

Multiple-trait analysis for conformation and other non-dairy-production traits; preliminary report¹

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Introduction

To date international genetic evaluation studies have considered only dairy production traits. However, availability of international genetic evaluations for additional traits would better serve breeding goals around the world. Problems often associated with such traits are lack of records in some countries and differences in the trait definition among countries.

This report summarizes projects currently undertaken by the INTERBULL Centre that address the issue of international evaluations for non-dairy-production traits.

Non-dairy-production traits in Nordic and North American countries

This exercise is part of a more comprehensive project initiated in 1992, in collaboration with the Nordic Farmers Advisory Committee. The aim of the project is to develop joint evaluations for bulls progeny tested in the Nordic countries. Holstein-Friesian bulls from Denmark, Finland, and Sweden and Red-and White (Ayrshire type) bulls from Finland, Norway, and Sweden are considered. A first study (Banos et al, INTERBULL Bulletin No. 8, 1993) indicated that Holstein-Friesian bull records from common exporting countries, especially the USA, are required for joint evaluation of Nordic bulls. This was due to lack of direct genetic connections among the Nordic Holstein bull populations. A similar study with Ayrshire bulls concluded that genetic connections were stronger among Nordic and among North American (USA and Canada) bull populations than between countries belonging to different geographic groups. However, simultaneous genetic evaluation of bulls from all countries was still possible.

Non-dairy-production traits have always been important attributes of the breeding goals in the Nordic countries and to some extent (conformation) in North America. Before deciding which particular traits to consider in this study, countries were surveyed on data availability and trait definitions (INTERBULL Bulletin No. 6, 1992). Based on responses to the survey, the following traits were selected:

1. Conformation traits:
 - 1.1. Stature (S)
 - 1.2. Body depth (BD)
 - 1.3. Rump (R)
 - 1.4 Rump width (RW)
 - 1.5 Rear leg set (RLS)
 - 1.6 Feet (F)
 - 1.7 Fore udder attachment (FU)
 - 1.8 Rear udder height (RUH)
 - 1.9 Central ligament (CL)

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- 1.10 Udder depth (UD)
- 1.11 Front teat placement (TP)
- 1.12 Front teat length (TL)
2. Female fertility
3. Stillbirth rate
 - 3.1. Direct (sire effect)
 - 3.2. Maternal (maternal grand-sire effect)
4. Mastitis related traits
 - 4.1. Clinical mastitis cases
 - 4.2 Somatic cell lactation score
5. Temperament

Choice of the conformation traits was also influenced by the World Holstein Friesian Federation definition of linear type traits. National evaluations for only a few of the above traits (feet and legs and udder related traits) are routinely available in all countries involved. Groups of countries will be jointly considered according to trait availability.. The above traits are considered important in the Nordic countries, but future international genetic evaluations will not be limited to them.

Data are currently being collected. Two data sets consisting of conformation records (January 1994 bull national evaluations) from the USA and Canada (CAN) were considered in a pilot study to test the methodology. These bulls were AI progeny tested in either country; 3779 bulls born 1960-1989 were from CAN and 11513 bulls born 1972-1989 from USA. Table 1 describes the trait to trait correspondence in the two countries and the genetic correlation computed from national proofs of bulls commonly tested in the two countries, adjusted for the accuracy of the evaluation.

TABLE 1: Conformation traits as defined by INTERBULL, USA, and CAN, and genetic correlation (r_g) between USA and CAN traits; the latter was computed from national proofs of bulls commonly tested in the two countries, adjusted for the accuracy of the evaluation.

INTERBULL trait	USA trait	CAN trait	r_g
Stature	Stature	Stature	.96
Body depth	Body depth	Capacity	.95
Rump width	Thurl Width	Rump width	.92
Rear leg set	Rear leg set	Set of rear legs	.90
Feet	Foot angle	Foot	.80
Fore udder attachment	Fore attachment	Fore udder attachment	.88
Rear udder height	Rear udder height	Rear attachment height	.85
Central ligament	Udder Cleft	Median suspensory ligament	.85

The following model of evaluation considered national proofs from different countries as different traits with correlations equal to those in Table 1 (suggested by Schaeffer and Zhang, INTERBULL Bulletin No. 8, 1993):

$$y_i = \mu_i 1 + Z_i Q g_i + Z_i s_i + e_i \quad [1]$$

where: y_i =unregressed adjusted daughter averages in the i^{th} country
 μ_i =the overall mean in the i^{th} country
 g_i =phantom parent genetic group effect in the i^{th} country
 s_i =bull genetic effect in the i^{th} country; $\text{Var}(s)=A^*G$, A =bull additive relationship matrix, G =trait genetic (co)variance matrix
 e_i =residual effect in the i^{th} country, $\text{Var}(e)=R^*e$, R =diagonal matrix with diagonals equal to the reciprocal of the number of daughters in a proof
 Z, Q =incidence matrices

The overall mean reflected the genetic base definition in each country. Phantom parent groups were defined by the country of origin and birth year of the bulls; 20 such groups were formed.

Unregressed adjusted daughter averages were computed within country from the national proof (P) as follows:

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

where k =residual to sire variance ratio in each country. Equation 2 can be derived from modified mixed model equations (Quass and Pollak, JDS 64:1868,1981) pertaining to Model 1. Please note that the Q matrix does not have to be formed explicitly in Equation 2.

Initial values for sire variances in each country were estimated by taking the geometric mean of national proofs and unregressed daughter averages from Equation 2. Then 10 iteration rounds of REML using sire solutions from Model 1 were used to derive final estimates. Genetic correlations were fixed to values shown in Table 1 and only sire variances were allowed to change. For each REML iteration, 600 iterations on the data were considered before accepting the solutions for the sire and other effects.

Within year correlations between national and international proofs were in all cases higher than .99. Table 2 shows means and standard deviations of national and international proofs for the above traits in each country.

Standard deviation appeared to be the same, suggesting that the variance ratio associated with the unregressed daughter averages computed with Equation 2 was similar to that of the phenotypic records. International proof means turned out .01-.05 standard deviations lower than corresponding national proof means for both countries.

In conclusion, multiple-trait analysis with Model 1 seemed to work well provided that genetic correlation estimates between countries were correct. More work is needed to provide a precise method for estimating these genetic correlations.

TABLE 2: Means and standard deviations (STD) of national (PRF) and international (IPRF) proofs for several conformation traits in CAN and USA; values are not comparable between countries; see text for trait abbreviation.

Trait	MEAN-USA		STD-USA		MEAN-CAN		STD-CAN	
	PRF	IPRF	PRF	IPRF	PRF	IPRF	PRF	IPRF
S	-.04	-.04	1.00	1.00	.01	-.03	5.04	5.03
BD	-.15	-.20	1.00	1.01	.02	-.10	5.02	4.98
RW	-.22	-.28	1.03	1.04	.05	-.05	4.97	4.95
F	-.22	-.27	1.13	1.14	.01	-.01	5.03	5.03
RLS	.02	.01	1.11	1.11	-.07	-.29	5.01	5.01
FU	.14	.21	1.04	1.06	.01	-.10	4.98	4.99
RUH	.12	.09	1.18	1.17	-.01	-.22	5.01	4.97
CL	.06	.05	1.18	1.17	-.07	-.34	4.95	4.96

Beef production traits in the Simmental breed

This project is currently being set up in collaboration with the World Simmental Federation. Wide range of trait definitions in various countries, different breeding goals (dual purpose or beef only breed), and diverse methods of recording and evaluation (progeny tests, performance test, or combination of both) have necessitated a survey to improve the knowledge on the subject. Thirteen (13) countries have responded to this date: Argentina, Czech Republic, France, Germany, Ireland, Italy, New Zealand, Spain, Sweden, Switzerland, Brazil, Slovakia, and Uruguay. A summary of traits and genetic evaluation schemes in these countries is presented in Table 3.

Some of the countries responded so far consider both, progeny and performance test in genetic evaluation. Further, Table 3 assists in appreciating the diversity of traits and breeding goals with regards to beef production. Among all traits, growth related characters (e.g. daily gain) appear to be the most interesting and frequently evaluated, followed by conformation and carcass quality traits.

Responses from a few more countries are expected. The plan is to use Model 1 in analysis of national proofs based on progeny test. Modification of this model will be needed to consider data based on performance (individual) test. Data layout and a progress timetable for the project will be decided upon completion of the survey.

TABLE 3: Number of countries with Simmental sire evaluations for beef production traits by progeny (PG) and performance (PF) test.

Trait	Number of countries	Number of countries by evaluation method	
1. Weights			
Birth	2	2 PG	
Weaning	1	1 PG	
Yearly	2	1 PG	1 PF
Final	1		1 PF
Carcass	1	1 PG	
Other	2	2 PG	
2. Growth traits			
Daily gain	10	6 PG	7 PF
Net daily gain	7	5 PG	2 PF
3. Carcass characteristics			
Quality/Index/Value	5	5 PG	1 PF
Lean meat %	2	2 PG	
Dressing %	4	3 PG	1 PF
4. Conformation			
EU score	3	2 PG	1 PF
Other scoring	6	3 PG	4 PF
5. Feed conversion	3		3 PF