

# Developing a Genetic Evaluation for Fertility Using Angularity and Milk Yield as Correlated Traits

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## Introduction

Several countries around the world have already implemented a genetic evaluation for female fertility (Interbull, 2005). This is a response to the increasing concern amongst farmers, who are suffering severe reduction in income due to reproductive failure of their cows. Positive experiences from the Nordic countries (Andersen-Ranberg *et al.*, 2005) demonstrate that genetic improvement of fertility can be attained. However, female fertility is quite a complex trait, not only because it is influenced by and related to several factors (physiological, nutritional or genetic) but even because, as outlined by VanRaden and colleagues (2004), trait definition differs across countries. Genetic evaluation for fertility eventually depends on what is recorded at national level. If the ultimate objective is to obtain an accurate estimation of an animal breeding value, a multiple trait approach, which consider direct fertility traits as well as correlated traits, seems to be the best option. Literature evidence do exist, showing that the use of correlated traits such as body condition score, milk yield or type traits can be beneficial because they can help overcome management biases that may be present in the fertility data (Wall *et al.*, 2004; Biffani *et al.*, 2004) as well as increase the accuracy of genetic evaluation (Kadarmideen *et al.*, 2003; Biffani *et al.*, 2004).

The purpose of this paper is to present the methodology and the traits used in Italy for the development of a national genetic evaluation for cow fertility.

## Material and Methods

### Data

Data on Holstein reproductive traits of first calving cows, born in year 1990 to 2002, were extracted from the national database stored at the Italian Holstein Breeders Association (ANAFI)

and matched to pedigree, lactation and linear evaluations to be able to calculate the traits of interest. The traits selected for the genetic evaluation were as follows: days from calving to first insemination (**DTFS**), calving interval (**CI**), first-service non return rate to 56 d (**NR56**), angularity (**ANG**) and mature equivalent milk yield at 305 d (**ME305**). A detailed description of the rules used to validate fertility traits that relied on insemination information (**DTFS**, **CI**, **NR56**) is given in Biffani *et al.* (2003). After editing, the data set consisted of approximately 2,800,000 records plus 3,200,000 animals in the pedigree file. Descriptive statistics for each trait are illustrated in table 1.

Previous analyses have shown that **ANG** is genetically related to body condition score and that their correlation with fertility traits are moderate to high and not statistically different from each other (Biffani *et al.*, 2004, Dechow, 2003). Furthermore, body condition score is not available at national level whilst linear evaluation

**Table 1:** Summary statistics of the data included in the national genetic evaluation

| TRAIT        | cows    | min  | max   | mean  | std  |
|--------------|---------|------|-------|-------|------|
| <b>ANG</b>   | 2088408 | 1    | 50    | 27    | 5,4  |
| <b>CI</b>    | 1615591 | 267  | 1594  | 418   | 86,7 |
| <b>DTFS</b>  | 2088408 | 21   | 250   | 88    | 40,4 |
| <b>NR56</b>  | 2030672 | 1    | 2     | 64,9% | 48%  |
| <b>ME305</b> | 2088408 | 2505 | 21856 | 9955  | 2022 |

of all primiparous cows began in 1985.

### Variance components estimation

Genetic parameters were estimated using the restricted maximum likelihood (REML) program REMLF90 written by Misztal (1998). A multivariate animal model with all traits fitted simultaneously was used to estimate (co)variances between traits. Specific single traits model for particular traits are given in table 2. The model for **ANG** is the one currently used in the official evaluation of type traits in Italy. All fertility traits included the fixed effect of herd-year-season of calving and the effect of age (in month) by year of calving. This interaction was included in the

model to take into account the decreasing trend in age at first calving observed over the last years in Italy. The inclusion of this interaction improved the fit of the model. Month of calving was included in the model for **CI** and **DTFS**, while month of insemination was used for **NR56**. Due to computing limitations, estimation of variance components using all data was unfeasible and eight samples were chosen among farms with at least 200 records.

**Table 2:** Fixed effect for multiple-trait variance component estimation and genetic evaluation of ANG, CI, DTFS, NR56 and ME305

| Effect                               | Trait |           |             |            |            |
|--------------------------------------|-------|-----------|-------------|------------|------------|
|                                      | ANG   | Ci (days) | DTFS (days) | NR56 (0/1) | ME305 (kg) |
| Herd-year-round of classification    | X     |           |             |            |            |
| Age at calving by stage of lactation | X     |           |             |            |            |
| herd-year-season of calving          |       | X         | X           | X          | X          |
| month of calving                     |       | X         | X           |            |            |
| month of insemination                |       |           |             | X          |            |
| age at calving by year of calving    |       | X         | X           | X          |            |

### Breeding value estimation

Data from the complete dataset (Table 1) were used to estimate multitrait BLUP EBV. The model was the same used for variance component estimation. Genetic groups were fitted for all unknown parents. Assignment to genetic groups was based upon sex, year of birth, and country of origin according to the same rules used in the official evaluation for yield and type. An *ad-hoc* program, based on the BLUPF90iod by Mizstal and colleagues (Tsuruta, 2001), was written in C++ (G. Jansen, personal communication) and used to get solutions for fixed and random effects. Each EBV was adjusted by subtracting a base value equal to the average EBV of cows born in 2000 that had a record for **CI**. Average EBVs of cows born in 2000 and their relative standard deviation are given in table 3. This genetic base approach is analogous to that used for yield and type proofs in Italy. A 3-trait model, including only fertility traits, was also implemented in order to verify the effect of using **ANG** and **ME305** as correlated traits.

**Table 3.** Average EBVs and their relative SD of cows born in 2000

| Trait | mean   | STD   |
|-------|--------|-------|
| ANG   | 2,4    | 1,3   |
| CI    | 14,8   | 10,4  |
| DTFS  | 4,5    | 4,4   |
| NR56  | -0,012 | 0,027 |
| MILK  | 962    | 449   |

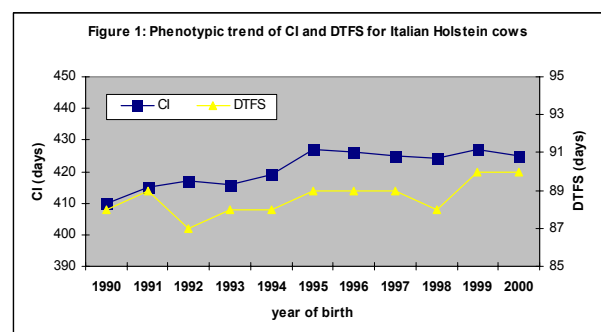
## Results and Discussion

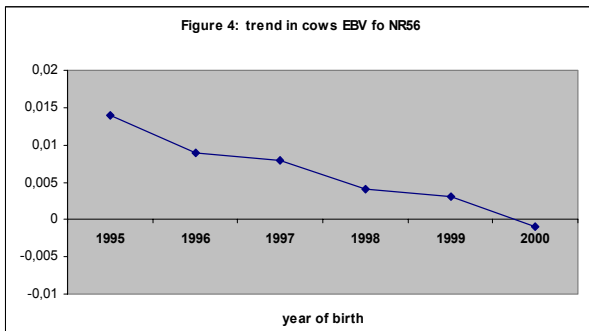
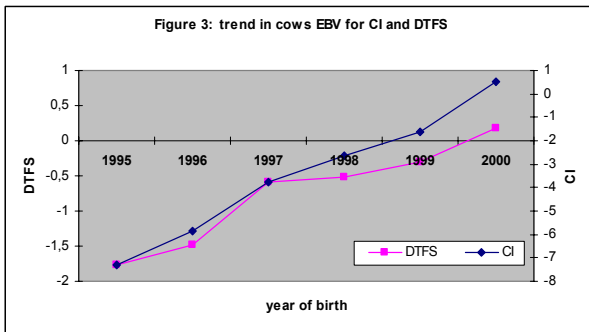
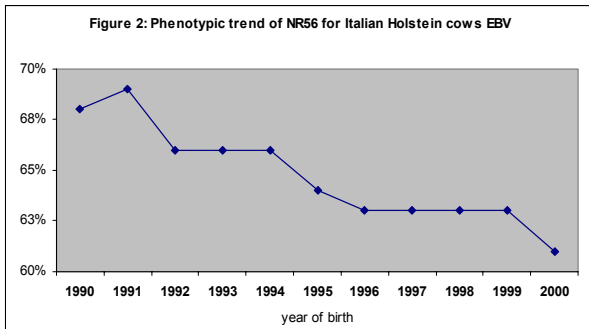
Table 4 provides genetic and residual correlations, SD and heritabilities for traits included in the analyses. The results obtained in this study followed, in general, results of other works (Wall *et al.*, 2004; Dechow, 2003) and confirm previous findings from the same authors (Biffani *et al.*, 2004). The relationship among fertility traits, namely **CI** and **DTFS**, with **ANG** is unfavourable, confirming the hypothesis that **ANG** can efficiently substitute BCS, when this information is missing, as indicator of change in the cow energy balance. Collard *et al.* (2000) and Veerkamp *et al.* (2000) stressed the fact that an excessive mobilization of body reserves may have adverse effects on cow fertility and health. Genetic correlation between **ANG** and **NR56** is null (.03) while it is -.25 (unfavourable) between **ME305** and **NR56**. These results support the idea that, notwithstanding the high genetic correlation between **ME305** and **ANG**, both traits should be included in the analyses.

**Table 4.** Estimates of h<sup>2</sup>, genetic SD (diagonal), genetic correlations (below diagonal), and residual correlations (above diagonal) for ANG, CI, DTFS, NR56 and ME305.

| Trait | ANG  | CI    | DTFS  | NR56  | MILK  | H2   |
|-------|------|-------|-------|-------|-------|------|
| ANG   | 1,99 | 0,04  | 0,05  | 0,00  | 0,22  | 0,17 |
| CI    | 0,38 | 22,27 | 0,36  | -0,24 | 0,02  | 0,07 |
| DTFS  | 0,36 | 0,58  | 8,65  | 0,00  | -0,01 | 0,06 |
| NR56  | 0,03 | -0,15 | -0,08 | 0,09  | 0,01  | 0,03 |
| MILK  | 0,60 | 0,37  | 0,33  | -0,21 | 608   | 0,20 |

Figure 1 through figure 4 depict the phenotypic and genetic trends for the 3 fertility traits. Both phenotypic and genetic trends are unfavourable with an increase in the interval traits, namely **CI** and **DTFS**, and a decrease in **NR56**. The latter seems to be more dramatic and can possibly have heavier negative economic consequences on the farmer revenue.





The effect of using a multiple trait model with correlated traits can be observed in figure 5, which depicts the trends for NR56 EBV of bulls born from 1990 to 1998 estimated with a 3-trait and a 5-trait model. When not considering the correlated traits, bulls EBVs for CI, DTFS and NR56 are, on average, underestimated by 9.26%, 1.30% and 22% respectively. NR56, which has the lowest  $h^2$ , is by far the most affected trait. Correlations between bulls EBVs from reduced (3 traits, only fertility) and complete model (5 traits, fertility + correlated traits) are given in table 5 and are lower than one for the fertility traits, confirming previous findings by the same authors on a smaller dataset (Biffani *et al.*, 2004) and by Kadarmideen *et al.* (2003). As expected, multiple-trait analyses with 5 traits improved accuracy of estimated breeding values (EBVs) for each trait in the model by reducing their variances of prediction error (PEV). Considering only bulls with at least 15 daughters, accuracy was, on

average, 5.5%, 9.9% and 10.8% higher for the complete model (5 trait).

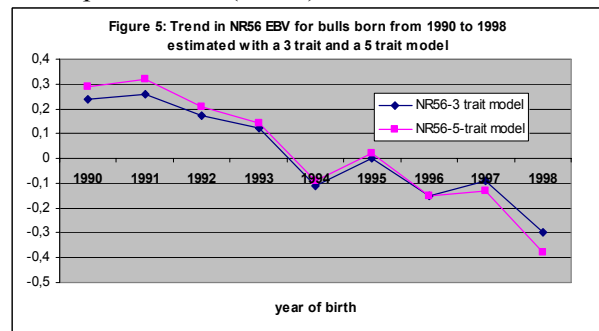


Table 5: Spearman correlation between bulls EBV from 3 and 5 trait model

| complete multiple trait | reduced multiple trait (only fertility) |      |      |
|-------------------------|---|------|------|
|                         | ci                                      | dtfs | nr56 |
| ci                      | 0,97                                    |      |      |
| dtfs                    |   | 0,98 |      |
| nr56                    |   |      | 0,95 |

## Conclusion and Future Developments

Due to the complexity of the trait, a multiple-trait approach should be considered when evaluating cow fertility.

Correlated traits, like angularity and milk yield, should be taken into account and used to supplement the predictions of genetic merit for fertility. In this way we can possibly approximate what happens for a highly multi-genic trait like reproduction.

Results from the genetic evaluation will be eventually combined in an aggregate index. The definition of the breeding objective is therefore crucial and selection index theory can be used to calculate the index weights to be applied to the selection criteria.

Some options are available as breeding objective: pregnancy rate (which measures the percentage of cows in a herd that become pregnant every 21-day period past the voluntary waiting period), non-return rate at 56 days or conception rate at first service. The principal feature of a breeding objective should be its simplicity. The farmer should eventually be able to understand what he is doing when using such an aggregate index.

Conception rate is probably the best solution. Pregnancy rate is inflated by management decision while non-return rate is not as clear as conception rate is.

Computation of index weights to be applied to **ANG, CI, DTFS, NR56** and **ME305** in order to maximize the response on the breeding objective is the next step of the development of the genetic evaluation for female fertility in Italy. Next June the technical committee of ANAFI will approve the overall plan that will lead to the first official publication of such an index.

## Reference

- Andersen-Ranberg, I.M. *et al.* 2005 Heritabilities, Genetic Correlations, and Genetic Change for Female Fertility and Protein Yield in Norwegian Dairy Cattle. *J. Dairy Sci.* 88,348–355.
- Biffani, S. *et al.* 2003. Data Quality assessment and preliminary investigations on fertility in the Italian Holstein Friesian. *Interbull Bulletin* 30, 89-95. Proceedings of The Interbull Technical Workshop BELTSVILLE, MD, USA March 2-3, 2003
- Biffani, S. *et al.* 2004. Genetic Evaluation of Fertility Using Direct and Correlated Traits in Italian Holstein. Pilot Study. *Proceedings of the 55<sup>th</sup> EAAP meeting*, 69.
- Dechow, C. 2003. Body condition score and dairy form as indicators of dairy cattle disease and reproductive performance, *Ph.D. thesis*. The University of Tennessee, Knoxville
- Collard, B.L. *et al.* 2000. Relationships between energy balance and health traits of dairy cattle in early lactation. *J. Dairy Sci.* 83, 2683–2690.
- Interbull. 2005. Description of national genetic evaluation systems for dairy cattle traits as practised in different Interbull member countries. [http://www-interbull.slu.se/national\\_ges\\_info2/framesida-ges.htm](http://www-interbull.slu.se/national_ges_info2/framesida-ges.htm). Accessed May 20, 2005.
- Kadarmideen, Haja N. *et al.* 2003. Genetic parameters and evaluations from single- and multipletrait analysis of dairy cow fertility and milk production. *Livest. Prod. Sci.* 81, 183–195.
- Misztal, I. 1998. *REMLF90 Manual*. Animal and Dairy Science, University of Georgia, Athens, Georgia
- Tsuruta, S. *et al.* 2001. Use of preconditioned conjugate gradient algorithm as a generic solver for mixed-model equations in animal breeding applications. *J. Anim. Sci.* 79, 1166-1172.
- VanRaden, P.M. *et al.* 2004. Development of a National Genetic Evaluation for Cow Fertility. *J. Dairy Sci.* 87, 2285–2292.
- Veerkamp, R.F. *et al.* 2000. Genetic correlation between days until start of luteal activity and milk yield, energy balance, and live weights. *J. Dairy Sci.* 83, 577–583.
- Wall, E. *et al.* 2003. Genetic Evaluation of Fertility Using Direct and Correlated Traits. *J. Dairy Sci.* 86, 4093–4102.