**Estimation of genomic breeding values**

**Animals included in genomic evaluation**
For genomic breeding values prediction (gBV) the animal genotype by Illumina BovineSNP50 v1 or v2 is used. The use of other formats can lead to problems with the inclusion into genetic evaluation resulting in lower accuracy. This is due to a lower number of SNPs available for calculation.

**Milk yield**
Genomic breeding values for milk yield are estimated per kg of milk, kg of fat and kg of protein. Genomic breeding values for milk content (protein and fat) are calculated from genomic breeding values per kg of milk using the same method as in conventional breeding values. The model for genomic evaluation is the same as for conventional breeding values: ST-ML-RR-TD-BLUP-AM. The model equation is the same for classical conventional breeding values. The difference between conventional and genomic estimation is that the matrix of relation is modified.
The genomic evaluation method for milk, fat and protein was validated at Interbull in September 2015.

**Somatic cell counts**
Genomic breeding values for somatic cell counts use the same model and the same model equation as the conventional estimation of breeding values. The difference between conventional and genomic estimation is that the relationship matrix is modified.

**Conformation**
For prediction of genomic breeding values the same model and model equation as for conventional genetic evaluation is used: ST – BLUP – AM. The same traits are used as in conventional genetic evaluation. The only difference between conventional and genomic estimation is that the relationship matrix is modified.

**Fertility**
Genomic breeding value is estimated for 4 traits: own fertility – heifers, own fertility – cows, fertility of daughters – heifers, fertility of daughters – cows. The model and model equation are the same as for conventional genetic evaluation: ST – BLUP – AM. Genomic breeding values for own fertility of females and fertility of daughters are calculated by using a simple average and not a weighted average. The reason is due to the frequent unavailability of insemination information of cows and daughters. The only difference between conventional and genomic estimation is that the relationship matrix is modified.

**Longevity**
Blending method is used for evaluation. These breeding values are estimated through Institute of Animal Science, Uhrineves-Prague. In future, evaluations will be performed at the Plemdat, ltd.

**Relationship matrix**
For prediction of all genomic breeding values, except gBVs for longevity, no changes have been made to the model or model equation. This approach with modified relationship matrix is called ssGBLUP (Single Step Genomic BLUP).

$$H^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \lambda(\mathbf{G}^{-1} - \mathbf{A}_{22}^{-1}) \end{bmatrix}$$

H    – Modified relationship matrix
A    – Conventional relationship matrix
G    – Genomic relationship matrix
$A_{22}$ – Pedigree relationship matrix for genotyped animals
λ    – Weight
-1   – Matrix inversion

The genomic relationship matrix is created on the basis of genotype data and pedigrees. The genomic relationship matrix is added to the conventional relationship matrix.

**gSIH – Genomic Selection Index**
For Genomic Selection Index calculation, the same method as for conventional index SIH is used. If genomic breeding values for some traits are not available, then average breeding value is used.

**Base and standardisation**
Genomic breeding values are related to basis of cows born in 2005. For genomic breeding values for milk the same standard deviation 600 as in conventional evaluation is used. For other relative breeding values the mean of basis year as 100 and standard deviation 12 is used. The Genomic Selection Index is standardised according to the parameters of the conventional selection index (SIH).

**Publication of results**
Results for bulls are published every second month. The bulls without conventional Interbull breeding values (MACE), younger than 7 years; and with daughters in less than 5 herds (for milk and conformation) are published with genomic breeding values.