

Estimation of HF sire breeding values

(April 2024)

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Production traits and somatic cell score

Model

Breeding values for production traits and somatic cell score are estimated according to a single-trait multi-lactation (limited to first three lactations) random regression test-day animal model:

$$Y_{ijklm} = HTD_i + \sum_{n=1}^3 b_{jln}x_{jln} + \sum_{n=1}^3 a_{kln}z_{kln} + \sum_{n=1}^3 p_{kln}z_{kln} + e_{ijklm}$$

where:

- Y_{ijklm} is the yield of milk, fat, protein, lactose or SCS on test-date m of cow k , in lactation l , within herd-test date effect i , belonging to the j -th class of calving age x calving season x breed of cow x class of calving year of lactation l ,
- HTD_i is fixed effect of the i -th herd-test-date,
- b_{jln} are fixed regression coefficients specific to subclass j of calving age x calving season x breed of cow x class of calving year for lactation l ,
- x_{jln} are terms of the Wilmink function,
- a_{kln} are random regression coefficients specific to the additive genetic effect of cow k in lactation l ,
- p_{kln} are random regression coefficients specific to the permanent environmental effect of cow k in lactation l ,
- z_{kln} are Legendre polynomials on days in milk (DIM),
- e_{ijklm} is residual effect for the test-day observation.

Heterogeneous herd variances are adjusted prior to the estimation of breeding values.

Breeding values for fat, protein and lactose percentage are calculated from the respective yields.

Data

Test-day yields included in the evaluation have been accumulated starting with cows that calved on January 1, 1995. Test-day yields from milk recording type AT4 have 80% weight compared to test days from A4 and A8 recordings.

Somatic cell count is transformed to somatic cell score with the following formula:

$$SCS = \log_2(SCC/100000) + 3$$

Genetic groups

Genetic groups are based on sex, birth year and HF percentage.

Adjustments for heterogeneous variance

Adjustments for heterogeneous variance within herds are applied.

Genetic parameters

Genetic parameters used in estimation of breeding values are presented in Table 1.

Table 1. Genetic parameters for lactational milk, fat, protein and lactose yields and SCS.

Lactational				
Milk	Fat	Protein	Lactose	SCS
0.33	0.29	0.29	0.30	0.32

Expression of genetic evaluation

Lactational breeding values for each of three lactations are obtained by summing up breeding values for days 5 to 305. Variances of second and third lactations are standardized to the first lactation variance; then the mean of lactational breeding values is calculated.

Genetic base

The average breeding value of cows born in 2015 was assumed as a fixed base.

Reliability

Reliabilities are calculated using the multiple trait effective daughter contribution method.

Publication criteria

Reliability \geq 50% and daughters in at least 10 herds.

F+2P index [kg]

$$\text{F+2P index [kg]} = \text{BV Fat[kg]} + 2 * \text{BV Protein[kg]}$$

Production subindex

$$\text{Production subindex (PS)} = \text{RBV Fat[kg]} + 2 * \text{RBV Protein[kg]}$$

Breeding values for yield traits are expressed as relative breeding values (RBV) standardized with mean 100 and standard deviation 10. The genetic reference base was defined as the mean breeding value of bulls born in 2009–2011 with at least 20 daughters in 10 herds.

The production subindex is calculated based on Interbull breeding values. If Interbull BVs are not available, national BVs are used.

Conformation

Table 2 lists the evaluated descriptive and linear conformation traits.

Table 2. Scores and heritabilities of conformation traits.

Trait	Score		h ²
	MIN	MAX	
Size	50	100	0.50
Type and conformation	50	100	0.33
Feet and legs	50	100	0.11
Udder	50	100	0.14
Overall conformation	50	100	0.25
Stature (cm)	(cm)		0.54
Body depth	1	9	0.21
Chest width	1	9	0.21
Rump angle	1	9	0.28
Rump width	1	9	0.30
Rear leg set side view	1	9	0.13
Foot angle	1	9	0.09
Rear leg set rear view	1	9	0.09
Fore udder	1	9	0.21
Rear udder height	1	9	0.24
Udder support (central ligament)	1	9	0.20
Udder depth	1	9	0.33
Udder width	1	9	0.19
Front teat placement	1	9	0.29
Teat length	1	9	0.36
Rear teat placement	1	9	0.29
Dairy character	1	9	0.28
BCS	1	9	0.24
Locomotion	1	9	0.10

Model

Breeding values for conformation traits are estimated according to a single-trait BLUP animal model including random additive genetic effect of cow, fixed effect of genetic group, linear and quadratic regression on age at calving, fixed effect of herd-year-season-classifier, and fixed effect of lactation stage.

Breeding values are estimated for cows having known sires and calved between 18 and 48 months of age. Cows are scored between days 15 and 180 of first lactation. This period is divided into 11 intervals.

Genetic groups

Genetic groups are based on unknown parents, sex, birth year and HF percentage.

Breeding values

Breeding values for conformation traits are expressed as relative breeding values (RBV) standardized with mean 100 and standard deviation 10.

Genetic base

The genetic reference base for conformation traits was defined as the mean breeding value of bulls born in 2009–2011 with at least 10 daughters in 5 herds.

Reliability

Reliability was approximated using selection index methodology.

Publication criteria

Published breeding values are based on at least 10 daughters.

Conformation subindexes

Table 3 lists five composite subindexes with assigned weights.

Table 3. Conformation subindexes

Frame subindex (FS)	weight
Rump angle	40%
Stature	25%
Rump width	20%
Chest width	15%
Dairy strength subindex (DS)	
Dairy character	50%
Chest width	25%
Body depth	15%
Stature	10%
Feet & legs subindex (FLS)	
Foot angle	45%
Rear leg set rear view	35%
Rear leg set side view	20%

Udder subindex (US)	
Udder depth	35%
Fore udder	18%
Rear udder height	15%
Udder support (central ligament)	10%
Udder width	10%
Rear teat placement	6%
Front teat placement	3%
Teat length	3%
Conformation subindex (CS)	
Udder subindex (US)	50%
Feet & legs subindex (FLS)	30%
Dairy strength subindex (DS)	10%
Frame subindex (FS)	10%

Conformation subindexes are standardized with mean 100 and standard deviation 10. The genetic reference base was defined as the mean breeding value of bulls born in 2009–2011 with at least 20 daughters in 10 herds.

Subindexes FS, DS, FLS, and US are calculated based temporarily on national breeding values. If at least one of the national BVs is not available, the corresponding subindex is calculated based only on Interbull BVs.

Female fertility

The following female fertility traits are evaluated:

Conception rate, heifer	CRh
Conception rate, cow	CRc
Days between calving and first insemination	CTFI
Days open	DO

Conception rates are coded as follows:

CR = 100/number of inseminations from the first to the last. If more than 15 inseminations were made or no insemination was marked as effective, CR = 100/16.

Table 4. Heritability (diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for fertility traits

Trait	CRh	CRc	CTFI	DO
CRh	0.027	0.483	0.581	-0.012
CRc	0.056	0.025	0.024	0.022

CTFI	-0.003	0.043	0.053	0.713
DO	-0.005	-0.215	0.609	0.080

Model

Breeding values for fertility traits are estimated by a multiple-trait BLUP animal model. The linear model for conception rates includes fixed effect of month of insemination, fixed regression on age of first insemination, random effect of herd-year of first insemination, and random additive genetic effect.

The linear model for days between calving and first insemination (CTFI) and days open (DO) includes fixed effects of herd-year and month of calving, regression on age at calving, and random additive genetic effect.

Breeding values for fertility traits are expressed as relative breeding values (RBV) standardized with mean 100 and standard deviation 10.

For CRh and CRc, greater breeding value means that, on average, fewer insemination are needed for the effective insemination of his daughters. Greater breeding values for CTFI and DO mean shorter intervals.

Genetic base

The genetic reference base was defined as the mean breeding value of bulls born in 2009–2011 with at least 50 daughters in 30 herds.

Reliability

Multiple-trait approximations.

Publication criteria

Published breeding values are based on at least 10 daughters.

Fertility subindex

$$\text{Fertility subindex FS} = 0.7 \times \text{CRh} + 0.1 \times \text{CRc} + 0.1 \times \text{CTFI} + 0.1 \times \text{DO}$$

The fertility subindex is standardized with mean 100 and standard deviation 10.

The fertility subindex consists of CRh (if based on at least 10 effective daughters), CRc, CTFI and DO (with minimum repeatability of 0.10). In the case of young bulls, CRc, CTFI and DO are not available and breeding values are obtained from the multitrait model through genetic correlations.

The fertility subindex is calculated based on Interbull breeding values. If at least one of the Interbull BVs is not available, the subindex is calculated based only on national BVs.

Calving ease and calf mortality

Data are routinely collected in the national milk recording system.

Calving traits are coded as follows:

Calving ease scores: 1 – unassisted, 2 – with assistance, 3 – with veterinary aid, 4 – difficult calving, caesarean or abortion

Calf mortality (stillbirth) scores: 1 – live, 2 – stillborn or died within 24 hours after birth

Calving records since calving year 2007 are included.

Calving records in first three parities are included.

Snell transformation is applied.

The following calving traits are evaluated:

- calving ease – direct effect
- calving ease – maternal effect
- calf mortality – direct effect
- calf mortality – maternal effect

Table 5. Heritability for calving traits (first parity)

Trait	h^2
calving ease – direct effect	0.05
calving ease – maternal effect	0.04
calf mortality – direct effect	0.03
calf mortality – maternal effect	0.05

Model

Breeding values for calving traits are estimated by a linear multiple-trait BLUP animal model. A total of 12 traits are evaluated: calving ease, stillbirth rate – each for 1st, 2nd, 3rd parity – each direct and maternal genetic effect. The linear model includes for each trait*parity combination: fixed effects of herd-year, calving_year_classes*calving_season*sex_of_calf, calving_year*calving_month*calving_age_classes*sex_of_calf and random additive genetic effect.

Genetic groups defined based on birth year and selection path.

Breeding values are expressed as relative breeding values (RBV) standardized with mean 100 and standard deviation 10. Greater breeding values for calving ease mean less difficult calvings, and for stillbirth fewer stillborn calves.

Only first-parity calving breeding values are published.

Genetic base

The genetic reference base was defined as the mean breeding value of bulls born in 2009–2011 with at least 50 daughters/calves in at least 10 herds.

Reliability

Multiple-trait approximations.

Publication criteria

Published breeding values are based on at least 50 daughters/calves (up to 3rd parity) in at least 10 herds.

Direct longevity

Trait definition

Functional longevity is defined as length of productive life measured by the number of days from first calving to culling (culling date) or censoring (last test-day date), adjusted for phenotypic production. Based on the disposal codes reported in the SYMLEK milk recording system, a longevity record is considered to be completed (uncensored) if the cow was culled for any reason other than being sold to another herd outside the milk recording system. Otherwise it is regarded as censored.

Model

Genetic evaluation of sires for functional longevity of their daughters is carried out using survival analysis methodology (Survival Kit 3.1) applying a mixed Weibull proportional hazard model (single-trait sire model).

The effects included in the model are random additive genetic sire effect (time-independent, following multivariate normal distribution, with variance-covariance matrix $A\sigma^2_s$), random time-dependent effect of herd-year-season (following log-gamma distribution), fixed time-independent effect of age at first calving, fixed time-dependent effect of lactation number \times stage of lactation, fixed time-dependent effect of year-season, fixed time-dependent effect of yearly change of herd size, and fixed time-dependent effect of fat and protein yield relative to herd mean.

Table 5. Genetic and Weibull distribution parameters

Weibull distribution	
ρ	2.07
λ	0.007
HYS distribution	
γ	2,23

Genetic parameters	
Sire variance σ_s^2	0.0451
Heritability h^2_{orig}	0.19

Breeding values for direct longevity are transformed (multiplied by -1) so that higher EBV indicates better longevity, and then expressed as relative breeding values (deviations from the base) standardized with mean 100 and standard deviation 10.

Genetic base

The genetic reference base was defined as the mean breeding value of bulls born in 2009–2011 with reliability $\geq 50\%$.

Reliability

Approximate reliability R , derived from selection index theory, incorporates information from the bull and bull's sire according to the formula:

$$R = (\frac{1}{4} * R_{bs} + R_b - 2 * \frac{1}{4} R_{bs} * R_b) / (1 - \frac{1}{4} * R_{bs} * R_b)$$

where

$$R_b = N_b / (N_b + (4 - h^2) / h^2)$$

N_b – number of culled daughters of bull

$$R_{bs} = N_{bs} / (N_{bs} + (4 - h^2) / h^2)$$

N_{bs} – number of culled daughters of bull's sire

h^2 – heritability (0.19).

Publication criteria

Relative breeding values of bulls with at least 20% reliability are published.

Workability

The following workability traits are evaluated:

- milking speed
- temperament

Milking speed is subjectively scored on a scale of 1 to 5.

Temperament is scored on a scale of 1 to 3.

Both traits are scored in the first lactation of the cow at the second test-day by a classifier.

Table 6. Heritability (h^2) for workability traits

Trait	h^2
Milking speed	0.12
Temperament	0.09

Model

Breeding values for workability traits are estimated by a multiple-trait BLUP animal model. The linear model includes linear and quadratic regression on age at calving, herd-year-season-classifier (fixed), lactation stage (fixed) and random additive genetic effect.

Breeding values for workability traits are expressed as relative breeding values (RBV) standardized with mean 100 and standard deviation 10.

For milking speed a higher breeding value of the bull means that his daughters milk faster than the average. A higher breeding value for temperament means that daughters of this bull are calmer than the average.

Genetic base

The genetic reference base was defined as the mean breeding value of bulls born in 2009–2011 with at least 20 daughters in 10 herds.

Reliability

Multiple-trait approximations.

Publication criteria

Published breeding values are based on at least 10 daughters.

PF index

The PF index (**P**roduction and **F**unctional traits) is defined according to the following formula:

$$\text{PF index} = 0.4 * \text{PS} + 0.25 * \text{CS} + 0.15 * \text{FS} + 0.1 * \text{SCS} + 0.1 * \text{LON}$$

where:

PS Production subindex
CS Conformation subindex
FS Fertility subindex
SCS Somatic cell score RBV

LON Longevity RBV

All breeding values and indexes are standardized with mean 100 and standard deviation 10.

Genomic breeding values

Data

Genotypes were generated by the use of Illumina BovineSNP50 Genotyping BeadChip, which consists of 54 001 SNPs. The applied SNP selection criteria comprised polymorphism, expressed by the minor allele frequency (MAF), with the minimum MAF of 0.01, and technical quality of an SNP, expressed by the minimum call rate of 90% within the analyzed sample of bulls. Phenotypic data were deregressed national proofs of estimated breeding values (EBV), effective daughter contribution (EDC) and relationships (Szyda et al., 2011).

Model

Direct Genomic Value (DGV)

Direct genomic value (DGV) is defined as the sum of additive effects of SNPs estimated from the linear mixed model with random additive SNP effects.

Genomic Enhanced Breeding Value (GEBV)

The genomic enhanced breeding values (GEBV) were calculated as a combination of direct genomic value (DGV) and the pedigree index (PI) using a selection index approach.

Reliability

Reliability of Direct Genomic Value (DGV).

The reliability of DGV is calculated based on the Interbull validation results and is expressed as the squared Pearson correlation coefficient between DGV and deregressed EBV (DRP) divided by the average reliability of bull's daughters' EBV.

Reliability of Genomic Enhanced Breeding Value (GEBV).

The reliability of GEBV is a combination of reliabilities of DGV and PA using the selection index theory.

Index and Subindexes

Genomic enhanced breeding values (GEBV) are used to construct subindexes and the PF Index according to formulae previously described.

Publication criteria

Interbull genomic breeding values, if available, or national genomic breeding values with at least 50% reliability for milk production, are published.

References

Strandén I, Garrick DJ (2009) Technical note: Derivation of equivalent computing algorithms for genomic predictions and reliabilities of animal merit. *J Dairy Sci* 92:2971–2975

Szyda, J., Żarnecki, A., Suchocki, T. and Kamiński, S. (2011) *Journal of Applied Genetics* 52(3) pp. 363-366.

Single-step genomic evaluation of resistance to digital dermatitis (DD)

Phenotypic data

Claw health data are collected in herds participating in CGen trimming project founded by the Polish Federation of Cattle Breeders and Dairy Farmers.. Data are collected into the CGen trimming application by professional trimmers during a herd visit.

During trimming, the trimmer recognizes diseases in accordance with ICAR Claw Health Atlas. When the DD is diagnosed, information about the phase of the disease is provided, according to the following M-stages:

- M1 - early stage of the disease
- M2 - active
- M3 - recovery
- M4 - chronic
- M4.1 - chronic lesion with additional lesion in the early stage of the disease

A detailed description of the stages is included in the ICAR Claw Health Atlas - Appendix 1.

Data included in the breeding value evaluation are prepared in accordance with the EuroGenomics Cooperative - Golden Standard guidelines. Observations are collected from cows in lactations 1, 2 and 3+.

Heritability of resistance to digital dermatitis is 0.07.

Genomic data

To estimate breeding value, the animal's genomic information in the form of Single Nucleotide Polymorphisms (SNP) is included. Genomic data undergoes standard quality control to discard those genotypes and SNP's that provide the least information for the evaluation.

Model

Breeding values are estimated using a single-step method: single-trait, three-lactation model. In one evaluation phenotypic, genomic and pedigree information are included. Single-step genomic evaluation of claw health is performed in accordance with the guidelines of the

EuroGenomics Cooperative. These guidelines specify how to edit and filter data, with the list of effects and modeling methods. The following effects are included in the linear model,

fixed:

- calving age * year of observation
- visit
- trimmer * year of observation
- lactation phase * year of observation
- month * year of calving

random:

- animal's additive genetic effect
- permanent environmental effect

Breeding values are expressed as deviations from the base mean and then transformed into a variable with a mean of 100 and a standard deviation of 10. A higher breeding value means a higher genetic resistance of the animal to digital dermatitis.

Genetic base

Bulls born between 2009 and 2011 with at least 10 daughters are used as the base population for relative breeding values.

Reliability of Single-step Genomic Breeding Value (ssGEBV)

The reliability of the breeding value was calculated using the approximation of the diagonal elements of the matrix using the single-step method (ssGBLUP).

Publication criteria

Breeding values from single-step evaluation are published based on the ssGEBV accuracy for individual animals. In the case of resistance to digital dermatitis, the minimum accuracy level for females is 0.15 and for males 0.35.