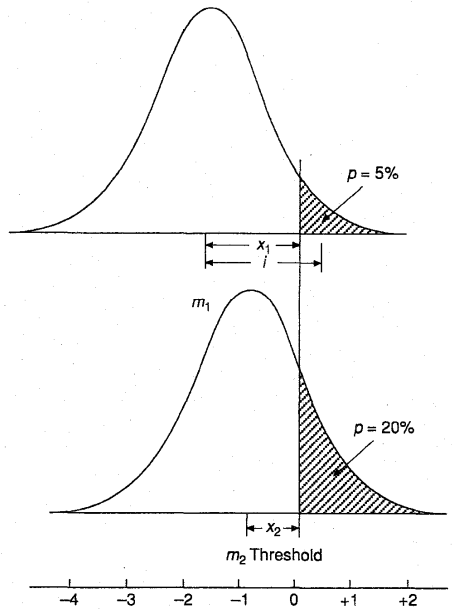
Book's Summary (3)

Liability and threshold

The clue to understanding the inheritance of such characters lies in the idea that the character has an underlying continuity with a threshold, which imposes a discontinuity on the visible expression.

Book's Summary (4)

When the underlying variable is below this threshold level the individual has one form of phenotypic expression, e.g., is 'normal'; when it is above the threshold the individual has the other phenotypic expression, e.g., is 'affected'.



Book's Summary (5)

The continuous variation of liability is both genetic and environmental in origin, and may be thought of as the concentration of some substance, or the rate of some developmental process - of something, that is to say, that could in principle be measured and studied as a metric character in the ordinary way.

It may be a compound of several different physiological or developmental processes but it is not necessary to know how these are combined to give the liability, or even to know what they really are.

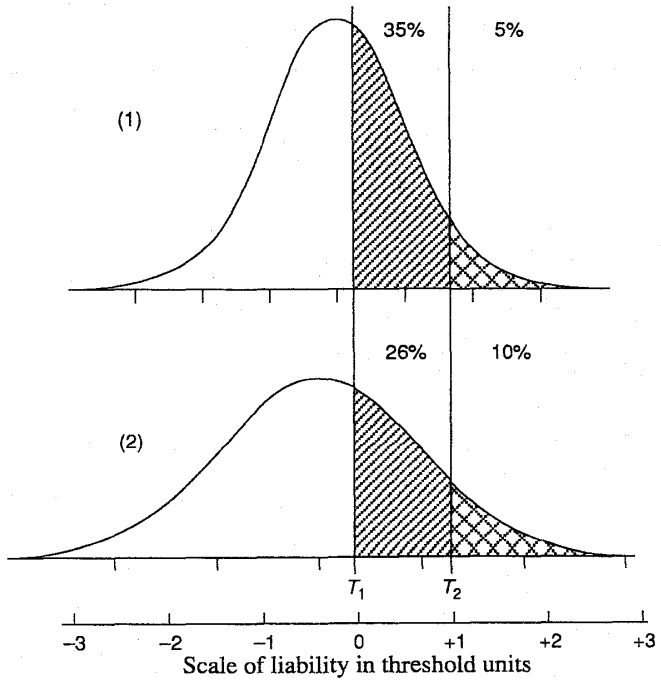
Book's Summary (6)

That the idea of an underlying variable is a realistic one can be appreciated by thinking of litter size. The litter size of mice or pigs, though in reality obviously discontinuous, can be treated as a continuous variable because there are a large enough number of classes.

The litter size of cows has only two classes, single and twin births, more than two calves being exceedingly rare. But there is no reason to think that the physiological causes of twinning in cattle are different from those of litter size in mice or pigs.

Book's Summary (7)

The underlying variable in both cases is made up mainly of the levels of circulating gonadotrophic hormones, which determine the number of eggs shed, the intra-uterine factors that affect embryonic survival and, in the case of cattle, the factors determining monozygotic twinning.



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Falconer & Mackay (1996)
Chapter 19

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Book's Summary (1)

Relationships between two metric characters, in particular with characters whose values are correlated - either positively or negatively in the individuals of a population.

Correlated characters are of interest for three chief reasons.

Book's Summary (2)

Firstly, in connection with the genetic causes of correlation through the pleiotropic action of genes: pleiotropy is a common property of major genes, but we have as yet had little occasion to consider its effects in quantitative genetics.

Book's Summary (3)

Secondly, in connection with the changes brought about by selection: it is important to know how the improvement of one character will cause simultaneous changes in other characters.

Book's Summary (4)

Thirdly, in connection with natural selection: the relationship between a metric character and fitness is the primary agent that determines the genetic properties of that character in a natural population.

Notation

X and Y:

r_P

r_A

r_E

cov

σ^2 and σ

h^2

e^2

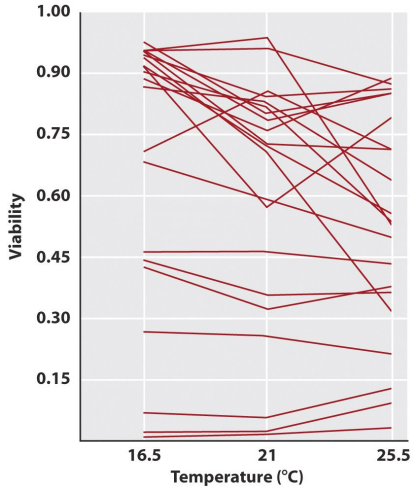
Not a so simple picture

r_P	r_A	r_E
0.20	0.07	0.31
−0.26	−0.38	−0.18
0.40	0.75	0.26
0.00	0.13	−0.18
0.66	0.69	0.64
0.33	0.42	0.23
0.01	−0.17	0.08
−0.05	−0.31	0.02
0.45	0.29	0.56
0.14	0.41	0.06

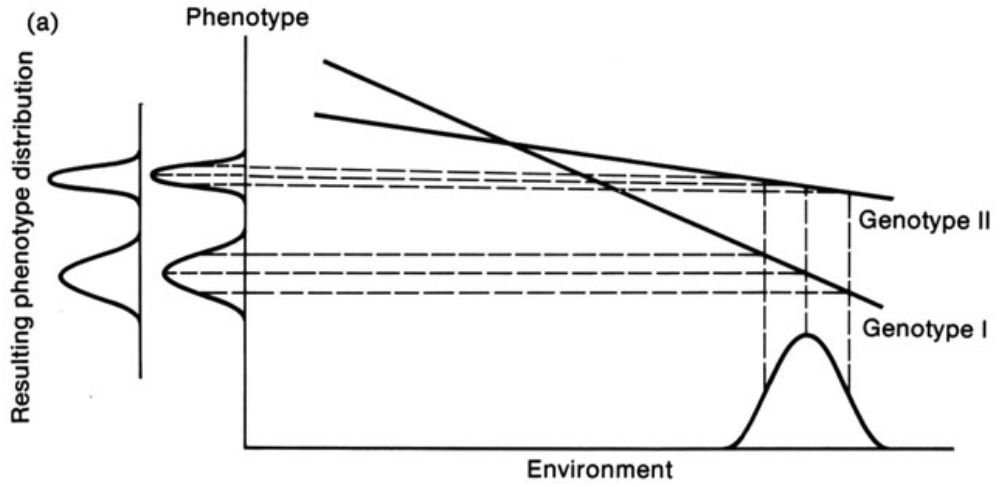
Correlated response

$$CR_Y = ih_X h_Y r_A \sigma_{PY} \quad \ldots [19.6]$$

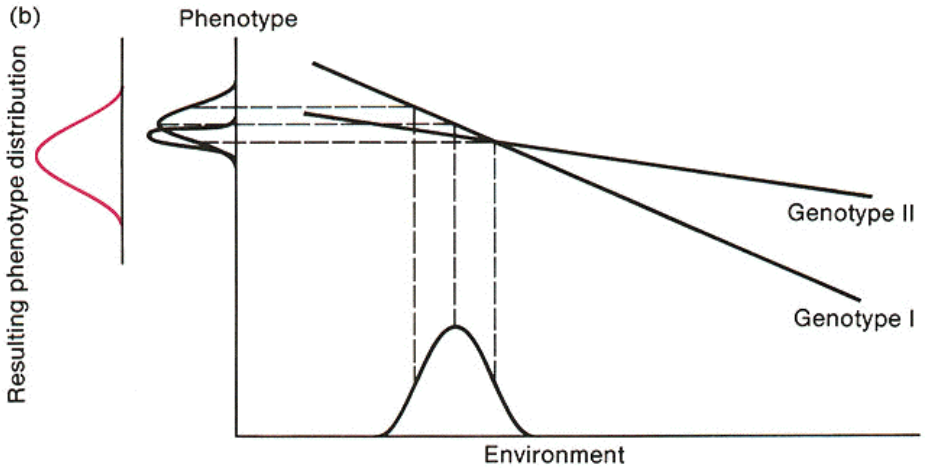
Genotype x Environment Interaction



Genotype x Environment Interaction



Genotype x Environment Interaction



Selection & production environments

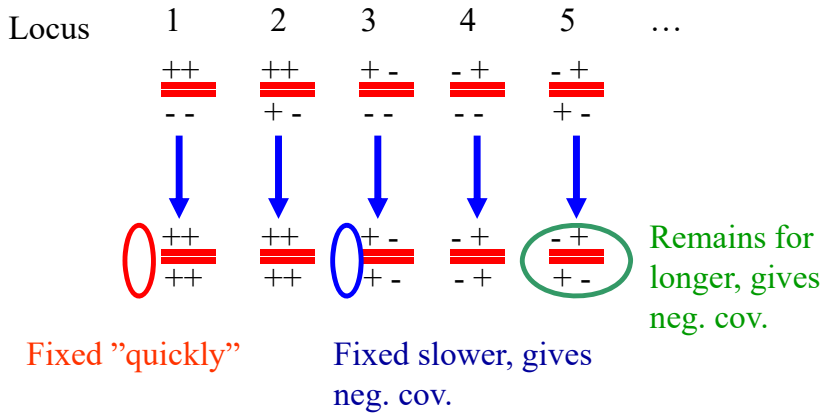
Selection		*Response*			*Sensitivity*
Direction	*Diet*	*Growth on good diet*	*Growth on bad diet*	*Mean of both diets*	*Effect of diet*
Up	good	2.3	*0.6*	1.45	5.4
Up	bad	*1.6*	3.1	2.35	3.5
Down	good	−2.8	−2.9	−2.85	3.6
Down	bad	*−1.2*	−3.2	−2.20	6.8

Index selection

$$
\left.
\begin{aligned}
b_1P_{11} + b_2P_{12} + \ldots + b_mP_{1m} &= a_1A_{11} + a_2A_{12} + \ldots + a_nA_{1n} \\
b_1P_{21} + b_2P_{22} + \ldots + b_mP_{2m} &= a_1A_{21} + a_2A_{22} + \ldots + a_nA_{2n} \\
&\cdot \\
&\cdot \\
b_1P_{m1} + b_2P_{m2} + \ldots + b_mP_{mm} &= a_1A_{m1} + a_2A_{m2} + \ldots + a_nA_{mn}
\end{aligned}
\right\} \ldots [19.15]
$$

Selection and genetic correlations

Consider alleles in various loci that have different pleiotropic effects



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Chapter 20

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Book's Summary (1)

Throughout the discussion of the genetic properties of metric characters, very little attention has been given to the effects of natural selection.

The absence of differential viability and fertility was specified as a condition in the theoretical development of the subject: that is to say, natural selection was assumed to be absent.

Book's Summary (2)

Though for many purposes this assumption may lead to no serious error, a complete understanding of metric characters will not be reached until the effects of natural selection can be brought into the picture.

Book's Summary (3)

The operation of natural selection on metric characters has a much wider interest than just as a complication that may disturb the simple theoretical picture and the predictions based on it.

It is to natural selection that we must look for an explanation of the genetic properties of metric characters, which hitherto we have accepted with little comment.

Book's Summary (4)

The genetic properties of a population are the product of natural selection in the past, together with mutation and random drift. It is by these processes that we must account for the existence of genetic variability;

It is chiefly by natural selection that we must account for the fact that characters differ in their genetic properties, some having proportionately more additive variance than others, some showing inbreeding depression while others do not.

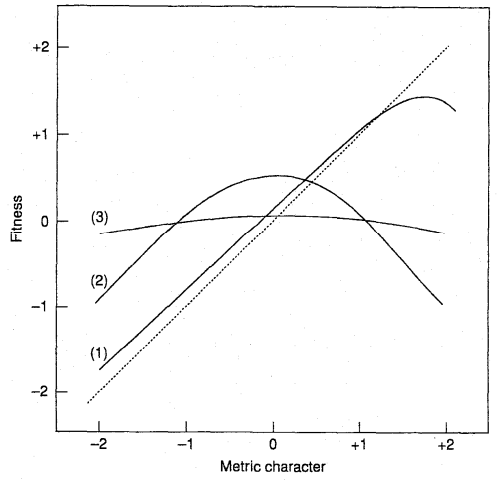
Book's Summary (5)

These, however, are very wide problems which are still far from solution, and in this chapter we can do little more than indicate their nature. Before considering the ways in which natural selection affects metric characters, we shall give a brief account of natural selection itself and what it means.

Mathematical concept of fitness

1	2	3	4
Fitness	Total number of offspring born (Fertility)	Viability	Disease resistance Predator avoidance
		Mating success	
		Litter size	Ovulation rate Embryo survival
		Frequency of litters	
		Number of litters	
	Quality of offspring weaned (Maternal performance)	Milk-yield	Mammary-gland size
		Maternal behaviour	

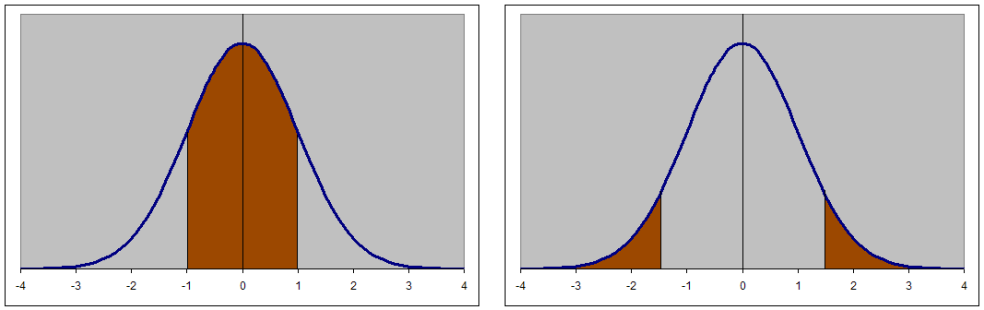
Fitness profiles



Selection? Can you prove it?

$$j = (V_P^* - V_P)/V_P \qquad \ldots [20.7]$$

Establish the presence of selection



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Chapter 21

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Book's Summary (1)

The preceding chapters has considered only the aggregate effects of all the loci causing the variation.

A complete description needs to take account of the properties of the loci individually - their allele frequencies and the magnitude of their effects on the trait of interest.

The loci cannot be studied individually using the methods of classical Mendelian genetics because their effects are lost in the statistical 'fog' of all other background variation.

Book's Summary (2)

In the absence of knowledge about the individual properties of loci we had to make some unrealistic assumptions:

a) Allele frequencies at all loci are more or less the same,

b) Alleles' effects and dominance relations are all about the same,

c) There are an indefinitely large number of loci affecting the trait.

Book's Summary (3)

Recently, however, methods have become available for studying the individual loci; these loci are known as Quantitative Trait Loci, or QTLs.

This chapter will explain the methods for identifying QTLs and of estimating their effects on quantitative traits. We shall see, however, that what is identified as a QTL is a segment of chromosome affecting the trait, not necessarily a single locus.

Book's Summary (4)

Identification of the individual loci could lead to several useful applications.

First, it could improve the efficacy of selective breeding, especially for traits with low heritability or that can only be measured in one sex

Second, transgenic technology might be applied to quantitative traits.

Third, in medicine, the identification of alleles causing predisposition to common multifactorial diseases, such as heart disease or diabetes, could lead to improved methods of prevention.

Fourth, **quantitative genetic theory will be made more realistic** when the numbers and properties of the genes are known, and the more realistic theories will improve our understanding of evolution

Book's Summary (5)

Major Genes

QTLs

Book's Summary (6)

The future for understanding quantitative traits in terms of complex genetics rather than statistical descriptions is bright.

The various genome projects are yielding very dense linkage maps for humans, model organisms and species of agricultural importance that often show remarkable conservation of linkage groups across taxa.

With the development of improved statistical methods for analysis of experimental crosses and pedigrees to detect segregating QTLs associated with molecular markers, and with the potential to resolve QTLs to the level of single genes, the description of the Mendelian genetic basis of quantitative variation is within reach.

Detecting departure from normality

Normal?

Who?

Me?

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