GENETIC RELATIONSHIP AMONG BODY CONDITION SCORE, TYPE, FERTILITY AND PRODUCTION TRAITS IN SWISS HOLSTEIN CATTLE

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SUMMARY
Genetic parameters for body condition score (BCS), 27 linear type, 5 milk production and 2 fertility traits were estimated for Swiss Holstein cattle. Data set consisted of 25126 records and 80329 animals in pedigree. Heritabilities (h^2), permanent environmental variances (c^2) and genetic correlations (r_g) were estimated via repeatability animal models. Estimates of h^2 and c^2 for BCS were 0.23 and 0.21, respectively. Estimated h^2 ranged from 0.09 to 0.50 for type traits and 0.21 to 0.57 for production traits. The range of estimated r_g of BCS with type traits was -0.69 to 0.58, with production traits was -0.27 to 0.17, and with fertility traits was 0.002 to 0.289. Results showed that cows with lower body condition scores have genetically poor fertility. Type and production traits are favourably and unfavourably related to BCS, respectively. Based on the results from this study it could be concluded that BCS could be used as a potential indicator of functional and fertility traits.
Key words: Body condition score, type and fertility traits, genetic analysis, dairy cattle

INTRODUCTION
Functional traits (e.g. health or fertility) in breeding goals are increasingly becoming an integral part of livestock breeding strategy and have been shown to maximize profit, by reducing costs and improving efficiency of production (Kadarmideen et al. 2002). Recent studies have shown that Body Condition Score (BCS) can be used in selecting robust and profitable animals, due to its strong genetic relationship with other functional traits such as body weight and feed efficiency (Coffey et al. 2001), type traits (e.g. Veerkamp et al. 1997), energy balance or metabolic stability (Coffey et al. 2001) and fertility (Pryce et al. 2000). BCS is routinely recorded from 2001 by Holstein Switzerland. The main objective of this work was to estimate heritability for BCS and its genetic and other correlations with 27 type, 5 production and 2 fertility traits.

MATERIALS AND METHODS
Data. BCS is recorded on 1-5 scale (1=very thin; 5=very fat) with an increment of 0.25. Heifers are assessed once during the lactation. For animals with a BCS record, data on all 27 linear type (and composite) traits and 5 milk production records were also obtained. Also, Estimated Breeding Values (EBV) of sires for daughter's non-return rates 56 day post insemination (NRR) and days to first service (DFS) were obtained from the Holstein Switzerland. These estimates of sire breeding values for daughters NRR and DFS are based on the individual animal model (AM) as reported by Schnyder and Stricker (2002). There were 25126 records (5483 herd-year-season, 7516 herd-year-visits) and were 5 lactation classes. Pedigrees were traced as far back as possible which included 80329 animals.

Statistical models and analyses. Estimation of genetic and environmental parameters was accomplished by defining three types of models / analysis as given below:

Univariate repeatability animal models. To estimate heritability and permanent environmental variance, the following repeatability animal models [1] and [2] were used for type + BCS and production traits, respectively.

$$y_{ijklmnopq} = m + HYV_i + L_j + S_k + M_l + \sum_{m=1}^{5} b_m at_m + b_n hp + a_o + w_p + e_{ijklmnopq} \quad \ldots\ldots[1]$$

Where: y = BCS or type traits; m = the overall mean; HYV = herd-year-visit of classifier; L = lactation number, S = stage of lactation (in months from calving date) at the time of classification; M = month of calving; at_m = age (in days) at condition scoring or type classification nested within m^{th} lactation and b_m is the regression coefficient for at_m for $m=1$ to 5; hp = percentage of Holstein genes and b_n is the regression coefficient for hp; a_o = random genetic effect of animal; w_p = random permanent environmental effect of animal; and e = residual error term.

$$y_{ijklmn} = m + HYS_i + L_j + \sum_{k=1}^{5} b_k ac_k + a_l + w_m + e_{ijklmn} \quad \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots[2]$$

Where: y = milk production traits; m = the overall mean; HYS_i = herd-year-season of calving; ac_k = age (in days) at calving nested within k^{th} lactation and b_k is the regression coefficient for ac_k for $k=1$ to 5 and all other terms are as in Model [1].

Bivariate repeatability animal models. Two-trait genetic models were used to estimate variances, covariances and correlations for genetic, permanent environmental and residual effects specified under the univariate models [1] and [2]. Terms in model [1] and [2] were used jointly in the bivariate model but applying only corresponding model terms for each trait.

Genetic regression models. The statistical model used for all type and BCS traits and was

$$y_{ijklmnopq} = m + HYV_i + L_j + S_k + M_l + \sum_{m=1}^{5} b_m at_m + b_n hp + b_o EBV_{NRR} + b_p EBV_{DFS} + e_{ijklmnopq} \quad .[3]$$

Genetic regressions for all milk production traits were the same and was

$$y_{ijklmn} = m + HYS_i + L_j + \sum_{k=1}^{5} b_k ac_k + b_l EBV_{NRR} + b_m EBV_{DFS} + e_{ijklmn} \quad \ldots\ldots[4]$$

Where: EBV_{NRR} is the estimated breeding value of the sire for daughters' non-return rate 56 day post insemination and β_o or β_l is the corresponding regression coefficient. Similarly, EBV_{DFS} is the estimated breeding value of the sire for daughters' interval (in days) between calving and first service and β_p or β_m is the corresponding regression coefficient. All other terms are as in models (1 and 2).

Implementation and Software: All parameters for models [1] to [4] were estimated using the software package, ASREML (Gilmour et al. 2001). It was not our aim to compute correlations among type traits or between type and milk production traits, as they were already estimated for Swiss Holsteins.

RESULTS AND DISCUSSION

Heritabilities and permanent environmental variances. Heritability (h^2) and permanent environmental variance (c^2) from univariate repeatability AM are given in Table 1. Heritabilities and c^2 for BCS was 0.23 and 0.21, respectively. Among type traits, heel depth had the lowest h^2 (0.09) and rump width had the highest h^2 (0.50). Udder traits had h^2 of 0.20 to 0.31, 'feet &leg' traits had h^2 of 0.15 to 0.18 and 'rump' traits were highly heritable with a range of 0.25 to 0.50. The c^2 estimates were generally higher than h^2 estimates and were the highest for stature (0.87) and lowest for rump width (0.26). The h^2 estimates were significant for all 27 type traits and BCS, with their standard error being small ($= 0.03$). Similarly, the c^2 estimates were significant for all 27 type traits and BCS, with their standard error being small ($= 0.04$). For milk production traits, estimates of h^2 were the highest for fat percentage (0.57) and lowest for fat yield (0.21). Estimates of h^2 and c^2 production were generally lower than those for type traits. Estimates of h^2 for BCS and type trait are similar to literature estimates (e.g. Veerkamp et al. 1997, Berry et al. 2002). As for permanent environmental variances, literature estimates based on multiple lactation records for BCS are scarce.

Table 1: Phenotypic means (Mean), standard deviations (S.d.), h^2 and c^2 with their standard errors (s.e (h^2), s.e.(c^2)), genetic and phenotypic correlations[1] with their standard errors, (r_g (s.e.), r_p (s.e.)) for body condition score (BCS)[2], type[3] and production traits, based on 25126 records.

Trait	Mean	S.d	h^2	h^2 s.e.	c^2	c^2 s.e.	r_g (s.e.) of BCS with	r_p (s.e.) of BCS with
BCS	2.7	0.4	0.23	0.03	0.21	0.04	-	-
Stature	145.5	5.9	0.09	0.01	0.87	0.01	0.01 (0.09)	0.02 (0.01)
Heart girth	197.1	8.8	0.28	0.03	0.54	0.03	0.52 (0.06)	0.28 (0.01)
Strength	5.3	1.2	0.26	0.03	0.42	0.03	0.58 (0.06)	0.34 (0.01)
Body depth	6.2	1.0	0.33	0.03	0.32	0.03	-0.05 (0.08)	0.04 (0.01)
Loin	5.9	1.0	0.28	0.03	0.37	0.03	-0.63 (0.05)	-0.29 (0.01)
Rump angle	4.6	0.9	0.32	0.03	0.45	0.03	0.08 (0.07)	0.03 (0.01)
Rump width	6.2	1.2	0.50	0.03	0.26	0.03	-0.15 (0.06)	-0.06 (0.01)
Dairy char	6.0	0.9	0.21	0.02	0.41	0.03	-0.44 (0.07)	-0.20 (0.01)
Rear leg side view	5.7	0.7	0.18	0.02	0.40	0.03	-0.24(0.08)	-0.09 (0.01)
Pastern	4.5	0.8	0.18	0.02	0.37	0.03	0.10 (0.08)	0.02 (0.01)
Heel depth	5.2	0.8	0.09	0.02	0.28	0.03	0.38 (0.09)	0.10 (0.01)
Rear leg rear view	5.3	1.1	0.17	0.02	0.38	0.03	0.11 (0.08)	0.09 (0.01)
Fore udder attach	5.7	1.2	0.20	0.02	0.48	0.03	0.02 (0.08)	0.08 (0.01)
Rear udder height	5.2	1.3	0.28	0.03	0.44	0.03	-0.07 (0.07)	-0.03 (0.01)
Rear udder width	5.7	1.0	0.25	0.03	0.32	0.03	-0.09 (0.07)	-0.01 (0.01)
Udder cleft	5.9	1.0	0.20	0.02	0.49	0.03	-0.09 (0.08)	-0.09 (0.01)
Udder depth	5.3	1.3	0.31	0.03	0.40	0.03	0.08 (0.07)	0.01 (0.01)
Udder quality	5.9	1.0	0.29	0.03	0.33	0.03	-0.48 (0.06)	-0.19 (0.01)
Teat length	4.8	0.9	0.37	0.03	0.37	0.03	-0.12 (0.07)	-0.01 (0.01)
Teatposition front	4.8	1.0	0.28	0.03	0.47	0.03	-0.16 (0.07)	-0.04 (0.01)
Teat position rear	6.4	0.9	0.24	0.03	0.38	0.03	-0.41 (0.06)	-0.10 (0.01)
Capacity	80.4	5.9	0.41	0.03	0.48	0.03	0.23 (0.06)	0.17 (0.01)
Rump	81.8	4.6	0.24	0.03	0.49	0.03	0.06 (0.08)	0.02 (0.01)
Dairy	82.0	3.5	0.28	0.03	0.42	0.03	-0.69 (0.04)	-0.31 (0.01)
Feet & legs	81.2	3.5	0.14	0.02	0.54	0.03	0.17 (0.08)	0.07 (0.01)
Udder	80.7	3.5	0.17	0.02	0.67	0.02	0.03 (0.08)	-0.01 (0.01)
Final class	80.9	3.3	0.30	0.03	0.54	0.03	0.13 (0.07)	0.07 (0.01)
Milk yield	7299	1658	0.26	0.02	0.33	0.03	0.17 (0.00)	0.31 (0.00)
Fat yield	285	66	0.21	0.03	0.31	0.02	-0.27 (0.04)	-0.08 (0.00)
Protein yield	262	69	0.27	0.01	0.29	0.03	-0.19 (0.03)	-0.03 (0.00)
Fat percent	3.93	0.42	0.57	0.03	0.20	0.03	0.19 (0.06)	0.05 (0.01)
Protein percent	3.19	0.21	0.47	0.03	0.18	0.03	0.17 (0.05)	0.04 (0.01)

[1]Permanent environmental and residual correlations between BCS, type and production traits are not shown;
[2]BCS was on 1 to 5 scale; [3]All type traits were on 1 to 9 scale except stature, heart girth and composite traits;

Correlations of body condition score with type and production traits. *Genetic correlations:* Estimates of genetic correlations (r_g) of BCS with type and production traits are given in Table 1, along with phenotypic correlations, r_p. BCS had lower positive estimates of r_g with stature, pastern,

right leg rear view, fore udder attachment, rump, rump angle, udder, udder depth, final class, feet & leg. Moderate to high positive r_g were found with heart girth, strength, heel depth and capacity. This indicates that cows with good BCS tend to have good heart girth, capacity etc., at the genetic level. BCS had lower negative estimates of r_g with body depth, rump width, rear udder height, rear udder width, udder cleft, teat length, teat position front and moderate to high negative estimates of r_g with dairy character, loin, udder quality, teat position rear, right leg side view and dairy. Genetic correlations with milk production traits were such that higher BCS increase milk yield but decrease fat and protein yield. Fat and protein percent also showed positive moderate genetic correlations. Generally, estimates of r_g between BCS and type traits were favourable suggesting that selection for good BCS would increase a chance of having desired type. *Phenotypic correlations* Estimates of phenotypic correlations (r_p) are also given in Table 1. In general, estimates of r_p were lower than estimates of r_g. Absolute estimates of r_p with type traits ranged from 0.00 for teat length to 0.34 for strength. Estimated correlations agree with earlier estimates (e.g. Veerkamp et al. 1997).

Genetic relationship of body condition score with fertility. The estimated regression coefficients ß for regressing BCS on the EBV_{NRR} was 0.002 (s.e.=0.001). Similarly, ß for regressing BCS on the EBV_{DFS} was -0.004 (s.e. 0.001). Estimate of ß indicates that for each unit increase in EBV_{NRR}, BCS increased by 0.002 and that for each unit increase in EBV_{DFS}, BCS decreased by 0.004. With ß's, approximate estimates of r_g could be derived using genetic standard deviations of traits involved. Genetic regression methods for approximate r_g were also used by others studies (e.g. Kadarmideen and Pryce, 2001). Letting genetic standard deviations of BCS, DFS and NRR as, s_{g_BCS}, s_{g_DFS} and s_{g_NRR}, respectively, the r_g between BCS and DFS was $r_{g\_BCS,DFS} = ß_{BCS,DFS}$ (s_{g_DFS}/s_{g_BCS})= - 0.269. Similarly, r_g between BCS and NRR was 0.002. Estimates for s_{g_DFS} and s_{g_NRR} for Swiss Holsteins were taken from Schnyder and Stricker (2002). For all type and production traits, ß's for NRR and DFS were available but are not reported here. Both ß and r_g for DFS show that cows with good body condition have genetically shorter time to recommence cycling after calving for first insemination. This result could also be extrapolated to the genetic relationship of BCS with calving interval since the latter has very strong genetic relationship with DFS (r_g of 0.90; Kadarmideen et al. 2000). In fact, Pryce et al. (2000) have reported r_g of -0.41 between BCS and calving interval. In general, genetic relationships of BCS with other traits show that the cows with lower BCS tend to have poor fertility, BCS is favourably related to type and unfavourably to milk production traits.

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