# Comparative analysis of selection schemes in small cattle populations

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## <u>Abstract</u>

Progeny testing has traditionally been considered not applicable to small populations, both for inability to obtain significant genetic gains and low profitability. Genetic improvement in small populations can contribute to sustainable utilisation of genetic resources. The objective of this study was to compare genetic gain under three selection schemes: no progeny test, with selection of sires on pedigree index (NPT); progeny test of sires of sires of sires (PT3); classical progeny test of sires of sires of dams (PT5). Selection response per year in populations from 1,000 to 15,000 recorded females was deterministically analyzed with a constraint of 1% inbreeding per generation. PT4 gives higher responses from 1,000 to 15,000 females. Superiority of PT4 is strictly connected with the accuracy of evaluation of candidates. NPT scheme reaches genetic gains lower than PT3 and PT4 even with small number of recorded females (1,000). Costs analysis shows the high increment of cost of schemes with progeny test mainly due the cost of incentive payments.

## **Introduction**

Breeding programs and genetic improvement is generally associated to large populations and management of local small breeds is seen as maintenance of the current genetic profile, however, selection may increase sustainability of local breeds. Selection schemes in these populations should consider maintenance of genetic variation and risks associated with high inbreeding increments. Traits proposed for selection should be evaluated for their genetic correlations with those traits that determine the conservation value of the breed (Gandini et al., 2005). A theoretical framework has been developed in the last years to design breeding schemes that maximise genetic gain while limiting the rate of inbreeding (Woolliams, 2006), however they mainly refer to intensively selected nuclei. The objective of this study was to compare expected genetic gain and relative costs for different selection schemes in simulated small populations of cattle. In general, the schemes differed according to the amount of information available for selection.

#### **Methods**

*Genetic gain* - Genetic progress in a milk trait was deterministically computed in simulated cattle populations of 1,000 to 15,000 recorded females undergoing three alternative selection schemes, with a constraint on effective population size. The following selection schemes were analysed: i.) absence of progeny test, with sires and dams selected on pedigree index (NPT); ii.) progeny test on young males to select sires of sires (SS), dams of sires (DS) selected among females with one lactation record, dams of dams (DD) selected on pedigree index, corresponding to a progeny test scheme with three selection pathways (PT3); iii.) as for PT3, but with a proportion of progeny test, corresponding to a classic four pathways progeny test

scheme (PT4). Genetic and demographic parameters common to all schemes are given in Table 1. The expected genetic gain ( $\Delta$ G) per year, expressed in units of standard deviation, was calculated following Rendel and Robertson (1950), accounting for inbreeding. Generation interval was set at 2, 4, and 5.2 years for sires (in NPT), all dams pathways (in NPT, PT3, PT4), and SS (in PT3, PT4), respectively. Generation interval of SD pathway (in PT4) was computed as weighted mean between the generation interval of females used for progeny test (2 years) and those mated to proven bulls (6.5 years). Accuracy of pedigree indexes was set at 0.25, the heritability of the selected trait. Accuracies of genetic indexes for PT3 and PT4 schemes were computed using standard formulas (e.g. Falconer and Mackay, 1996). The expected genetic gain ( $\Delta$ G) for each selection scheme and population size was computed for all combinations of proportions of selected parents (in NPT, PT3, PT4) and proportions of females (in PT4) allocated to progeny. For each female population size, among the selection combinations analysed, the case producing the highest  $\Delta$ G, under the constraint of Ne = > 50 corresponding to an inbreeding rate per generation of 0.01, was kept.

Table 1. Genetic and demographic parameters of the simulated populations

25%
25%
0.85
0.5
0.95
0.6
0.8
0.9

Effective number of individual of sex s was computed following Santiago and Caballero (1995) as,

$$N_{e,s} = 4Ns \left/ \left[ \frac{1}{\mu_{sm}} + \frac{1}{\mu_{sf}} \right] \times (1 - \alpha_{I,s}) + \left[ \frac{S^2_{sm}}{\mu_{sm}^2} + \frac{2S_{sm,sf}}{\mu_{sm}^2} + \frac{S^2_{sf}}{\mu_{sm}^2} + 4Q^2 C^2_{s} \right] \times (1 + \alpha_{I,s} + 2\alpha_0)$$

where  $N_s$  is the number of parents of sex s,  $\mu_{su}$  and  $S_{su}^2$  the mean and variance of offspring number of sex u (= m or f) from parents of sex s, respectively,  $S_{sm,sf}$  is the covariance between numbers of male and female offspring from parents of sex s,  $C_s^2$  is the variance of selective advantage among families of parents of sex s, Q is the accumulation of selective advantages over generations, approximated to 2,  $\alpha_{l,s}$  is the deviation from Hardy Weinberg proportions of the correlation between genes within individuals and  $\alpha_0$  is the correlation between genes in pair of parents.  $C^2$  was approximated as  $C_s^2 = i^2 \times h^2/4$ , and i was estimated as mean between selection intensities of the pathways involved. Covariances and the  $\alpha_0$  and  $\alpha_{l,s}$  terms were assumed equal to zero. The Santiago and Caballero (1995) formula accounts for mass selection, therefore probably it underestimates the effects of index selection, but it was chosen because it allows taking into account the variances of reproductive success for all pathways, that can be affected by selection scheme. Finally, effective population size was computed as (Crow and Denniston, 1988):

$$N_e = \frac{4 \times N_{e,m} \times N_{e,f}}{N_{e,m} + N_{e,f}}$$

*Costs* - The analysis focused on current costs of the selection scheme, without considering returns from semen sale and genetic gain. Costs for trait recording and for computation of genetic indexes were not considered because common to all schemes. It was assumed the use of artificial insemination (AI) in the whole recorded population and the presence of an AI station. For the two progeny test schemes, PT3 and PT4, two bull management strategies were simulated: the first assumed that bulls were culled after the semen doses required for their progeny test and their possible future use were collected, the second that bulls were kept alive until progeny tested and thereafter additional semen was collected from the selected animals. Costs per year (CY) of each selection scheme and population were estimated as the sum of i.) semen production costs, ii.) incentive payments to farmers for using PT semen and keeping PT daughters, and iii.) costs for maintenance of AI bulls or semen storage. Unitary costs used in the simulation are given in Table 2.

Table 2. Unitary costs used in the simulation.	
<b>.</b>	Value
Cost for renting young bulls, Euro/ bull	800
Proportion of young bulls giving semen	0.9
Cost to evaluate the health status of bulls, Euro/bull	120
Cost of bull's training, Euro/bull	570
Cost of labour for semen collection, Euro/collection	25
Cost of bull maintenance between two semen collections, Euro/bull	14
Cost of producing the semen dose, Euro/dose	0.09
Number of semen doses per collection	200
Cost (incentive payment) for females from bulls under progeny test, Euro/female	30
Costs to incentive the use the semen of bulls undergoing progeny test, Euro/dose	1

#### **Results and Discussion**

Figure 1 shows the genetic gain ( $\Delta$ G) per year, as a function of selection scheme and female population size. PT4 scheme produced the highest genetic gain at all population sizes simulated, with PT3 scheme lying between PT4 and NPT. Genetic gain increased by augmenting female population size. Results for PT4 were within the ranges obtained by Meuwissen (1997) and Villanueva (2006) with similar constraints on inbreeding rate. Proportional increments of genetic gains obtained by augmenting the number of females, in all schemes decreased rapidly up to 6,000 females, from 10% to 1%, and reached a mean value across schemes of 0.4% at 14,000 females. This indicates that below a few thousands females, increasing the size of the recorded population can produce substantial additional genetic gains. Accuracy was assumed constant in the NPT scheme and in dam pathways in PT3 and PT4. Index accuracies showed similar values in SD (in PT4) and in SS (in PT3 and PT4) pathways, increasing on average from 1.48 (1,000 females) to 1.58 (15,000 females). Higher variation across schemes and populations was observed for selection intensity in the

pathways SD (in PT4), DS (in PT3) and Sires (in NPT), increasing on average from 1.87 (1,000 females) to 2.48 (15,000 females). Contributions of the pathways dams of dams (DD) slightly decrease by increasing number of females. Contributions of sires were very high for NPT and then decreased as more phenotypic information was available for selection (PT3 to PT4).

Cost analysis revealed large differences among selection schemes and bull management strategies (Figure 2). Costs per year increase linearly with population size with a divergent trend among selection schemes. NPT scheme had the lowest costs at all population sizes. Figure 3 shows how semen doses, semen storage or bull maintenance, and incentive payments contributed to total costs of the PT3 and PT4 schemes, with and without culling of bulls. When bulls were culled, proportional contribution from semen storage was low, almost absent in PT3. Moreover by increasing female population size, the contribution of incentive costs increased. When bulls were kept alive, proportional costs for keeping bulls was consistent, approximately 80% at 1,000 females (PT3 and PT4), than reduced to 45% and 32% respectively in PT3 and PT4 at 15,000 females. The decrease, by increasing population size, of the proportional contribution to total costs of the costs of semen doses was partly due to the fact that numbers of payment incentives increased, but also to the variation of the unitary cost of the semen dose.

Figure 4 shows the cost of the semen dose as a function of selection scheme and population size. The unitary costs decreased as the female population size increased, the cost of the dose at 1000 females was 8.4 Euro for NPT, 8.6 Euro in PT3 and 2.3 in PT4. This difference is function of the number of doses produced per bull that differs among scheme: at 1,000 females, the number of doses collected per bull was 200 in NPT, 196 in PT3 and 775 in PT4. Expected genetic gain per year is plotted, in Figure 5, against costs per year for the three selection schemes as a function of population size. In Figure 5, for the PT3 and PT4 schemes, only the cheaper strategy of culling bulls is reported. With no progeny test (NPT), by augmenting population size from 1,000 to 15,000 females, genetic gain increased from 0.102 to 0.135 and costs incremented on average by 5,363 Euro per 1/100 of SD unit of genetic gain. With the progeny test schemes PT3 and PT4, costs incremented per 1/100 SD units of genetic gain on average by 12,395 and 23,718 Euro up to approximately 6,000 females, respectively for PT3 and PT4. Than up to 15,000 females, costs incremented by 65,599 and 174,946 Euro per 1/100 SD unit, respectively for PT3 and PT4. At small population sizes PT4 seemed to produce consistent higher genetic gain with reasonable cost increments. At higher population sizes, genetic gains were still higher, but costs increased considerably.

Figure 1. Expected genetic gain ( $\Delta G$ ) per year as a function of selection scheme and female population size.

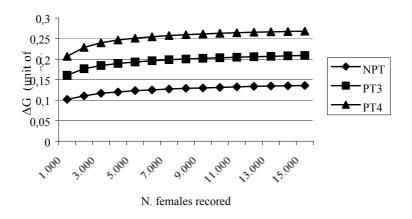


Figure 2. Cost per year (CY), by selection scheme, bull management strategy and population size.

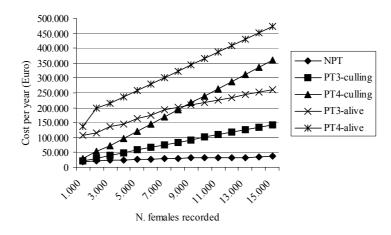
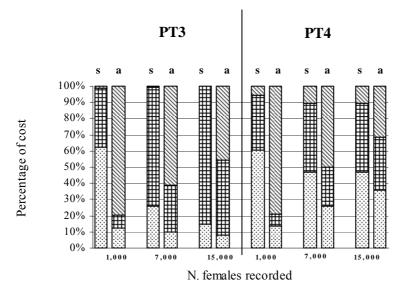
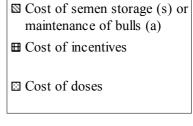


Figure 3. Breakdown of costs per year (CY) for PT3-PT4 schemes, as function of bull management strategy (s = semen storage; a = maintenance of bulls).





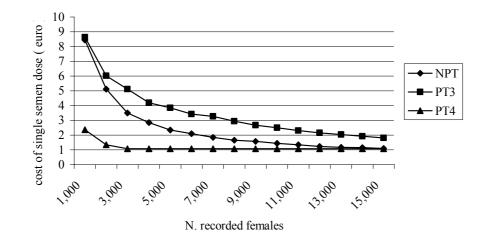
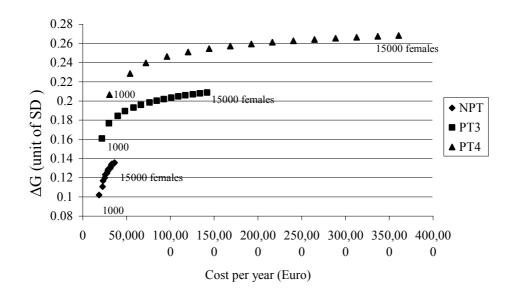


Figure 4. Cost of the semen dose as a function of selection scheme and population size.

Figure 5. Combined trend of genetic gain per year ( $\Delta G$ ) and cost per year (CY), by selection scheme.



## **References**

- Crow J.F. and C. Denniston, 1988. Inbreeding and variance effective population numbers. Evolution 42:482-495.
- Falconer, D. S., and T. F. C Mackay, 1996. Introduction to Quantitative Genetics. 4th ed. Longman Group, Essex, U.K.
- Gandini G., R. Rizzi, A. Bagnato, A. Montironi, F. Panzitta, F. Pizzi, A. Stella, G. Pagnacco, 2006. "Local breeds and genetic improvement", Animal Product from the Mediterranean area, EAAP publication No. 119, Wageningen Academic Publisher.
- Goddard M.E., 1987. Policy of selecting bulls to breed bulls. Anim. Prod. 44:29-38.
- Meuwissen T.H.E., 1997. Maximising the response of selection with a predefined rate of inbreeding. J. Anim. Sci. 75: 934-940
- Rendel, J. M., and A. Robertson, 1950. Estimation of genetic gain in milk yield by selection in a closed herd of dairy cattle. J. Genet. 50:1–8.
- Santiago E. and A.Caballero, 1995. Effective size of populations under selection. Genetics 139: 1013–1030.
- Villanueva B., S. Avendaňo and J.A. Woolliams, 2006. Prediction of genetic gain from quadratic optimization with constrained rates of inbreeding. Genet. Sel. Evol. 38: 127-146
- Woolliams J.A., 2006. Designs and evaluations for managing genetic diversity in breeding programs. 8<sup>th</sup> WCGALP, Belo Horizonte.