

1 **Genomic selection in dairy cattle simulated populations**

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Abstract

Genomic selection is the most promising tool to improve domestic animals genetic gain in the last few decades. However obtaining genomic information is an expensive process. The aim of this study was to evaluate the economic impact related to the implementation of genomic selection in a simulated dairy cattle population. The software QMSim was used to simulate genomic and phenotypic data. The genome simulated contained 30 chromosomes with 100 cM each, 1,666 SNPs markers equally spread and 266 QTLs randomly designated for each chromosome. The numbers of markers and QTLs were designated according information available from: Animal QTL (<http://www.animalgenome.org/QTLD>) and Bovine QTL (<http://bovineqtl.tamu.edu/>). The allelic frequency changes were assigned in a gamma distribution with alpha parameters equal to 0.4. Recurrent mutation rates of $1.0e^{-4}$ were assumed to markers and QTLs. A historic population of 1,000 individuals was generated and the total number of animals was reduced gradually along 850 generations until obtain a number of 200 animals in the last generation, characterizing a bottleneck effect. Progenies were created along generations from the random mate of the male and female gametes, assuming the same proportion of both genders. Than the population was extended for another 150 generations until we obtained 17,000 animals, with only 320 male individuals in the last generation. After this period a 25 year of selection was simulated taking in account a trait limited by sex with heritability of 0.30 (i.e. milk yield), one progeny/cow/year e variance equal to 1.0. Annually, 320 bulls were mated with 16,000 dams, assuming a replacement rate of 60 and 40% for males and females, respectively. Selection and discard criteria were based in four strategies to obtain the EBVs assuming as breeding objective to maximize milk yield. The progeny replaced the discarded animals creating a overlapping generation structure. The selection strategies were: RS) selection based in random values; PS) selection based in phenotypic values; Blup) selection based in EBVs estimated by BLUP; and selection based in genomic estimated breeding values (GEBVs) in one step, using high (GBlup) and low (GBlupi) density panels. Results indicated that the genetic evaluation using the aid of genomic information could provide better genetic gain rates in dairy cattle breeding programs as well as reduce the average inbreeding coefficient in the population. The economic viability indicators showed that only Blup and GBlup/GBlupi strategies, the ones that used milk control and genetic evaluation were economic viable, considering a discount rate of 6.32% per year.