**Answers exercise Inheritance of variability**

1. When the population derives from a single sire and dam, the between family variance equals zero. Moreover, when sire and dam are fully inbred, the genetic variance due to Mendelian segregation is also zero. Hence, in this population, the genetic variance equals zero. Thus Var(P) = Var(E) = 0.7, and the phenotypic standard deviation equals 0.84, indicating a proportional reduction of 16%. Hence, fully removing the genetic variance has relatively little impact on variability.

2. In this population, the environmental variance equals 0.7 + 0.1 = 0.8. Because it is a clone, there is no genetic variance within the population. Thus phenotypic variance equals 0.8.

3. The sire explains 25% of the additive genetic variance. Hence, within family variance equals 0.75Var($A_M$) + Var(E). The offspring on average inherit half the breeding value of the sire for environmental variance. Hence, in the offspring expected Var(E) = 0.7 + 0.5*0.1 = 0.75. This value is larger than Var(E), illustrating that this sire produces offspring that are more variable than on average. The full within family variance equals 0.75*0.3 + 0.75 = 0.975. For "the average" sire, the within-family variance would equal 0.925.

4. The exponential model is approximately multiplicative. Hence, $A_{v,add}$ = Var(E)*$A_{v,exp}$ , so that 0.1 ≈ 0.7* $A_{v,exp}$, given $A_{v,exp}$ = 0.14.

5. When breeding values differ approximately a factor Var(E), then the variance of breeding values must differ approximately a factor Var(E)$^2$. Hence, Var($A_{v,add}$) = Var(E)$^2$Var($A_{v,exp}$) giving Var($A_{v,exp}$) = 0.0204.

6. $GCV_v$ = sd($A_v$)/Var(E)_average = 0.1/0.7 ≈ 0.14.

7. In the exponential model, the $GCV_v$ is given by the genetic standard deviation of the variance, $GCV_v$ = √0.0204 ≈ 0.14. The the exponential model directly gives an estimate of the $GCV_v$, you should not divide by the mean environmental variance (This is because the model is multiplicative).

8. You can judge this by considering the genetic coefficient of variation, sd($A_v$)/Var(E). This equals 0.1/0.7 = 0.14, indicating that the genetic standard deviation is 14% of the mean trait value (the trait being Var(E)). This quite large, larger than for most usual traits in livestock. If we would have an intensity of 2 and an accuracy of 0.5, we could reduce Var(E) by 14% in a single generation.

9. On the standard deviation scale, the genetic coefficient of variation is half as large as on the variance scale; $GCV_{SD} = \frac{1}{2}GCV_v = 0.07$. Thus reducing the standard deviation goes slower than reducing the variance. In other words, if you reduce the variance by e.g. 10%, then the standard deviation is reduced by only ~5%. Usually we are interested in the standard deviation ☹.

10. -1 x 0.5 x 0.14 = -0.07 = minus 7%.

11. The selection differential is the difference in P$^2$ before and after selection. Because the mean P is zero, the mean P$^2$ equals the variance. Thus P$^2$ before selection equals 1. The lowest value we can ever get is P$^2$ = 0, which occurs when all selected animals precisely have the average phenotype of P = 0. Hence, when selecting against P$^2$ we can never get a selection differential greater than S = −1.

12. $h_v^2 = 0.01/(2*1^2 + 3*0.01) = 0.0049$.

13. With mass selection on $P^2$, the accuracy is the square root of the heritability of the variance, $r_{IH}$ = sqrt(0.01/(2*1$^2$ + 3*0.01) = 0.07. Because heritability for variance is the regression coefficient of Av on $P^2$, we can use R = $h_v^2$ S = 0.0049*-1 = -0.0049. Thus, Var(E) in the next generation equals 0.695, a very small reduction. This illustrates that stabilizing selection reduces the variance only very slowly. This slow response has two reasons: First, accuracy is very small. Second, the selection differential is limited to -1.

14. Even though there is no genetic correlation between effects on the mean and variance, we will be getting response in the variance, because selection on P also creates a selection differential on $P^2$. Animals with high breeding values for variance are more likely to be in the tail of the distribution, and are thus preferentially selected when applying truncation selection. Thus mass selection for higher trait-values will also increase the variance of trait values.