OPTIMIZING ALLOCATION OF TEST PLACES IN MULTIPLE TRAIT PROGENY TESTING SCHEMES

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SUMMARY

Alternative strategies on how to allocate a limited amount of progeny test places are discussed. In the example used, all males are progeny tested for a composite trait (eg. a combination of weight and carcass measurements). A much smaller number of test places is available for more intensive measurements, in this case eating quality of meat. A limited number of sons of each grandsire can be tested for a limited number of offspring. Information on males' EBV for eating quality could arise from a progeny test, from progeny tested sibs, and information from correlated traits. The proportion of sons to be tested from each grandsire family was evaluated for merit and the lower limit of a 95 %-confidence interval of true breeding value for eating quality (LL95). LL95 was low for untested sires when genetic correlation with other traits was small. In that case, also tested sires had low LL95 when a large proportion was tested with few progeny per son. Selecting a larger proportion of sons from each grandsire family reduced LL95 of tested sons, but did not affect LL95 of untested sons. With a high economic value of eating quality, investing in more testing places would be justified if genetic correlation with other traits were low.

Keywords: Progeny testing, test place allocation

INTRODUCTION

An important type of decision concerning the efficiency of animal improvement is related to trait measurement. Obtaining measurement constitutes the majority of the operating costs of breeding programs. Rules to decide on which animals should be measured, and for which traits, may be just as important for the success of the breeding program as rules for selecting animals. An example of a decision problem with respect to data collection is which animals should be progeny tested. Progeny testing is generally costly and always is constrained by limited resources. Particularly progeny tests for traits that are laborious and expensive to measure, such as feed intake, extensive carcass measures or measurement of eating quality allow generally a small number of test places.

Decisions with respect to the optimization of test places are based on selection intensity, selection accuracy and family structure, and the main assessment criteria are genetic merit obtained (this may include inbreeding issues), and the cost and risk involved. When more selection stages are involved, selection at the first stage based on EBV alone is not optimal (Van Raden *et al.* 1982, Goddard and Howarth, 1994). The possible outcome of a second selection depends then not only on mean, but also on variance of the animals selected in the first stage. The variance of the outcome at the second

stage, indicated as risk, is often part of a decision criterion. Therefore, in deciding which animals should be progeny tested, mean and variance at both selection stages are relevant.

We present an example of assigning test places for eating quality in meat sheep. There is a limited number of test places available for this trait but it is assumed that all young rams are progeny tested for other traits than eating quality trait (eg. a combination of weight and carcass measurements). Therefore, ultimately, all males will obtain an EBV for eating quality. Information for this EBV will be based on correlated traits, on progeny tested sibs, and possibly on an own progeny test. Young males are generally sons of a limited number of selected males (here indicated as grandsires). The question becomes then how many young sires should be progeny tested, and how many should be progeny tested from each grand sire family. Testing more young sires allows larger selection intensity in the second stage of selection, but a lower accuracy of selection. Testing a lower proportion of sires per grandsire family allows more families to be tested. The main arguments in this case will be obtained by simple analyses of alternative static designs, and evaluation of accuracy obtained in multi-trait selection.

MATERIALS AND METHODS

Different alternatives were investigated analytically We assumed a breeding program where 500 young males from 50 grandsires are progeny tested annually for production traits such as weaning weight and meat quality measurements on live animals (Eye muscle depth, Cfat). Genetic merit for such traits is summarized in a 'composite trait'. The number of test places available for eating quality (EQ) is limited to 1000. The heritability for the composite trait is assumed 25 %. And heritability for EQ is also assumed 0.25. Genetic correlation between EQ and the composite trait is poorly known and was varied. The environmental correlation was assumed zero. The proportion of sons tested per grandsire was varied at 0.2, 0.5 and 0.8 (assuming equal merit for each grandsire) Number of sires tested for EQ and progeny per tested son are in Table 1. The economic value per unit of standard deviation of EQ was assumed 50 % of the aggregate genetic value for the composite trait.

A groups of rams was selected as elite breeders (for the sires of sires pathway) being 10 % of the tested rams. Selection was by truncation across tested and untested sons for an aggregate genotype for eating quality and the composite trait. For this group mean genetic merit lower limit of the 95 % confidence interval of true breeding value (LL95) for eating quality were calculated. If the estimated breeding value is $\hat{u}$, with accuracy $r_{TI,}$ then LL95 $= \hat{u}$-SEP*1.65. SEP is the standard error of prediction, calculated as $\sqrt{(1-r_{TI}^2)}$ times the genetic standard deviation. Merit and LL95 were expressed in units of genetic standard deviation.

RESULTS

Accuracy, mean merit and LL95 for EQ is given in Table 2. LL95 is generally negative, indicating that the selection superiority is smaller than the confidence interval based on SEP. For example, with 60 % accuracy, the SEP would be 0.80. An animal with no information has an EBV of 0 and a LL95 of –1.65. LL95 can become smaller for negative correlations, as selection for the composite trait will then reduce EQ. This effect is stronger with more intense selection. Whether or not sons were progeny tested for EQ did not greatly affect the accuracy of total merit index (not shown), and, as a

consequence, relatively equal proportions of tested and untested sons were selected. In general, selection differentials for EQ are lower for rams not progeny tested for EQ (untested sons). Results show that untested sons have lowest LL95, but differences are not much lower than those from tested sons when many of them (80 %) were tested (Table 2). Testing a smaller proportion of sons of each grandsire family increases the number of progeny per young male, and consequently increases accuracy, selection response and LL 95 for EQ-EBV's of tested sons. There is no difference in LL95 of untested sons for different proportions tested. Hence, there is little difference between the information coming from few sibs with more progeny, and more sibs with less progeny. Testing less sons per grandsire family will therefore increase the LL95 of tested animals, but it will also increase the number of untested sons. With higher genetic correlations, the difference between tested and untested sons becomes smaller. For small or zero correlation, untested sons, and even tested sons with few progeny, have a considerable risk of having a low breeding value for EQ.

Table 1. Number of sires tested and number of progeny per son for varying proportions tested per grandsire family

	Eating quality		Other traits	
Proportion tested	**No. of sires tested**	**Progeny per tested son**	**No. of sires tested**	**Progeny per tested son**
.20	**100**	**10**	**500**	**50**
.50	**250**	**4**	**500**	**50**
.80	**400**	**2.5**	**500**	**50**

Table 2. Accuracy, mean EBV for EQ and LL95 for eating quality (EQ) for selected males based on progeny test, distinguishing whether there was a progeny test for EQ available or not, and with varying proportion tested and genetic correlation

Genetic	Proportion	Accuracy EQ		Mean EBV-EQ		LL95-EQ	
correlation	tested	Tested	Untested	Tested	Untested	Tested	Untested
0	.80	.48	.34	0.17	0.06	-1.27	-1.49
0	.50	.54	.34	0.23	0.05	-1.16	-1.50
0	.20	.67	.32	0.37	0.05	-0.85	-1.51
0.60	.80	.64	.59	1.00	0.95	-0.25	-0.37
0.60	.50	.67	.59	1.03	0.95	-0.20	-0.37
0.60	.20	.74	.59	1.10	0.95	-0.0	-0.38

DISCUSSION

The problem outlined in this paper focussed on the information that can be obtained from correlated traits and from tested sibs. Information from correlated traits could be very valuable if genetic parameters were favorable, ie. a moderate genetic correlation and some difference between genetic and environmental correlations. The value of information from half sibs progeny tested for EQ was low and did not have a significant effect on accuracy of untested sibs. Therefore, if genetic correlations between EQ and other traits are not moderate to high, there will be very little information available for rams not tested for EQ. If EQ constitutes a significant part of the variation of the total breeding objective, then investment of increasing the number of test places for EQ would

be justified. For moderate to high correlations, the risk of using untested rams with a low BV for EQ becomes lower.

We looked at the lower limit of true breeding value as a criterion to compare different alternatives. This criterion is conservative and emphasizes customer satisfaction with regard to ram buyers. In the medium and long term, rate of genetic improvement is of main concern for the survival of the breeding program. Smaller proportions of sons tested would increase selection differentials for EQ with LL95 even additionally increased due to smaller PEV. However, if risk of low BV for EQ was a concern, untested sons would then need to be excluded from selection. Effective selection intensity would be decreased in the small group of tested sons. Again, if eating quality has considerable economic value, and if correlations with other traits were low, more extensive progeny testing would be needed to make sufficient rates of genetic gain compatible with a strategy of producing 'low risk' rams.

We have assumed no difference in average merit of grandsire families and no information available to distinguish between sons within family. In practice, this will be the case and better grandsires will have more sons tested. As information from progeny tested half sibs seemed irrelevant for an untested son's accuracy of EBV, the number of sons per family is not relevant for merit. Selection within family can be optimized versus selection from different grandsire families. Within grandsire families, better sons can be distinguished based on their dam or, alternatively, a test based on genetic markers or on a physiological trait measurable on young males. Early selection could partly be based on BLUP EBV's, although using this criterion alone is often shortsighted. Several studies have discussed selection of young males for single trait progeny testing, emphasizing that low accuracy at first stage would benefit the selection differentials in a second stage (Van Raden *et al.* 1987). More sophisticated dynamic selection rules might include effects of inbreeding or risk, as pointed out by Goddard and Howarth (1994). Kinghorn and Shepherd (1999) have proposed methodology that uses dynamic rules to obtain maximum genetic merit under a series of constraints such as inbreeding, costs and logistics. Such tools would be also applicable in multiple trait progeny testing schemes and could be applied in dynamic decision making in practice. However, this paper has illustrated that comparison of static designs provides information about strategic decisions related to investment in data collection and progeny testing schemes. Such decisions typically require sufficient knowledge of economic and genetic parameters of the production system.

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