Genetic Progress In Simulated Dairy And Dual Purpose Cattle Breeds With Small Population Sizes

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Introduction

Selection for genetic improvement is generally restricted to populations with rather high numbers of breeding females, mainly because of the risk of high inbreeding rates associated to selection in small populations. However, selection could improve viability of local cattle breeds and consequently increase breed profitability and stimulate interest in farming. It is obvious that selection goals should be in agreement with conservation aims and genetic variability should be preserved (e.g. Gandini and Oldenbroek (2007)). Tools to select farm populations with inbreeding control are available (e.g. Meuwissen (1994); Grundy et al. (2000)). The objective of this study is to develop simulated selection schemes which, due to their simplicity, could be applied to dairy and dual purpose local cattle breeds in an European context.

Material and methods

A computer simulation of several scenarios of selection schemes was developed in Fortran90 language.

Simulated Populations. We simulated dairy and dual-purpose populations of 500 to 3,000 breeding females, demographically structured in nine age classes. Selection was performed on a single lactation trait (h^2 = 0.3) (dairy populations), or alternatively on a lactation trait and a growth trait (h^2 = 0.4). A genetic correlation among traits of -.30, zero and .15 (dual purpose populations) was assigned. Twenty-five years of selection were simulated, although results were considered on the interval from year 15 to year 25. Number of iterations was 100.

Breeding schemes. In the dairy populations, dams of sires (DS) and sires of sires (SS) were selected by optimizing genetic contributions with a penalty on relationship (OC-selection). Number of young sires (YS) was predefined. The number of SS was determined by OC-selection. In the dual-purpose populations, dams of sires (DS) and sires of sires (SS) were also selected by optimizing genetic contributions with a penalty on relationship (OC-selection). YS were selected among males performance tested males with OC-selection or alternatively with truncated selection.

In both types of populations, minimum and maximum age of sires was predetermined. Moreover, we simulated one mate per dam per year, and the number of mating per sire was allowed unlimited.

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Genetic model. We simulated an infinitesimal genetic model, with Estimated Breeding values (EBVs) estimated with a BLUP animal model for repeated records (dairy trait). Genetic contributions were optimized with a penalty on relationship, by optimizing the following function: $C = v_1 * c' EBV - v_2 * c' A c$, where v1 and v2 are the cost factors, c is the vector of the genetic contributions of candidates, EBV is the vector of the BLUP estimated breeding values of the candidates, and A is the matrix of additive genetic relationships among selection candidates.
The optimization limited the rate of inbreeding to .3% per year, corresponding, across the different models simulated, to an inbreeding rate per generation from 1% to 1.4%. Optimal contributions were computed using Monte-Carlo sampling of sets of selected mating pairs. Conditional to optimal genetic contributions, minimization of mating relationship was performed.

Results and discussion

Figure 1 shows the dynamics of genetic gain in SD units per year for increasing population size (from 500 to 3,000 breeding females). Genetic progress increased rapidly by increasing number of breeding females until population size reached 2,000 females. Thereafter increments seem marginal when schemes based on DS and DD selection and no progeny test of sires are applied.

Figure 1: Genetic gain in dairy cattle populations selected for a milk trait, as a function of population size.

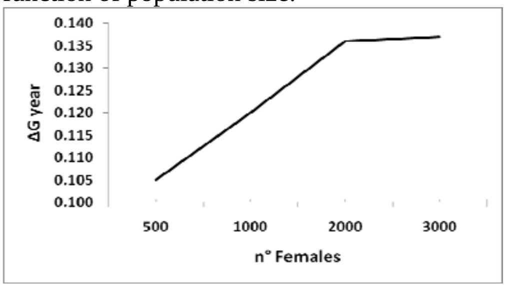

Figure 2: Genetic gain in dual-purpose cattle populations of 500 females, as function of genetic correlation between traits.

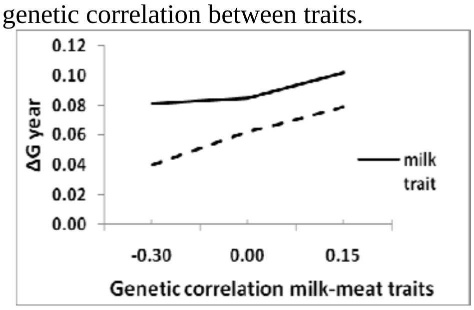

Figure 2 shows genetic gain per year (SD units) in dual-purpose populations of 500 breeding females in the milk and meat traits, as a function of the genetic correlation among milk and meat traits, varying from -.3, as reported for carcass quality, to .15, as reported for growth rate (Liinamo et al. (1999)).

Table 1 reports year genetic gain and inbreeding rate in populations of 500 breeding females when truncation selection or, alternatively, OC-selection was simulated among YS after performance test. Results demonstrated that, in order to control inbreeding at a rate of .3 per year, with a number of YS as low as 8, OC selection must be applied to select YS after performance test. With higher numbers of YS it was possible to control inbreeding rate at a level of .3 by selecting only DS and SS with OC-selection and selecting YS after performance test with truncation selection.

Table 1: Inbreeding rate and genetic gain in dual purpose populations of 500 females and eight YS, when using truncation selection or OC-selection on performance tested young males.				Table 2: **Inbreeding rate and genetic gain in dairy populations of 500 females and sixteen YS, when min and max age of SS is 1-1-and 5-10.**		
Schemes (see text)	**ΔF**	**ΔG milk**	**ΔG meat**	**Scheme (see text)**	**ΔF**	**ΔG milk**
Truncation sel.	.32	.09	.07	SS age:1-1	.30	.11
OC-sel.	.30	.09	.07	SS age 5-10	.30	.11

Table 2 illustrates the relationship between genetic gain and inbreeding rate, and age of SS. When the age of SS was set from a minimum of 5 years to a maximum of 10, forcing SS to be evaluated on daughters' first lactations, genetic gain per year was 0.11 SD units. If maximum age of SS was restricted to 1 year, genetic gain was comparable to the previous scenario. This is explained by the fact that, although SS index accuracy increased in the 5 to 10 years situation, generation length of SS increased from 2 years to 7.6 years. We also compared the use of SS of only 1 year of age with the use of SS from one to ten years of age, and also in this case we did not observe significant differences in genetic gain.

Conclusion

These results show that some genetic progress can be achieved in populations as low as a few hundred breeding females. Interestingly, in dual-purpose cattle populations, optimal contribution selection can be applied only to selection of dams of sires and sires of sires and sires of dams performance tested can be selected with truncation selection. Additional simulations are necessary in order to evaluate the most profitable selection schemes, for a given population size, in terms of both genetic gain and easiness of field implementation.

References

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