

Genetic Correlated Traits for Female Fertility Evaluations in Spanish Holsteins

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1. Introduction

Genetic evaluation for female fertility in Holsteins is officially calculated in Spain since January 2005. It is based on days open data, calculated from calving interval and available for all milk recorded herds. A single trait repeatability animal model is used. Low heritability (4,5%) and late availability of data, because of the need to know subsequent calving, limit the reliability of young bulls or even they do not get proof at all.

Other traits correlated with female fertility are available and may help to improve the accuracy of genetic merit prediction. This is the case of production traits, that can help also in taking into account the effect of heavy selection on these traits (de Jong, 2005; Biffani *et al.*, 2005). Ratio of milk fat to protein may be an interesting option, as it has been indicated to be negatively correlated with energy balance at least at a phenotypic level (Grieve *et al.*, 1986) and it is available for all milk recorded cows. Angularity and body condition score (BCS) have been reported to be indicators of negative energy balance, but maybe other type traits can contribute to increase accuracy. Subclinical and clinical mastitis have been reported to reduce reproductive performance of lactating cows (Schrick, 2001) and this two kinds of mastitis are present at a high rate during the first 90 days of lactation (Schrick, 2001). So, somatic cell count (SCC) may be also an indirect measure to consider. Milk urea nitrogen (MUN) measured with wet chemistry (WC) has been reported to be genetically correlated with days open (Mitchell *et al.*, 2005). Infrared technology data (IR) has been used for estimating genetic parameter jointly with milk production traits but no genetic correlations were reported with female fertility traits (Wood *et al.*, 2003). In Spain IR urea is available only at one region, but it may be also interesting to analyze it's genetic correlation

with female fertility traits in the view of a possible recommendation to spread it's analysis at a national basis.

Right now, insemination data is being gathered at the national database for start analyzing them with the goal of being incorporated into female fertility evaluations, although in many regions it has not been collected in a routine basis and data quality may be very heterogeneous. Inseminations are compulsory to be recorded in milk recorded herds since April 2005.

The objective of this paper is to estimate genetic correlations between days open and several traits, as production, type, BCS, SCC and urea for it's possible incorporation into a multiple trait genetic evaluation for female fertility.

2. Materials and methods

2.1. Data

A random sample of herds was chosen based on last digit of herd code, from first calvings belonging to years 2001-2003 and with data available for production, type traits, somatic cell count and body condition score. BCS data collection by classifiers started officially in 2002 and data was included since march 2002. Only animal with known sire and dam were included in the analysis, as for routine evaluations. A previous requirement was imposed for herds to had been on on-going milk recording since 1987, as their pedigrees are more complete and there is a better trace back for estimating genetic (co)variances of the unselected population (Pena *et al.*, 2000). The final data set had near 20.000 cows with data.

For calculation of days open only calving intervals between 300 and 600 days were used.

Data with less than 50 days was set to 50 days to reduce the impact of recording errors and those greater than 250 days were set to 250 (VanRaden *et al.*, 2004).

Production traits related to first 100 days of lactation were used instead of 305 days, because this measure is more related with energy balance than the latter and because pregnancy affects mainly the last part of the lactation. Also it avoids bias due to length of lactation when analyzing 305 day data (Pena *et al.*, 2005). Fleischman method was used with an adjustment for days in milking at first available test. Kg milk and ratio percentage fat over percentage protein was calculated for first 100 days in lactation.

Previous to analysis, test day somatic cell count were transformed into somatic cell linear scores (Schutz, 1994) and adjusted for days in milk and month of the test, with adjustment factors calculated in a preliminary analysis. An average of linear scores belonging to first 100 days of lactation was then calculated (SCS100). Weights were assigned based on number of test, for considering the reduction in variance as number of test increases. Reference variance was considered as the one that correspond to the average number of tests in the first 100 days, 2,85.

Urea data was available only for one region (Asturias) and was obtained with a Fosomatic 4000 by Infrared technology. Data was available as mgr urea/Kg and was transformed to mgr nitrogen/dL dividing by 2.14. Values were required to be at least 0,5 and not greater than 40. Average values were calculated for first 100 days in milk (MUN100) and weights were assigned as for SCS100.

2.2. Parameter estimation

A series of bivariate animal model analysis were run, using software AIREMLF90 (Tsuruta and Misztal, 1999). Fixed effects considered in the model for type traits were age at calving, lactation stage (11 classes) and herd-date-classifier. For rest of the traits age at calving (except for days open), calendar month at calving and herd-year. In all traits only

animal and residual were considered as random.

3. Results

Estimated heritabilities for new traits are shown in table 1. Heritability for days open was in all analysis between 4 and 5%. Heritability for kg milk in first 100 days is much lower than 305 days figures (0,36) what can be explained because of lower heritability of milk production during the first part of the lactation.

Table 1. Heritabilities for new traits.

Trait	heritability
Kg milk 100 days	0,20
Fat/protein ratio 100 days	0,19
SCS 100 days	0,09
MUN 100 days	0,19
Body Condition Score	0,21
Loin Strength	0,24

Genetic correlations between days open and measures for first 100 days in milk were 0,47 with kg milk, 0,31 with fat/protein ratio and 0,38 with urea. Genetic correlations between urea and fat/protein ratio was only 0,27. Urea was less correlated with milk (0,12) than fat/protein ratio (-0,23).

Genetic correlations between days open and body traits was relatively high (0,25-0,43), but partly due to correlations between body traits and milk production. But for Loin Strength (not a standard linear trait recommended by WHFF) the genetic correlation was 0,43 and genetic correlation with milk production in first 100 days was 0,27, indicating it may contribute some extra information to female fertility. Angularity is very correlated with days open (0,58) but also with production (0,48). Body Condition Score is less correlated with days open (-0,28) but similarly correlated with production than angularity. Correlation between angularity and BCS was -0,54. Genetic correlation between days open and rump angle was nearly zero. A relatively high correlation was found between days open and foot angle (0,42). Genetic correlations between days open and SCS100 and udder depth were lower than 0,20 in absolute value.

4. Conclusions

Although some traits seems to be of interest to incorporate into a multiple trait model with days open, whole set of correlations between all considered traits should be estimated before final conclusions can be drawn. Some apparently interesting correlations may be explained by correlations through other traits. Also some more samples may be used for the estimations. Calculations or modelling of production traits in first 100 days and some details on the effects fitted to other traits should also be improved.

Finally, insemination data will be soon incorporated into the analysis.

5. References

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