Genetic parameters for intermediate optimum type traits

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Introduction

In most countries conformation traits are routinely recorded on linear scales. These scales cover the biological range between two extremes and do not reflect desirability. For some type traits, mid-scores are more desired than extreme scores. In the population of Polish Holstein-Friesian cows, 6 of 16 type traits evaluated linearly have intermediate optima.

In this paper the routine linear scoring system of type traits with intermediate optima is compared with scoring on a modified scale in which the most desirable form of trait receives the highest score.

Material

Data were type evaluations of 8,041 primiparous cows in western Poland, daughters of 359 sires. The cows calved for the first time in 2008 and were classified in 1,110 herd-year-season classifier subclasses. Six type traits with intermediate optima (body depth, rump angle, rear leg-side view, foot angle, fore udder attachment and udder depth) were evaluated by classifiers using linear and modified scales. The descriptive type traits were also included in the analysis.

Method

A multi-trait animal model was used and a Bayesian approach with Gibbs sampling was applied to estimate (co)variance components for all traits (Misztal, 1999).

(Co)variance components of type traits were estimated based on the following linear model:

y = Xb + ZQg + Zu + e

where **y** is the vector of observations, **g** is the vector of fixed effects of genetic groups, **b** is the vector of fixed effects of herd-year-season of calving-classifier, stage of lactation and fixed regression on age at calving, **u** is the vector of additive animal genetic effects, **e** is the vector of residual error, and **X**, **Z** and **Q** are coincidence matrices. Matrix $\mathbf{G} = \mathbf{A} \otimes \mathbf{G}_0$, where \mathbf{A}^{-1} is the numerator relationship matrix and \mathbf{G}_0 the genetic (co)variance matrix between traits.

It is assumed that $E(\mathbf{u}) = \mathbf{0}$, $E(\mathbf{e}) = \mathbf{0}$, $V(\mathbf{u}) = \mathbf{G}$, $V(\mathbf{e}) = \mathbf{R}$, $Cov(\mathbf{u}, \mathbf{e}) = \mathbf{0}$, and $E(\mathbf{y}) = \mathbf{X}\mathbf{b}$, $V(\mathbf{y})=\mathbf{Z}\mathbf{G}\mathbf{Z'}+\mathbf{R}$. Matrix $\mathbf{R} = \mathbf{I} \otimes \mathbf{R}_0$, where \mathbf{R}_0 is the residual (co)variance matrix between traits and \otimes is the Kronecker product. Animals with unknown parents were assigned to genetic groups. Genetic groups were formed according to the sex of the unknown parent and

the birth year of its offspring. Two groups for male and four for female unknown parents were formed.

Results

The characteristics of type traits are shown in Table 1. Modified scores had larger means than the respective linear traits. The largest mean was found for modified rump angle (7.7), and the smallest for linear rump angle (2.0). Standard deviations of modified traits ranged from 1.6 for rump angle to 2.0 for udder depth, and were higher than the standard deviations of the respective linear traits (1.2 to 1.6).

On the modified scale the most desirable form suggested by breeders receives the highest score, regardless of the biological character of the trait. Such an appraisal does not precisely describe the conformation of the cow and is similar to a descriptive scoring system. It is easier to use in selection indices and reflects the tendency of farmers to associate high scores with excellent animals.

Heritabilities of linear scores, shown in Table 1, ranged from 0.16 for foot angle to 0.44 for udder depth, and were consistent with earlier estimates in this population. The highest heritabilities were obtained for height at rump (0.62) and two descriptive traits: size (0.53) and overall conformation score (0.42). Feet&legs and descriptive udder had lower heritability (0.15 and 0.19 respectively).

Modified evaluations of traits with intermediate optima showed lower heritabilities than the respective linear scores. The largest heritabilities in this group were estimated for udder traits (0.31 for udder depth and 0.30 for fore udder height) and the lowest for rump angle (0.09). Leg traits showed moderate heritability: 0.14 for rear legs and 0.15 for foot angle.

Genetic correlations between modified scores and the descriptive traits were largest for udder traits (Table 2.). Modified udder traits showed the highest correlations with descriptive udder (0.71 for fore udder height and 0.66 for udder depth), final score (0.54 and 0.63 respectively) and feet&legs (0.44 and 0.52 respectively). Modified leg traits were also strongly correlated with descriptive traits. These traits showed large correlations with feet&legs (0.67 for rear legs and 0.58 for foot angle), final score (0.42 and 0.45 respectively) and udder (0.38 and 0.34 respectively).

Modified score of body depth showed low correlations with all descriptive traits (from 0.22 with feet&legs to 0.29 with final score); the correlations between modified score of rump angle and descriptive traits were close to zero.

Genetic correlations between modified scores and respective linear type traits are shown in Table 3. The largest correlations were obtained for foot angle (0.96) and udder traits: 0.95 for fore udder height and 0.91 for udder depth. The optimum score located at the right end of the linear scale might be the reason for high correlations of these traits. Much lower genetic correlations were found for body depth (0.52) and rump angle (0.26), which have optima closer to the middle of the scale. The genetic correlation between modified rear legs-side view and the respective linear trait was large and negative (-0.73). On the linear scale, straight legs are related to the lowest score and sickled ones to the highest. The optimum value for this trait is in the middle of the scale; however, sickled legs (scores higher than optimum) are less favorable than straight (scores lower than optimum). The negative correlation between modified and linear rear leg score is a consequence of this relation.

Conclusions

Heritabilities of modified scores were lower than those for the respective linear traits. Modified scores of udder and legs were strongly correlated with descriptive traits. Genetic correlations between modified and linear scores were higher for traits with optima close to the right end of the scale, and smaller or negative for traits with optima in the middle of the scale.

Trait	x	SD	h^2
Descriptive traits (50-100)			
Size	81,6	5,5	0,53
Overall conformation	79,1	4,4	0,42
Feet&Legs	78,9	4,1	0,15
Udder	77,3	5,1	0,19
Final score	78,5	3,9	0,29
Height at rump	143,1	4,3	0,62
Linear Scale (1-9)			
Body depth	5,9	1,4	0,32
Rump angle	5,0	1,2	0,40
Rear legs - side view	5,4	1,2	0,23
Foot angle	5,1	1,3	0,16
Fore udder height	5,5	1,4	0,35
Udder depth	5,4	1,6	0,44
Modified scale (1-9)			
Body depth	7,3	1,7	0,12
Rump angle	7,7	1,6	0,09
Rear legs - side view	7,4	1,8	0,14
Foot angle	5,6	1,8	0,15
Fore udder height	6,3	1,9	0,30
Udder depth	6,5	2,0	0,31

Table 1. Means (\overline{x}) and standard deviations (SD) and heritabilities (h^2) of descriptive, linear and modified type traits (N=8,041)

Table 2. Genetic correlation between descriptive and modified traits

Trait	Modified scores					
	Body	Rump	Rear legs -	Foot	Fore udder	Udder
	depth	angle	side view	angle	height	depth
Size	0,230	-0,040	0,120	0,320	0,140	0,370
Overall conformation	0,250	-0,090	0,280	0,330	0,190	0,380
Feet&Legs	0,220	-0,040	0,670	0,580	0,440	0,520
Udder	0,260	-0,030	0,380	0,340	0,710	0,660
Final score	0,290	-0,040	0,420	0,450	0,540	0,630
Height at rump	0,140	-0,010	0,120	0,350	0,130	0,390

Trait	Modified scores						
	Body depth	Rump angle	Rear legs - side view	Foot angle	Fore udder height	Udder depth	
Body depth	0,520	0,040	0,030	0,080	-0,070	-0,090	
Rump angle	-0,170	0,260	-0,110	-0,100	-0,340	-0,190	
Rear legs - side view	-0,160	-0,030	-0,730	-0,130	-0,090	-0,060	
Foot angle	0,190	0,170	0,090	0,960	0,260	0,190	
Fore udder height	0,070	0,070	0,410	0,320	0,950	0,680	
Udder depth	0,030	-0,020	0,200	0,210	0,600	0,910	

Table 3. Genetic correlation between linear and modified traits