

## SHORT-TERM GAIN AT THE EXPENSE OF LONG-TERM RESPONSE WITH SELECTION OF IDENTIFIED LOCI

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### SUMMARY

Selection experiments were performed *in silico*, with model populations subject to selection on individual phenotypic or progeny test information, with or without additional information on genotype at a single locus. Simulations were deterministic, with inheritance under an additive infinitesimal model plus a single bi-allelic locus. The development of gametic phase disequilibrium and of associations between genotypes and average infinitesimal effects were accounted for. When single locus information was available, the latter associations were either ignored during genetic evaluation (direct selection), or assumed estimated without error (maximum accuracy selection). Both direct and maximum accuracy selection improved short-term response compared to having no information on genotype (control), but control selection always gave better long-term responses. The long-term responses with direct, maximum accuracy and control selection ranged from 25 to 75, from 50 to 75 and from 64 to 84% of the fixable gene effect compared to populations without the locus segregating. The poorest responses were for genes of intermediate to small effect. Optimum utilisation of single locus information will depend on the time horizon.

### INTRODUCTION

Advances in molecular genetic technologies have greatly increased the chances of identifying economic trait loci (ETL), or of markers linked to such loci, in livestock species. Information on individual loci or their marker loci could be combined with estimated breeding values (EBV) based on quantitative genetic variation to produce a single selection criterion. The value of the single locus information will clearly depend on the size of the gene effect and its accuracy and bias of estimation. Work on methods of estimating ETL effects has progressed (e.g. Cantet and Smith, 1991; Hofer and Kennedy, 1993; Hoeschele, 1993). In contrast, the time dependent contributions to selection response of an ETL with effects known without error, remains unclear.

I here report on experiments *in silico* which indicate that use of information on an ETL genotype in selection gives more rapid short-term response but less long-term response than ignoring ETL genotype.

### METHODS

Deterministic computer simulations were constructed for populations under selection with inheritance of a single trait controlled under an additive infinitesimal model (quantitative genetic effect) plus a single bi-allelic locus with predefined genotype effects. Each cohort of animals coming forward for selection is initially described in terms of the frequency, the mean associated quantitative genetic effect and the mean associated quantitative genetic variance of each of the three genotypes. The means and variances of estimated breeding values (EBV) are derived, assuming various combinations of individual phenotypic or progeny test information, with or without knowledge of genotype at the ETL. It is assumed that, in practice, regression of information toward the mean to obtain EBV would involve a single

perhaps, intensity is reduced to slow progress of the favoured allele and hence capture a greater long-term response than would occur without genotype selection. For loci of small effect, selection on genotype will improve short-term response, but the absolute gains will be small and the penalties in reduced long-term response relative to the size of the locus effect will be severe. These results are currently being extended to multi-locus selection models, where the extent of these problems is predicted to depend on the proportion of variation explained by identified loci. Nevertheless, the current results clearly add to the arguments for using genotype information at a separate stage of selection (e.g. Kashi et al., 1991; Gomez-Raya and Gibson, 1993).

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**Table 1.** Additional response<sup>1</sup> at fixation or after 20 generations (in parenthesis) due to segregating single locus with additive action<sup>2</sup> under control, direct or maximum accuracy selection

Gene effect <sup>3</sup>	Individual Performance			Progeny Test		
	Control	Direct	Maximum Accuracy	Control	Direct	Maximum Accuracy
2	.824	.683	.685	.732	.659	.662
1	.805	.509	.546	.696	.528	.572
.5	.798	.357	.496	.687	.439	.542
.25	(.49) <sup>4</sup>	.272	.482	(.561) <sup>4</sup>	.389	.526

<sup>1</sup> Additional response expressed as proportion of fixable gene effect. Fixable gene effect =  $2qd$  where  $q$  is initial favourable allele frequency and  $2d$  is additive genetic difference between the two homozygotes.

<sup>2</sup> Initial allele frequency,  $q = .05$ .

<sup>3</sup> Difference between homozygotes (=  $2d$ ).

<sup>4</sup> Frequency of increasing allele at generation 20 was .637 for individual performance and .836 for progeny test.