

Inbreeding Depression for Global and Partial Economic Indexes, Production, Type and Functional Traits in the Walloon Region of Belgium

C. Croquet,^{*,†} P. Mayeres,[†] A. Gillon,[†] S. Vanderick,[†] N. Gengler,^{*,†}

^{*}National Fund for Scientific Research, B-1000 Brussels, Belgium

[†]Animal Science Unit, Gembloux Agricultural University, B-5030 Gembloux, Belgium

Introduction

With the use of modern genetic selection programs and the development of new reproductive technologies, the best animals accumulate in pedigrees. Today, it is practically impossible in a given dairy breed to find animals without any relationships this leads to increasing inbreeding in the majority of the dairy cattle populations.

One of the main economic consequences of inbreeding is inbreeding depression, the reduction of the mean phenotypic value for economically important quantitative traits.

The objective of this research was to estimate the effect of inbreeding on production, type and SCS traits. This was done by the inclusion of a linear regression into the current models used in the calculation of breeding values for Walloon dairy cattle. These individual estimations were then combined into to estimate the effect of inbreeding on the current partial and global economic indexes.

Materials and Methods

Data

Data consisted of test-day records for milk production traits, type traits and SCS for the Holstein breed and for the February 2004 Walloon official evaluation. For production and SCS computations are multibreed, regression of inbreeding were however breed specific. Only results for Holsteins are reported here.

Table 1. Statistics on the Holstein data used for Walloon official evaluation for Holsteins in February 2004.

Traits	Type of data	Number
Production	Test-day records	7,842,796
	Cows	916,347
SCS	Test-day records	6,885,443
	Cows	825,167
Type	Classifications	75,373
	Cows	69,246

Table 1 reports statistics on the Holstein data used for this study.

Total pedigree file used contained information for 956,516 animals, a large part of the recently born animals are Holsteins. In 2000 the proportion of Holstein was 83.7%.

Estimation of inbreeding coefficient

An inbreeding coefficient for each animal in the Walloon pedigree file was computed using a simplified version of the method of Auvray *et al.* (2001) integrated into the Meuwissen and Luo (1992) algorithm.

The method of Auvray *et al.* (2001) allowed to estimate inbreeding of the individual with one or two missing parents. This method considered that inbreeding of animals with unknown parents was equal to half of the average relationship between genetic groups of his phantom parents.

The genetic groups are based on variables able to explain the gene composition (sex, year of birth, breed and country of origin) and groups animals that are expected to have similar inbreeding.

Models

Models used in this study were the same models used in the Walloon evaluations for production, type and for SCS.

Genetic model for production traits. A multilactation, multitrait random regression test-day model (**RRTDM**) is used in the Walloon Region of Belgium. The model used currently can be written as :

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Q}(\mathbf{Wh} + \mathbf{Za} + \mathbf{Zp}) + \mathbf{e}$$

where, \mathbf{y} is a vector of precorrected milk, fat and protein test-day records, \mathbf{b} is a vector of fixed effects (herd*test date, stage of lactation, stage of lactation*age at calving*season of calving, gestation stage), \mathbf{h} is a vector of herd*period of calving random regression coefficients, \mathbf{a} is a vector of additive genetic random regression coefficients, \mathbf{p} is a vector of permanent environmental random regression coefficients, \mathbf{e} is a vector of random residuals, \mathbf{X} , \mathbf{W} and \mathbf{Z} are incidence matrices, \mathbf{Q} is the covariate matrix for the second order Legendre polynomials. The precorrection is applied to account for environmental effects of age within lactation*stage*breed classes. This allowed correction for maturity differences within lactation according to breed composition. More details are in Auvray *et al.* (2002).

Genetic Model for SCS. The genetic evaluation model is a multilactation **RRTDM** similar to the one used for milk, fat and protein. There are only two major modifications, no common herd environment effect is defined as previous research showed that this effect is very small for SCS and the model is only multilactation, not multitrait. Also an iterative weighting of SCS records by a function expressing the probability of a mastitis event was introduced in the genetic evaluation model (Gengler *et al.*, 2003). This modification is significant because it allows the transition from a purely descriptive evaluation of somatic cells to an evaluation which allows a better expression of the relationship between mastitis incidence and given test-day.

The RRTDM for SCS is written as :

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Q}(\mathbf{Zp} + \mathbf{Za}) + \mathbf{e}$$

where, \mathbf{y} is the vector of daily SCS, \mathbf{b} is a vector of fixed effects (the same as for the production model), \mathbf{p} is a vector of permanent environmental random regression, \mathbf{a} is a vector of additive genetic random regression.

Genetic Model for Type Traits. The genetic evaluation model used for type traits is based on the one used for the genetic evaluation of non-Holstein breeds in the US (Gengler *et al.*, 1999; Gengler *et al.*, 2001a; Gengler *et al.*, 2001b). This genetic evaluation method consists of three interdependent iterative systems which solve regular mixed model equations on a canonical scale allowing the update of canonical traits to account for missing original traits. Integrated into this system is the adjustment for heterogeneous variance. The general model on a canonical scale can be written as :

$$\mathbf{y}_Q = \mathbf{Xh} + \mathbf{Ss} + \mathbf{Cc} + \mathbf{Zp} + \mathbf{Za} + \mathbf{e} = \mathbf{Mm}_Q + \mathbf{e}$$

where for a particular type trait, \mathbf{y}_Q is the vector of canonical type trait records adjusted for heterogeneity; \mathbf{h} is the vector of fixed effects of herd, date scored, and parity (first or later) group (contemporary group); \mathbf{s} is the vector of system specific fixed effects for age and lactation stage within parity group (first or later); \mathbf{c} is the vector of classifier specific fixed effects for age and lactation stage; \mathbf{p} is the vector of random effects of permanent environment; \mathbf{a} is the vector of random additive genetic effects of animals and genetic groups; \mathbf{X} , \mathbf{S} , \mathbf{C} and \mathbf{Z} are the common incidence matrices for all traits that associate \mathbf{h} , \mathbf{s} , \mathbf{c} , \mathbf{p} , and \mathbf{a} , respectively, with \mathbf{y} ; and \mathbf{e} is the vector of random residual effects. Computation of canonical type trait records adjusted for heterogeneity during iterations can be written as $\mathbf{y}_Q = \mathbf{\Gamma}^{-1}[\mathbf{Q}_1(\mathbf{y} - \bar{\mathbf{y}}) + \mathbf{Q}_2\mathbf{\Gamma M}\hat{\mathbf{m}}_Q]$ where $\mathbf{\Gamma}$ is the multiplicative scaling matrix, its inverse being the adjustment matrix, $\bar{\mathbf{y}}$ is a vectors containing the means of the traits, \mathbf{Q}_1 and \mathbf{Q}_2 are the transformation matrices defined as in Ducrocq and Besbes (1993) obtained from the transformation matrix \mathbf{Q} and $\hat{\mathbf{m}}_Q$ are the current solutions on a canonical scale. More details can be found in Gengler *et al.* (2001c).

Partial and Global Economic Indexes

In the Walloon region of Belgium a global economic index called **V€G** is currently used. It reflects expected lifetime economic profitability. This global economic index is subdivided into a partial economic index milk (**V€L**) for the milk production traits, a partial economic index type (**V€T**) for the morphology traits and a partial economic index functionality (**V€F**) for the functional traits index, where **V€G** is the sum of **V€L**, **V€T** and **V€F**. At the moment, the **V€L** contains milk, fat and protein yields, the **V€T** contains the 19 type traits evaluated by INTERBULL, and the **V€F** contains only SCS. The partial index **V€T** is itself subdivided into three second order indexes: partial economic index udder (**V€P**) for the udder traits, partial economic index body (**V€C**) for the development and frame traits, and partial economic index feet and legs (**V€M**) for the feet and legs traits. These indexes provide a simple tool for the Walloon breeders to choose parents despite the presence of over 30 different evaluated traits. They embody their economic selection goal of overall profitability over the productive life, as well as its components.

Estimation of inbreeding depression

Inbreeding depressions for production, type traits and SCS were estimated by adding a linear regression of phenotypic performances on inbreeding coefficient to the genetic evaluation models.

The combination of the effects of inbreeding on separate traits in the Walloon genetic evaluations and the use of adequate weights allowed the estimation of effects of inbreeding on different partial indexes and the global economic index expressed per 1% increase in inbreeding.

Results and Discussion

Effects of 1% increase in inbreeding on yield traits and SCS are shown in Table 2.

Table 2. Estimated inbreeding depression for yield traits (305 d in kg) and SCS per 1% increase in inbreeding during the first three parities of Holstein cows

Lactation	Milk	Fat	Protein	SCS
1	-18.81	-0.91	-0.65	+0.005
2	-20.57	-0.99	-0.75	+0.005
3	-19.67	-0.99	-0.68	+0.006
Average	-19.68	-0.96	-0.69	+0.005

The losses per lactation for milk yields caused by inbreeding estimated in this study were lower than values cited in North American literature (Smith *et al.*, 1998; Wiggans *et al.*, 1995; Miglior *et al.*, 1995). An explanation could be that the scale of inbreeding depression is not a constant value but is relative to the amount of production. In consequence, in less productive populations as the Walloon dairy cattle compared to North American dairy cattle, one would also expect less inbreeding depression.

The inbreeding depression on SCS was relatively low. However, on average, inbred animals tended to have higher SCS than non inbred animals, therefore, as SCS is a parameter related to mastitis events this may mean that inbred animals tended to be more sensitive to mastitis perhaps because of a weakening of immune system due to inbreeding (Miglior *et al.*, 1995).

Table 3 presents the inbreeding depression for Interbull type traits.

For type, inbreeding depression tended to be small for all evaluated traits. However, inbred cows seemed to be smaller and less heavy than non inbred cows. The type traits most affected by inbreeding were overall development, overall conformation score, overall feet and leg score, overall rear udder, stature and body depth. As for Misztal *et al.* (1997), the estimates were positive for several type traits; the largest being for udder depth. As for SCS, small levels of inbreeding depression for type traits could be associated with small dominance variance (Misztal *et al.*, 1997). Also less production could put less stress on udders that are then less deep.

Table 3. Estimated inbreeding depression for type traits on a standardized scale per 1% increase in inbreeding and for Holstein cows

Trait	Standardized units per 1% inbreeding	Effect of inbreeding
Stature	-0.025	Shorter
Chest width	-0.075	Narrower
Body depth	-0.048	Shallower
Rump angle	+0.001	Lower
Rump width	-0.034	Narrower
Foot angle	-0.048	Lower
Rear leg set	+0.014	Straighter
Rear leg rear v.	-0.062	More hocked-in
Udder depth	+0.031	Shallower
Udder support	-0.013	Weaker
Fore udder	+0.005	Stronger
Front teat plac.	+0.016	More inside
Teat length	-0.013	Shorter
Rear udder hgt	-0.003	Lower
Rear teat plac.	+0.001	More outside
Angularity	+0.002	More angular
Ov. feet & leg	-0.049	(-)
Ov. udder	-0.015	(-)
Ov. Conform.	-0.038	(-)

Most interesting in our study was the effect of inbreeding on indexes. Table 4 presents effects of inbreeding on the V€G and the different partial indexes used in the Walloon region. As all indexes are expressed in monetary units (euros) this gives a raw indication of the financial impact.

Table 4. Effects of 1% increase in inbreeding on different partial index (first and second order) and global economic index

Index	Partial	Second order partial	€ per 1% inbr.
V€G			-6.13
	V€L		-4.77
	V€T		-1.23
		V€P	+0.54
		V€C	-0.63
		V€M	-1.14
	V€F		-0.13

The influence of inbreeding on V€L was - 4.77 € the largest of all the indexes. This was expected as V€L represent 55% of the V€G.

The inbreeding depression for V€F was rather low as expected given the limited influence of inbreeding on SCS. The inbreeding depression for V€T was negative despite a positive value for V€P. In total, the loss resulting in 1% increase in inbreeding on the V€G summed to -6.13 €.

Obviously, this result is an underestimation of the real economic impact because traits such as fertility, longevity and health that are expected to show high inbreeding depression are not yet accounted for in the V€G.

However, this result means also that given the current selection indices if we choose between two bulls for a mate every percent difference in inbreeding in their offspring has to be compensate by 12.26 V€G points, e.g. if one bull creates 6% inbreeding compared to other 1%, the difference the first one has to compensate is over 61 V€G points. This example shows the important ranking differences that may occur when breeding values are adjusted for inbreeding. However it might already be very difficult to find outcross bulls that have only a relationship of 2 to an average. Holstein cow. Also a potential outcross bull can only be locally outcross. Currently the lowest relationship in the USA is for HIGHLAND-H STORMIN NORMAN HOLUSAM000122217650 with 3.6%. He is however a STORM x ASTRE dam x ASTRO-JET grand dam representing Canadian ancestors, which means that is R-value (relationship to the population) in Canada is very high with 12 with means that expected inbreeding of future progeny is 6%.

Acknowledgments

Coraline Croquet who is Research Fellow and Nicolas Gengler, who is Research Associate of the National Fund for Scientific Research (Brussels, Belgium), acknowledge their support. Additional support was provided through Grant 2.4507.02 F (2) of the National Fund for Scientific Research. The authors gratefully acknowledged the support of the Walloon Breeding Association (AWE) and the Walloon Regional Ministry of Agriculture (MRW-DGA, especially projects : RW1009, D31-1039).

References

- Auvray, B., Wiggans, G.R., Miglior, F. & Gengler, N. 2001. Method to establish average relationships among Holstein bull populations over time. *J. Dairy Sci.* 84 (Suppl.1), 215(abstr. 891).
- Auvray, B. & Gengler, N. 2002. Feasibility of a Walloon test-day model and study of its

- potential as tool for selection and management. *Interbull Bulletin* 29, 123-127.
- Ducrocq, V. & Besbes, B. 1993. Solution of multiple trait animal models with missing data on some traits. *J. Anim. Breed. Genet.* 10, 81-92.
- Gengler, N., Wiggans, G.R. & Wright, J.R. 1999. Animal model genetic evaluation of type traits for five dairy cattle breeds. *J. Dairy Sci.* 82, 1250.
- Gengler, N., Dusseldorf, T., Wiggans, G.R., Wright, J.R. & Druet, T. 2001a. Heterogeneity of (co)variance components for Jersey type traits. *J. Dairy Sci.* 84, 1772.
- Gengler, N., Wiggans, G.R., Wright, J.R. & Druet, T. 2001b. Simultaneous accounting for heterogeneity of (co)variance components in genetic evaluation of type traits. *J. Dairy Sci.* 84 (Suppl.1), 247 (abstr.1022)
- Gengler, N., Dusseldorf, T., Wiggans, G.R., Wright, J.R. & Druet, T. 2001c. Multitrait genetic evaluation of Jersey type with integrated accounting for heterogeneous (co)variance. *Interbull Bulletin* 25,123-127.
- Gengler, N. & Mayeres, P. 2003. Use of a weighted random regression Test-Day model to better relate observed somatic cell score to mastitis infection likelihood. *Interbull Bulletin* 31, 92-96.
- Miglior, F., Burnside, E.B. & Dekkers, J.C.M. 1995. Non-additive genetic effects and inbreeding depression for somatic cell counts in Holstein cattle. *J. Dairy Sci.* 78, 1168-1173.
- Misztal, I., Lawlor, T.J. & Gengler, N. 1997. Relationships among estimates of inbreeding depression, dominance and additive variance for linear traits in Holsteins. *Genet. Sel. Evol.* 29, 319-326.
- Smith, L.A., Cassell, B.G. & Pearson, R.E. 1998. The effects of inbreeding on the lifetime performance of dairy cattle. *J. Dairy Sci.* 81, 2729-2737.
- Wiggans, G.R., VanRaden, P.M. & Zurbier, J. 1995. Calculation and use of inbreeding coefficients for genetic evaluation of United States dairy cattle. *J. Dairy Sci.* 78, 1584-1590.