



Implementation of genomic selection in small populations - Croatian case

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Abstract

Dual purpose Simmental breed represents dominant part of Croatian cattle population which is mainly raised in a limited number of countries (Germany, Austria, Czech Republic, north Italy, Slovenia, and Croatia). Holstein is the second largest breed population in Croatia. In order to maintain and improve production of young Simmental bulls based on a genomic breeding value of young calves, Croatia joined German-Austrian system of genomic evaluation in July 2013. The inclusion was justified since the breeding of Croatian Simmental is closely related to Austrian and Bavarian breeding. Bull's sires and bull's dams are coming from these populations and there is a long-standing import of breeding heifers and bull's semen for artificial insemination. In contrast to Simmental, the main goal of genomic improvement in Holstein population is based on female calves in order to identify potential dams at a young age. Croatia does not have a sufficiently large reference population. Therefore the potential female candidates were included in German Holstein genomic evaluation system, starting from 2016.

Young male and female candidates were chosen based on parent average, interesting bull lines, as well as dam exterior. Based on these criteria, 254 young Simmental and 96 Holstein calves were selected, genotyped and genomic breeding values were estimated for them. Additional benefits of genomics, beside genomic evaluation, are parentage verification and information about major gene/disease defects specific for Simmental and Holstein populations. The recommended criterion for entry of potential young Simmental bull in the centres for AI is total merit index over 130. Furthermore, candidates should not be carriers of known genetic defects or recessive for them. On the basis of agreed criteria, seven young bulls were selected as potential bulls for AI. The recommended criteria for selection of Holstein female candidates are a total merit index of 150, without gene defects and so far none of them reached these standards.

Croatian Agricultural Agency as milk recording organization is deeply included in genomic services through collecting recording data, breeding value estimation and consequently parent average calculations, processing and publishing of the genomic evaluation results. At the farm level, genomics for females becomes an attractive option to capitalise on the benefits of using this technology. At the national level, Croatia has gone from a country that imported most of its genetics to a country which now uses own semen. The usage of genomic bulls has increased from 8% of all used bulls in 2012 to 23% in 2016. In addition, Croatian AI companies are now marketing semen of two young bulls internationally.

Key words: genomic selection, Simmental and Holstein breed, male and female calves,

Introduction

Dairy cattle population in Croatia (CAA, 2017) is composed of Simmental (62.8%), Holstein (24.3%), and Brown Swiss (2.8%) breeds. The remaining proportion includes crossbreeds (5.6%), and other minor breeds (4.3%) including indigenous breeds. Although the number of cows decreased in the past ten years (from 234,671 to 167,628), the number of cows in milk recording was constant. Dual-purpose traits, adaptability and long breeding tradition of Simmental (SIM) breed have a great relevance to the Croatian cattle production. SIM cows represent around 57.5% of all cows in milk recording. Holstein (HOL) cows are the second most important cattle population in Croatia. This breed is used mainly on enterprises specialized in milk production. The enlargement of existing farms, establishment of new farms, as well as the transition of medium sized and dual-purpose farms has led to a constant increase of specialized milk producing facilities. The proportion of HOL cows in milk recording was nearly 40% in 2016.

Phenotypic data collected through various recording schemes (milk and fertility recording, type classification, etc.), together with pedigree information, provide a basis for breeding value estimation (EBV). In the past decades, genetic progress in Croatian SIM and HOL cattle population has been low. Breeding organizations were not sufficiently powerful during the transition period to define rules of conducting the breeding program. At that time massive and, in most of the cases, unnecessary imports of heifers have occurred. Beside the justified use of bulls with a high BV, a lot of bulls used in artificial insemination could not provide expected genetic gain due to low BV. At that time, production of young bulls from the national breeding program was reduced to a minimum.

During the past five years, breeding organizations started to grow and recognized the importance of genomic selection program, which opens the possibility of revitalization through the production of competitive young bulls. The most important breed for Croatia is dual-purpose SIM, which is also raised in a limited number of countries (Germany, Austria, Czech Republic, northern Italy and Slovenia). Due to generally small population, the inclusion to joined German-Austrian genomic evaluation system in July 2013 was a reasonable solution. The participation was justified since bull's sires and bull's dams are coming from this population and there is a long-standing import of heifers and bull's semen. In contrast to SIM, the main goal of genomic improvement in HOL population is based on female calves in order to identify potential dams at a young age. These dams will be further inseminated via ET and usage of sexed semen to produce replacement heifers and to insure the market of female breeding material. For that purpose, selected Croatian female calves were included in the German Holstein genomic evaluation starting from March 2016. The inclusion was reasonable due to pedigree connection with German population through the long-standing import of breeding heifers.

The objectives of this study were to describe the steps in an implementation of genomic selection in a small population of Croatian SIM and HOL breed and to show the results of its implementation for Croatian candidates.

Material and methods

Agreement for Implementation of genomic selection is the main act which defines the rules and obligations of all participants involved in the implementation of genomic selection for Simmental and Holstein breed. The participants are: Simmental and Holstein breeding associations (BA's), Croatian Agricultural Agency (CAA), artificial insemination centres (AIC's), and scientific institutions (SI's). BAs are involved in the selection of potential candidates (male and female calves) and for using of semen of selected young bulls. CAA participates in the selection of potential candidates, updating

the herdbook and preparing the pedigree of candidates, performs analysis of genomic BV and is responsible for the publication of results. AIC's are also involved in the selection of potential candidates, they collect and send biological samples (blood or tissue) to the official laboratory, as well as purchase and hold the genomically tested young bulls. SI's have advisory and educational function in the implementation of genetic-population parameters. The main step in the implementation of genomic selection is a selection of potential candidates and all participants are involved in this step. Young male and female candidates are selected based on following criteria: a) they are progenies of the most interesting genomically and progeny tested sires; b) pedigree is important since the interesting sire and dam lines are considered; c) parent average is calculated in the case of Croatian sires; d) dam exterior has to be scored.

Altogether 260 SIM and 109 HOL calves were selected, genotyped and included in the genomic evaluation system. Genotyping is carried out using standard IlluminaBovine50K chip. Genotypes are bases for further genomic evaluation of candidates. For SIM breed, genomic evaluation is conducted monthly in German-Austrian genomic evaluation system for a total of 44 traits. A two-step approach using G-BLUP (VanRaden, 2008) is used for genomic evaluation of all traits. Direct genomic values (DGV) are estimated for all genotyped animals. These DGV are further blended with the conventional breeding values (EBV) or parent averages (PA) in combined genomic breeding values (GEBV) as described by VanRaden *et al.* (2009) including modifications (Edel *et al.*, 2010). Genomic evaluation has been routinely conducted for German Holstein breed since 2010 for a total of 44 traits. The evaluation is based on a BLUP SNP model with a trait-specific residual polygenic variance as described by Liu *et al.* (2011). DGV and PA were combined based on selection index method (Liu *et al.*, 2011) to obtain GEBV for all traits. GEBV are the officially published breeding values of a genotyped animal, either of SIM or HOL breed.

For the Croatian SIM population, GEBV and DGV were estimated for 254 calves which are progenies of 60 bulls mostly of German or Austrian origin. In the case of HOL breed, 96 females with estimated GEBV and DGV were progenies of 51 bulls. The distribution of sires by year of birth in SIM and HOL breed is shown in figure 1.

Results and discussion

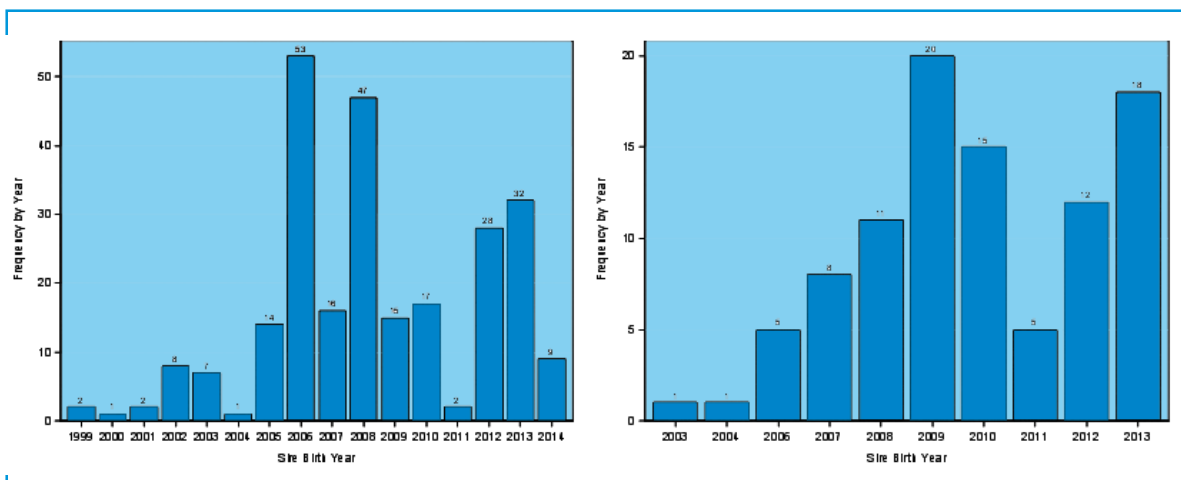


Figure 1. Number of progenies per bull in SIM and HOL breed

Distribution of GEBV (Figure 2a) showed a similar proportion of animals by classes of the standard deviation of GEBV by the trait group. The highest proportion of animals has GEBV which is one standard deviation from the average. The recommended criterion for entry of young SIM bulls in the centre for AI is total merit index over 130. On the basis of agreed criteria, seven young bulls were selected as bulls for AI. The figure 2a represents GEBV from the last monthly evaluation where only three animals have passed criterion. However, since the GEBV changes over time, the selected animals had met the criteria set in the given monthly evaluation. As a result of higher selection intensity on genomic bulls, the 1:35 ratio of selected and genotyped male candidates was observed which is similar to the ratio in other countries. At the national level, Croatia moved from a country that imported most of its genetics to a country which now uses own semen. The usage of genomic bulls has increased from 8% of all used bulls in 2012 to 23% in 2016. In addition, Croatian AI companies are now marketing semen of two young bulls internationally.

When calves were ranked based on GEBV, around 10% of them were incorrectly assigned to the top of the list compared to the rank based on PI evaluated in the genomic system. However, it is hard to compare PI between the national genetic evaluation and genomic evaluation since some bulls selected as sires are not progeny tested in our population. Furthermore, GEBV were not transformed to the Croatian scale due to the lack of transformation formula for many of traits. Another criterion for selection of candidates as bulls for AI is that they should not be carriers of known genetic defects or be recessive for them. In the German-Austrian genomic evaluation system, nine genetic defects specific for SIM breed were discovered. However, there

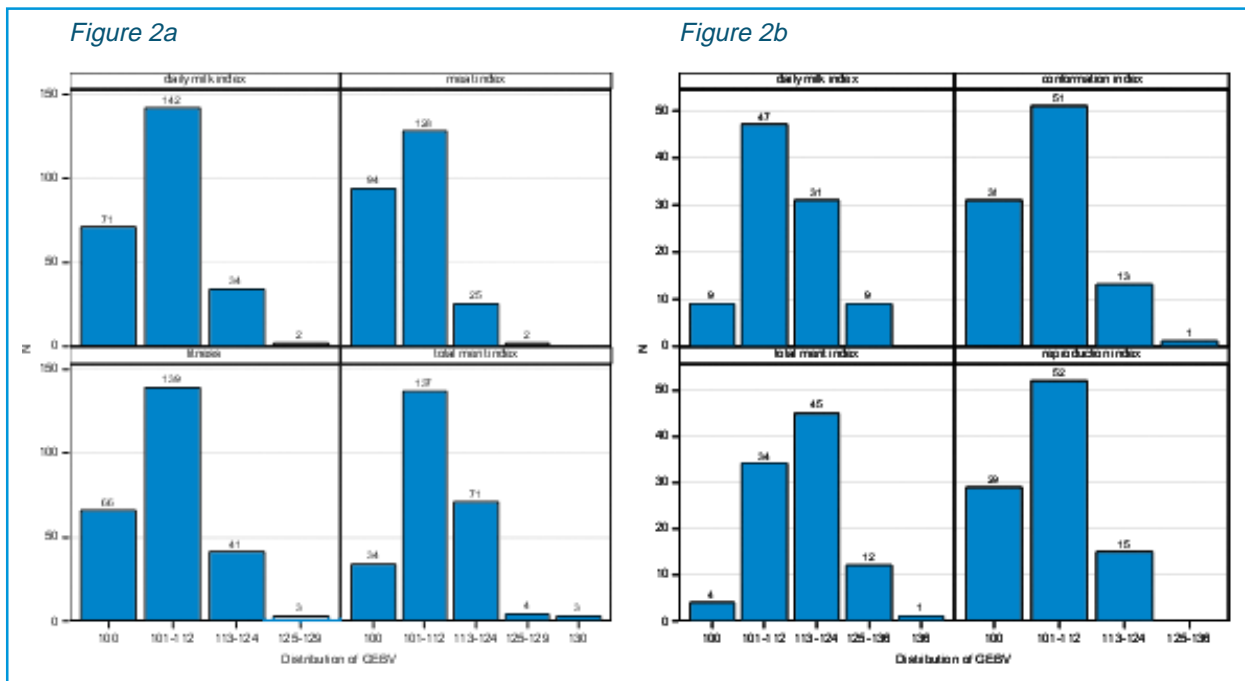


Figure 2a Distribution of GEBV for main group of traits in SIM breed .

Figure 2b Distribution of GEBV for main group of traits in HOL breed

are also data on traits like polled and kappa casein, which should be expanded over populations. The proportion of animals that carry one or more of genetic defects or is recessive for them decreased in the genotyped population since sires having defects are no longer used on genotyped animals or should not be in the dam's pedigree.

The recommended criteria for selection of HOL female candidates are a total merit index of 150, without gene defects and so far none of them reached these standards. Distribution of GEBV for the main group of traits (Figure 2b) was similar to SIM breed: the highest proportion of animals belonged to the group within one standard deviation from the average. However, there are selected HOL with a high genetic potential since animals having GEBV with two or three standard deviations better than average existed. Eight of genetic defects specific for HOL breed, were also detected using genomic information. The proportion of animals that are carriers of a specific defect was low.

An additional benefit of genomics, beside genomic evaluation and information about gene/disease defects, is parentage verification. The proportion of animals with pedigree conflict was low in SIM breed (0.04%). However, the proportion is higher (1%) in HOL breed which is coming from large farms. In the most of the cases pedigree was updated based on genomic data and offered potential sire which exists in German base.

Despite all benefits, some obstacles exist in the implementation of genomic selection in Croatia. Although genomics brings back to the breeders confidence in the national breeding program, the number of active breeders is small. There is still insufficient use of the bulls with a respectable either EBV or GEBV as bull sires. The price of implementation of genomic selection in SIM breed is still high. Furthermore, GEBV, DGV, and PI are given on German scale and one of the future steps will be an adaption of German system to the national. Since the past year, our population is dealing with lumpy skin disease threat and obligatory vaccination. Breeding Associations are in negotiations with a Ministry of Agriculture to exclude genomic calves from vaccination.

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Conclusions

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