Appendices to Selection and Genetic Change

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Appendix 1. Calculation of selection intensity from the proportion selected individuals.

In order for the following procedure to work we need to assume that the selection criterion is ***normally distributed***. (This is not a strictly valid assumption in all situations, e.g., when the candidates are the retained individuals from a previous step of selection.). We also have to assume ***truncation selection***, i.e. all individuals above (or below) a certain value are retained, they get equal number of offspring, and all other individuals are discarded. This is not always the case in practice because individuals which should have been selected might be discarded due to some additional information about them and others, not qualified according to the selection criterion might be selected owing to some other reason. In such a situation, the point where the distribution of selection criteria for the candidates is truncated into selected and not selected is consequently not distinct. An approximate truncation point can however be found from the proportion selected.

Figure 1 illustrates the situation where a upper proportion p is selected according to a selection criterion X. Note that X can be ***any*** selection criterion, e.g., a phenotypic value, a selection index based on information on several traits and sources of information, or a predicted breeding value from a mixed linear model. In Figure 1 the variable X is transformed to a standardized variable x where $x = (X - \mu_X)/\sigma_X$, i.e. a variable with mean zero and standard deviation equal to unity. The purpose of the standardization is to enable use of the standardized normal curve as reference distribution.

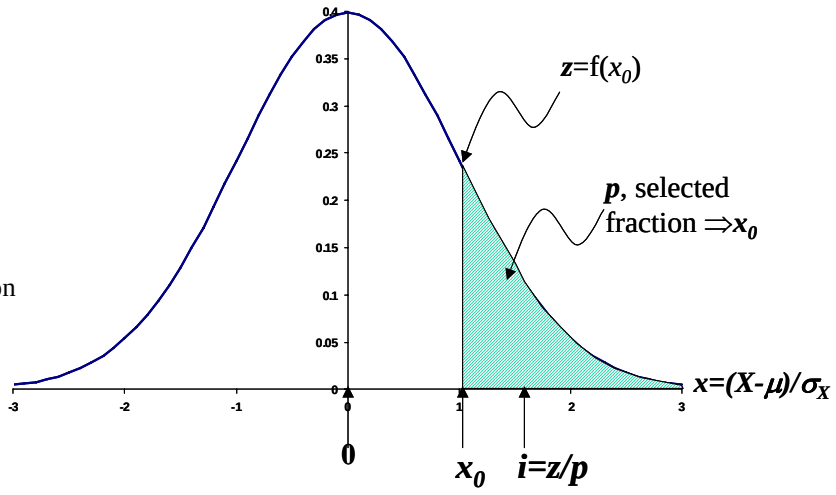

Figure 1. Graphic illustration of the calculation of selection intensity (i) from the proportion selected (p) for a standardized selection criterion x.

The selected fraction p corresponds to a truncation value x_0, above which all individuals are selected. We now need to find the selection differential in terms of the x-scale, being the same as the mean of x for the fraction above x_0. The average is found as a weighted mean of the x-values between x_0 and ∞, using the "frequency" or density of each possible x-value as weights:

$$i = \frac{\int_{x_0}^{\infty} f(x)\, x\, dx}{\int_{x_0}^{\infty} f(x)\, dx} = \frac{f(x_0)}{p} = \frac{z}{p} \qquad [1]$$

The result turns out to be very simple, i.e. the ratio of the normal density function or "height of the normal curve", z, at the truncation value and the proportion p

that is selected. The standardized selection differential obtained here is called the ***selection intensity*** and it is the selection differential of the selected group expressed in standard deviation units of the selection criterion.

Values of z can be calculated from the normal density equation for a given threshold value x_0:

$$z = f(x_0) = \frac{1}{\sqrt{2\pi}} \exp(-\frac{x_0^2}{2}) \qquad [2]$$

and selection intensity can be calculated from [1].

A more common approach to calculate selection intensity values is to use tabulated values of i for various proportions selected. One such tabulation is given in Table 1.

Table 1. Truncation point (x_0) and selection intensity (i) for different proportions selected (p in %) in large samples. Based on Falconer and Mackay (1996)

p (%)	x_0	i	p (%)	x_0	i	p (%)	x_0	i
0.01	3.719	3.960	1.0	2.326	2.665	16	0.995	1.521
0.02	3.540	3.790	1.2	2.257	2.603	17	0.954	1.489
0.03	3.432	3.687	1.4	2.197	2.549	18	0.915	1.458
0.04	3.353	3.613	1.6	2.144	2.503	19	0.878	1.428
0.05	3.291	3.554	1.8	2.097	2.459	20	0.842	1.400
0.06	3.239	3.507	2.0	2.054	2.421	21	0.806	1.372
0.07	3.195	3.464	2.2	2.014	2.386	22	0.772	1.346
0.08	3.156	3.429	2.4	1.977	2.353	23	0.739	1.320
0.09	3.121	3.397	2.6	1.943	2.323	24	0.706	1.295
0.1	3.090	3.367	2.8	1.911	2.295	25	0.674	1.271
0.12	3.036	3.313	3.0	1.881	2.268	26	0.643	1.248
0.14	2.989	3.273	3.2	1.852	2.243	27	0.613	1.225
0.16	2.948	3.234	3.4	1.825	2.219	28	0.583	1.202
0.18	2.911	3.201	3.6	1.799	2.197	29	0.553	1.180
0.20	2.878	3.170	3.8	1.774	2.175	30	0.524	1.159
0.22	2.848	3.142	4.0	1.751	2.154	31	0.496	1.138
0.24	2.820	3.117	4.2	1.728	2.135	32	0.468	1.118
0.26	2.794	3.093	4.4	1.706	2.116	33	0.440	1.097
0.28	2.770	3.070	4.6	1.685	2.097	34	0.413	1.078
0.30	2.748	3.050	4.8	1.665	2.080	35	0.385	1.058
0.32	2.727	3.030	5.0	1.645	2.063	36	0.359	1.039
0.34	2.706	3.012	5.5	1.598	2.023	37	0.332	1.020
0.36	2.687	2.994	6.0	1.555	1.985	38	0.306	1.002
0.38	2.669	2.978	6.5	1.514	1.951	39	0.279	0.984
0.40	2.652	2.962	7.0	1.476	1.918	40	0.253	0.966
0.42	2.636	2.947	7.5	1.440	1.887	41	0.228	0.948
0.44	2.620	2.932	8.0	1.405	1.858	42	0.202	0.931
0.46	2.605	2.918	8.5	1.372	1.831	43	0.176	0.913
0.48	2.590	2.905	9.0	1.341	1.804	44	0.151	0.896
0.50	2.576	2.892	9.5	1.311	1.779	45	0.126	0.880
0.55	2.543	2.862	10	1.282	1.755	46	0.100	0.863
0.6	2.512	2.834	11	1.227	1.709	47	0.075	0.846
0.65	2.484	2.808	12	1.175	1.667	48	0.050	0.830
0.70	2.457	2.784	13	1.126	1.627	49	0.025	0.814
0.75	2.432	2.761	14	1.080	1.590	50	0.000	0.798
0.8	2.409	2.740	15	1.036	1.554	60	-0.253	0.644
0.85	2.387	2.720				70	-0.524	0.497
0.90	2.366	2.701				80	-0.842	0.350
0.95	2.346	2.683				90	-1.282	0.195
1.0	2.326	2.665				95	-1.645	0.109

To calculate values of i for p greater than 50%:

Take x_0 and i tabulated for (1-p), give x_0 a negative sign, multiply i by (1-p)/p retaining the positive sign

E.g. for p =80%, take x_0 for 20% and change sign (-0.842), and multiply 1.4(1-0.8)/0.8= 0.35

Appendix 2. Calculating selection intensity for several fractions

It is not uncommon that several fractions are selected for different purposes from the same population. For instance, a top fraction p_1 of tested sires may be chosen for intensive use in an artificial insemination program while a fraction p_2 below them is selected as natural service sires within individual farms. With the symbols given in Figure 2 the selection intensity for the top fraction is:

$$i_1 = \frac{z_1}{p_1} \qquad [3]$$

and the selection response can be predicted as described previously.

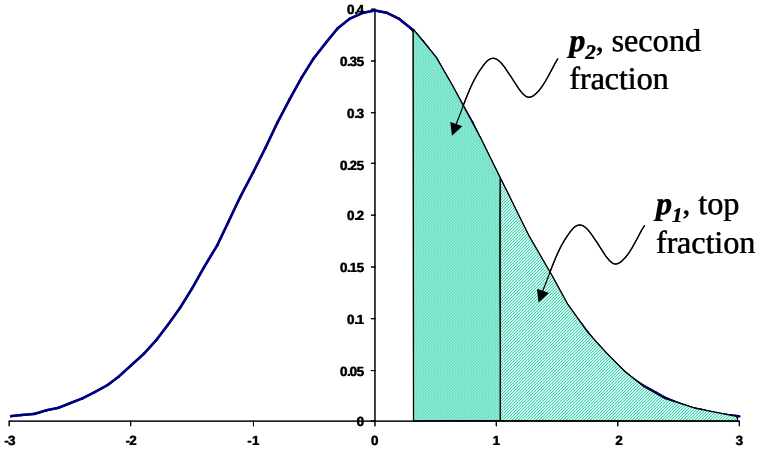

Figure 2. Graphic illustration of selection from two top fractions.

We can calculate the selection intensity i_2 for the second fraction p_2 from the selection intensity, i, for the two top fractions together (which can be found from Table 1 for a fraction (p_1+p_2)). This selection intensity can actually be thought of as the weighted mean of the selection intensities i_1 and i_2 of the two fractions separately, weighted by their respective relative proportions, i.e.:

$$i = \frac{p_1}{p_1 + p_2} \times i_1 + \frac{p_2}{p_1 + p_2} \times i_2 = P_1\, i_1 + P_2\, i_2 \qquad [4]$$

where $P_1 = p_1/(p_1 + p_2)$ and $P_2 = p_2/(p_1 + p_2)$ are the weights or relative sizes of the two fractions. Solving for i_2 gives:

$$i_2 = \frac{i - P_1\, i_1}{P_2} \qquad [5]$$

and the selection response can be predicted as before.

Example: Assume that both top proportions constitute 38%, and the top proportion p_1=15% (i.e. p_2=23%). From, i=1.002 and i_1=1.554, then:

$$i_2 = \frac{1.002 - \frac{0.15}{0.38}1.554}{\frac{0.23}{0.38}} = 0.642$$

Appendix 3. Selection intensity in small samples

The values in Table 1 are exactly correct only when the number of individuals among which to select is large (at least 500). When few individuals are measured, the probability of finding extreme animals is decreased, and thus a certain proportion selected will deviate less from the mean than when selecting the same proportion from a large population.

If we assume that we select the top ten percent from a large population we would expect a selection intensity of 1.755 (Table 1). However, if we only have 100 individuals measured and select 10 of those (i.e. 10%) we would only get a selection intensity of 1.73, and if we selection the best one of 10 measured individuals i=1.539. If we have few individuals to select among, the effect can be a quite drastically reduced selection intensity, compared with that computed from Table 1, and we should be careful not to overestimate the expected genetic gain from the selection.

Tables for selection intensity in small samples are found in e.g. Becker (1984) or from order statistics (Fisher and Yates, 1963). A rough approximation given by Henderson, is to take i for the large sample size (e.g. Table 1) and subtract 0.25/n, where n is the number of individuals selected, i.e.:

$$i^{*}_{\text{small sample}} = i_{\text{large sample}} - \frac{0.25}{\text{Number of individuals selected}}$$

If we do that for the two examples above we get 1.73 and 1.505 (cf. 1.73 and 1.539).

Appendix 4. Calculation of selection response in each breeding goal trait

The general equation ($i\, r_{TI}\, \sigma_T$) gives the response in the total breeding goal. Sometimes it is, however, interesting to get the response in each breeding goal trait separately, for instance to check whether the response in each trait is favourable. We can calculate that by regressing each breeding goal trait (*j*) on the selection response in the index:

$$\Delta T_{gj} = b_{T_j/I} i\sigma_I = \frac{\mathrm{cov}(I,T_j)}{\sigma_I^2} i\sigma_I = \mathrm{cov}(I,T_j)\, i/\sigma_I \qquad [6]$$

Now, the covariance between the index and a certain breeding goal trait *j* can be written as:

$$\mathrm{cov}(I,T_j) = \mathrm{cov}(\mathbf{b}'\mathbf{X},T_j) = \mathbf{b}'\mathrm{cov}(\mathbf{X},T_j) = \mathbf{b}'\mathbf{g_j} \qquad [7]$$

where **b'X** is the vector of index weights multiplied by the column vector of index traits and $\mathrm{cov}(\mathbf{X},T_j)$ (the covariances between index traits and the breeding goal trait T_j) is that column of the matrix **G** (from selection index equations **Pb=Gv**) which corresponds to trait *j*, $\mathbf{g_j}$. Thus equation [6] becomes:

$$\Delta T_{gj} = \mathbf{b}'\mathbf{g}_j\, i/\sigma_I \qquad [8]$$

or:

$$\mathbf{\Delta T_g} = \mathbf{b}'\mathbf{G}\, i/\sigma_I \qquad [9]$$

where $\mathbf{\Delta T_g}$ is a row vector of genetic responses in each of the *m* breeding goal traits.

Appendix 5. Genetic gain with different number of progeny within path

In dairy cattle both young bulls (bulls that are subjected to progeny testing) and proven bulls may produce daughters. However, the young bulls will only get one batch of daughters, whereas the selected bulls also will get a second batch, some years after. In this situation we can calculate ***a weighted average*** of the two fractions of bulls producing daughters (path SD), both for the selection response and the generation interval:

$$\Delta T_{SD} = p_{YB}\Delta T_{YB} + (1 - p_{YB})\Delta T_{PB}$$

and

$$L_{SD} = p_{YB}L_{YB} + (1 - p_{YB})L_{YB}$$

where p_{YB} is the proportion of daughters produced by young bulls (with ΔT_{YB} and L_{YB}) and (1 – p_{YB}) the proportion produced by proven bulls (with ΔT_{PB} and L_{PB}). In this example we can assume that ΔT_{YB}=0.

Appendix 6. Efficiency of indirect versus direct selection

In the main text we have seen that the response to indirect selection is:

$$\Delta T_{2/I_1} = r_{g_{12}} i_1 \; r_{TI_1} \; \sigma_{T_2} \qquad [10]$$

where trait 2 is the trait we want to improve by selecting on trait 1. If we instead select directly on trait 2 the direct response to selection is:

$$\Delta T_2 = i_2 \; r_{TI_2} \; \sigma_{T_2} \qquad [11]$$

The efficiency of indirect response relative to the direct response is then:

$$\frac{\Delta T_{2/I_1}}{\Delta T_2} = \frac{r_{g_{12}} \; i_1 \; r_{TI_1} \; \sigma_{T_2}}{i_2 \; r_{TI_2} \sigma_{T_2}} = \frac{r_{g_{12}} i_1 \; r_{TI_1}}{i_2 \; r_{TI_2}} \qquad [12]$$

If we for simplicity assume that we can select as intensely indirectly as directly (i.e. $i_1 = i_2$) then the efficiency is dependent on the genetic correlation between the two traits and the ratio of accuracies of indirect and direct selection. If the genetic correlation is high and the accuracy of indirect selection is higher than that for direct selection, indirect selection can be more efficient that direct selection.

If we have selection on phenotypic values (when $r_{TI}^2 = h^2$) the efficiency becomes:

$$\frac{\Delta T_{2/P_1}}{\Delta T_2} = \frac{r_{g_{12}} i_1 \; h_1}{i_2 \; h_2} \qquad [13]$$

where h_1 and h_2 are the square root of the heritabilities for the indirect and direct traits, respectively.

Appendix 7. Selection and change in genetic variation

To have a meaningful discussion on how selection influences genetic variation, we first need to determine what kind of genetic model we assume. The two main models are called the *finite locus model* and the *infinitesimal model*.

The finite locus model

The finite locus model is the one commonly used in traditional population genetics, and the simplest version is the single-locus model. This is fully described in population genetics texts, e.g. in Falconer and Mackay (1996), and here we will just show the most important features.

We assume a locus with two alleles, A_1 and A_2, with allele frequencies in the population of p and q, respectively. The genotypes A_2A_2, A_1A_1, and A_1A_2 have genotypic values –a, a, and d, respectively. If we have Hardy-Weinberg equilibrium the genotype frequencies are q^2, p^2, and $2pq$. The genotypic values are all expressed as deviations from the average of the two homozygotes. If d is not equal to zero, there is dominance for the trait (Figure 3).

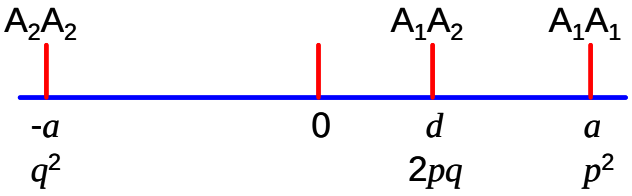

Figure 3. Illustration of single locus genetic model.

Effects on additive genetic variance

The (additive) genetic variance in the finite locus model is a function of the gene frequencies and the genotypic values:

$$\sigma_A^2 = 2pq[a + d(q - p)]^2 \qquad [14]$$

If selection is changing the gene frequencies, then the genetic variance is also changing with selection. If we also have an environmental influence on the trait, then heritability will also change with selection. In Figure 4 the change in additive genetic variance with changing gene frequencies is described for two situations: complete dominance or no dominance (d=1 or 0).

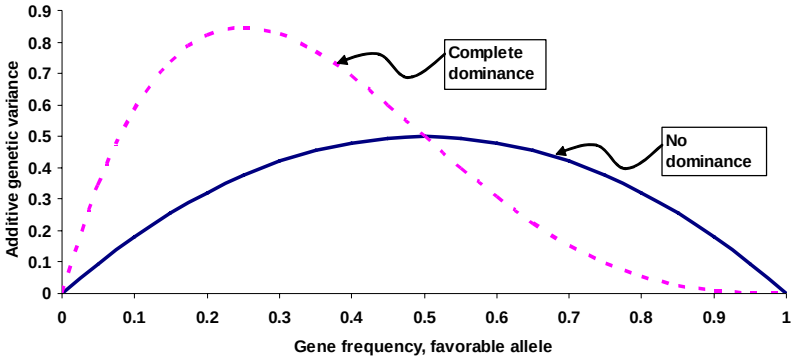

Figure 4. Illustration of the additive genetic variance as a function of gene frequency p for the favorable allele. Two situations: complete or no dominance.

If there is no dominance, the additive genetic variance is largest at the intermediate gene frequency (i.e. p=q=0.5). This can be seen in equation [14], which when d=0 reduces to $2pqa^2$, which is at maximum when p and q are equal[1]. If there is dominance, then the maximum is not at p=0.5 but at lower values (in the graph at p=0.25). Regardless of whether there is dominance or not, one can see that as the gene frequency approaches zero or one, the genetic variance goes to zero. Equally interesting is that, depending on the actual gene frequency at the beginning of selection, selection can actually ***increase*** the genetic variance, even in the single locus model. If we have more than one locus affecting the trait, and the gene frequencies are at different point at the start of selection, and the genotypic effects differ between the loci, the change in genetic variance with selection might be quite unexpected.

Previously, we have seen that we predict selection response by using the heritability; in the simplest case, if we select on phenotypes we predict the response as h^2S. Strictly speaking, this equation only holds for one generation of selection, and if we have the finite locus model, the same initial heritability may not give the same long-term response, because the change in genetic variance may be different. This is illustrated in Figure 5, where various numbers of loci are assumed.

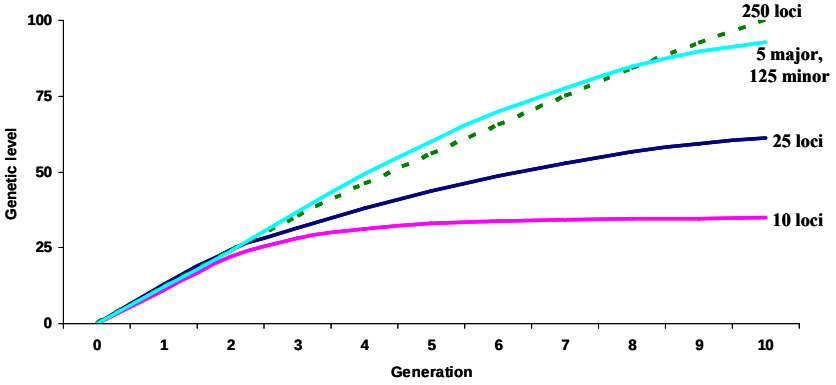

Figure 5. Selection response to phenotypic selection in four populations where the trait is affected by different number of loci but the same heritability. Adapted from Walsh and Lynch (2000)

In the situation with 10 loci all starting at intermediate frequencies, the genetic variance is soon depleted. When 25 loci are affecting the trait, the response is continuing for a longer period, but slows down after some generations. For a situation where 250 loci, all with equal effects are affecting the trait, we have more or less constant and continuous selection response. When there are 5 loci which have large effect on the trait (starting frequency of favourable allele 0.25), and 125 loci with small effects, the response is larger than for the situation with 250 loci with small effects for some generations but then (as the major genes move closer to fixation) the response slows down.

Another complication can arise when the trait is influenced by dominance. If we assume complete dominance of the favorable allele and a high gene frequency of that allele, upward selection may not give any appreciable selection response (Figure 6). This could lead us to believe that we have reached a selection plateau owing to depleted genetic variance. However, if we select downward instead, we can see a fast selection response, showing that there indeed is additive genetic variation.

[1] This can be seen by searching for the maximum of pq by differentiating this with respect to e.g. q: $pq = (1-q)q = q - q^2$; $\dfrac{\partial(q-q^2)}{\partial q} = 1 - 2q = 0$; $q = 0.5$

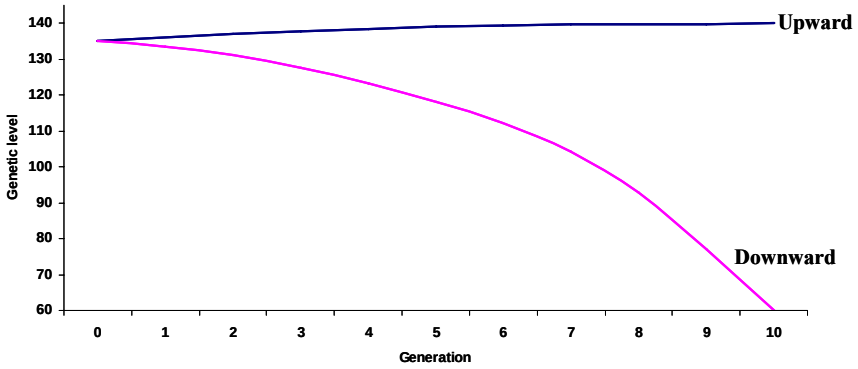

Figure 6. Selection response for a trait with complete dominance of the favorable allele, and a starting frequency of that allele of 0.8. Adapted from Walsh & Lynch (2000).

This phenomenon can intuitively be explained as follows. The genotypes A_1A_2 and A_1A_1 are indistinguishable from each other if we look at their genotypic values. That means that if you select only individuals with the high genotypic values you get both alleles in the proportion they occur in the population. If we assume Hardy-Weinberg equilibrium for simplicity, this would mean that $0.8^2 = 0.64$ are A_1A_1 and $2\times0.2\times0.8 = 0.32$ are A_1A_2. This means that about 17% of the alleles selected are A_2 alleles (compared with 20% before) even though we tried to select only the A_1 allele. On the other hand, if we select only the individuals with the low genotypic values, A_2A_2, we will only select A_2 alleles. Now, with selection on phenotypic rather than genotypic values (with environment blurring the picture), the response will not be as large in any direction, but the same logic still applies. This is the same reasoning which explains why it is so hard to eradicate a recessive allele from the population, the recessive allele will always hitch-hike on the other allele in the heterozygote.

One phenomenon that may help avoid fixation is if there is over-dominance, i.e. if the heterozygote is better than the best homozygote. This is also called *heterzygote advantage*. If this is true for a locus, gene frequencies will stay at intermediate levels, unless the locus becomes fixed by drift.

Effects on genetic covariance

In the previous examples we have seen what happens with the genetic variance when selection is operating – an equally interesting question is what happens to the genetic covariance between two traits, especially when we are trying to improve both traits?

In Figure 7 five types of loci are shown which all are pleiotropic, i.e. they influence both traits. Locus 1 has two alleles, one with positive effects on both traits (++) and one allele with negative effects on both traits (--). Locus 2 has one ++ allele but one which acts increasing on trait 1 and decreasing on trait 2 (indicated by +-). And so on. All of these loci (and there may be several within each type) contribute both to the variance of each trait (the + and – for each trait can be thought of as *a* and *–a* of Figure 3) and to the covariance between them[2]. When an allele has an effect on both traits *in the same direction* (++ or --) this allele contributes to a *positive* covariance. When an allele has a positive effect on one trait and a negative effect on the other (+- or -+), it contributes to negative covariance.

[2] Remember that the covariance between x_1 and x_2 is : $\sum(x_1-\bar{x}_1)(x_2-\bar{x}_2)/(n-1)$

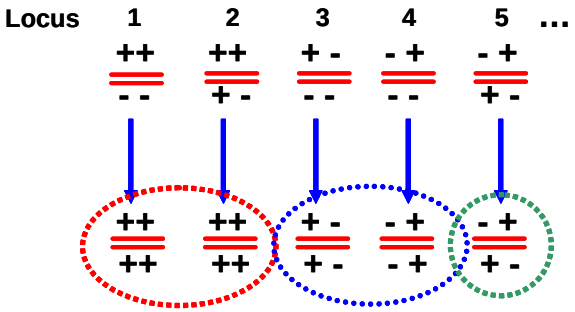

Figure 7. Illustration of five types of pleiotropic loci and how their gene frequencies change as a result of selection for increased value of the trait in question.

Let us assume that when we start out (upper part of Figure 7) the combination of gene frequencies and allelic effects contributes to an overall covariance of zero[3]. As we select for increased value of ***both*** traits the following will happen. In locus 1 and 2 we will favour the allele ++. After some generations these alleles will contribute mainly positive covariance, however, they will also become fixed rather quickly (especially in locus 1 where ++ is much better than --). When the alleles become fixed they contribute nothing to the genetic variance and covariance.

For loci of type 3 and 4, the road towards fixation is longer, especially compared with locus 1. As the favourable allele (+- or -+) increases in frequency, it will contribute to negative covariance, but eventually it will also be fixed.

For locus 5, the situation is more difficult to predict. When we select for increased value for both traits, we will sometimes favour the -+ allele and sometimes the +- allele. The change in gene frequency towards fixation for either one of them is slow and hard to predict. It is possible that the alleles will stay at intermediate frequencies. While they still are unfixed, both alleles are contributing to a negative covariance, and if all other alleles (at other loci) are fixed, the total covariance will be negative.

So, the take-home message is: ***if we select for increased value for two traits, the genetic covariance between the traits will move towards negative values***. In our description above we started out assuming a covariance of zero, this is as you probably have understood by now, not necessary. It is important, however, to remember that the expectation is that the covariance *will move towards* negative values: that means that if we start out with a genetic correlation of 0.5, the correlation (and the sign of the correlation depends on the covariance) will not necessarily have become negative after a few generations of selection, perhaps it has gone down to 0.4. But it has moved downwards, towards negative values!

So, here's question for you: what will happen if we select for increased value of trait 1 (say milk yield) but decreased value of trait 2 (mastitis incidence)?

When selection is for increased value of a complex trait (say, some fitness-related trait) which consists of a combination of subtraits (e.g. number of born and viability of the offspring), there might arise a situation where the subtraits become so negatively correlated that we seem to have reached a selection plateau; even if we select the best individuals to become parents we make no progress. However, there may still be substantial genetic variation left in the subtraits.

Other phenomena affecting genetic variance

The description above has focused on the effect of selection on genetic (co)variance, but there are also other phenomena that affect the overall outcome.

As you probably remember from population genetics, there are four "forces"

[3] This is not a critical assumption, see later

affecting a population: ***selection, genetic drift, mutation, and migration***. Genetic drift acts in a similar way as selection, inasmuch as it will also lead to fixation. However, whereas selection favours fixation of the desired alleles, drift is a purely random process.

Mutation is naturally an extremely important process in an evolutionary context. It is also one force that prevents that the finite locus model always ends up at the dead-end of fixation. It has been shown that a balance between mutation and drift evolves in populations of a given size. In any given generation *t* the loss of genetic variation due to drift is proportional to $1/2N_e$ where N_e is the effective population size, but at the same time new additive genetic variation due to mutation (σ_m^2) is created :

$$\sigma_{A_t}^2 = (1-\frac{1}{2N_e})\sigma_{A_{t-1}}^2 + \sigma_m^2 \qquad [15]$$

As the loss in genetic variation is proportional to what is left (the smaller the variance left becomes, the smaller the loss due to drift) but the mutational variance is constant, there comes a point where the loss is equal to the newly created variance. This can also be shown mathematically by expanding the recursive equation [15] all the way back to the starting generation:

$$\sigma_{A(t)}^2 \approx 2N_e\sigma_m^2 + \left[\sigma_{A(0)}^2 - 2N_e\sigma_m^2\right]\exp(-t/2N_e) \qquad [16]$$

The development of genetic variance over time is given in Figure 8 (a graphic description of equation [16]). The exponential part of [16] will go towards zero, the quicker the smaller the population size, and the equilibrium genetic variance will be attained faster for small populations. That variance will be:

$$\sigma_{A,m(\infty)}^2 \approx 2N_e\sigma_m^2 \qquad [17]$$

With an assumed σ_m^2=0.005 (in relation to environmental variance σ_e^2=1) and an effective population size of 100 this equilibrium genetic variance becomes 2×100×0.005=1.0.

The interpretation of equation [17] is that the larger the population, the larger influence will mutation have on creating additive genetic variance that can be exploited by selection.

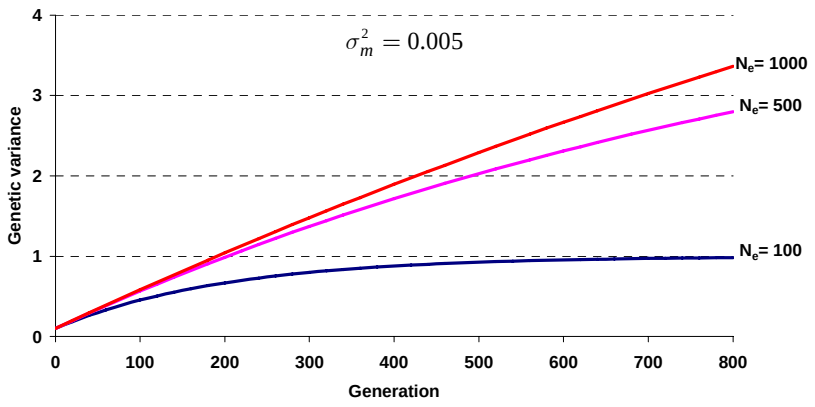

Figure 8. Development of additive genetic variance as a balance between genetic drift and mutation.
Mutation variance $\sigma_m^2 = 0.005$,
starting value for $\sigma_a^2 = 0.3$
(all related to $\sigma_e^2 = 1$)

Finally, a few words about ***migration***. Immigration of unrelated individuals can be a powerful way of counteracting inbreeding and genetic drift. Actually, in an ideal population, one immigrant every or every other generation is enough to keep the populations from becoming totally inbred. Strangely enough, this is regardless of population size! One way to explain this is that in a large population one individual has a small impact on the total population, but the risk that the genes of this individual will be lost due to drift is small. In a small population, one individual would make a larger impact if selected, but the risk of losing those genes due to drift is larger. These two counterforces – migration and drift – actually balance each other perfectly.

The infinitesimal model

Another very common genetic model is the so-called infinitesimal model. This model was initially introduced by R.A. Fisher in 1918. The assumptions are that there are an infinite number of genes. As the number of genes goes to infinity, the effect of each gene goes towards zero. Thus the assumption is also that all genes have identical and infinitesimal (i.e. very close to zero) effects. As the number of genes is infinitely large and each effect is infinitesimally small, selection will not change the gene frequency (or at least we can ignore that change as it is infinitesimally small).

In this model the genotypic values become normally distributed. This is because of the assumption of many loci contributing to the total genotypic value. If we also have a normally distributed environmental component, the phenotypic values are also normally distributed. If we select a proportion (*p)* of the animals we can calculate the phenotypic variance of the selected animals (σ^2_{P*}) as:

$$\sigma^2_{P*} = \sigma^2_P(1-k) \qquad [18]$$

where σ^2_P is the phenotypic variance before selection, and $k = i(i-x)$, where *i* is the selection intensity and *x* is the truncation point as deviation from the mean zero in a normal distribution with variance equal to 1 (Figure 9).

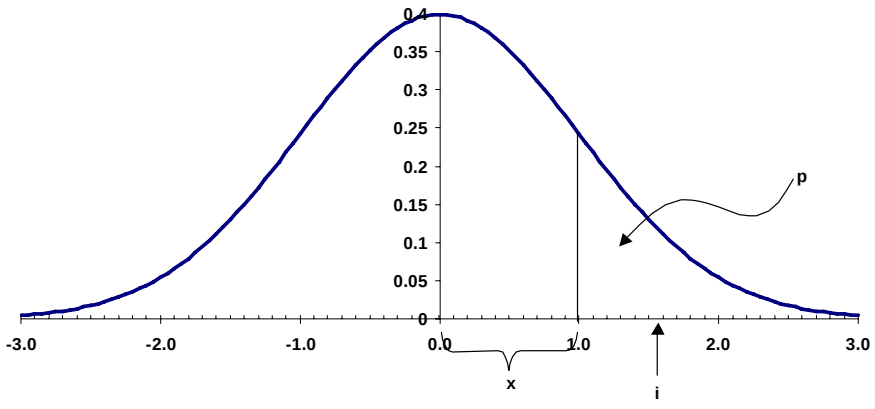

Figure 9. Illustration of truncation selection on normally distributed phenotypic values with mean zero and variance 1. Individuals above a value *x* (here 1.0) are selected. They have a mean of *i* (selection intensity) and constitute a proportion *p* of all individuals.

The parameter *k* in equation [18] describes the proportional decrease in phenotypic variance as a result of selection, and the smaller proportion selected (the higher selection intensity) the higher *k* (Figure 10).

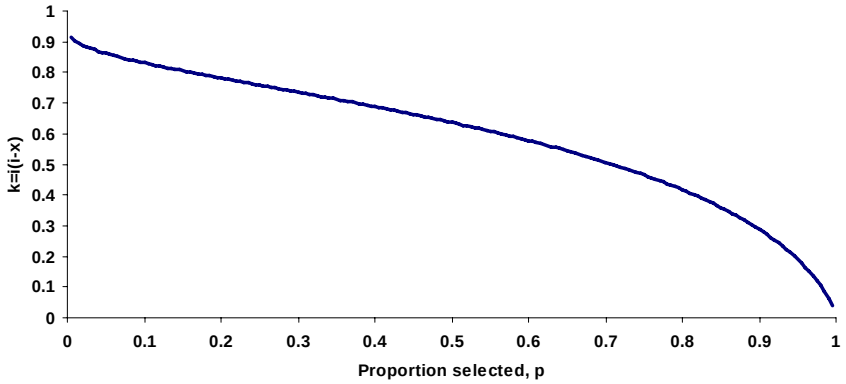

Figure 10. Proportional reduction in phenotypic variance ((*k=i(i-x)*) as a function of proportion selected (*p)*

So, the phenotypic variance is reduced to σ^2_{P*} but all of that reduction is not seen at the genetic level. The additive genetic variance among the selected individuals (parents) becomes:

$$\sigma^2_{A*} = \sigma^2_A(1-h^2k) \qquad [19]$$

In the creation of gametes to create the next generation, half of the loss in additive genetic variance is restored by the random recombination of alleles (Mendelian sampling), so the genetic variance in the offspring generation becomes:

$$\sigma^2_{A*} = \sigma^2_A(1-\frac{1}{2}h^2k) \qquad [20]$$

As we have seen in the compendium Genetic Evaluation we can write the breeding value as:

$$A_i = \frac{1}{2}\mathrm{A_s} + \frac{1}{2}\mathrm{A_d} + \mathrm{A_{MSsi}} + \mathrm{A_{MSdi}}$$

where $\mathrm{A_s}$ and $\mathrm{A_d}$ are the breeding values for the sire and dam, respectively, and $\mathrm{A_{MSsi}}$ and $\mathrm{A_{MSdi}}$ are the Mendelian sampling terms. The Mendelian sampling terms are unaffected by selection because they are restored every generation; together they make up 50% of the original additive genetic variation. This is inherent in the infinitesimal model, as we assume that selection does not change gene frequencies.

The reasoning behind the decrease in genetic variance with selection in the infinitesimal model is usually attributed to Sir Michael Bulmer (Bulmer, 1971), and therefore this phenomenon is often referred to as the ***"Bulmer effect"***. The reasoning goes as follows.

Assume that the genotypic value for a trait is composed of the sum of genotypic values from an infinite number of loci:

$$G = G_1 + G_2 + \ldots$$

The genetic variance then becomes:

$$\sigma^2_G = \sigma^2_{G1} + \sigma^2_{G2} + \ldots + \sigma_{G12} + \sigma_{G13} + \ldots \qquad [21]$$

In a random mating population (which we assume we have at the start) there is no association between the genotypic value at one locus with that at another locus, i.e. all the covariances are zero and the total variance is just the sum of the variances at each separate locus. If we only care about the distribution of the genotype combinations at any two loci (haplotypes, e.g. AB, ab, Ab, aB), we can say that there is ***linkage equilibrium***, because these haplotypes occur in the frequency we would expect from their respective gene frequencies. This term is also called *joint equilibrium* or *gametic phase equilibrium*. If you want to refresh your memory on linkage equilibrium and disequilibrium, have a look in appendix 8.

Now, when we have selection on the total genotype (or the phenotype) we will create linkage disequilibrium between loci, and as a result we will also create ***negative covariances*** between loci. This means that the total sum in [21] will be lower than before and the genetic variance (σ_G^2) has decreased.

In the following we will try to explain why selection on the sum of two (or more) values creates a negative covariance. In Figure 11 (upper graph) 500 individuals' genotypic values from two loci are plotted against each other. The assumption is that in each locus there are many alleles and thus many possible genotypic values. In the total population there is no covariance (nor correlation) between the genotypic values at the two loci – the points are scattered around the centre in a circle. If you select a point at the x-axis, say at +1.0, the points are equally spread with

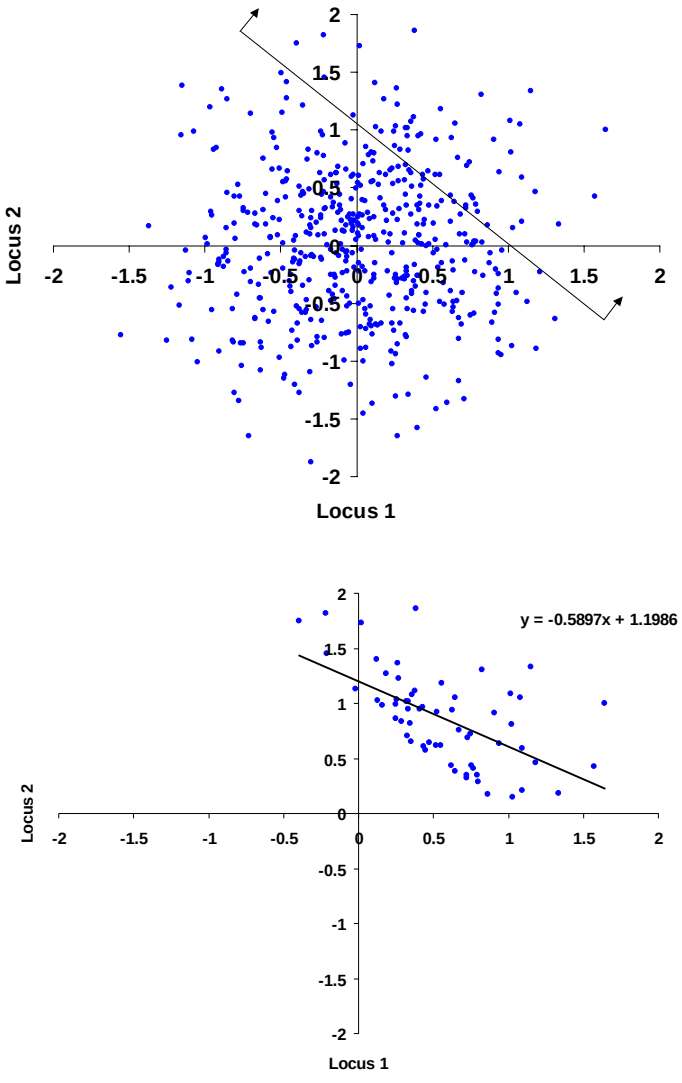

Figure 11. Illustration of the Bulmer effect. The upper graph shows the genotypic values from two loci plotted against each other. The assumption is that in each locus there are many alleles and thus many possible genotypic values.

In the lower graph only the selected individuals are shown. If we try to summarize these values with a line it has a negative slope, which indicates a negative covariance between genotypic values at the two loci

respect to the y-axis. If there had been a negative correlation, one would have expected that values at the y-axis would be low (because x is above average).

If we select on the sum of genotypic values and choose individuals with sum values greater than 1.0, we would choose individuals above the line drawn in the graph. Now, with respect to all points, these individuals are chosen because they have high values for both locus 1 and locus 2. Therefore, it might be natural to think that the correlation (and covariance) between these genotypic values is positive. However, if we take away the individuals that were not selected and only keep the "parents" we get the picture in the lower part of Figure 11. If we try to summarize these points by a regression line, we see that it has a *negative slope*, which indicates a negative covariance between genotypic values at the two loci.

The above reasoning applies for directional selection and also for stabilizing selection (when individuals around the mean are selected). However, with disruptive selection, a positive covariance is created (Figure 12).

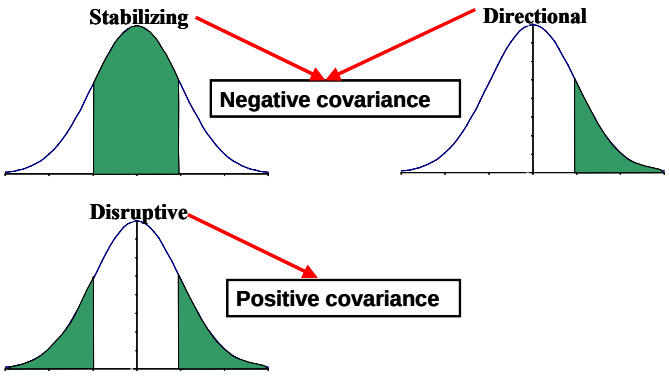

Figure 12. Illustration of various types of selection and their effect on covariance between genotypic values at different loci.

The effect of selection on the genetic variance is quite fast, after the first two generations of selection there is hardly any change in genetic variance (Figure 13). The interesting thing is that if you stop selecting, the variance returns to the base population value again, as the linkage equilibrium is restored by half the amount for every generation of Mendelian sampling (Figure 13). This means that in the infinitesimal model, as opposed to the finite locus model, the lower genetic variance is not permanent, it only exists as long as you continue selecting!

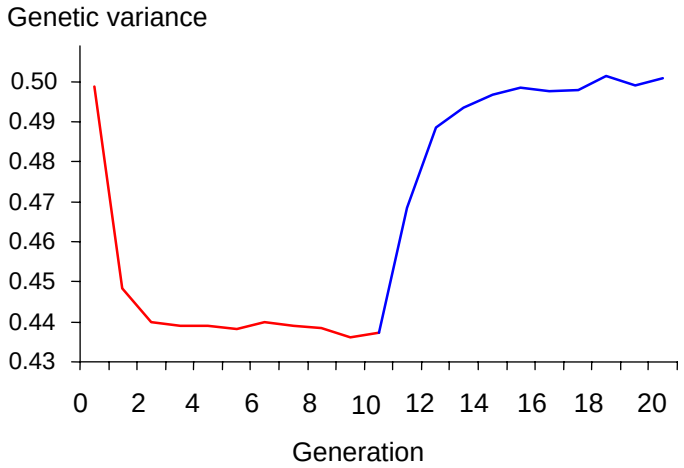

Figure 13. Change in genetic variance owing to the Bulmer effect. Base population variance 0.5, selection for 10 generations, thereafter random mating

Selection on two traits at the same time has a similar effect as in the finite locus model, the covariance between the traits moves in the negative direction (Figure 14). However, in the same way as the genetic variance returns to its initial value after one has stopped selecting, so does the genetic covariance.

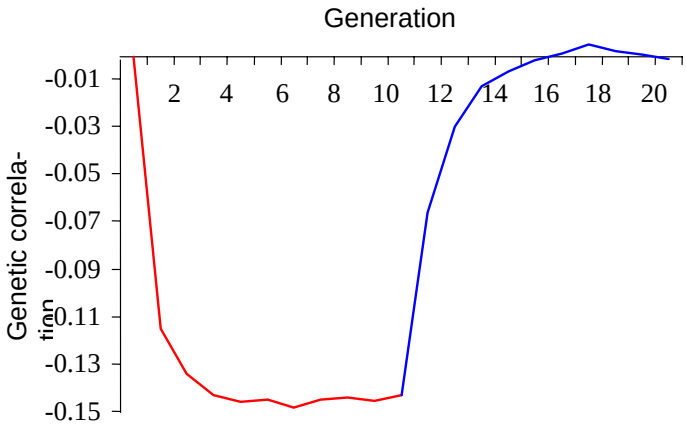

Figure 14. Change in genetic correlation owing to the Bulmer effect. Base population correlation 0.0, selection for 10 generations, thereafter random mating.

What about the selection response? Is that affected by the changes in genetic variance owing to the Bulmer effect? Is the selection response permanent or does that also revert to the base population level? The answer to the last question is thankfully: No! The genetic level, after, say 10 generations of selection followed by random mating, stays at the level it was at generation 10 (Figure 15).

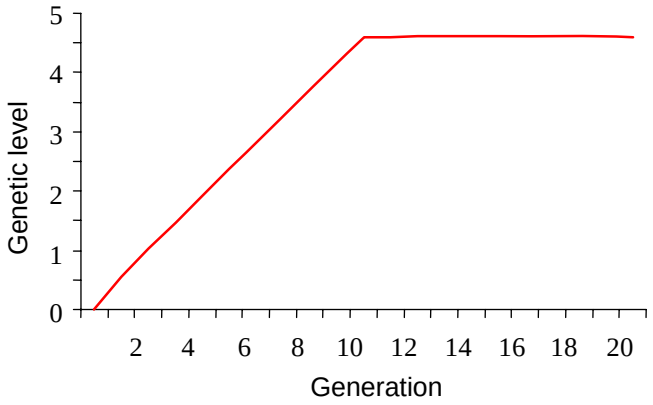

Figure 15. Change in genetic level as a result of selection, assuming the infinitesimal model. Selection for 10 generations, thereafter random mating.

In Figure 15 it seems that the selection response per generation is constant for the first 10 generations. However, if we plot the response per generation we can see that this is not true – the selection response is higher the first generation owing to the higher additive genetic variance (and thus heritability) in the base generation (Figure 16).

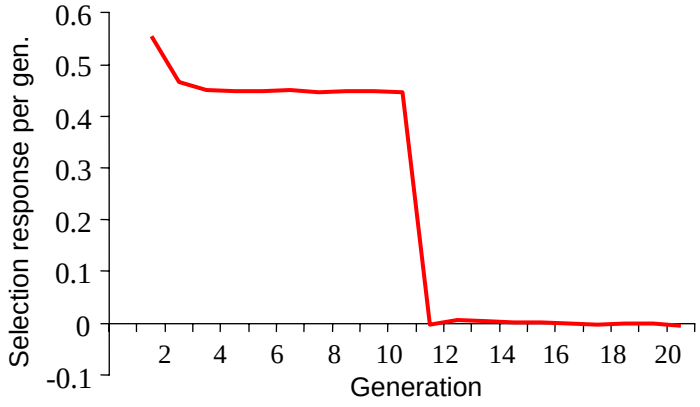

Figure 16. Change in selection response per generation over generations assuming an infinitesimal model.

Another factor that affects the change in genetic variation due to selection is whether the selected animals are mated randomly or assortatively. If the best males (among the selected) are mated to the best females (again of those selected) we have positive assortative mating. If the best males are mated to the worst of the selected females, we have negative assortative mating (Figure 17).

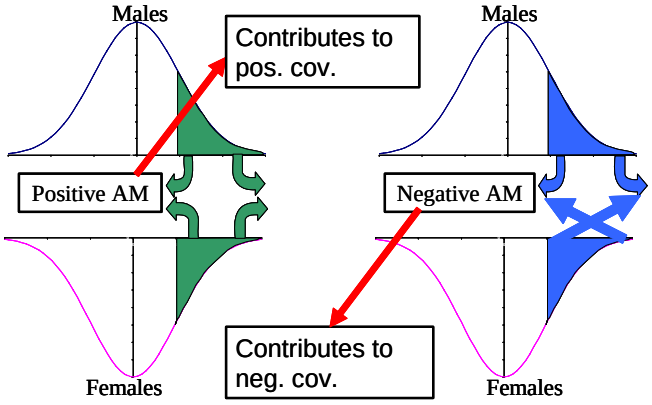

Figure 17. Illustration of positive and negative assortative mating among the selected animals

As positive assortative mating contributes to *positive* covariance, the genetic variance is not decreased as much as for random mating. On the other hand, with negative assortative mating, the decrease in genetic variance is even larger than for random mating (Figure 18).

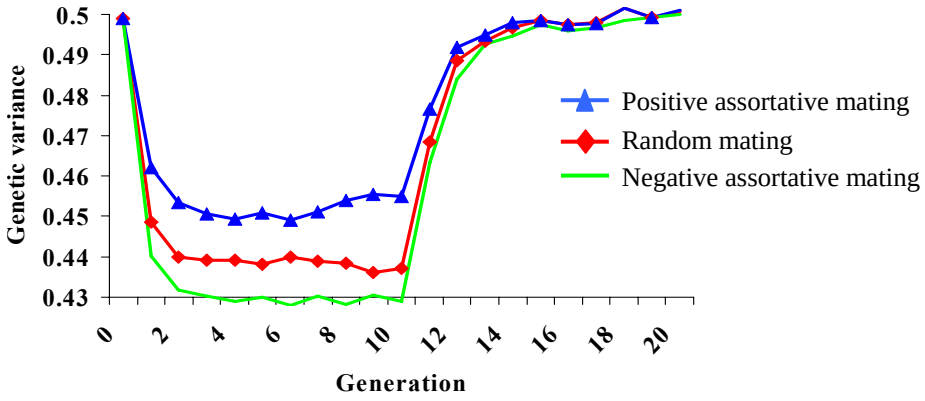

Figure 18. Change in genetic variance owing to the Bulmer effect for different types of mating.
Base population variance 0.5, selection for 10 generations, thereafter random mating.

In accordance with the results for genetic variance, the genetic response to selection is also higher with positive assortative mating than with random mating or negative assortative mating (Figure 19).

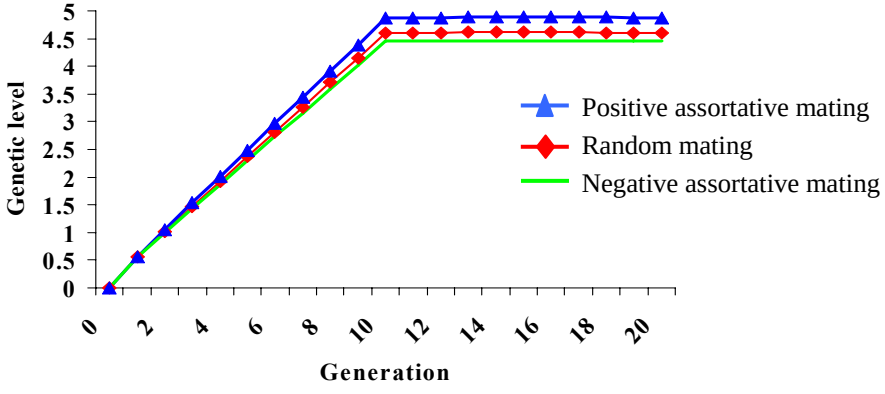

Figure 19. Change in genetic level as a result of selection, assuming the infinitesimal model, for different types of mating.among the selected animals.
Selection for 10 generations, thereafter random mating.

Appendix 8. Linkage disequilibrium

If we only look at one locus, we have the well-known Hardy-Weinberg equilibrium after just one generation of random mating, i.e. given that the allele frequencies are p and q, the genotype frequencies are p^2, q^2, and $2pq$, for the two homozygotes and the heterozygote, respectively. However, such a quickly attained equilibrium does not appear if we look at more than one locus jointly.[4]

Suppose we start out with two populations, one which only consists of genotypes $A_1A_1B_1B_1$, and one which only consists of $A_2A_2B_2B_2$ individuals. If we allow these two populations to mate at random (i.e. not only cross them) then the outcome would be as in Figure 20.

		Gametes			
		A_1B_1	A_1B_2	A_2B_1	A_2B_2
Gametes	A_1B_1	$A_1A_1\ B_1B_1$			$A_1A_2\ B_1B_2$
	A_1B_2				
	A_2B_1				
	A_2B_2	$A_2A_1\ B_2B_1$			$A_2A_2\ B_2B_2$

Figure 20. Outcome of mating of two "inbred" lines, consisting of only $A_1A_1\ B_1B_1$ and $A_2A_2\ B_2B_2$ individuals, respectively. Only gametes A_1B_1 or A_2B_2 are created.

Given the two alleles at both loci, there are potentially 9 different genotypes, but only three of them will occur – the original two homozygotes and the "double" heterozygote $A_1A_2B_1B_2$. If these two alleles have effects on the same trait, this would look like there is only one gene controlling the trait.

With continued random mating, the "missing" genotypes will appear, as you see now gametes of type A_1B_2 can be created from the heterozygote. If the two loci are linked the equilibrium will take longer to reach.

The disequilibrium described above is called *gametic phase disequilibrium* or *linkage disequilibrium*. The latter name is shorter and more commonly used, but it has the disadvantage that one might believe that there need to be linkage for linkage disequilibrium to exist. That is not the case, linkage disequilibrium can appear between loci that are on different chromosomes, thus with recombination frequency of 0.5.

As we have seen, linkage disequilibrium can be produced by intermixture of populations with different gene frequencies, but it can also be created by random drift in small populations and by selection. This is described in appendix 7.

[4] The description of linkage disequilibrium in this appendix is mainly based on Falconer and Mackay (1996, p 19-)

How quickly is linkage *equilibrium* attained? Let's consider the two locus case again. We assume gene frequencies for A_1 and A_2 to be p_A and q_A, respectively, and corrspondingly p_B and q_B for B_1 and B_2. In Table 2 the equilibrium frequencies of the gametic types are given together with some assumed actual frequencies, *r*, *s*, *t*, and *u*. The population is in equilibrium if the gametes are only a function of the respective gene frequencies.

We also need some measure of disequilibrium. Here we measure it as the deviation of the actual frequency from the expected. It actually turns out that the deviation (r - p_Ap_B) is the same as (u - q_Aq_B), and that the other deviations have the same size but opposite sign.

Table 2. Equilibrium and actual gametic frequencies for the two locus case.

Gametic types	A_1B_1	A_1B_2	A_2B_1	A_2B_2
Equilibrium frequencies	$p_A\ p_B$	p_Aq_B	q_Ap_B	q_Aq_B
Actual frequencies	*r*	*s*	*t*	*u*
Difference from equilibrium	D	-D	-D	D

Anyway, let's have a look at one of the gametic types, A_1B_1 (the same reasoning applies to all of them). In the progeny generation of a random mating population this gamete may have been created in two ways:

1. As a non-recombinant from the genotype A_1B_1/A_xB_x. The frequency for this occurrence is $r(1-c)$, where c is the recombination frequency. The *x* subscript means any of the alleles could be present (also allele 1).

2. As a recombinant from A_1B_x/A_xB_1. The frequency of chromosome A_1B_x is p_A and the frequency of A_xB_1 is p_B. So the frequency with which occurs this way is $p_A\ p_Bc$. If we sum these two ways we get the new frequency of A_1B_1:

$$r_1 = r(1-c) + p_A\ p_Bc = r - cD \qquad [22]$$

and the new disequilibrium:

$$D_1 = r_1 - p_A\ p_B = r(1-c) + p_A\ p_Bc - p_A\ p_B = r(1-c) - p_A\ p_B(1-c) =$$
$$= (r - p_A\ p_B)(1-c) = D(1-c)$$

So, in the next generation the original disequilibrium has been decreased by a factor $(1-c)$, where c is the recombination rate. For unlinked loci, this is 0.5, so disequilibrium is halved every generation. For closer linkage, the decrease is slower. In generation t the disequilibrium is :

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

where D_0 is the disequilibrium at the beginning of random mating (e.g. after selection or intermixing of two populations).

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