Quantitative Genetics I

Phenotypic value Genotypic value Environmental deviation P = G + E $P_i = G + E_i$, i = 1, 2, ..., n ($\sum E_i = 0$) $\sum P_i = \sum G + \sum E_i$ $= \sum G$ $= nG \longrightarrow \overline{P_i} = G$

Mean phenotypic value = genotypic value



No dominance : d = 0Complete dominance : d = aOverdominance : d > aDegree of dominance : $\frac{d}{a}$

Example 7.1 : a = 4, d = 2

	Genotypes			
	++	+pg	pg pg	
Weight in grams	14	12	6	

Population mean

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Genotype	Frequency	Value	Freq.×Val.
A_1A_1	p^2	а	p^2a
$A_1 A_2$	2 <i>pq</i>	d	2 pqd
$A_2 A_2$	q^2	- <i>a</i>	$-q^2a$
		a(p-q)+2 dpq

contributed by heterozygote

$$M = a(p-q) + 2 dpq$$

$$(n)$$

$$M = a(1-2q) \quad \text{if} \quad d = 0 \quad (\text{ no dominance })$$

 $M = a(1-2q^2)$ if d = a (complete dom.)

Example 7.2 (pg 111): p = 0.9, M = 3.56 (13.56) p = 0.4 M = 11.76 q = 0 (pygmy gene is eliminated), M = 4 (14)

Genotypic value :

Multiple loci :

Assuming no epistasis,

 $\mathbf{M} = \sum a_i (p_i - q_i) + 2 \sum dpq$

Total range in the absence of overdominance is $2 \sum a_i$ Theoretical limits of potential variation (selection limits) are $(-\sum a_i, \sum a_i)$

Example 7.3 : Color genes in mice

	<i>B</i> –	bb	$2a_B$
С-	95	90	5
$c^{e}c^{e}$	38	34	4
$2a_c$	57	56	

Conclusion : no epistasis between B and C.

Average effect of a particular allele

Parents pass on their genes and not their genotype to next generation. Average effect of a particular allele depends on genotypic values and gene frequencies.

Type of Gamete	Geno and	otypic v freque	values ncies	Mean value	Population mean	Average effect
	A_1A_1	A_1A_2	A_2A_2			
	a	d	a			
A_1	p	q		pa + qd	М	q[a+d(q-p)]
A_2		р	q	-qa + pd	Μ	- $p[a+d(q-p)]$

Definition of average effect :

$\alpha_1 = pa + qd - [a(p-q) + 2dpq]$
= q[a + d(q - p)]
$\alpha_2 = -p[a + d(q - p)]$

Multiple alleles :

Average effect of the gene substitution :

$$A_{1}A_{2} \rightarrow A_{1}A_{1} \qquad p(a-d)$$

$$d \qquad a$$

$$A_{2}A_{2} \rightarrow A_{1}A_{2} \qquad q(d+a)$$

$$-a \qquad d$$

$$\alpha = p(a-d) + q(d+a) = a + d(q-p)$$
Relationship between α, α_{1} and α_{2} :
$$\alpha = \alpha_{1} - \alpha_{2}$$

$$\alpha_{1} = q\alpha$$

 $\alpha_2 = -p\alpha$

Example 7.4 : (pg 114)

	q = 0.1	q = 0.4
Average effect of +: $\alpha_1 =$	+0.24	+1.44
Average effect of pg: $\alpha_2 =$	-2.16	-2.16
$\alpha = \alpha_1 - \alpha_2 = $	2.40	3.60

Breeding value of an individual

The value of an individual, judged by the mean value of its progeny, is called the breeding value of an individual.

Average value refers to allele, and breeding value refers to genotype.

The breeding vale of an individual is the average effect of the two alleles it carries.

Genotype	Breeding value
A_1A_1	$2\alpha_1 = 2qd$
$A_1 A_2$	$\alpha_1 + \alpha_2 = (q - p)\alpha$
A_2A_2	$2\alpha_2 = -2p\alpha$

Example 7.5 : (pg 115)

	М	Breeding ve	Breeding values		
41 		++	+pg	pg pg	
q = 0.1	13.56	+0.48	-1.92	-4.32	
q = 0.4	11.76	+2.88	-0.72	-4.32	

One can't speak of an individual's breeding value without specifying the population in which it is to be mated.

Multiple alleles :

Epistasis :

Mean breeding value is zero

 $p^{2}(2q\alpha) + 2pq(q-p)\alpha + q^{2}(-2p\alpha) = 0$

Variation in breeding value = additive effects of genes Preading value is denoted by A

Breeding value is denoted by A.

Expected breeding value of an individual is the average of the breeding values of its parents.

Different offspring of the same parents will differ in breeding value.

Breeding value = expected phenotypic value

$$\overline{P}_0 = \overline{A}_0 = \frac{1}{2}(A_s + A_d)$$

Dominance deviation

G = A + D

The dominance deviation arises from the property of dominance among the allele at a locus.

Dominance deviations are interactions between alleles, or within – locus interaction.

Example 7.6 :

	q = 0.1	M = 13.5	56	q = 0.4: $M = 11.76$			
	++	+pg	pg pg	++	+pg	pg pg	
Frequency	0.81	0.18	0.01	0.36	0.48	0.16	
Genotypic value, G	+0.44	-1.56	-7.56	+2.24	+0.24	-5.76	
Breeding value, A	+0.48	-1.92	-4.32	+2.88	-0.72	-4.32	
Dominance dev., D	-0.04	+0.36	-3.24	-0.64	+0.96	-1.44	

Figure 7.2 : linear regression of genotypic value on number of genes



 Table 7.3
 Values of genotypes in a two-allele system, measured as deviations from the population mean.

. Population mean: M = a(p - q) + 2dpq

• Average effect of gene substitution: $\alpha = a + d(q - p)$

	Genotypes			
	$\overline{A_1A_1}$	A ₁ A ₂	A ₂ A ₂	
Frequencies Assigned values	p^2 a	2pq d	q^2 -a	
Deviations from population mean:	pa-alp-g).	-2dpg = acp2-p+ = acpcp-12	+93-aC-P8+6	
Genotypic value	$\begin{cases} 2q(a-pd) \\ 2q(\alpha-qd) \end{cases}$	a(q-p) + d(1-2pq) (q-p)\alpha + 2pqd	$\frac{-2p(a+qd)}{-2p(\alpha+pd)}$	
Breeding value	$2\kappa\alpha$	$(q-p)\alpha$	$-2p\alpha$	
Dominance deviation	$-2q^{2}d$	2pqd	$-2p^2d$	

Sum of dominance deviation is zero

Interaction deviation

$$G = G_A + G_B + I_{AB}$$
$$G = A + D + I$$
$$\sum A = \sum D = \sum I$$

Example 7.7:

	B-	bb	Diff.
C-	1.44	0.77	0.67
c ^e c ^e	0.94	0.77	0.17
Diff.	0.50	0.00	

Homework: If there were a locus, overdominant with respect to a metric character, with the genotypic values given below, (1) what gene frequency would give a random-mating population its maximum mean value, and what would the mean be? (2) Find the breeding values and dominance deviations of the three genotypes when the mean is at its maximal value.

A_1A_1	A_1A_2	A_2A_2
110	150	90