Example 1.1 2-1

The M-N blood groups in man are determined by two alleles at a locus, and the three genotypes correspond with the three blood groups, M, MN, and N. The following figures, taken from the tabulation of Mourant (1954), show the blood group frequencies among Eskimos of East Greenland and among Icelanders as follows:

		Blood group			Number of individuals
		M	MN	N	
Frequency, %	Greenland	83.5	15.6	0.9	569
	Iceland	31.2	51.5	17.3	747

Clearly the two populations differ in these genotype frequencies, the N blood group being rare in Greenland and relatively common in Iceland. Not only is this locus a source of variation within each of the two populations, but it is also a source of genetic difference between the populations.

Example 1.2

To illustrate the calculation of gene frequencies from genotype frequencies we may take the M–N blood group frequencies given in Example 1.1. The M and N blood groups represent the two homozygous genotypes and the MN group the heterozygote. The frequency of the M gene in Greenland is, from equation [1.1], $0.835 + \frac{1}{2}(0.156) = 0.913$, and the frequency of the N gene is $0.009 + \frac{1}{2}(0.156) = 0.087$, the sum of the frequencies being 1.000 as it should be. Doing the same for the Iceland sample, we find the following gene frequencies in the two populations, expressed now as percentages:

	Gene	
	M	N
Greenland	91.3	8.7
Iceland	57.0	43.0

2-2

Thus the two populations differ in gene frequency as well as in genotype frequencies.

Table 1.2

Male gametes and their frequencies	Female gametes and their frequencies: A_1 p	A_2 q
A_1 p	A_1A_1 p^2	A_1A_2 pq
A_2 q	A_1A_2 pq	A_2A_2 q^2

2-3

2-3A

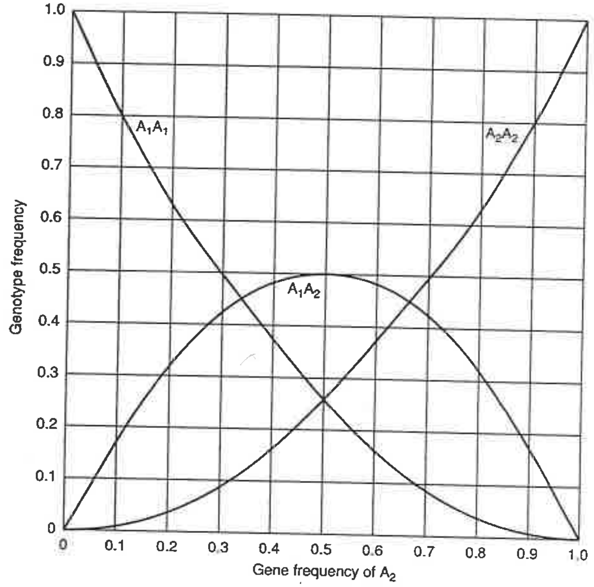


Fig. 1.1. Relationship between genotype frequencies and gene frequency for two alleles in a population in Hardy–Weinberg equilibrium.

2-4

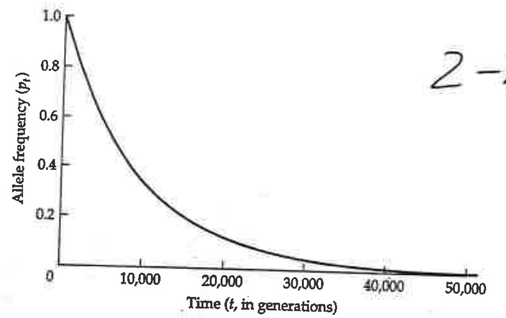


Figure 5.1 Change in frequency under mutation pressure. In this example, an allele A mutates to a at a rate of $\mu = 1 \times 10^{-4}$ per generation; p_t is the allele frequency of A in generation t. We assume that $p_0 = 1$. With the given value of μ, the allele frequency decreases by half every 6931 generations.

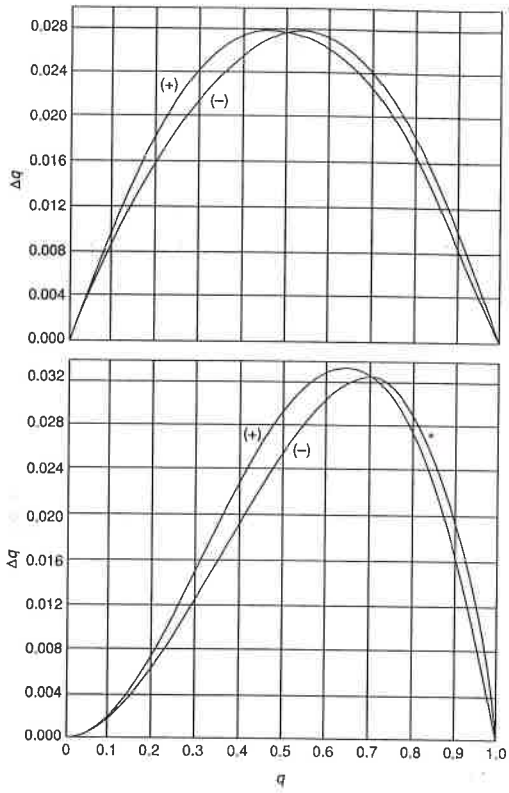


Fig. 2.2. Change of gene frequency, Δq, under selection of intensity $s = 0.2$, at different values of initial gene frequency, q. Upper figure: a gene with no dominance. Lower figure: a gene with complete dominance. The graphs marked (−) refer to selection against the gene whose frequency is q, so that Δq is negative. The graphs marked (+) refer to selection in favour of the gene, so that Δq is positive. (*After Falconer, 1954.*)

Pilt 2-3B.

Genotüüpide sagedused esimeses järglaspõlvkonnas, kui kokku saavad kaks populatsiooni, millest kummaski on kahes erinevas lookuses fikseerunud erinev alleel (vanemate genotüübid siis $A_1A_1B_1B_1$ ja $A_2A_2B_2B_2$. Vaid kolme genotüübi (üheksast võimalikust) esinemine järglaskonnas on näide *gametic phase disequilibrium*'ist. Servmises reas ja tulbas on gameetide haplotüüpide sagedused.

	50% A_1B_1	**0% A_1B_2**	**0% A_2B_1**	**50% A_2B_2**
50% A_1B_1	25% $A_1A_1B_1B_1$	0% $A_1A_1B_1B_2$	0% $A_1A_2B_1B_1$	25% $A_1A_2B_1B_2$
0% A_1B_2	0% $A_1A_1B_1B_2$	0% $A_1A_2B_2B_2$	0% $A_1A_2B_1B_2$	0% $A_1A_2B_2B_2$
0% A_2B_1	0% $A_1A_2B_1B_1$	0% $A_1A_2B_1B_2$	0% $A_2A_2B_1B_1$	0% $A_2A_2B_1B_2$
50% A_2B_2	25% $A_1A_2B_1B_2$	0% $A_1A_2B_2B_2$	0% $A_2A_2B_2B_1$	25% $A_2A_2B_2B_2$

	Sagedus 1. plvk	Tasak. sagedus
$A_1A_1B_1B_1$	0.25	1/16
$A_1A_1B_1B_2$	0	2/16
$A_1A_1B_2B_2$	0	1/16
$A_1A_2B_1B_1$	0	2/16
$A_1A_2B_1B_2$	0.5	4/16
$A_1A_2B_2B_2$	0	2/16
$A_2A_2B_1B_1$	0	1/16
$A_2A_2B_1B_2$	0	2/16
$A_2A_2B_2B_2$	0.25	1/16

Sources of Varia

Figure 5.15 Change of allele frequency with one-way migration assuming that an allele A is initially fixed in the recipient population and absent in the source population. The migration rate is $m = 0.01$. Note that this is the same curve as in Figure 5.1 except that the horizontal axis is compressed to 500 generations. The time scale is different because, generally speaking, the migration rate m is much larger than the mutation rate μ.

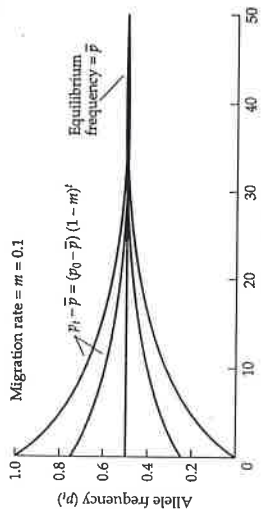


Figure 5.16 Change of allele frequency with time in five subpopulations exchanging migrants at the rate $m = 0.1$ per generation. Note the rapid convergence to a common equilibrium frequency.

Table 2.1 Selection against a recessive gene.

	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	$2pq$	$q^2(1 - s)$	$1 - sq^2$

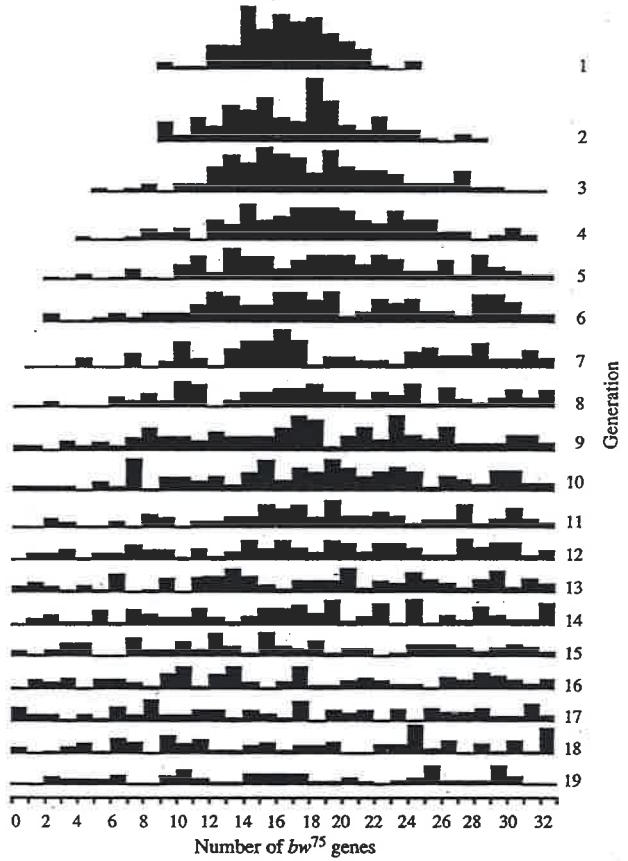


Fig. 3.3. Distributions of gene frequencies in 19 consecutive generations among 105 lines of *Drosophila melanogaster*, each of 16 individuals. The gene frequencies refer to two alleles at the 'brown' locus (bw^{75} and bw), with initial frequencies of 0.5. The height of each black column shows the number of lines having the gene frequency shown on the scale below, previously fixed lines being excluded. (*After Buri, 1956.*)

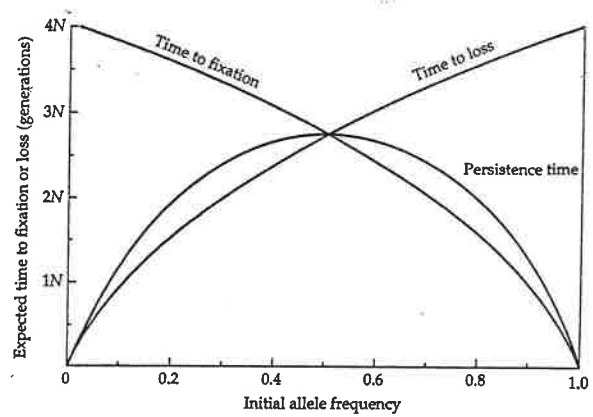
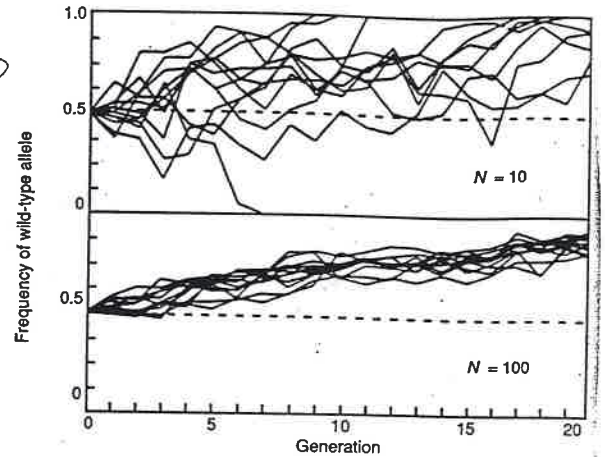


Figure 7.8 Average persistence of a neutral allele in an ideal diploid population of size N, plotted against initial allele frequency.



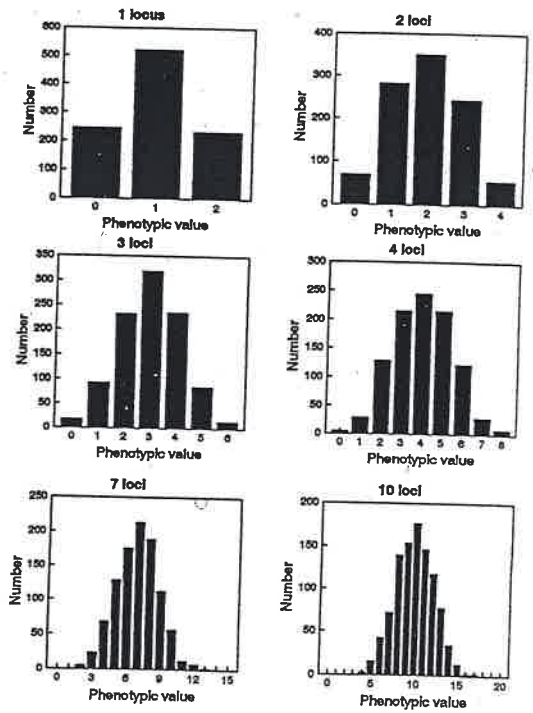


Figure 1.3 Distributions of phenotypic values for a genetic model in which there are n loci with two alleles per locus, one allele contributing 0 to the phenotypic value and the other contributing 1, the overall genotypic (=phenotypic, as no environmental effects are assumed) value being the sum of the allelic values. Each distribution is generated by drawing at random 1000 individuals with n loci with allelic frequency per locus of 0.5. The theoretical distribution can be generated by using the coefficients of the binomial expansion $(p + q)^n$, where p is the frequency of one allele and $q = 1 - p$.

Pilt 2-14A

Keskne hajuvusstatistik on **dispersioon** (***variance***). Populatsiooni dispersioon on defineeritud valemiga

$$\sigma^2 = \sum_{i=1}^{N} (x_i - \mu)^2 / N$$

ehk siis on iga üksiku objekti väärtus lahutatud populatsiooni keskmisest, vahed on ruutu tõstetud, kokku liidetud ja jagatud objektide arvuga. Mida suurem on dispersioon, seda suurem on hajuvus populatsioonis, ehk siis seda rohkem objektid üksteisest erinevad.

Dispersiooni saab jagada komponentideks.

Näide. Olgu meil elukate (viis tükki) fenotüübiväärtus jagatud genotüübiväärtuseks ja keskkonnahälbeks. Näeme, et genotüübiväärtuste dispersioon ja fenotüübiväärtuste dispersioon annavad kokku fenotüübiväärtuste dispersiooni, just nii nagu vastavad väärtused ise seda teevad. Komponente võib väljendada ka protsentides.

nr.	gen. v.	kesk. h.	fen. v.
1	11	-1	10
2	12	0	12
3	13	2	15
4	14	0	14
5	15	-1	14
disp	**2.5**	**1.5**	**4.0**
	62.5%	**37.5%**	**100%**

2-27

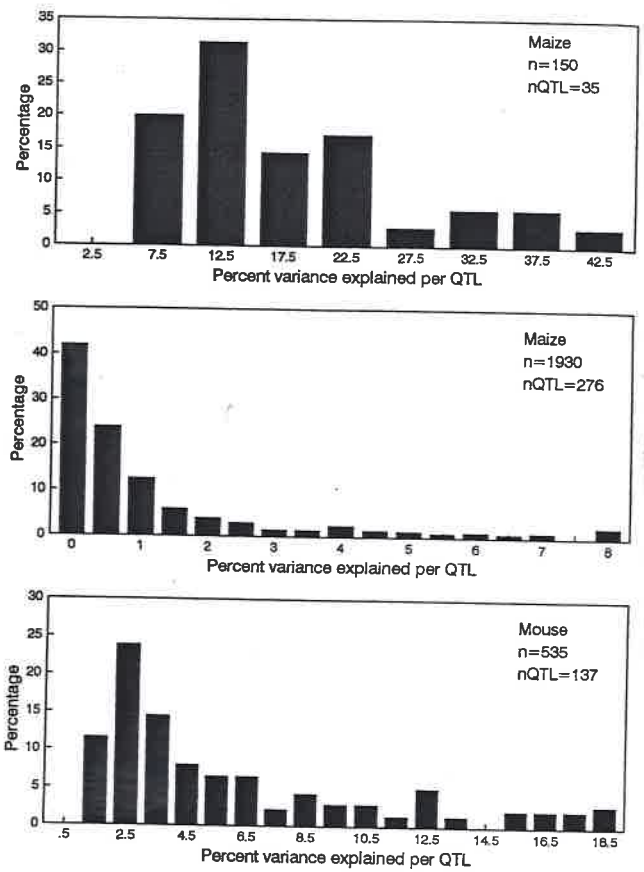
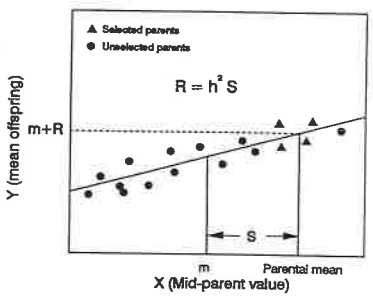


Figure 1.11. Distribution of the magnitude of individual QTL effects. The number of traits examined are 8 [maize, upper plot; Veiboom and Lee (1994)], 25 [middle plot; Edwards et al. (1987)], and 10 [bottom plot; Cheverud et al. (1996)]. Because of overlap of QTL effects, the summed value per trait can exceed 100% (the data shown in Table 1.7 correct for this).

Table 10.1 Approximate values of the heritability of various characters in various animal species. The estimates are rounded to the nearest 5 per cent; their standard errors range from about 2 per cent to about 10 per cent.

	h^2(%)	Ref.
Man		
Stature	65	(1)
Serum immunoglobulin (IgG) level	45	(2)
Cattle		
Body weight (adult)	65	(3)
Butterfat, %	40	(4)
Milk-yield	35	(4)
Pigs		
Back-fat thickness	70	(5)
Efficiency of food conversion	50	(5)
Weight gain per day	40	(5)
Litter size	5	(6)
Poultry		
Body weight (at 32 wks)	55	(7)
Egg weight (at 32 wks)	50	(7)
Egg production (to 72 wks)	10	(7)
Mice		
Tail length (at 6 wks)	40	(8)
Body weight (at 6 wks)	35	(8)
Litter size (1st litters)	20	(9)
Drosophila melanogaster		
Abdominal bristle number	50	(10)
Body size	40	(11)
Ovary size	30	(12)
Egg production	20	(11)



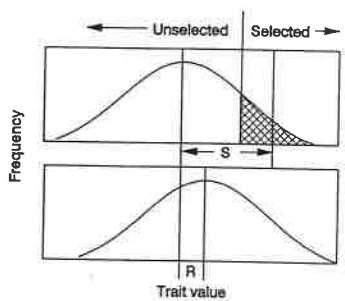


Figure 4.2 Response to directional selection illustrated using the mean offspring on mid-parent regression. The regression is shown in the top panel. The mean value of the population is m, the mean value of the parents is X, and the difference between them is the selection differential S. From the regression, the value of the offspring is $m + R$, where R is the response to selection. The lower two panels show truncation selection. All individuals (or a random selection of the specified group) greater than a certain value are selected as parents. Parents are represented by the hatched region on the right tail of the distribution. The distribution of offspring values is shown in the bottom panel, the mean value having shifted R units with respect to the mean value in the previous generation.

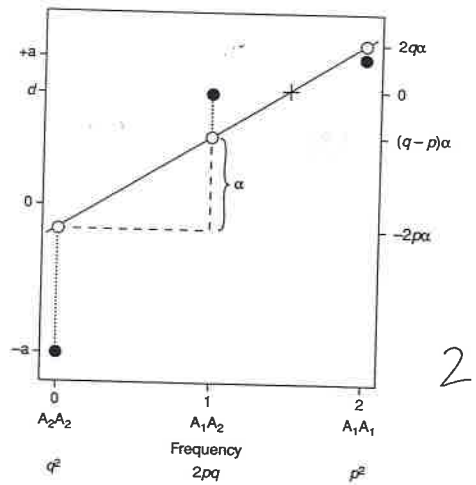


Fig. 7.2. Graphical representation of genotypic values (closed circles), and breeding values (open circles), of the genotypes for a locus with two alleles, A_1 and A_2, at frequencies p and q, as explained in the text. Horizontal scale: number of A_1 genes in the genotype. Vertical scales of value: on left – arbitrary values assigned as in Fig. 7.1; on right – deviations from the population mean. The figure is drawn to scale for the values: $d = \frac{3}{4}a$, and $q = \frac{1}{4}$.

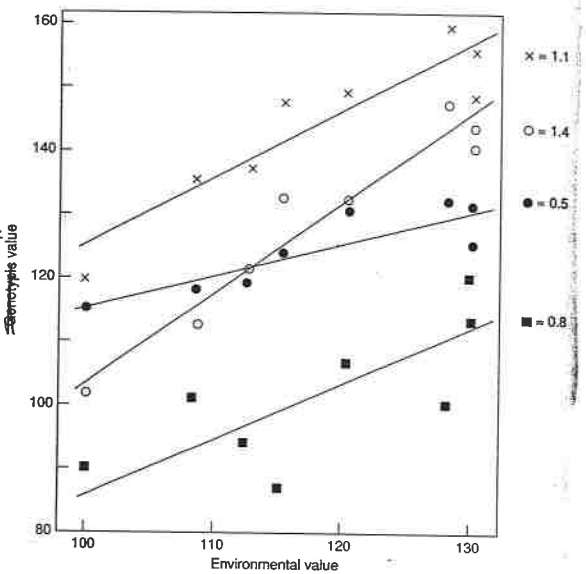


Fig. 8.2. Plant height (cm) of *Nicotiana rustica* genotypes grown in eight specific environments as explained in Example 8.3. (These are genotypes numbered 3, 6, 7, 10 in Tables 42 and 44 of Mather and Jinks, 1982.)

Table 10.2

Relatives	*Covariance**	*Regression (b) or correlation (t)*
Offspring and one parent	$\frac{1}{2}V_A$	$b = \frac{1}{2}h^2$
Offspring and mid-parent	$\frac{1}{2}V_A$	$b = h^2$
Half sibs	$\frac{1}{4}V_A$	$t = \frac{1}{4}h^2$
Full sibs	$\frac{1}{2}V_A + \frac{1}{4}V_D + V_{Ec}$	$t \geq \frac{1}{2}h^2$

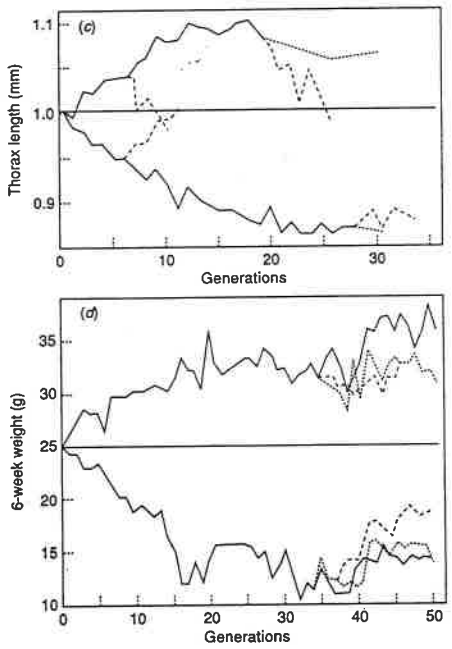
*The contributions of epistatic interactions are ignored, and so are the possible environmental contributions to relatives other than full sibs.

1-21

Table 19.1 Some examples of phenotypic, genetic, and environmental correlations. The estimates quoted refer to particular populations in particular circumstances; they should not be taken as generally applicable.

	r_P	r_A	r_E
Man (Grundbacher, 1974)			
Serum immunoglobulin levels, IgG: IgM	0.20	0.07	0.31
Cattle (Barker and Robertson, 1966)			
Milk-yield: butterfat % (1st lactation)	−0.26	−0.38	−0.18
Milk-yield in 1st: 2nd lactations	0.40	0.75	0.26
Pigs (Smith, King, and Gilbert, 1962)			
Weight gain: backfat thickness	0.00	0.13	−0.18
Weight gain: efficiency	0.66	0.69	0.64
Poultry (Emsley, Dickerson, and Kashyap, 1977)			
Body weight: egg weight	0.33	0.42	0.23
Body weight: egg production	0.01	−0.17	0.08
Egg weight: egg production	−0.05	−0.31	0.02
Mice (Rutledge, Eisen, and Legates, 1973)			
Body weight: tail length	0.45	0.29	0.56
Drosophila melanogaster (Sheridan *et al.*, 1968)			
Bristle number, abdominal: sternopleural	0.14	0.41	0.06

2-22



(c) *Drosophila melanogaster*, thorax length. (*After F. W. Robertson, 1955.*)
(d) Mouse, six-week body weight. (*Adapted from Roberts, 1966b.*)
Dashed lines are responses to selection in the reverse direction; dotted lines are responses to natural selection, with artificial selection suspended.
(*All figures redrawn from the above sources with permission of the authors and publishers.*)

2-13

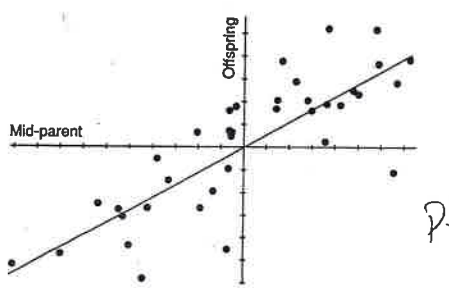


Fig. 10.1. Regression of offspring on mid-parent for wing length in *Drosophila*, as explained in Example 10.2. Mid-parent values are shown along the horizontal axis, and mean value of offspring along the vertical axis. (*Drawn from data kindly supplied by Dr E. C. R. Reeve.*)

Pset 2-20