Estimation of HF sire breeding values

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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-lactational (limited to first three lactations) random regression test-day animal model:

$$Y_{ijklmo} = HTD_{io} + \sum_{n=1}^{5} b_{jno} z_{mnlo} + \sum_{n=1}^{3} c_{kno} z_{mnlo} + \sum_{n=1}^{3} a_{mno} z_{mnlo} + \sum_{n=1}^{3} p_{mno} z_{mnlo} + e_{ijklmo}$$

where:

Y_{ijklmo}	is the yield of milk, fat, protein or SCS on test-day *l* of cow *m*, in lactation *o*, within herd-test day effect *i*, belonging to herd-year class *k* and the *j*th class of age and season of calving-fraction of HF genes,
HTD_{io}	is the random herd-test-day effect,
b_{jno}	are fixed regression coefficients specific to age-season-HF subclass *j*,
c_{kno}	are fixed regression coefficients specific to herd-year *k*,
a_{mno}	are random regression coefficients specific to the additive genetic effect of cow *m*,
p_{mno}	is the random permanent environmental effect,
z_{mnlo}	are Legendre polynomials on DIM and *n* represents the order of fit for age-season, herd-year, additive genetic, and permanent environment curves, respectively,
e_{ijklmo}	is the residual effect for each observation.

Lactation curves in the age-season-fraction of HF genes subclasses are modeled by 4th-order Legendre polynomials; the remaining lactation curves are modeled by 2nd-order Legendre polynomials. Homogeneity of error variances for consecutive lactation days and no correlations between them are assumed. Random error effects are not correlated between and within lactations.

Evaluations are performed using TDM Poznan System software.

Breeding values for fat and protein 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 herd-year subclasses 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 and protein yields and SCS.

Lactational			
Milk	Fat	Protein	SCS
0,33	0,29	0,29	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 2010 was assumed as a fixed base.

Reliability

Equivalent numbers of progeny for each lactation are assigned equal weights, and the reliability of the estimated breeding value for the average yield in the first three lactations is then calculated.

Publication criteria

Reliability >= 50% and daughters in at least 10 herds.

F+2P index [kg]

F+2P index [kg] = BV Fat[kg] + 2* BV Protein[kg]

Production subindex

Production subindex (PS) = RBV Fat[kg] + 2* 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 2004-2006 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

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 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 2004- 2006 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:

Nonreturn rate at 56 days at first insemination, heifer	NRh
Nonreturn rate at 56 days at first insemination, cow	NRc
Days between calving and first insemination	CTFI
Days open	DO

Nonreturn rates are coded as follows:

- lack of estrus until 56th day after first insemination = 1
- estrus observed before 56th day of insemination = 0

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

Trait	NRh	NRc	CTFI	DO
NRh	0.020	0.103	0.581	-0.006
NRc	0.031	0.021	0.013	0.007
CTFI	-0.001	0.325	0.053	0.713
DO	-0.003	-0.193	0.609	0.080

Model

Breeding values for fertility traits are estimated by a multiple-trait BLUP animal model.

The linear model for nonreturn rates includes fixed effect of herd-year, fixed effect of month, and regression on heifer/cow age of first insemination after calving.
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, and regression on age at calving.

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

For NRh and NRc, greater breeding value means a higher percentage of daughters with successful first insemination. 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 2004-2006 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

Fertility Subindex FS = 0.7 × NRh +0.1 × NRc + 0.1 × CTFI + 0.1 × DO

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

The fertility subindex consists of NRh (if based on at least 10 effective daughters), NRc, CTFI and DO (with minimum repeatability of 0.10). In the case of young bulls, NRc, 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.

Phenotypic characteristics of calving ease and calf mortality

Calving ease

The phenotypic characteristics of calving ease of bull daughters (min. 50 daughters) and cows sired by the bull are coded as follows:

1. Without assistance
2. With assistance
3. With veterinary assistance
4. Difficult calving
5. Abortion
6. Caesarean section

Calf mortality

The phenotypic characteristics of calf mortality of bull daughters (min. 50 daughters) and cows sired by the bull are coded as follows:

1. Alive
2. Stillborn or died within 24h

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 x 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^2_s	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 2004-2006 with reliability >= 50%.

Reliability

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

$R = (¼ * R_{bs} + R_b - 2 * ¼ R_{bs} * R_b) / (1 - ¼ * R_{bs} * R_b)$

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.

PF index

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

PF index = 0.4 * PS + 0.25 * CS + 0.15 * FS + 0.1 * SCS + 0.1 * 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 a 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 direct genomic value (DGV) was estimated following the approach of Strandén and Garrick (2009).

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) Fitting and validating the genomic evaluation model to Polish Holstein-Friesian cattle. Journal of Applied Genetics 52(3) pp. 363-366.