Genetic correlations between three countries for conformation traits

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Introduction

Extensive exchange of dairy cattle germ-plasm (semen, embryos, live animals) currently takes place between countries and have prompted the need for accurate bull comparisons. To date several procedures (like conversion formulas and linear model comparisons (LMC)) have been followed in order to tackle that issue. These methods suffer from several limitations, which are mostly overcome by Schaeffer and Zhang's (1993) extension of the LMC procedure; multi-trait across country evaluation (MACE). Knowledge of genetic parameters across coutnry is required by this method.

To date international genetic evaluation studies in dairy cattle have considered only production traits. However, availability of international genetic evaluations for additional traits would better serve breeding goals around the world. Problems often associated with additional traits are lack of records in some countries and different trait definitions among countries (Banos and Sigurdsson, 1994).

The aim of this study is to estimate genetic variances and covariances between Denmark, Canada and the United States of America for conformation traits in Holstein bulls.

Material and Method

Data

Data were Holstein bull evaluations for 8 linear scored conformation traits from Denmark (DNK), Canada (CAN) and the United States of America (USA). Bulls were born between 1950 and 1990. Proofs obtained in both country of first sampling of the bull and importing countries were included. Although imported proofs might be biased, they are necessary in order to provide direct genetic links for the estimation of genetic correlations (Sigurdsson and Banos, 1995). Proofs were required to be based on more than 5 daughters. The conformation traits data set consisted of 4 479 Canadian, 1 639 Danish and 14 671 US bull evaluations. Of these evaluations, 70 bulls had evaluations in both Canada and Denmark, 605 in Canada and USA and 74 in Denmark and USA. Total number of bulls in this data set was 20 118.

The relationship matrix is assumed to provide ties among bulls from different countries. Most exchange of semen has occurred among Nordic countries and among North American countries, while export from North America to the Nordic countries has provided genetic links between the two continents.

Bull pedigree records included the identification of sire, dam, maternal grandsire and maternal granddam. Information about national origin of ancestors was used to determine the national origin of each bull as follows: one-half the origin of the sire plus one-quarter the origins of the maternal grandsire (MGS) and maternal granddam (MGD). Thus only unknown parents need to be assigned to genetic groups, which were defined by national origin, birth year and path of selection (sire, maternal grandsire and maternal granddam). Ancestor-bulls without own proofs were traced back two generations from the oldest bulls with proofs in order to increase across country connections.

Method of analysis

National proofs were first de-regressed within country and then analyzed jointly with a linear model (Schaeffer and Zhang, 1993):

$$y_i = \mu_i 1 + Z_i Q g_i + Z_i s_i + e_i \tag{1}$$

where: y_i : vector of unregressed proofs from the ith country;
μ_i : scalar for the ith country;
g_i : vector of genetic group effects of phantom parents;
s_i : vector of random sire transmitting abilities for the ith country, var(s) = A*G, A: bull additive genetic relationship matrix, G: trait genetic (co)variance matrix;
e_i : vector of residual effects in the ith country; var(e) = R*e_i, R: diagonal matrix with diagonals equal to the reciprocal of the total number of daughters in a proof;
Z_i : matrix that relates proofs to sires;
Q : matrix that relates sires to phantom parents groups.

Unregressed proofs were computed within country form the national proof as follows:

$$y = R[A^{-1}k - A^{-1}kQ(Q'A^{-1}kQ)^{-1}Q'A^{-1}k + R^{-1}]P \tag{2}$$

where k is the residual to sire variance ratio in each country, calculated as $(4-h^2)/h^2$, where h^2 is the heritability used in the national evaluation. Data sub sets inluding bulls with multiple proofs and full-sib families with members in different countries were used to estimate genetic correlations between countries. A multivariate (considering all countries together) and a bivariate (considering only two countries together) model was used to estimate ReML genetic correlations (Sigurdsson and Banos, 1995).

Results and Discussion

Heritabilities, estimated sire variances and proof type for the 8 conformation traits are shown in Table 1.

Table 1: Proof type, assumed heritabilities (h^2) and estimated sire variances (σ^2_s) for conformation traits in Canada (CAN), Denmark (DNK) and USA.

Trait	CAN		DNK		USA	
	h^2	σ^2_s	h^2	σ^2_s	h^2	σ^2_s
Stature	0.40	29.64	0.61	7.87	0.42	1.35
Rump	0.30	35.12	0.39	0.69	0.28	1.66
Rump width	0.24	30.02	0.27	0.54	0.26	1.40
Rear leg set	0.16	42.01	0.21	0.53	0.16	2.71
Foot	0.07	40.67	0.21	0.46	0.13	2.38
Fore udder	0.14	37.15	0.23	0.72	0.24	1.84
Central ligament	0.15	30.23	0.15	0.41	0.10	2.89
Teat placement	0.24	31.52	0.36	1.21	0.22	1.96
Proof type	STA[1]		AM-SOL		PTA	

[1] STA: standardized transmitting ability; AM-SOL: animal model solutions; PTA: predicted transmitting ability

Table 2: Number of bulls with proofs and total number of bulls (including ancestors) in data sets used for estimating genetic correlations for conformation traits for multi- and bivariate method.

Method	Number of bulls	Total number of sires
Multivariate	1339	1665
Bivariate		
CAN-DNK	72	141
CAN-USA	1294	1620
DNK-USA	107	180

The number of bulls with proofs and the total number of bulls (including ancestors) for the conformation traits data subsets are shown in Table 2.

The estimated genetic correlations for the eight linear scored conformation traits, based on the bivariate method, and the difference between the bi- and multivariate method are in Table 3. For the small data sets (CAN-DNK and DNK-USA) leaving out redundant data gave increased genetic correlations. Difference in methods for CAN-DNK ranged between +0.02 and -0.20, and for DNK-USA between -0.07 and -0.14. Genetic correlations between CAN and USA were equal for both methods. High correlation for the linear scored conformation traits were expected, since scoring of those traits was harmonized between countries (Cnossen *et al.*, 1993). REML estimates agreed fairly good with proof correlations for bulls with multiple proofs.

Table 3: Genetic correlations between countries for conformation traits based on bivariate analysis; between bracket difference between estimates based on multi- and bivariate analysis.

Trait	CAN-DNK		CAN-USA		DNK-USA	
Stature	0.83	(-0.08)	0.95	(0.00)	0.84	(-0.10)
Rump	0.88	(-0.11)	0.92	(0.00)	0.91	(-0.11)
Rump width	0.90	(-0.20)	0.87	(-0.01)	0.84	(-0.14)
Rear leg set	0.84	(-0.17)	0.94	(0.00)	0.79	(-0.11)
Foot	0.64	(-0.14)	0.84	(0.00)	0.55	(-0.08)
Fore udder	0.78	(-0.07)	0.94	(0.00)	0.86	(-0.14)
Central ligament	0.79	(-0.12)	0.93	(0.00)	0.86	(-0.17)
Teat placement	0.77	(0.02)	0.95	(0.00)	0.83	(-0.07)

Genetic correlations based on the bivariate analysis were used for a MACE-evaluation for the three countries. Correlations between international and national proofs were 0.99 for all traits for USA, but lower for CAN and DNK. The lowest correlations for foot angle might be related to the low genetic correlation between countries for that trait. However, this did not affect the correlation between national and international proofs for USA. The expectation of those correlations is almost unity, as de-regressed proof are regressed in MACE with the same factors used in the de-regression.

To show the impact of genetic correlations less than unity on the ranking of sires within countries, an additional evaluation with genetic correlations of unity was run. Product moment and rank correlation between international proofs based on genetic correlations of unity and bivariate estimates were above 0.95, except for foot in CAN. Table 4 shows the number of bulls in the top 100 for USA that also ranked in the top 100 for CAN and DNK for both methods. As expected genetic correlation less than unity gave different ranking of sires in different countries: when using genetic correlation of unity more sires rank in the top 100 in all three countries than using estimated genetic correlations. Traits with lowest genetic correlations showed largest difference in rankings. North American bulls without proofs in DNK got high international proofs in DNK, due to high assumed genetic correlation. Using estimated genetic correlations in the international evaluation international proofs of those bulls were much lower, and more local bulls ranked in the top. The difference for CAN was less because most of those North American bulls had a national proof in CAN as well as in the USA.

Table 4: Number of top 100 bulls in USA which also rank in top 100 in Canada (CAN) and Denmark (DNK), averaged over all conformation trait, for genetic correlation of unity and estimated correlation.

Genetic correlation	Number of USA top 100 bulls with ranking < 100 in:	
	CAN	DNK
unity	85	92
estimated	73	62

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