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## THE INFLUENCE OF THE GENOMIC DATA ON THE BREEDING VALUES ESTIMATION IN THE SLOVAK REPUBLIC

### VPLYV GENOMICKÝCH DÁT NA ODHAD PLEMENNÝCH HODNÔT V SLOVENSKEJ REPUBLIKE

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**Abstract:** We investigated the influence of these factors: the herd-year-season of calving (HYS), the breed type (BT), the milk production, the lactation length and the single nucleotide polymorphism effect (SNP) on the fertility trait interval from the calving to the first service (CTFS) of the Holstein cattle in the Slovak Republic. A highly significant coefficient of determination ( $P < 0.0001$ ) estimated by linear model was observed when the SNP effect and the quadratic effect of the milk production and the lactation length was included. The coefficient of heritability of CTFS in HYS2 and HYS4 increased after the first calving when the SNP effect was included (0.0079 and 0.0093, respectively). When the SNP effect was included, positive trends of the breeding values of CTFS were observed. We can conclude that the inclusion of genomic data could have a significant influence on the estimation of breeding values and heritability in the future.

**Key words:** cattle, SNP, genomic, breeding values

The genomic prediction represents a revolutionary advancement in the animal improvement by providing a means of improving the accuracy of the estimated genetic merit for the selection candidates with no individual or offspring records (Garrick, 2010). The genomic prediction combines genotypic, phenotypic, and pedigree data to decrease the generation interval (Van Raden et al., 2009). The genomic selection based on single nucleotide polymorphism (SNP) allows us to select juvenile animals in a greater accuracy in comparison with the traditional genetic evaluation systems. It can significantly increase the accuracy of pre-selection of breeding animals (Meuwissen, et al., 2001) and it can lead to increased genetic gain from the incorporation of the genomic information in the dairy cattle breeding programs (Harris and Johnson, 2010).

The genome-wide genetic evaluation might involve the computation of BLUP-like estimations, potentially including thousands of covariates (i.e., single-nucleotide polymorphism markers) for each record (Legarra and Misztal, 2008). Similarly as published by Meuwissen et al. (2001), the best linear unbiased prediction (BLUP) or Bayesian methods can be used to simultaneously estimate the effect of each contiguous SNP interval (interval effect). To estimate the breeding values and heritability, Blonk et al. (2010) prepared the relationship matrix from the molecular relatedness method and offered it to the ASReml as a generalized inversed matrix. To obtain convergence in ASReml, they made a positive definite matrix using the bending method before inverting.

The aim of our work was to observe the influence of the genomic data in breeding values estimation in the national Holstein cattle population.

## Material and methods

We received the data for genetic evaluation from results of the dairy milk recording in the Slovak Republic and the Breeding services of the Slovak Republic. We have divided the data set

according to the season of calving into subsequent groups. In the first group (HYS2), the population was divided into two seasons of calving (1 from April to September; 2 from October to March) and in the second group (HYS4), it was divided into four seasons of calving (1 from December to February; 2 from March to May; 3 from June to August; 4 from September to November). This separation was used after the first and second calving. Cows had to fulfil subsequent requirements: minimum 10 records for each HYS effect, the interval from calving to first service between 30 and 365 days, the age at first calving from 720 to 1200 days. The resulting data set contained 38931 and 21157 records for HYS divided into two and four seasons after 1<sup>st</sup> calving, respectively. For HYS divided into two and four seasons after 2<sup>nd</sup> calving, the data set contained 35614 and 19636 records, respectively. We observed the influence of the joint herd-year-season of the calving effect, the breed type, the sire, the milk production, the days in milk and the simulated SNP effect on the interval from the calving to first service in a linear model.

We have divided the cows according to their breed type into subsequent groups:

- H<sub>0</sub> – cows with proportion of Holstein genes more than 93.75%
- H<sub>1</sub> – cows with proportion of Holstein genes from 87.5% to 93.74%
- H<sub>2</sub> – cows with proportion of Holstein genes from 75 to 87.4%
- H<sub>3</sub> – cows with proportion of Holstein genes from 50 to 74.9%

### Model equations (relationship between the factors and the interval from calving to the first service)

Model 1.1 (without the SNP effect):

$$Y_{ij} = HYS_i + BT_j + b(milk)_{ij} + c(dim)_{ij} + e_{ijm}$$

Model 1.2 (with the SNP effect):

$$Y_{ijk} = HYS_i + BT_j + SNP_k + b(milk)_{ijk} + c(dim)_{ijk} + e_{ijkm}$$

Model 2.1 (the quadratic effect of the milk production and the quadratic effect of the days in milk without the SNP effect):

$$Y_{ij} = HYS_i + BT_j + b_1(milk)_{ij} + b_2(milk)^2_{ij} + c_1(dim)_{ij} + c_2(dim)^2_{ij} + e_{ijm}$$

Model 2.2 (the quadratic effect of the milk production and the days in milk with the SNP effect):

$$Y_{ijk} = HYS_i + BT_j + SNP_k + b_1(milk)_{ijk} + b_2(milk)^2_{ijk} + c_1(dim)_{ijk} + c_2(dim)^2_{ijk} + e_{ijkm}$$

#### Model equations for the computation of the breeding values

Model 3.1 (without the SNP effect):

$$Y_{ijl} = HYS_i + BT_j + b(milk)_{ijl} + c(dim)_{ijl} + a_l + e_{ijlm}$$

Model 3.2 (with the SNP effect):

$$Y_{ijkl} = HYS_i + BT_j + SNP_k + b(milk)_{ijkl} + c(dim)_{ijkl} + a_l + e_{ijklm}$$

Model 4.1 (the quadratic effect of the milk production and the quadratic effect of the days in milk without the SNP effect):

$$Y_{ijl} = HYS_i + BT_j + b_1(milk)_{ijl} + b_2(milk)^2_{ijl} + c_1(dim)_{ijl} + c_2(dim)^2_{ijl} + a_l + e_{ijlm}$$

Model 4.2 (the quadratic effect of the milk production and the quadratic effect of the days in milk with the SNP effect):

$$Y_{ijkl} = HYS_i + BT_j + SNP_k + b_1(milk)_{ijkl} + b_2(milk)^2_{ijkl} + c_1(dim)_{ijkl} + c_2(dim)^2_{ijkl} + a_l + e_{ijklm}$$

where:

- $Y$  is the interval from the calving to the first service,  $HYS_i$  is a fixed effect of the herd by the year of birth and the season of calving;  $BT_j$  is the effect of the breed type;  $SNP_k$  is the effect of the simulated single nucleotide polymorphism;  $b(milk)$  is the linear effect of the milk production;  $c(dim)$  is the linear effect of the days in milk;  $b(milk)^2$  is the quadratic effect of the milk production;  $c(dim)^2$  is the quadratic effect of the days in

milk;  $a_l$  is a random animal additive genetic effect;  $e$  is a random error term.

These models were used for the first and second calving and for the joint HYS effect with two and four seasons of calving.

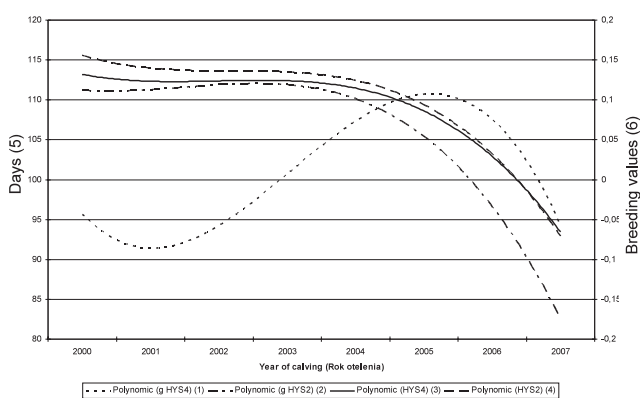
The basic statistic analysis, factor analysis, distribution analysis and data edition was performed using the program SAS 9.1 Enterprise Guide 3.0. The computation of the breeding values and the simulation of the SNP effect were performed by the Misztal pack programs.

## Results and discussion

The Holstein cows in the data set were calved for the first time during the years 2000 and 2007. The average age at the first calving and the average interval from the calving to the first service had a decreasing tendency during the years of calving in all groups. This is in contrast with the findings of another author, who observed an opposite trend of the CTFS (Van Doormaal et al., 2004; Melendez a Pinedo, 2007). We can observe positive trends in the simulated breeding values when the SNP effect was used.

We found a very low heritability of the CTFS (0.0076 and 0.0077) for two and four seasons after the first calving. When the effect of the simulated SNP was included, the heritability increased (0.0079 and 0.0093, respectively). The heritability of the CTFS for two and four seasons after the second calving was higher (0.0107 and 0.0308, respectively). It was similar with the low heritability in the interval from the calving to the first service, as was published by Wall et al. (2003), Andersen-Ranberg et al. (2005), Jorjani (2006) and Berry et al. (2007).

The phenotypic and genetic trends of CTFS are shown in Figure 1 and 2. The phenotypic and genetic trends for the HYS2 according to the years of the first calving (Figure 1) have a similar decreasing tendency. For the HYS4, the phenotypic

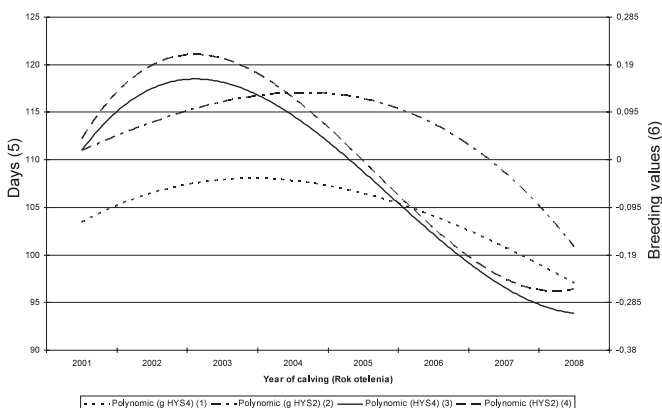


**Figure 1** The phenotypic and genetic trends of the interval from the calving to the first service after the first calving

- (1) the genetic trends for cows divided into four seasons of calving,
- (2) the genetic trends for cows divided into two seasons of calving,
- (3) the phenotypic trends for cows divided into four seasons of calving,
- (4) the phenotypic trends for cows divided into two seasons of calving

**Obrázok 1** Fenotypové a genetické trendy pre insemináčny interval po prvom otelení

- (1) genetické trendy kráv rozdelených na štyri sezóny telenia, (2) genetické trendy kráv rozdelených na dve sezóny telenia, (3) fenotypové trendy kráv rozdelených na štyri sezóny telenia, (4) fenotypové trendy kráv rozdelených na dve sezóny telenia, (5) dni, (6) plemenné hodnoty



**Figure 2** The phenotypic and genetic trends of the interval from the calving to the first service after the second calving

- (1) the genetic trends for cows divided into four seasons of calving,
- (2) the genetic trends for cows divided into two seasons of calving,
- (3) the phenotypic trends for cows divided into four seasons of calving,
- (4) the phenotypic trends for cows divided into two seasons of calving

**Obrázok 2** Fenotypové a genetické trendy pre insemináčny interval po druhom otelení

- (1) genetické trendy kráv rozdelených na štyri sezóny telenia, (2) genetické trendy kráv rozdelených na dve sezóny telenia, (3) fenotypové trendy kráv rozdelených na štyri sezóny telenia, (4) fenotypové trendy kráv rozdelených na dve sezóny telenia, (5) dni, (6) plemenné hodnoty

and genetic trends did not have a similar tendency, probably because of the number of animals. But from the year 2005, they had a similar decreasing tendency. According to the years of the second calving, the phenotypic and genetic trends of the CTFS had a decreasing tendency (Figure 2).

The correlation coefficients between the true breeding values and the simulated breeding values for the HYS2 after 1<sup>st</sup> and 2<sup>nd</sup> calving were 0.67318 ( $P < 0.0001$ ) and 0.54853 ( $P < 0.0001$ ), respectively. For the HYS4, the correlation coefficients between the true and the simulated breeding values after 1<sup>st</sup> and 2<sup>nd</sup> calving were 0.61494 ( $P < 0.0001$ ) and 0.59627 ( $P < 0.0001$ ), respectively. Kolbehdari et al. (2007) found the correlations between the genomic breeding values and the true breeding values increased with an increase in heritability. The correlation coefficients between the breeding values were high when the SNP information was included (Veerkamp et al., 2010).

The coefficient of determination estimated by the linear model was significant ( $P < 0.0001$ ) for two and four seasons after 1<sup>st</sup> calving. In the group with 4 seasons after 2<sup>nd</sup> calving, when the quadratic effect of the milk production and the lactation length and the SNP effect were included, the coefficient of determination increased significantly ( $P < 0.0001$ ), about 5%. We observed a similar increase ( $P < 0.0001$ ) of the  $R^2$  when the simulated breeding values were used.

### Conclusion

The phenotypic and genetic trends of the CTFS suggest a decreasing trend for this trait. But in comparison with the findings of other authors, the length of the interval from the calving to the first service is still very high. We found a very low heritability of the CTFS for two and four seasons after 1<sup>st</sup> calving and slightly a higher heritability for two and four seasons after 2<sup>nd</sup> calving. The heritability was slightly higher when the simulated SNP effect was included but only for groups after 1<sup>st</sup> calving. A significantly higher coefficient of determination about 5% ( $P < 0.0001$ ) estimated by the linear model was observed for the HYS with four seasons of calving when the SNP effect and the quadratic effect of milk production and the quadratic effect of lactation length were included.

The aim of our work was to observe the influence of the genomic data through the simulated SNP effect in the breeding values estimation in national Holstein cattle population in the Slovak republic. On the basis of our results, we can conclude that the inclusion of genomic data into the estimation of breeding values could be significant.

### Súhrn

Sledovali sme vplyv faktorov stádo – rok – sezóna telenia, plemenný typ, produkcia mlieka, dĺžka laktácie a efekt jednoduchého polymorfizmu na báze nukleotidov (SNP) na insemináčny interval holštajnského plemena na Slovensku. Po zahrnutí efektu SNP a kvadratického efektu produkcie mlieka a dĺžky laktácie do lineárneho modelu sme pozorovali vysoko preukazný koeficient determinácie ( $P < 0,0001$ ). Po zahrnutí SNP efektu koeficient dedivosti pre insemináčny interval po prvom otelení v skupine s dvoma sezónami telenia bol 0,0079 a v skupine so 4 sezónami telenia 0,0093. Tiež boli pozorované pozitívne trendy v plemenných hodnotách insemináčného intervalu po zohľadnení SNP efektu. Môžeme teda konštatovať, že

zahrnutie genomických dát by mohlo mať v budúcnosti významný vplyv pri odhade plemenných hodnôt a plodnosti.

**Kľúčové slová:** hovädzí dobytok, SNP, genomika, plemenné hodnoty

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### Literature

- ANDERSEN-RANBERG, I. M. – KLEMETS DAL, G. – HERINGSTAD, B. – STEINE, T. 2005. Heritabilities, genetic correlations, and genetic change for female fertility and protein yield in Norwegian dairy cattle. In: Journal of dairy science, vol. 88, 2005, p. 348–355.
- BERRY, D. P. – COUGHLAN, S. – EVANS, R. D. 2007. Preliminary genetic evaluation of female fertility in Ireland. In: Interbull Bulletin, no. 37, 2007, p. 125–128.
- BLONK, R. J. W. – KOMEN, H. – KAMSTRA, A. – VAN ARENDONK, J. A. M. 2010. Estimating breeding values with molecular relatedness and reconstructed pedigrees in natural mating populations of Common Sole, *Solea Solea*. In: Genetics, vol. 184, 2010, p. 213–219.
- GARRICK, D. J. 2010. Consequences of genomic prediction in cattle. In: Interbull Bulletin, no. 41, 2010, p. 1–8. ISSN 1011-6079.
- HARRIS, B. L. – JOHNSON, D. L. 2010. The impact of high density SNP chips on genomic evaluation in dairy cattle. Interbull meeting in Riga, In press, 2010.
- JORJANI, H. 2006. International genetic evaluation for female fertility traits. In: Interbull Bulletin, no. 34, 2006, p. 57–64.
- KOLBEHDARI, D. – SCHAEFFER, L. R. – ROBINSON, J. A. B. 2007. Estimation of genome wide haplotype effects in half-sib designs. In: Journal of animal breeding and genetics, vol. 124, issue 6, 2007, p. 356–361. ISSN 0931-2668.
- LEGARRA, A. – MISZTAL, I. 2008. Computing strategies in genome-wide selection. In: Journal of dairy science, vol. 91, 2008, p. 360–366.
- MELLENDEZ, P. – PINEDO, P. 2007. The association between reproductive performance and milk yield in Chilean Holstein cattle. In: Journal of dairy science, vol. 90, 2007, p. 184–191.
- MEUWISSEN, T. H. E. – HAYES, B. J. – GODDARD, M. E. 2001. Prediction of total genetic value using genome-wide dense marker maps. In: Genetics, vol. 157, 2001, p. 1819–1829.
- VAN DOORMAAL, B. J. – KISTEMAKER, G. – FATEHI, J. – MIGLIOR, F. – JAMROZIK, J. SCHAEFFER, L. R. 2004. Genetic evaluation of female fertility in Canadian dairy breeds. In: Interbull Bulletin, no. 32, 2004, p. 86–89.
- VAN RADEN, P. M. – VAN TASSELL, C. P. – WIGGANS, G. R. – SONSTEGARD, T. S. – SCHNABEL, R. D. – TAYLOR, J. F. – SCHENKEL, F. S. 2009. Reliability of genomic predictions for North American Holstein bulls. In: Journal of dairy science, vol. 92, 2009, p. 16–24.
- VEERKAMP, R. F. – VERBYLA, K. L. – MULDER, H. A. – CALUS, M. P. L. 2010. Simultaneous QTL detection and genomic breeding value estimation using high density SNP chips. In: BMC Proceeding: Proceedings of the 13<sup>th</sup> European workshop on QTL mapping and marker assisted selection, vol. 4, suppl. 1, 2010, p. 1–4.
- WALL, E. – BROTHERSTONE, S. – WOOLLIAMS, J. A. – BANOS, G. – COFFEY, M. P. 2003. Genetic evaluation of fertility using direct and correlated traits. In: Journal of dairy science, vol. 86, 2003, p. 4093–4102.

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