

Guernsey International Genetic Evaluation Using Performance Records: Preliminary Report

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Introduction

Current methods for routine international evaluations are based on pre-processed information like national evaluation results. This limits the amount of information available for comparisons; for instance, no cow information can be utilized. It also enforces the comparison to be made on genetic evaluation unit bases. Neighboring countries with similar production environments cannot be treated as genetically identical traits, and environmental variation within country cannot be utilized.

Access to individual performance records allows for international evaluations that can bypass the shortcomings of pre-processed input. Projects have been initiated to study the use of lactation records for international evaluations in the Holstein breed, focusing on optimal ways to model environmental variation (Rekaya *et al.*, 1999^b; Weigel & Rekaya, 2000). Recently also a project was started to investigate the feasibility of international evaluations based on performance records for the Guernsey breed. This paper reports on that project, and discusses the available data, genetic ties between countries and preliminary results for genetic parameters.

Material and Methods

Data

Test day data on milk yield for the first three lactations for cows with a first lactation between January 1990 and december 1999 was available

from four countries: Australia (AUS), Canada (CAN), United States (USA) and South Africa (ZAF). Table 1 presents the number of cows, test day records and herds in each data set prior to edits.

Table 1. Descriptive statistics of data before edits

	# cows	# test day records	# herds
AUS	10,343	147, 197	606
CAN	7,097	97,641	154
USA	87,608	922,931	1,863
ZAF	3,030	32,216	56

After data edits, incomplete lactation records were extended to 305 day lactation length, and analyses were based on 305 day lactation yields. Data was only included in the extension procedure for lactations with a first and second test day by 90 and 180 days in milk, respectively. Age at calving was required to be between 20 and 42 months for first lactation records. For later lactations, length of preceding calving interval was bound between 9 and 18 months. Lactation yields were only included in subsequent analyses for cows sired by bulls with daughters in at least 10 herds. This was done to assure that pedigree information was available for bulls. Pedigree records for bulls were taken from the February 2000 routine international evaluation for the Guernsey breed.

Genetic ties

Number of common bulls for each country pair and percentage genes by population of origin were used as a crude ways to assess genetic ties between countries. Two other techniques were employed to measure genetic connectedness. Genetic similarity for countries pairs was computed, defined as number of daughters sired by common bulls divided by the total number of daughters in both countries (Rekaya *et al.*, 1999^a). In addition, average genetic relationships within and between countries (Kennedy and Trus, 1993) were estimated. Average relationships were estimated from a sample of 1,000 cows from each country. For the estimation of within country relationships herds were restricted to be present in only one sample.

Extension of lactations

Incomplete lactations were extended to 305 days for all countries. Inspection of the data revealed that in all countries at least 50% of the lactations had the last test day after 290 days in milk. For incomplete lactations, yield on missing test days was predicted based on a standard lactation curve, regressions on the difference between predicted and actual lactation yield, and yield at last known test day. Wood's lactation function (Wood, 1967) was used to model the lactation curve:

$$y(t) = a \cdot b^t \cdot \exp(-c \cdot t)$$

Coefficients for standard lactation curve and regressions were based on complete lactations, and were estimated within age at calving × season of calving × average herd production subclasses.

Variance component estimation

Variance components were estimated for a sire model in which multiple lactations were treated as repeated records. Fixed effects in the model were herd-year of calving, year-season of calving, age at calving, breedcode class, lactation length, and random sire effect. For the herd-year effect levels were grouped together if the number of observations was less than five. Four seasons of equal length were considered. Breed code class was considered to account for heterosis. For each animal the genetic constitution by breed was determined from two generations of pedigree, and each breed combination formed a different class.

Two different analyses were carried out. First, genetic effects in different countries were assumed to be uncorrelated, hence variance components were estimated within country. Second, genetic effects in the four countries treated as genetically correlated traits, and genetic correlations between countries were estimated. VCE 4.2 (Neumaier & Groeneveld, 1998) was used to estimate variance components.

Results and Discussion

Genetic ties

Table 2, 3, 4 and 5 show the number of common bulls, genetic constitution, genetic similarity and average genetic relationships, respectively.

Table 2. Number of common bulls

	CAN	USA	ZAF
AUS	47	54	14
CAN		110	27
USA			40

Table 3. Percentage genetic constitution

Cows in	Population of origin				
	AUS	CAN	USA	ZAF	OTH
AUS	19	10	29		39
CAN		39	52		8
USA		<1	87		12
ZAF		<1	22	59	17

Table 4. Genetic similarity

	CAN	USA	ZAF
AUS	.532	.209	.257
CAN		.474	.216
USA			.392

Table 5. Average genetic relationships within and between countries (off-diagonals $\times .01$)

	AUS	CAN	USA	ZAF
AUS	1.26	1.50	1.14	0.80
CAN		1.97	2.00	1.20
USA			2.30	1.34
ZAF				1.68

Number of common bulls between ZAF and the other countries was small, due to the size of the ZAF data set. Genetic similarity and average genetic relationships were also lower for ZAF, nevertheless on a level indicating that imported bulls had a relatively large influence in the South African Guernsey population. Strong genetic links existed between USA and Canada. USA appeared to be the primary source for import among the countries included in this study. Percentage genes for which the origin is unknown was relatively high for Australia (37%). Overall, average genetic relationships between countries were higher than for the Holstein breed, and suggest sufficient links exist for international evaluations.

Table 6 summarizes lactation yield per lactation in the four countries.

Table 6. Number of lactation records by country and parity, and their mean and standard deviation

	Lactation								
	1			2			3		
	#	μ	σ	#	μ	σ	#	μ	σ
AUS	8432	2996	1527	4618	3435	1722	2418	3645	1744
CAN	6417	4577	1276	3731	5064	1400	1812	5191	1485
USA	51493	5295	1235	28804	5912	1389	13417	6127	1463
ZAF	2279	3550	1246	1185	3982	1469	560	4084	1491

The lowest average milk production is realized in the countries practicing grazing systems. Standard deviation is highest for Australia, and is for the other countries very similar to each other. As expected, both mean and standard deviation increased for later lactations.

Results from both variance component estimations are in Tables 7 and 8, and the resulting variance ratios in Table 9 and 10. Standard errors for the heritabilities were smaller than .05, and ranged from .01 to .10 for the genetic correlations.

Despite the large standard deviation of lactation yields in Table 6, Australia had the lowest phenotypic variance. Residual and phenotypic variance were consistent for both analyses. However, genetic and permanent environmental variances appear to be redistributed, the genetic variance being higher in case genetic effects were assumed to be correlated. The same pattern was found for heritabilities and c^2 . Heritabilities are lower than the ones used in the national evaluations, however, those might have been inferred from other breeds because of the size of Guernsey data sets. The residual variance for Canada is high, resulting in lower than expected heritability. This possibly indicates that one or more systematic effects are ignored in the model. Ignoring the third level interaction between herd, year and season could be one of those, and this will be further investigated.

Table 7. Estimated phenotypic, genetic, permanent environmental and residual variance ($\times 1,000$) for sire model with lactations as repeated observations and uncorrelated genetic effects

	AUS	CAN	USA	ZAF
σ_p^2	686.6	1,094.5	1,111.6	812.7
σ_e^2	491.9	809.5	690.2	589.4
σ_{PE}^2	78.3	175.7	210.1	89.3
σ_a^2	116.5	109.3	211.3	134.0

Table 8. Estimated phenotypic, genetic, permanent environmental and residual variance ($\times 1,000$) for sire model with lactations as repeated observations and correlated genetic effects

	AUS	CAN	USA	ZAF
σ_p^2	690.2	1,104.9	1,112.3	821.9
σ_e^2	491.6	810.1	690.2	586.5
σ_{PE}^2	66.8	140.3	208.2	47.9
$\sigma_{a_{ij}}$	131.9	141.0	155.9	156.0
		154.5	165.1	154.2
			214.0	157.2
				181.5

Table 9. Variance ratios for genetic and permanent environmental effects for sire model with lactations as repeated observations and uncorrelated genetic effects

	AUS	CAN	USA	ZAF
c^2	0.11	0.16	0.19	0.11
h^2	0.17	0.10	0.19	0.16

Table 10. Variance ratio for genetic and permanent environmental effects for sire model with lactations as repeated observations and correlated genetic effects

	AUS	CAN	USA	ZAF
c^2	.10	.13	.19	.06
h^2/r_g	.19	.89	.84	.99
		.14	.99	.81
			.19	.74
				.23

The relatively high residual variances and low heritabilities suggest that improvements in the model might be possible, and this will be the next step in this project. Data from the United Kingdom and Island of Guernsey has been received, and will be included in further analyses. These analyses will involve studies to utilize variation in production systems, using

herd clustering and structural models for genetic covariances, expanding the current procedures with a dimension for time to accommodate data on multiple lactations.

References

- Neumaier, A. & E. Groeneveld. 1998. Restircited maximum likelihood estimation of covariances in sparse linear models. *Genet. Sel. Evol.*, 30, 3-26.
- Rekaya, R., Weigel, K.A. & Gianola, G. 1999^a. Bayesian estimation of a structural model for genetic covariances for milk yield in five regions of the USA. *50th Meeting of the EAAP, Zurich, Switzerland, 22-26 August 1999.*
- Rekaya, R., Weigel, K.A. & Gianola, G. 1999^b. Estimation of parameters of structural model for genetic covariances in international genetic evaluations. *Interbull Bulletin* 22, 25 - 30.
- Schaeffer, L.R. 1994. Multiple-country comparison of dairy sires. *J. Dairy Sci.*, 77, 2671-2678.
- Weigel, K.A. & Rekaya, R. 2000. A multiple-trait herd cluster model for international dairy sire evaluation. *J. Dairy Sci.*, 83, 815-821.
- Wood, P.D.P. 1978. Algebraic model of the lactation curve in cattle. *Nature*, 216, 164.