

## MARKER ASSISTED SELECTION IN A POULTRY BREEDING PROGRAM

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### SUMMARY

Marker assisted selection responses were computed for a poultry breeding program. Covariances between information sources used for breeding value estimation were conditioned on marker information. The marker was located 5 cM from a Quantitative Trait Locus (QTL) explaining 20% of the additive genetic variance. Selection was for a sex-limited trait (egg number) with a heritability of .3. Effect of selection on genetic (co)variances was accounted for. Additional selection response due to the use of a marker was 5% in the generation in which marker information was used for the first time. The extra response decreased to 1-2% in later generations. After 10 generations QTL variance was reduced by 30% and polygenetic variance by 17%.

### INTRODUCTION

The use of information on genetic markers which are associated with a quantitative trait of interest can increase genetic progress (e.g., Solter, 1978). Genetic markers explaining a considerable amount of the genetic variance within a population have been found for livestock species (e.g., Bovenhuis and Weller, 1994). Several studies quantified the extra selection response due to marker information (Kashi et al., 1990; Meuwissen and Van Arendonk, 1992). These studies focused on dairy cattle breeding schemes and did not allow for the effect of selection on genetic (co)variances. In this study, response to selection using an index incorporating marker information and the effect of selection on QTL variance is computed for a closed poultry breeding nucleus. Recombination rate between the marker and QTL and amount of variation explained by the QTL are assumed known.

### GENETIC MODEL

The model for additive genetic effects is:

$$a_i = v_i^p + v_i^m + u_i$$

where  $a_i$  = additive genetic effect of animal  $i$ ,  $v_i^p$  = effect of paternal QTL allele,  $v_i^m$  = effect of maternal QTL allele and  $u_i$  is polygenetic effect. Genetic effects are random and normally distributed. A marker linked to the QTL is available. The recombination fraction between marker and QTL is  $r$ , variation due to allelic effects at the QTL is  $\sigma_v^2$  and variation explained by the two alleles of the QTL is  $\sigma_q^2$  (the QTL variance). The covariance between the QTL effects of animals is conditioned on marker information (Fernando and Grossman, 1989):

$$\text{cov}(v_i^p, v_j^p) = P(Q_i^p = Q_j^p | M) \sigma_v^2$$

where  $P(Q_i^p = Q_j^p | M)$  is the probability that the two QTL alleles are identical by descent given the marker information.

The variance of a paternal QTL allele effect for animal  $i$  in a new generation is:

$$\text{var}(v_i^p) = (1-d) \text{var}(v_s^p) + d \text{var}(v_s^m) \quad (1)$$

where  $d$  is  $r$  if sire  $s$  transmits the paternal marker allele and  $(1-r)$  if the sire transmits the maternal marker allele. For a maternal QTL effect the same development can be made. In this model QTL variance is completely determined by the QTL variance in the (selected) parents in the previous generation.

#### DETERMINISTIC SIMULATION

Selection index theory is used to compute response to (marker assisted) selection. Index information sources are: estimated parent genetic effects ( $\hat{v}_s^p, \hat{v}_s^m, \hat{v}_d^p, \hat{v}_d^m, \hat{u}_s, \hat{u}_d$ ), observations on full-sibs and half-sibs and own performance if available. A sibship is divided in 4 groups of equal size based on inherited marker alleles.

Let  $\mathbf{C}$  be a  $n \times 3$  matrix with covariances between  $n$  information sources and the three genetic effects ( $v^p, v^m, u$ ) of the selection candidate and  $\mathbf{V}$  the covariance matrix among information sources. In that case  $\mathbf{W} = \mathbf{C}'\mathbf{V}^{-1}\mathbf{C}$  is the (co)variance matrix of estimated genetic effects (Henderson, 1984). The selection index is  $I = \hat{v}_i^p + \hat{v}_i^m + \hat{u}_i$  and the variance of the index ( $\sigma_i^2$ ) is  $(1 \ 1 \ 1) * \mathbf{W} * (1 \ 1 \ 1)'$ . Let  $\mathbf{R}$  be a vector with selection responses for the three genetic effects then  $\mathbf{R} = \hat{i} / \sigma_i * \mathbf{W} * (1 \ 1 \ 1)'$  where  $\hat{i}$  is the selection intensity and  $\sigma_i$  the standard deviation of the selection index. Selection intensities are corrected for finite population size. Reductions of (co)variances due to selection are computed using Cochran (1951) and these effects are incorporated in the  $\mathbf{V}$  matrix for a next generation. Variance of QTL alleles in offspring of selected parents is computed using (1) with  $\text{var}(v_s^{p(m)})$  replaced by  $\text{var}(v_s^{p(m)})^*$ , the variance of QTL alleles after selection.

#### BREEDING PROGRAM

The effect of marker information is illustrated for an egg layer poultry breeding program. A QTL explaining 0 or 20% of the additive genetic variance of egg number in the unselected base population is located 5 cM from a 'perfect' marker (marker inheritance can be traced for all animals). Additive genetic variance, including QTL variance, is 30% of the phenotypic variance. Per generation, the breeding nucleus has 50 sires, 6 dams per sire and 30 offspring (15♂, 15♀) per dam. Selection took place after female selection candidates completed their production record. Only the 5 first born male offspring per dam were available for selection. The number of female offspring selected per dam was unrestricted. Marker information was introduced in generation 0 or 5. All animals in the breeding nucleus were typed for the marker from generation 0 or 5 onwards, depending on the alternative. For each generation response to selection of males and females was computed. Reductions of genetic and phenotypic (co) variances were accounted for.

#### RESULTS

Table 1 gives genetic (co)variances in selection candidates for a QTL explaining 0 or 20% of the genetic variance in the base population. For the QTL explaining 20%, selection response is given for a program without marker information and for a program in which marker information is used from generation 5 onwards. Generation 0 is the unselected base population. The phenotypic variance of the base population is 1.

Additive genetic variance stabilized after generation 4 when all variance was polygenetic.

Table 1. QTL variance ( $\sigma_q^2$ ), polygenetic variance ( $\sigma_u^2$ ), covariance between QTL and polygenes ( $\sigma_{uq}$ ) and additive genetic variance ( $\sigma_a^2$ ) in the selection candidates

Generation	$\sigma_q^2 = 0$	$\sigma_q^2 = .2 * \sigma_a^2$ in generation 0; no marker information				$\sigma_q^2 = .2 * \sigma_a^2$ in generation 0; marker available from generation 5 onwards			
	$\sigma_a^2$	$\sigma_q^2$	$\sigma_u^2$	$\sigma_{uq}$	$\sigma_a^2$	$\sigma_q^2$	$\sigma_u^2$	$\sigma_{uq}$	$\sigma_a^2$
0	.300	.060	.240	0	.300	.060	.240	0	.300
4	.235	.053	.198	-.020	.231	.053	.198	-.020	.231
5	.235	.052	.198	-.020	.230	.052	.198	-.020	.230
6	.235	.051	.198	-.020	.229	.050	.200	-.024	.226
10	.235	.047	.197	-.018	.226	.042	.200	-.023	.219

A steady decrease was found, however, for variation at the QTL also when marker information was not used. Selection introduced negative covariances between QTL and polygenic effects. Marker assisted selection increased the negative covariance and the reduction of QTL variance.

Selection responses for three programs with a QTL explaining 20% of the genetic variance are given in Table 2. Responses for programs 2 and 3 are relative to responses for program 1, a breeding program in which no marker information is used. In program 2 marker information was used from generation 5 onwards, i.e. marker information was introduced in an ongoing breeding program which is what will happen in reality. In program 3 marker information was available from generation 0 onwards. Maximum extra response due to marker assisted selection was 5% in generation 5 for program 2 and 4% in generation 1 for program 3. Additional cumulative response over the first five generations after introducing markers, generation 0 to 5 for program 2 and generation 5 to 10 for program 3, was 3.4% for program 2 and 3. Thus, additional response was independent of the moment of introducing marker information

Table 2. Selection response for programs with: 1) no marker information; 2) marker information from generation 5 onwards and 3) marker information from generation 0 onwards. QTL variance is 20% of genetic variance in base population. Responses for 2. and 3. are given in % of response for 1.

Generation	1) no marker information	2) marker available from generation 5 onwards	3) marker available from generation 0 onwards
0	.680	100.0	103.0
1	.524	100.0	104.4
5	.498	104.7	102.7
6	.496	103.8	102.5
10	.492	102.5	101.3
cum. 0-5 <sup>1</sup>	3.21	-	103.4
cum. 5-10 <sup>2</sup>	2.97	103.4	-

<sup>1</sup> cumulative response over generation 0 to 5; <sup>2</sup> cumulative response over generation 5 to 10

## DISCUSSION

The number of males selected per dam was restricted in the breeding program. Per family only the five first born male offspring were reared, as would be done in a commercial breeding program. The additional response due to marker information probably would have been higher in case all male offspring were reared and marker information was used for within family selection of 5 out of 15 males. Also additional responses could have been made by optimizing the breeding programme with respect to family structure, generation intervals, etc. The additional response described here is entirely due to increased selection accuracies and therefore the effect of marker assisted selection is underestimated.

A fundamental problem of accessing the value of marker assisted selection is the nature of the genetic variance associated with the marker. Here we assumed a QTL with normally distributed allele effects in the base and later generations. The fact that QTL variance will decrease over time was accounted for. The reduction of QTL variance was probably underestimated because the model implicitly assumes a infinite number of QTL-alleles. Even then, extra response due to marker information was moderate. The additional response decreased due to reduced QTL variance and increased negative covariance between QTL and polygenic effects. The effect of selection on (co)variances will be the same if a cluster of closely linked QTL's instead of one QTL is assumed to explain 20% of the genetic variance. For a cluster, selection will introduce negative covariances within the cluster which will hardly breakdown due to the close linkage between the QTL's. The reduction of QTL variance will be lower when several independent QTL are assumed to explain the same amount of variance. In that case, breakdown of negative covariances during the formation of a new generation will be larger.

In the simulated poultry breeding programs, a limited number of records was used to estimate QTL effects. Meuwissen and Van Arendonk (1992) assumed for a dairy cattle breeding nucleus that many grandoffspring could be used to estimate marker associated effects in grandsires. Using these data the selection index could explain an extra 10% of within family variance which is considerably higher than in the present study. In a poultry breeding scheme no data is routinely collected from outside the nucleus. The possibilities to collect more data to estimate marker associated effects should be evaluated in future studies.

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