

Adopting Partial Genomic Breeding Values in Selection Plan

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INTRODUCTION

Genomic selection has the revolutionary potential in dairy cattle breeding as the young animals may properly be chosen as the parents of the next generation, which reduces the generation interval and increases the rate of genetic gain. Moreover, due to possibility of better controlling of Mendelian Sampling and increased difference between the close relatives, the level of inbreeding decreases (De Roos 2011). In this study, the strategy of choosing chromosomes rather than whole genomes, followed by complementary mating of individuals with special chromosome attributes for the purpose of achieving the desirable genotype at the population level is appraised.

MATERIALS AND METHODS

In this study a population of 30000 dams and 200 sires were simulated as a base population for a trait with parameters similar to what can be seen for milk yield. The simulated genome includes 30 chromosomes. Each of them is 100cM in length to contain 3000 evenly distributed linked SNP markers ($r^2 \approx 0.2$) and 500 QTLs were distributed on the chromosomes (Jahan Bakhshi 2013). The conventional four-path (FP) selection was simulated through selection of 10% of the top sires as sires of sires (SS) and 2% of the best dams as dams of sires (DS) based on the total breeding value as the control group (Jahan bakhshi et. al., 2011). For the second strategy (PS), different but complementary partial genomes of sires and dams considered as selection index. The top 20% of sires for the chromosomes 1 to 15 were mated with the dams ranked for the chromosomes 16 to 30, and the male calves were ranked for the overall breeding value to replace active sires annually in the same rate as FP. Intended strategies were compared for 4, 16 and 32 MOET per DS in order to control it.

RESULTS AND DISCUSSION

At the entire levels of MOETs, the gain of PS was significantly higher ($p < 0.01$). A survey of average of final 10 years provides two other important results: first, with an increase in the number of MOETs, PS response becomes closer to FP. For example, in case of the best observed sire (BS) in MOET=4, the relative response was 80.8%, which with the addition of MOETs to 16 and 32 was raised to 83.2% and 84.4% respectively. Second, in presenting the best observed genotype, the PS was more efficient than the other parameters. The difference between these two strategies lies in the reverse for average inbreeding. The final 10 years of inbreeding caused by PS were only 56%, 60% and 75% of what were caused by FS for 4, 16 and 63 MOET respectively.

However computer RAM limited this study to simulated large number of MOET but the pattern of change in superiority by increasing MOET number hopefully proposed this idea that in the near future improvement in in vitro embryo production may lead breeding plans to account for partial genomes.

Keywords: Genomic Selection, Chromosomal Value, Breeding Plan

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