

Testing different genomic selection scenarios in a small cattle population by simulation

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Genomic selection increases genetic gain by reducing generation interval and increasing accuracy of selection. However, success of selection depends also on the extent and strategy of using genomic information in the breeding program. The questions relate to how many and which animals to genotype and in what extent to use the genomic information. We developed a simulator of realistic cattle population with overlapping generations and selection. We tested five sire selection scenarios including conventional and four genomic selection scenarios that differed in the criterion for sire selection (progeny / genomic testing). All five scenarios were tested within three sire use strategies differing in the number of sires selected per year and years kept in use. Scenarios were compared by genetic gain and efficiency of selection. The latter was defined as conversion of genetic variance into genetic gain. In all sire use strategies the increasing use of genomics increased the genetic gain. Using genomic information for pre-selection of calves for progeny testing increased genetic gain between 35% and 46% and using genomic information for the immediate selection of sires increased the gain up to 123% compared to the conventional scenario. These results were in line with the reduced generation interval. In the original sire use strategy (five bulls selected each year and used for five years) the conventional scenario was the least efficient and the complete genomic selection scenario was not the most efficient. Despite higher genetic gain, increasing intensity of selection (only one bull selected each year and used for five years) decreased the efficiency of selection due to larger loss in genetic variance. Reducing the generation interval even further (replacing all five bulls every year) remedied the low efficiencies - but they were still decreased compared to the original strategy due to a lower accuracy of prediction. The developed simulator will be used as a modelling tool for answering further questions regarding genomic selection in specific populations.