Opportunities of implementing the genomic selection in small populations - the Croatian case

Marija Špehar*, Zdenko Ivkić, Ivica Vranić, Josip Crnčić,
Maja Dražić, Davor Pašalić, Zdravko Barać

Croatian Agricultural Agency, Ilica 101, 10000 Zagreb, Croatia
*Corresponding author: E-mail: mspehar@hpa.hr

Abstract

The implementation of genomic selection (GS) together with the changes caused by globalization and trade liberalization of breeding material often raise the question of sustainability of breeding programs in small cattle populations/countries. The objective of this study was to describe the steps in the implementation of GS in small populations of Croatian Simmental (SIM) and Holstein (HOL) breeds; to show the results of its implementation; and to present the perspectives of GS for these populations. In order to improve the selection of SIM bulls, Croatia joined the German-Austrian genomic evaluation system in July 2013. The main goal of the GS in HOL population was selection of bull's dams at a young age which started in 2016 through the inclusion in German HOL genomic evaluation system. In total, 268 SIM and 96 HOL calves were selected, genotyped, and genomically tested until the end of 2017. The criterion for the entry of SIM bulls in the artificial insemination (AI) centres is the total merit index over 130 and candidates should not be carriers of specific monogenic defects or be recessive for them. Based on these criteria, seven young bulls were selected as for AI. The criteria for the selection of HOL females are the total merit index of 150, without monogenic defects and so far none of them reached these standards. The future perspective for HOL breed is international IgHol project for small HOL populations representing the possibility for cost-efficient solutions of GS. The implementation of GS brought opportunity to Croatian breeders to use semen of bulls from the national breeding program. Genomics for females becomes an attractive option to capitalise the benefits of using this technology.

Key words: genomic selection, Simmental and Holstein breed, direct genomic value, genomically enhanced breeding value

Introduction

The genetic improvement of quantitative traits (dairy, beef, conformation traits, longevity, etc.) is commonly based on phenotypic and pedigree information that are used to estimate breeding value (EBV). In dairy cattle, phenotypic data are collected through various recording schemes (milk and fertility recording, conformation scoring, etc.) on daughters of progeny tested bulls. The latter are four to six years old when the first crop of data on their daughters is collected. At that time the accuracy of bull EBV is 0.90 or more. Without progeny testing as a source of phenotypic information that pertains

to bulls, the accuracy of EBV using only pedigree information (i.e., average parental breeding values, PA) is around 0.60 (e.g. Schefers and Weigel, 2012).

The availability of affordable high-density panels of the single nucleotide polymorphisms (SNP's) showing a variation at a single position in a DNA has led to the abundant use of this information in selection decisions commonly called genome-wide or genomic selection (Meuwissen et al., 2001). Genomic selection is based on the inference of breeding values based on the sum of SNP effects related to the phenotype across the whole genome (Meuwissen et al., 2001; Solberg et al., 2008). The sum of all SNP effects represents an estimate of total additive genetic (breeding) value of an individual. In dairy cattle, this estimate is often called direct genomic value (DGV) and is based solely on genotypic information of individual animal based SNP effects. For the implementation of genomic selection, phenotyped and genotyped reference population of at least 1000 bulls is needed to estimate the SNP effects and assemble them in DGV prediction equation which is in turn used to estimate DGV for non-phenotyped individuals (Meuwissen et al., 2001; Goddard and Hayes, 2007). Different types of breeding value estimates (EBV based on PA or progeny testing and DGV from genomic information) could be blended into one value often called genomically enhanced breeding value (GEBV) using various approaches (VanRaden 2008; Kachman, 2008; Aguilar et al., 2010). The accuracy of genomic evaluation mainly depends on the number of genotyped and phenotyped individuals in the reference population (Goddard, 2009; Schefers and Weigel, 2012). Although the use of genomic data generally provides less information than phenotypic data from a progeny test and consequently lower accuracy of EBV, the advantage of using genomic data is to increase the accuracy of EBV of young or non-phenotyped animals from about 0.60 (PA) to 0.80 (Hayes et al., 2009). Even though these accuracies are still lower than with progeny test, the early use of genomically tested young bulls in artificial insemination (AI) shortens the generation interval considerably and increases therefore the genetic gain per unit of time (Schaeffer, 2006). An additional benefit of genomics, beside genomic evaluation is information about monogenic disor-

ders/defects and parentage verification. Namely, with decreasing the costs of genotyping, parentage verification based on SNPs replaced microsatellites (McClure et al., 2013; McClure et al., 2018). Furthermore, it is important to emphasize that genomic selection does not replace the current selection methods rather than upgrade them.

Implementation of genomic selection in small populations

In Croatia, the importance of introducing genomic selection in cattle has been recognised following European and world trends. However, chances for commercial implementation of genomic selection are limited in small populations. As already mentioned, the effectiveness of genomic selection depends on the size and the composition of the reference population used for genomic predictions. Since Croatia does not have large enough reference population, the inclusion in the genomic evaluation system of other countries or consortia was a reasonable solution. With the goal to increase genetic gain by selecting competitive young bulls and female calves as potential bull's dams based on genomic BV, the objective of this paper was to: a) describe a framework for the implementation of genomic selection in a small population of Croatian Simmental (SIM) and Holstein (HOL) breeds, b) to show the results of its implementation for Croatian candidates, and c) to present the future perspectives of genomics for these populations, d) to present future perspectives of genomic selection in dairy cattle.

A framework for the implementation of genomic selection

'Agreement for Implementation of the genomic selection at the national level' was the main act signed in 2012 which defined the rules and obligations of all participants involved in the implementation of genomic selection for the SIM and HOL breed. The participants were SIM and HOL

Breeding Associations (BA's), Croatian Agricultural Agency (CAA), Artificial Insemination Centres (AIC's), and Agricultural Faculties (AF's). BA's were involved into the selection of potential candidates (male and female calves) and for use of selected young bulls. CAA participated in the following activities: selection of potential candidates, updating the Herd book, collecting biological samples, analysing of genomic BV, and publication of genomic results. AIC's were also involved in the selection of potential candidates, collecting and sending biological samples to the official laboratory, as well as purchasing and holding genomically tested young bulls. AF's had advisory and educational function in the implementation of population genetic parameters. Meanwhile, two of the AIC's had been closed, while Semen Shops have been involved in the implementation of the activities recently. The recommended criterion for entry of the potential young SIM bull in the AI centres is total merit index over 130. Furthermore, candidates should not be carriers of known monogenic defects or be recessive for them. The recommended criteria for selection of HOL female candidates are a total merit index of 150, without gene defects.

The first step in the implementation of genomic selection was the selection of potential candidates. The Breeding Committee (representatives from BA's, CAA, and AIC's) carried out this activity by selecting young male and female calves based on several criteria. The criteria were: a) they were progenies of the most interesting genomically and progeny tested sires; b) belonged to the interesting sire and/or dam lines based on pedigree; c) PA was calculated for the Croatian sires, while BV estimated in originated country was used for foreign sires (i.e. GZW - GesamtZuchtWert from the DE/AT system); d) dam exterior had to be scored having high values for the main group of conformation traits. The next step was collecting biological samples (ear tissue) of calves for genotyping by AIC's and CAA employees. Biological samples were sent to an authorized laboratory (GeneControl in Grub for SIM and IFN Schönow, Berlin in Germany or Weatherbys, Johnstown in Ireland for HOL breed). The genotyping was performed using Illumina BovineSNP50K BeadChip® (version 1, 54001 SNP's) and Illumina BovineSNP50K BeadChip® (version 2, 54609 SNP's). After genotyping, several quality controls were applied to analyse the integrity and informativeness of SNP's as follows: genotyping the call rate by SNP and by the animal, the minor allele frequency, and the departure from Hardy-Weinberg equilibrium. Genomic data preparation also included checks on reasonable accordance of genotypes for related animals using direct comparison (parent-offspring) and marker-based IBD-coefficients (Wang, 2002).

In Croatia, dual purpose SIM breed represents dominant breed and largest cow population in milk recording (CAA, 2017) showing an advantage over the HOL in many traits such as health, fertility, meat quality, and longevity. Therefore, the implementation of genomics started earlier in SIM compared to HOL population.

Implementation of genomic selection for SIM breed

Implementation of genomic selection for SIM population has a goal to maintain and improve the production of young competitive bulls based on genomic BV whose semen could primarily be used to inseminate cow population in Croatia and in neighbouring countries. At the same time, genomically tested female calves could be used as bull's dams. Dual purpose SIM breed is mainly raised in a limited number of countries in Central and Eastern Europe (southern part of Germany i.e. Bavaria, Austria, Czech Republic, northern Italy, Slovenia, Croatia, Serbia, and Romania). Germany and Austria as the most important breeding areas have joint genetic evaluation system since 2002. The system was upgraded with an officially routine genomic German-Austrian (DE/AT) evaluation in August 2011 performed on monthly basis for the genotyped animals (Edel et al., 2010). Croatia and Bavaria have co-operated in the harmonization of the breeding program for the SIM breed for many years. Therefore, the inclusion of the Croatian SIM population in the DE/AT genomic evaluation system in July 2013 became a reasonable solution. The participation was justified since the breeding of Croatian SIM population was closely connected with the farming in Bavaria. In addition, bull's sires and bull's dams have been coming from this popu-

lation and there is a long-standing import of heifers and bull's semen.

Altogether 268 SIM calves (male and female) were selected, genotyped and included in the genomic evaluation system since 2013. These animals were born in the period from 2013 to 2017 (Figure 1). Male calves prevail (94 %) in the structure of genotyped animals since the main reason of implementation of genomic selection was to ensure a sufficient number of young genotyped bulls to be used for AI in the population of SIM cows in Croatia. Female calves were genotyped in order to check their acceptance as a possible bull's dams.

Genotyped SIM calves were progenies of 64 sires (Figure 2). Among genotyped calves, 237 of them were progenies of 50 sires having German origin (DE), while 26 claves originated from 10 Austrian sires (AT). These sires were chosen for insemination of Croatian SIM population based on either conventional or genomic BV for total merit index. Five calves were progenies of four sires having Croatian origin (HR).

The most of genotyped SIM calves were progenies of progeny tested bulls (Figure 3) born between 2005 and 2010. Among genotyped animals, there are also progenies of young genomically tested bulls born in 2013 and 2014 without progeny results, i.e. without conventional BV.

Routine genetic and genomic evaluation in DE/AT system has been performed in three evaluation centres the Institute in Grub, Bavaria (dairy and conformation traits, somatic cells, and milking speed), the Institute in Stuttgart, Baden-Württemberg (beef traits), and Zuchtdata in Vienna, Austria (longevity, calving ease, stillbirth, fertility, and total merit index). The validated and processed genotypes served as a basis for predicting DGV, PA, and GEBV for each genotyped animal. In total, 44 traits are used for genomic evaluation using G-BLUP two-step approach (VanRaden, 2008). DGV are estimated for all genotyped animals which is further blended with the conventional breeding values (EBV or PA) in GEBV as described by VanRaden et al. (2009) including modifications (Edel et al., 2010).

Distribution of GEBV for the main group of traits in SIM breed (milk, beef, and fertility index) as well as for total merit index is shown in Figure 4. The GEBV is given on DE/AT scale since Croatia
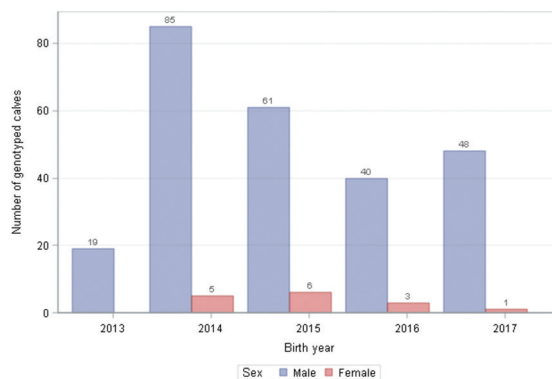

FIGURE 1. The number of genotyped calves by sex *per* birth year in the period from 2013 to 2017 for Croatian Simmental breed
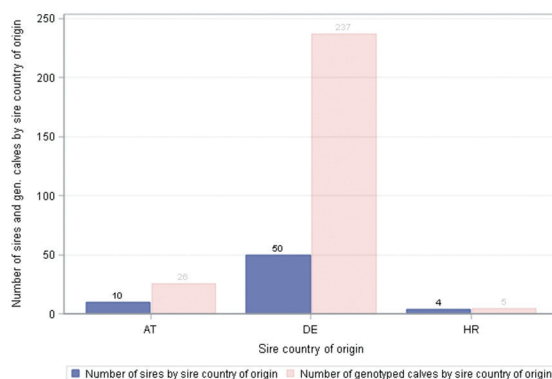

FIGURE 2. The number of sires by country of origin (AT- Austria; DE- Germany; HR-Croatia) and the number of genotyped Simmental calves borned in the period from 2013 to 2017 by the sire country of origin
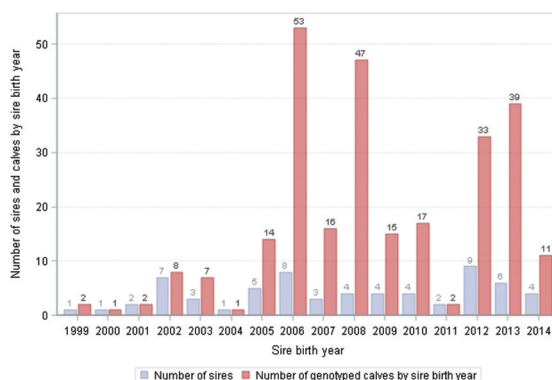

FIGURE 3. The number of sires borned in the period from 1991 to 2014 and the number of genotyped calves by sire birth year in Croatian Simmental breed

uses the same indexes for the main group of traits. The distribution of GEBV for all groups of traits was shifted to the right side of the normal distribution curve (the average is 100, with one standard devia-
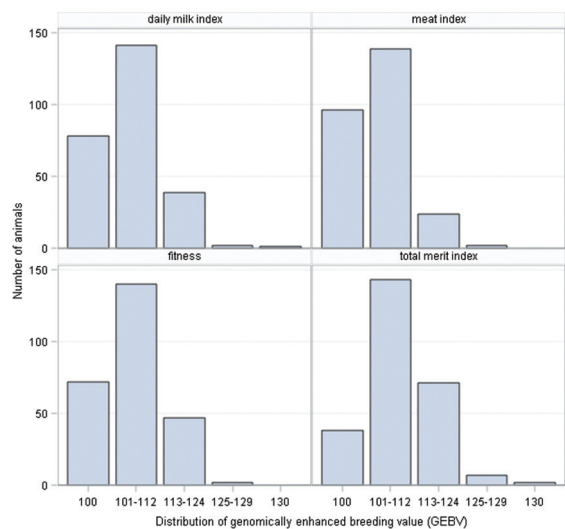
FIGURE 4.
The distribution of genomically enhanced breeding value (GEBV) for the main group of traits (daily milk index, meat index, fitness, and total merit index) for genotyped calves borned in the period from 2013 to 2017 in Croatian Simmental breed

of the GEBV for most of the traits included in the genomic evaluation for SIM breed was higher than the average reliability of the PA for the same traits (Figure 5). This suggests that SNPs contribute with additional information to the BV evaluation in comparison to pedigree data.
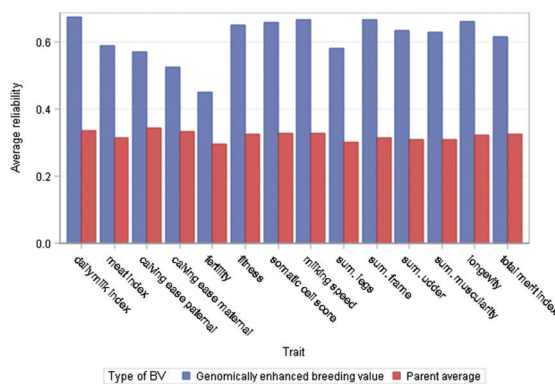

FIGURE 5. Average reliability of genomically enhanced breeding value and parent average by trait for genotyped calves borned in the period from 2013 to 2017 in Croatian Simmental breed

tion of 12 points) since the pre-selection of candidates was done. In the DE/AT system, the reference population consists of around 9,000 bulls having both, genotype and phenotype of the most traits (Plieschke et al., 2016). Several studies (Calus et al., 2013; Thomasen et al. 2014; Plieschke et al., 2016) reported that adding information from genotyped and phenotyped females in the reference population increases the reliability of breeding values of young selection candidates and also contribute to reduce the biasing effects of preselection.

The distribution of GEBV showed a similar proportion of animals by the classes of GEBV standard deviation for the main groups of traits (Figure 4). The highest proportion of animals had GEBV of one standard deviation from the average. Figure 4 represents GEBV from the latest monthly evaluation where only three animals had GEBV above 130 for the total merit index. However, since the GEBV change over time, the selected animals had met this criterion in the given monthly evaluation. GEBV is changing due to the re-calibration of the genomic system after conventional BV estimation three times per year (Edel et al., 2011).

An additional benefit of genomics, besides the increased genetic gain per unit of time due to shortened generation interval, is the increased accuracy of GEBV compared to PA. The average reliability

For the most of analysed traits, the average GEBV reliability was between 0.62 and 0.68 and was 29 % and 34 % higher than the average reliability of PA for the same traits. The exceptions were the functional traits (fertility, calving ease, and stillbirth) with a small difference in average reliability between GEBV and PA due to low heritability.

The results of genotyping also provide information on monogenic traits, i.e. monogenic characteristics and disorders. The term "monogenic trait" is used to describe a trait inherited by a single gene as the result of a mutation (Griffiths et al., 2012). Therefore, monogenic variants of κ- and β-casein, as well as bovine polledness, are determined by genotyping. Therefore, genetic testing provides additional information in order to improve selection and future breeding decisions with an impact on short and long-term profitability (Caroli et al., 2009). It became a standard that bull catalogues of AI companies contain information about monogenic characteristics. κ- and β-casein are associated with the cheese processing and quality of dairy products having a growing role in human nutrition and breeding in general. κ-casein as one of the non-whey proteins associated with the increased protein yield and percentage has three genotypes (AA, AB, or BB). Genotype BB is the most desirable since

it is associated with the higher cheese production (Bovenhuis et al., 1992; Azevedo et al., 2008). Some countries already included κ-casein into their breeding programs and started increasing the frequency of the B allele variant in order to improve milk quality and its cheese making characteristics (Potočnik, 2015). Gene testing for β-casein determines three genotypes: A1A1, A1A2, and A2A2 of which A2A2 is considered to have health benefits over the others genotypes of the protein (Bell et al., 2006). Although health benefits are under debate in the dairy industry (EFSA, 2009), milk having genotype A2A2 is selling in USA, New Zealand and Australian markets at a premium over standard milk. Genetic tests also determine the polledness in cattle and the belonging results are indicated by an asterisk (*), while the possible genotypes are PP* (a dominant homozygous animal which is hornless or polled), Pp* (heterozygous animal which is hornless or polled), and pp* (recessive homozygous animals which are horned).

Beside the monogenic characteristics, the genotyping results also provide information of monogenic disorders specific for the SIM breed in the DE/AT genomic testing system (Lfl, 2017). Therefore, SIM breed is tested against Arachnomelia, Bovine Male Subfertility, Dwarfism, Fleckvieh Haplotype 2, Fleckvieh Haplotype 4, Fleckvieh Haplotype 5, Thrombopathia, and Zinc deficiency-like syndrome. Proportion of animals that carry one or more of monogenic defects or are recessive for them, decreased in the genotyped population since sires having defects are no longer used or should not be in the dam's pedigree. If the potential calf sire is a carrier for a certain disorder, his progeny will not be chosen for genotyping. Furthermore, genotyping has also enabled parentage verification for genotyped animals. The proportion of genotyped animals having pedigree conflict according to marker-based IBD-coefficients was small (0.04 %). In the most of cases, the origin of these genotyped animals (i.e. sire or dam-sire) is corrected using genomic information and offering potential sire or dam-sire from the database.

Young SIM bulls with the estimated genomic BV after reaching maturity can be used in the centres for AI, if they meet criteria defined by the SIM Breeding Program as follows: GEBV of total merit index over 130 with reliability of >0.50, while candidates at the same time should not be carriers of disorders or recessive homozygous for them. The exceptions are candidates of interesting sire/dam lines (rarely represented lines) or progenies of dams having high production for the main group of traits. In this case, the GEBV for total merit index could be three to four points lower than, i.e. minimum 126. Furthermore, a young bull that is heterozygous for a disorder could be selected for AI only if they will be used in the mating programme. With respect to the agreed criteria, seven young bulls were selected as bulls for AI. As a result of higher selection intensity, the ratio of selected genotyped male candidates chosen for AI and all genotyped animals was 1:35 which is similar to the ratio in other countries. Due to the implementation of genomic selection, Croatia moved from a country that imported most of its genetics to the country which now uses semen of own young genotyped bulls. The usage of genomic bulls increased from 8% of all used bulls in 2012 to 23 % in 2016. Furthermore, two young bulls were included in the AI on the international level (Austria and Bavaria) which gives a possibility for double testing of these bulls.

Genomic selection implementation for Holstein breed

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 embryo transfer (ET) and usage of sexed semen to produce replacement heifers and to ensure of the market with the 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.

So far, 96 HOL calves were selected, genotyped and included into the genomic evaluation system. According to the breeding programme, the number

of genotyped animals are planned to be at least 100 per year. Genotyped female calves were born in 2016 (72 calves) and 2017 (24 calves) and were progenies of 51 bulls (Figure 6). The most of sires (21) have USA origin (US), followed by German (DE), Danish (DK), and Canadian (CA) sires. These sires are among the best bulls based on either conventional or genomic BV for the total merit index in the HOL population worldwide. In contrast to SIM, none of the genotyped calves was a progeny of sires having Croatian origin.

The most of genotyped calves were progenies of progeny tested bulls born between 2007 and 2010 (Figure 7). Similar to genomics practice in other countries, among genotyped animals, there are also progenies of young genomically tested bulls without progeny results, i.e. without conventional EBV.

Genomic evaluation for the selected HOL calves was carried out by the computer centre VIT (Verein-igte Informationssysteme Tierhaltung) in Verden. In this Centre, genomic evaluation has been routinely conducted for German HOL breed since 2010 for a total of 44 traits. The evaluation is based on a BLUP SNP model with a trait-specific residual polygen-ic variance as described by Liu et al. (2011). DGV and PA were combined based on the selection index method (Liu et al., 2011) to obtain the GEBV for all traits.

Distribution of GEBV for the main group of traits (milk, conformation, fertility and total merit index) in HOL breed (Figure 8) was similar to SIM. The highest proportion of animals belonged to the group within one standard deviation higher 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.

The average reliability of the GEBV for most of the traits included into the genomic evaluation for HOL breed was higher than the average reliabili-ty of the PA for the same traits (Figure 9). These differences were lower for milk and conformation traits. The functional traits (fertility, calving ease, and stillbirth) had a larger difference in average re-liability between GEBV and PA.
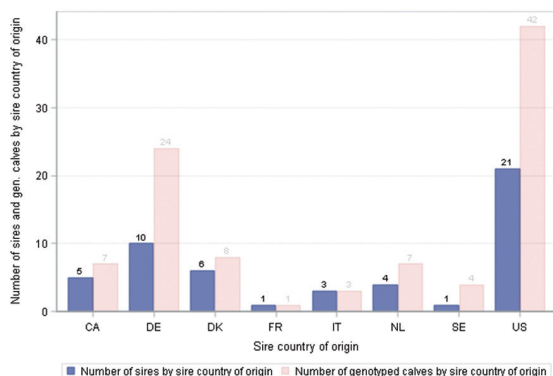

FIGURE 6. The number of sires by country of origin (CA-Canada; DE-Germany; DK-Denmark; FR-France; IT-Italy; NL-The Netherlands; SE-Sweden; US- United States) and the number of genotyped Holstein calves borned in the period from 2016 to 2017 by the sire country of origin
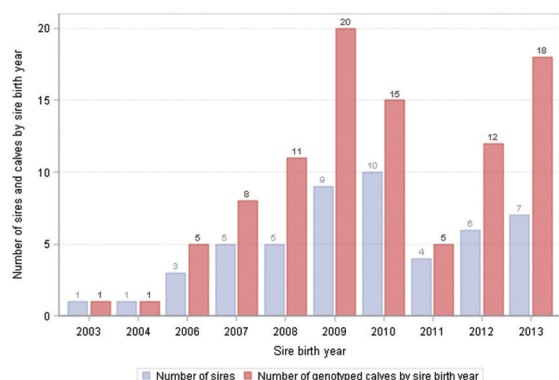

FIGURE 7. The number of sires borned in the period from 2003 to 2013 and the number of genotyped calves by sire birth year in Croatian Holstein breed
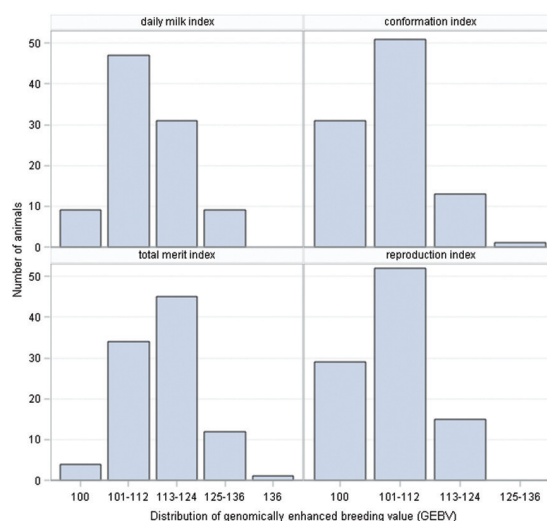

FIGURE 8.
The distribution of genomically enhanced breeding value (GEBV) for main group of traits (daily milk index, conformation index, total merit index, reproduction index) for genotyped calves borned in the period from 2016 to 2017 in Croatian Holstein breed
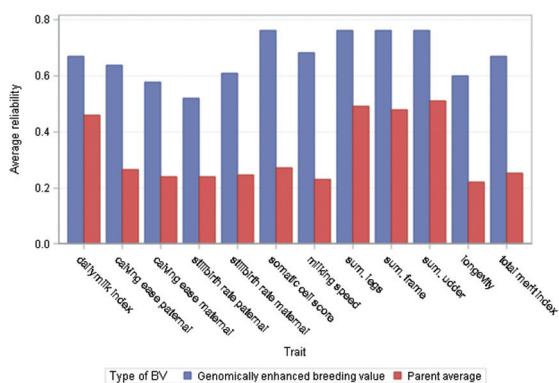
FIGURE 9. Average reliability of genomically enhanced breeding value and parent average by trait for genotyped calves borned in the period from 2016 to 2017 in Croatian Holstein breed

The results of genotypes also provide information of genetic disorders and characteristics specific for HOL breed as Bovine Leukocyte Adhesion Deficiency - BLAD, Brachyspina - BY, Holstein Haplotype for Cholesterol Deficiency - CDH, Holstein Haplotype 1 to 5 - HH1 to HH5, and Dominant Red or Variant Red Carrier - VR. Additionally, genetic variants of polled cattle and κ-casein were also determined during the genotyping following the same pattern as described for SIM breed.

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. However, there are selected HOL with a high genetic potential since animals having GEBV with two or three standard deviations better than average existed.

Despite all benefits, some obstacles exist in the implementation of genomic selection in Croatia. Although genomics brings back confidence of the breeders into the national breeding program, the number of active breeders is small. There is still insufficient use of bulls with a respectable either EBV or GEBV as bull sires, and consequently a small number of their progenies. Although the genotyping price decreased, the cost of genomic implementation selection is still high. Furthermore, GEBV, DGV, and PA are given on German scale and one of the future steps will be an adaption of the German system to the national. Also, from 2016, Croatian population is dealing with lumpy skin disease (LSD) threat and obligatory vaccination that resulted in a trade ban to countries free of LSD. Representatives of BA's and CAA are in negotiations with the Min-

istry of Agriculture and Department of Veterinary and Food Safety to exclude genomic calves from vaccination since AIC's could not accept vaccinated young bulls in. Negotiations also discussed the possibility of excluding cattle trade ban from farms involved in genomic selection since young bulls have to stay on the farm until the age of 10 to 12 months when AIC's could purchase young bulls.

New possibility for genomic selection in HOL population

Due to the low turnover in small populations, there is a limited chance for commercial implementation of genomic selection. Beside Croatian, other small HOL populations have been searched for possibilities of ensuring cost-efficient solutions for genomic selection. After the successful implementation of InterGenomics for Brown Swiss cattle provided by the International Bull Evaluation Service (or Interbull), the idea of implementing this methodology into small HOL populations has arisen. During 2017, Interbull proposed the project 'Implementation of InterGenomics methodology for small HOL populations (IgHol)' in order to start with a genomic evaluation. There are several benefits for the countries involved into the project as follows: a) establishment of a large reference population for applying genomic selection for traits evaluated nationally; b) accurate imputation of all lower density (LD) genotypes to higher density, which extends any national financial resources to genotyping more animals, especially females, using LD chip panels; c) access to both DGV and GEBV estimates, with associated reliability for all genotyped animals in IgHol; d) access to genomic prediction equations on the national scale for each trait evaluated in MACE; d) significantly reduced costs for establishing a genomic selection program nationally based on a large reference population; and e) benefits from international expertise and opportunities for further collaborations including continued technical improvements to IgHol methodologies. Target countries in the proposed IgHol project are Slovenia, Ireland, Belgium, Croatia, Portugal, Baltic countries (Estonia, Lithuania, and Latvia), the Czech Republic, Slovakia, the South African

Republic, Israel and Uruguay. This project proposes that each country should prepare data according to guidelines of the InterGenomics evaluation. After the data have been prepared, Interbull will make the test run evaluation. After the test run, partner countries will check the results and a coordination meeting will take place where the opportunity to invite or to join the project will be given also to other interested countries. Should the feedback be positive and costs for routine evaluation (Interbull service) acceptable, other details will be decided.

Effect of genomic selection on the dairy industry

Genomic selection affected the genetic improvement of dairy cattle during the last decade. Producers and AI organizations have accepted genomic evaluations where young bulls having genomic evaluations replaced progeny-test bulls in over a half of all mattings. Male and female calves are usually genotyped before they are one month old. Also, some embryos are genotyped before implantation and may have been purchased at a high cost. The age of parents has decreased since the start of the genomic selection. Bull sires became young bulls with genomic evaluations as well as heifers that become the bull dams at the age near the biological minimum. These reductions in parent age increase genetic improvement since the generation interval has been halved. The rate of improvement has almost doubled for HOL bulls from the implementation of genomic evaluation in 2010. The benefit of genomics is the greatest for traits with a low heritability and those that can be observed only late in life (such as longevity) due to the increased reliability provided by genomics (Garcia-Ruiz et al., 2016). For cows, a genomics brought a higher reliability of evaluation which is available shortly after birth, compared to the conventional evaluation based on cows own records. In order to avoid rearing costs of heifers and cows, the industry is interested in evaluation on a weekly base which became a practice in many countries.

Genomics can also be used for pedigree discovery, mating programs, and tracking of inbreeding. If ancestors have been genotyped, pedigree infor-

mation can be corrected for many animals. For example, in the USA, more than 80 % of bulls and 40 % of cows had a maternal grandsire confirmed by genotypes submitted for genomic evaluation in 2014 (VanRaden et al., 2013; VanRaden et al., 2014). Tracking of inbreeding is important due to its influence on the production efficiency and fertility. Genomic inbreeding which is easy to estimate from the genomic matrix can be used to control the inbreeding in the next generation of animals by computing genomic relationships for potential mate pairs through mating programs (Sun et al., 2013). Another benefit of genomics is the detection of carriers of undesirable recessive disorders and characteristics.

Future of genomic selection in dairy cattle

Although genomic selection gains genetic improvement, the dairy industry is faced with several challenges that will require the further adoption of new technologies. First, a potential issue in the genomic evaluation system could be addressed to the incorrect parentage in some herds. Furthermore, no economically feasible parentage testing is available for breed associations and producers. The current state of the genomic prediction has also reduced the milk recording. If the dairy industry reduces the recording of field data, a long-term negative effect is possible on the future accuracy of the genomic selection. On contrary, the amount of the on-farm data collected for other functional traits is growing. Sharing the research discoveries from new phenotypic data (feed efficiency, nitrogen excretion, reproductive longevity and efficiency, immune response to bovine respiratory disease, bacterial infection of the mammary gland, and resistance to heat stress) provides options for better selection of animals that fit their production environment. The investment in genomics has expanded and now includes funds for developing new diagnostics for whole-genome sequencing. A new technology that has a great potential for genetic improvement and has the potential to change the direction and intensity of the selection is genome editing (Bastiaansen et al., 2018). This technol-

ogy could also be used to fix additive traits such as milk production, which would greatly accelerate genetic progress by modifying multiple quantitative trait nucleotides in a single generation across multiple sire lines (Jenko et al., 2014).

Conclusions

Genomic selection has been successfully implemented into the Croatian SIM and HOL population. Seven young genomically tested SIM bulls, after genotyping and genomic evaluation, were selected with respect to the agreed criteria and used as bulls for AI of SIM cows in Croatia. At the farm level, implementation of genomic selection allowed breeders to use the semen of young genomically tested bulls from the national breeding program. At the national level, Croatia has gone from a country that imported most of its genetics to the country which now uses semen of own genomically tested bulls. Croatian AIC's are now marketing semen of two young bulls internationally (Austria and Bavaria), while one of them (Mozilla) was selected as bull's sire in Bavaria. Genotyped HOL female calves did not reach recommended criteria for selection

after the genomic evaluation in the German system. Genomic evaluation within the IgHol project will bring the possibility to identify potential dams at a young age and propagate them via ET and usage of sexed semen to produce young genomically tested bulls, replacement heifers, and to ensure the market of female breeding material. In dairy cattle, genomic selection enables faster genetic progress with higher accuracy and shorter generation interval. Genomics can also be used for pedigree discovery, and consequently in mating programs and tracking of inbreeding. Genotyping becomes more affordable due to continuous decrease of the costs and is expected to replace the use of microsatellites in parentage verification. Genome editing in combination with the genomic selection is a new technology that has great potential for genetic improvement and has the potential to change the direction and intensity of selection.

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Mogućnosti provedbe genomske selekcije za male populacije goveda - primjer Hrvatske

Sažetak

Tehnološki napredak i uvođenje genomske selekcije potaknuti globalizacijom i liberalizacijom tržišta rasplodnog materijala doveli su u pitanje održivost postojećih nacionalnih uzgojnih programa posebice u manjim državama. Cilj ovog rada je bio: opisati postupke pri uvođenju i provedbi genomske selekcije u malim populacijama simentalske (SIM) i holstein (HOL) pasmine goveda u Republici Hrvatskoj (HR); predstaviti rezultate uvođenja genomske selekcije; i prikazati perspektive koje genomika nudi za ove populacije. S ciljem unapređenja odabira SIM bikova, RH se pridružila sustavu genomskog vrednovanja Njemačke i Austrije u srpnju 2013. godine. Cilj uvođenja genomske selekcije za HOL populaciju temeljio se na odabiru potencijalnih bikovskih majki u ranoj dobi, a započeo je 2016. godine uključenjem u sustav njemačkog genomskog vrednovanja za HOL pasminu. Ukupno je 268 SIM i 96 HOL teladi odabrano, genotipizirano i za njih je bilo provedeno genomsko vrednovanje. Preporučeni kriterij za ulazak mladih SIM bikova u centre za umjetno osjemenjivanje je genomski optimizirana uzgojna vrijednost za ukupan selekcijski indeks iznad 130, a ujedno kandidati ne smiju ispoljavati genetske defekte niti biti nositelji istih. Na osnovi ovih kriterija, sedam je mladih bikova bilo uključeno u sustav umjetnog osjemenjivanja. Preporučeni kriterij za odabir ženskih grla HOL pasmine je ukupni selekcijski indeks iznad 150, a kandidatkinje ne smiju ispoljavati niti biti nositeljice genetskih defekata. Do sada niti jedno genotipizirano

žensko grlo nije zadovoljilo ove standarde. Alternativa njemačkom sustavu genomskog vrednovanja je međunarodni projekt za male HOL populacije (IgHol) koji predstavlja mogućnost ekonomski prihvatljive genomske selekcije. Provođenje aktivnosti genomske selekcije u RH omogućilo je korištenje sjemena bikova iz nacionalnog uzgojnog programa. Provođenje genomske selekcije za ženski dio populacije predstavlja mogućnost odabira najboljih jedinki u ranoj dobi i tako pridonosi ekonomičnosti proizvodnog ciklusa.

Ključne riječi: genomska selekcija, simentalska i holstein pasmina, direktna genomska vrijednost, genomski optimizirana uzgojna vrijednost

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