

**UNIVERSITY OF MARYLAND**  
**COLLEGE OF AGRICULTURE AND NATURAL RESOURCES**  
**ANSC327/627 (Molecular and Quantitative Animal Genetics), Spring 2007**  
**Final Examination (Siewerdt)**  
**College Park, May 12, 2007**

**ANNOTATED KEY**

**Question 1.**

There are  $m=4$  alleles (D1, D2, D3, and D4), so there are  $m=4$  different homozygotes and  $\frac{m(m-1)}{2} = 6$  different heterozygotes, for a total of 10 possible genotypes.

The homozygotes are: D1D1, D2D2, D3D3, and D4D4.

The heterozygotes are: D1D2, D1D3, D1D4, D2D3, D2D4, and D3D4.

**Question 2.**

Hardy-Weinberg Equilibrium is not affected by gene action, so the presence or absence of dominance is not an assumption for Hardy-Weinberg Equilibrium.

**Question 3.**

It is impossible for a population that has more than 50% of heterozygotes to be in Hardy-Weinberg Equilibrium, so the populations 1 and 5 can be eliminated without any calculations. Equilibrium in the other three populations can be verified by computing allele frequencies and then checking if the genotypic frequencies are determined by the allele frequencies. With only two alleles in the locus, it is sufficient to obtain the frequency of one allele (any one of them) and then try to compute the frequency of the corresponding homozygote genotype. If these numbers don't match, then the population will not be in Hardy-Weinberg Equilibrium.

Population 2:  $f(GG) = 0.16$ ,  $f(Gg) = 0.16$ ,  $f(gg) = 0.68$

Here,  $f(G) = f(GG) + \frac{1}{2} f(Gg) = 0.16 + \frac{1}{2} (0.16) = 0.24$

Now  $f(G) \times f(G) = 0.24 \times 0.24 = 0.0576$ , which is different from  $f(GG)$ .

Population 2 is not in Hardy-Weinberg Equilibrium.

Population 3:  $f(GG) = 0.36$ ,  $f(Gg) = 0.48$ ,  $f(gg) = 0.16$

Here,  $f(G) = f(GG) + \frac{1}{2} f(Gg) = 0.36 + \frac{1}{2} (0.48) = 0.60$

Now  $f(G) \times f(G) = 0.60 \times 0.60 = 0.36$ , which is equal to  $f(GG)$ .

Population 3 is in Hardy-Weinberg Equilibrium.

Population 4:  $f(GG) = 0.81$ ,  $f(Gg) = 0.18$ ,  $f(gg) = 0.01$

Here,  $f(G) = f(GG) + \frac{1}{2} f(Gg) = 0.81 + \frac{1}{2} (0.18) = 0.90$

Now  $f(G) \times f(G) = 0.90 \times 0.90 = 0.81$ , which is equal to  $f(GG)$ .

Population 4 is in Hardy-Weinberg Equilibrium.

For completeness, in population 1,  $f(G) = 0.45$ ; the predicted  $f(G) \times f(G) = 0.2025$  is different from  $f(GG) = 0.10$  (not in Equilibrium). In population 5,  $f(G) = 0.5$ ;  $f(G) \times f(G) = 0.25$  is different from the observed  $f(GG) = 0$  (not in Equilibrium either).

**Question 4.**

For backfat thickness, the phenotypic mean for the heterozygote genotype lays exactly at the midpoint between the two homozygote genotypes, so gene action in that locus is additive. For litter size, the phenotype of the heterozygote is larger than either of the homozygotes, so the gene action is of overdominance for this trait. You can also formally calculate the quantities  $a$  and  $d$  in each case and draw conclusions from those values:

Backfat thickness:  $a = \frac{1}{2}(32 - 22) = 5mm$        $d = 27 - \frac{1}{2}(32 + 22) = 0mm$

Litter size:  $a = \frac{1}{2}(9.2 - 10.3) = -0.55$  piglets       $d = 11.7 - \frac{1}{2}(9.2 + 10.3) = 1.95$  piglets

For backfat thickness  $d = 0$ , thus an additive effect. For litter size,  $d > a$  indicates overdominance.

### Question 5.

The coancestry of two full-sibs is 0.25, given that their parents are not related and the neither is inbred. This result can be found using the drawing on the right and the recurring formula for determination of coancestry:

$$f_{LM} = \frac{1}{4}(f_{AA} + f_{BA} + f_{AB} + f_{BB})$$

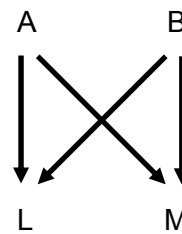
$$f_{LM} = \frac{1}{4}\left(\frac{1}{2} + 0 + 0 + \frac{1}{2}\right) = \frac{1}{4} = 0.25$$

The assumption that A and B are not inbred is necessary when  $f_{AA}$  and  $f_{BB}$  are computed. For example,

$$f_{AA} = \frac{1}{2}(1 + F_A) = \frac{1}{2}(1 + 0) = \frac{1}{2}. \text{ (The same result is valid for B)}$$

If A was inbred, than the coancestry of A with itself would be higher than  $1/2$  and that would, in turn, increase the coancestry between L and M.

(It is assumed that parents A and B are neither related nor inbred)



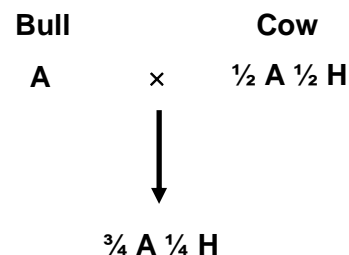
### Question 6.

The fraction of the phenotypic variance that is explained by the genotypic variance is the heritability, in the broad sense (not the repeatability) of a trait. But the repeatability is the upper limit of the heritability, so the heritability can be, at most,  $h^2 = 0.40$ ; that happens when all the genetic variation is additive in nature and when there is no variation due to permanent environmental effects. The improvement in accuracy by collecting a second record in each animal will not increase by the repeatability, but only by a fraction of it. Finally, genetic progress due to selection is a fraction of the selection differential; this fraction is the heritability of the trait, not the repeatability, so genetic progress can be, at most, 40% of the selection differential, not exactly 40% (it will usually be less).

### Question 7.

The progeny will have 50% individual heterosis because in half the loci it will receive an allele from the Holstein breed (from the cow) that will necessarily be combined with an Ayrshire allele (received from the bull). In the other half of the loci there will be two alleles from the Ayrshire breed, so no heterosis will be accrued.

The progeny will have 100% maternal heterosis because the mother has 100% individual heterosis (all her loci have one allele from the Holstein breed and one allele from the Ayrshire breed). There is no paternal heterosis expressed on the progeny because the bull is purebred.



**Question 8.**

Suggestion: Selection is aimed at accumulation of favorable alleles. Heritability tells us if selection for a trait will be successful. If most of the genetic action is of dominance, then crossbreeding may be a more suitable strategy because it is the combination of alleles in a single locus that yields higher production. These strategies are not mutually exclusive. Most commercial breeding programs combine selection in individual breeds or lines and then cross these lines to produce the animals for the market.

**Question 9.**

(a) There is no selection done on the males. This is equivalent to assuming random selection on males, thus there the selection differential on the males is zero:  $S_m = 0$  eggs. In the females the selection differential is:  $S_f = 267 - 227 = 40$  eggs. Since half of the genes in the progeny will come from either gender, the combined selection differential is the average of both selection differentials:

$$S = \frac{1}{2} (S_m + S_f) = \frac{1}{2} (0 + 40) = 20 \text{ eggs.}$$

(b) The predicted genetic progress is obtained by using the breeder's equation:

$$\Delta G = h^2 \times S = (0.18) \times (20) = 3.6 \text{ eggs.}$$

(c) After 5 generations of selection, the hens in this flock will be laying  $227 + 5 \times 3.6 = 245$  eggs.

**Question 10.**

Suggestion: The annual genetic progress is inversely proportional to the generation interval. When we replace breeders rapidly, or when we make early selection decisions, we reduce the generation interval and increase  $\Delta G_a$ . For example, if all rams are replaced every year, rather than only 50% of those, then the generation interval for males will be reduced from 1.5 years to 1 year, corresponding to an additional 50% of speed in genetic progress per time unit, on the males.

**Question 11.**

Suggestion: Epistasis is the interaction between alleles in different loci. Gene action in a locus may be variable depending on the genotype in another locus. The interaction (synergy) between enzymes produced by genes in different loci may trigger reactions that would not occur when only one of the enzymatic products is present.

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