Reflection of Genomic Selection in Practice – use of Genomic Brown Swiss Bulls in Slovenia

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Summary

For seven years Slovenia has been collaborating in international genomic Brown Swiss cattle evaluation - InterGenomics project. This research aimed to provide an estimation of practical contribution of genomic selection. For that purpose data records of routine breeding value evaluations (EBV12) for Slovenian Brown Swiss cattle were used. The data for years 2013 – 2016 were obtained for up to 877 herds. Region ($P = 0.0032$) and year ($P = 0.0063$) significantly affected percent of genomically evaluated bulls used in herd. This percent most greatly and significantly decreased with an increase of the average parity (b = -3.93%, $P < 0.0001$). Although these effects had no statistically significant effect, the increase in the estimated value for herd based on a test day milk yield evaluation breeding value and the total merit index for dual purpose justifies the use of genomically evaluated bulls to some extent (about 25% of all bulls). Results did not confirm connection between greater genetic gain and breeders' choice of genomically evaluated bulls.

Key words

genomic evaluation, Brown Swiss, InterGenomics, consequences

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Introduction

The rising success of genomic selection (GS), shown by improved production of dairy and beef cattle, has led to acceptance of genomic tools and integration of this selection method into breeding programs all over the world (Patry, 2011; Jonas and De Koning, 2015). Voluntary international collaboration projects (EuroGenomics, InterGenomics, DEA) formed on joint genomic bull sire evaluation have been functioning quite successfully (Emmerling, 2006; Lund et al., 2010; European Brown Swiss federation, 2017; Interbull, 2017).

Since the first submission of Brown Swiss (BSW) bulls' genotype data to the Interbull Centre as a part of InterGenomics project, seven years have passed. In 2010 multi-country data submission, Slovenia's included, has formed the international Brown Swiss bull reference population. The same year first genomic evaluation results were known. As combining the genomic predictions based on genotype information and phenotypes in form of deregressed classical estimated breeding values (obtained from Multiple Across Country Evaluation also performed by Interbull) resulted in highly reliable genomically enhanced breeding values – GEBVs, international genomic evaluation of BSW populations has undergone numerous official routine runs (Jorjani et al., 2012; Vandenplas et al., 2015). Until spring 2017, Slovenia has participated in 17 InterGenomics' evaluations.

Incorporation of GS is also a part of the endeavour made to reduce expenses as well as to shorten and thereby accelerate the selection process in cattle. Primarily due to the reduced generation intervals and declining costs of selection process, GS has been proven to contribute high genetic gain and high economic performance of a breeding program. A higher degree of selection response along with the financial advantages compensates for the somewhat lower accuracy of genomic breeding values. That justifies the high start-up costs of genomic breeding scheme application, even in small dairy cattle populations like Slovenian BSW (Buch, 2011; de Roos, 2011; Wensch-Dorendorf et al., 2011; Schöpke and Swalve, 2016; Kariuki et al., 2017). With provided genomic and progeny information (GEBV) and especially only genomic information (direct breeding value - DGV), more and more young, highly genomically estimated (genetically superior) bull sires emerge on the market (e.g. Dovea Genetics, 2017; German Genetics International, 2017) and take place of young bulls in sire catalogues (Dovea Genetics, 2017; German Genetics International, 2017; Kmetijsko gozdarski zavod Ljubljana, 2017).

An important factor affecting the use of GS in practice is, presumably still present, fear among the breeders in relation to risk, associated with lower reliability of DGVs. Young genomically estimated sires are believed to be lacking the reliability of information about productivity of their offspring, on account of having no milking daughters (Patry, 2011; Selner, 2013; Seiler, 2017). Nevertheless, there are some breeders that use young genomic sires with increasing frequency. They use proven sires only when they desire to improve specific traits or to sire the heifers (Seiler, 2017).

Aim of this research is to show an information on the uptake of genomically evaluated BSW bulls in Slovenia. Based on the Slovenian BSW population data, the number of the descendants of genomic sires in Slovenian herds was estimated and an overview of the implementation of GS in practice was made. To our knowledge, there is no similarly themed research, neither in Slovenia nor elsewhere. As genomic methodology is implemented worldwide in an increasing extent, it is important to consider early (current) consequences on animal traits of importance undergoing selection. Any possible existing impacts of Slovenian breeders' decision to utilise the genomically evaluated sires have yet to be assessed.

Material and methods

Data records of routine breeding value evaluations (EBV12) from a national cattle evaluation were used. The data records were obtained from the data warehouse of Biotechnical Faculty, University of Ljubljana. All breeding values and estimates for herd effect were represented by standardized estimated values with population mean of 100 points and one standard deviation of 12 points. Data records stemmed form years 2013 to 2016 and included traits: number of all calves in herd (herd size), number of calves from bulls that were genomically estimated in time of conception (percent of calves from genomically evaluated bulls used in herd (PCGB)), average parity and estimated value for herd based on a test day milk yield evaluation breeding value (herd management). Also, average estimated breeding values of cows per herd (herd average) were used, for traits: calving interval, protein and fat index, muscularity, exterior index for milk production, total merit index for milk production (TMIM) and total merit index for dual purpose (TMID). Data records of 877 herds for year 2013, 852 herds for year 2014, 815 herds for year 2015 and 802 herds for year 2016 were used.

Analysis of variance was made using MIXED procedure of statistical software program SAS/STAT 9.4. For the least squares means' differences pairwise comparison the Bonferroni adjustment test was used. Statistical model included only those studied effects which significantly affected PCGB:

$$y_{ijk} = \mu + R_i + L_j + b_I(s_{ijk} - \bar{s}) + b_{II}(u_{ijk} - \bar{u}) +$$
$$b_{III}(w_{ijk} - \bar{w}) + b_{IV}(x_{ijk} - \bar{x}) + b_V(z_{ijk} - \bar{z}) + e_{ijk}$$

In the model y_{ijk} represented PCGB; μ overall mean; R_i region as fixed effect (i = 1, 2, 3, 4, 5, 6, 7); L_j year of the data record as fixed effect (j = 2013, 2014, 2015, 2016); b_I linear regression coefficient for herd size; s_{ijk} herd size; b_{II} linear regression coefficient for average parity; u_{ijk} average parity; b_{III} linear regression coefficient for protein and fat index; w_{ijk} EBV12 for protein and fat index; b_{IV} linear regression coefficient for muscularity; x_{ijk} EBV12 for muscularity; b_V linear regression coefficient for TMIM; z_{ijk} EBV12 for TMIM, and e_{ijk} represented a random residual.

Results and discussion

Contrary to expectations, the more successful breeders (who, concluded on the estimated value for herd based on a test day milk yield evaluation breeding value, manage their herds with greater success) have not been proven to be the ones who more often decide to use genomically evaluated bulls. Also, a connection between greater genetic gain and breeders' choice of genomically evaluated bulls has not been confirmed.

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Descriptive statistics

In 2016, 59 herds (7.3%) had PCGB greater than 50% (group 1), 169 herds (21.1%) had PCGB between 50% and 25% (group 2), 243 herds (30.3%) had PCGB up to 25% (group 3) and 331 herds (41.3%) had no progenies of genomically evaluated bulls (group 4).

Herd size, interpreted as the number of calves born in the current year, has generally increased over observed 4-year period. In herds which belonged to group 1 an increase of 10.5% was noted, in group 2 12.1% increase, in group 3 20.5% increase and in group 4 1.5% increase in herd size was noted when comparing the data records for year 2013 to 2016. Herds where no genomically evaluated bulls were used have had the lowest increase of size, whereas herds where genomically evaluated bulls represented no more than one quarter of all bulls used have recorded the greatest increase of size.

Furthermore, the estimated value for herd based on a test day milk yield evaluation breeding value has generally decreased with exception of group 2, where increase of 0.56% was recorded. The largest decline was noted in group 1 (-2.88%) which could mean that the use of more than 50% genomically evaluated bulls have had deteriorating influence on the overall estimated value for herd. The most desired results were estimated in herds where 25% – 50% share of genomically evaluated bulls were used. Improvement of calving interval was only noted in group 1. EBV12 for average protein and fat index, and for exterior index for milk production have increased in all groups; the same was true for TMIM. Decrease in EBV12 for muscularity was recorded in all groups, whereas EBV12 for TMID has decreased in groups 1, 3, 4 and increased in group 2. Since Slovenian BSW cattle have lately been reared as dual purpose cattle, increase in EBV12 for TMID also confirms expediency of using genomically evaluated bulls in an extent of 25% – 50% share of all bulls used in herd.

In herds where genomically evaluated bulls have been used most often, average parity has slightly decreased (-0.26%). There is no evident reason for the decrease. An explanation of this phenomenon could be found in heifer genotyping (which is less costly than bull genotyping) and in concurrent extended utilisation of genotyped heifers in reproduction schemes.

Analysis of variance

Region and year of the data record significantly affected PCGB ($P = 0.0032$ and 0.0063, respectively).

Results have shown that PCGB is low and has been decreasing since 2013 (Table 1). The highest percent of genomically evaluated bulls used in herd by region (reflected by the highest percent of their progenies (PCBG = 26.3%)) was determined for Upper Carniola region. Similarly high PCBG (20.6%, 20.3% and 19.9%) for Styria (Savinjska), Littoral and Lower Carniola region, respectively, were determined. Central region had 16.7% and Podravje as another part of Styria region had 11.2% PCBG. Prekmurje (Pomurska) region had the lowest number (practically non-existent) of registered BSW animals.

The estimated relationships between independent variables shown in Table 2 and PCGB were statistically significant. Estimated regression coefficients for herd size and EBV12 for

Table 1. PCGB by the year of data record in least square means and standard errors (LSM ± SE)

Year	N	LSM ± SE	P - value
2013	877	21.2 ± 3.9	< 0.0001
2014	852	19.7 ± 3.9	< 0.0001
2015	815	18.2 ± 3.9	< 0.0001
2016	802	17.6 ± 3.9	< 0.0001

N: number of observations; STD: standard deviation

Table 2. Regression coefficients on PCGB and standard errors (b and SE) with corresponding p-values

Independent variable	b ± SE (%)	P - value
Herd size (number of calves)	0.14 ± 0.05	0.0105
Average parity	-3.93 ± 0.74	< 0.0001
Protein and fat index (EBV12)	0.44 ± 0.13	0.0008
Muscularity (EBV12)	-0.12 ± 0.06	0.0405
Total merit index for milk production (EBV12)	-0.41 ± 0.12	0.0004

protein and fat index on PCGB have shown to be positive. In contrary, estimated regression coefficients for average parity, EBV12 for muscularity and EBV12 for TMIM on PCGB have shown to be negative (Table 2). That means the breeders who manage larger herds and whose animals have higher EBV12 for protein and fat index use genomically evaluated bulls to a greater degree than the breeders who manage herds with higher average parity or herds of animals with higher EBV12 for muscularity and TMIM. Average parity has shown the greatest negative regression coefficient on PCGB (b = -3.93%, $P < 0.0001$).

Conclusions

Use of genomically evaluated bulls in Slovenia, when compared to countries with developed cattle breeding, is very limited. Results for Slovenia, by contrast, even indicate a negative trend. It has been shown that the majority of Slovenian breeders do not use genomically evaluated bulls, and that the number of breeders using only these bulls is rather small. Although the results justify the use of genomically evaluated bulls to some extent (about 25%), the comparison of breeders' results (EBV12 changes for traits of interest) is not yet relevant nor fruitful. On the other hand, the implementation period of genomic bull evaluation is relatively short. To enhance the certainty of commenting the consequences of genomically evaluated bulls' utilisation, the result tracking over the next few years will be necessary.

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