# ESTIMATES OF GENETIC PARAMETERS FOR FERTILITY TRAITS OF ITALIAN HOLSTEIN-FRIESIAN CATTLE

## S. Biffani, R Canavesi, A. B. Samore

**Summary**

Data from insemination and calving events of Italian Holstein cows and heifers collected from January 1996 until December 2002 were used to estimate phenotypic and genetic parameter for some fertility traits. A validation procedure of the data based on gestation length and information on service sire was used. According to these procedure, in Italy 75.9 % of the calvings are associated to service or inseminations events. Days to first service (DTPS), calving interval (CI), number of service per conception (NSC) and non return rate at 90 days (NRR90) were the main traits analysed. The effect of month and year of calving (or insemination), of sampling bull code, of age of cow and of herd-year-season of calving were included in the model and were significant for all the traits analysed. A decreasing efficiency in cow fertility was observed over the last 5 years, with a longer days to first service interval and a higher proportion of cows being re-bred after 90 days. Different data sets were successively defined according to the parities in order to validate the hypothesis that different parities have to be considered as different traits. Heritabilities for the five fertility traits were low ranging from 0,014 for NRR90 to 0,065 for CI. Estimates of c2 for score traits (NSC, NRR56 and NRR90) ranged from 0,010 to 0,025 and were lower than those for CI and DTPS. Genetic correlation were high between traits related to time period but were moderate between those traits and score traits. Heritabilities of interval traits (CI, DTPS) vary over parities, with some indication that higher parities show higher estimates. Results in terms of genetic correlations confirmed the high relationships with interval traits between parities.

*Introduction*

Over the last years selection for functional cows has become an important part of the breeding goals all over the world. Functionality refers to the ability

of the cow of producing milk in an efficient way, i.e. producing the same output of products reducing input costs. Among the traits which belong to the functional characters of an animal and which can inflate the production cost per cow, fertility plays an important role, being one of the main reason for the involuntary culling of a cow in Italy (Romeo, 1999). Previous studies have shown that fertility efficiency can be enhanced above all by means of a better management or applying particular hormonal protocol (Darwash et al., 2001) but that a part of the variation in fertility traits has genetic origin (Jansen, 1985). This means that selection can be practiced for such traits (Philipsson, 1981), even because, due to an increasing interest on animal welfare, hormonal treatment to correct fertility deficiencies will be less acceptable or possibly restricted in the future (Kardamideen et al., 2003).

As stressed by Kadarmideen and Coffey (2001), the improvement of fertility efficiency, whether managerial or genetic, relies both on the availability, accuracy and editing of field data (i.e, insemination date, calving date, etc) and on the appropriate statistical model used to estimate variance components and breeding values. In a recent paper, Biffani et al. (2003) proposed a validation procedure based on gestation length (GL) and information on service sire (SS). According to these procedure, in Italy 75.9 % of the calvings are associated to service or inseminations events, considering a GL within 240 and 300 days and with the sire equal to the SS. Using those data Biffani et al. (2003) verified an increasing (negative) phenotypic trend for days to first service (DTPS), calving interval (CI), number of service per conception (NSC) and non return rate at 56 or 90 days (NRR56, NRR90). Those results confirmed the Italian breeders concern about fertility problems and stressed the importance of including fertility in the present Italian breeding goal.

The heritability of reproductive traits is generally low and for this reason multiple-trait animal model within or across parity are advocated in order to maximise the amount of available information (Groen et al. 1997; Boichard et al., 1999; Kardamideen et al., 2003).

Bagnato and Oltenacu (1993, 1994) and Miglior et al. (1997) estimated both phenotypic and genetic parameters for fertility traits in Italian Holstein cows but their results have to be updated using the data edited with the new procedure. The objectives of this study are thus: 1) to re-estimate variance components and genetic parameters for days to first service, calving interval, number of service per conception and non return rate at 56 and 90 days using a multi-trait repeatibility animal model, 2) to estimate genetic parameters for days to first service and calving interval in different parities.

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*Material and methods*

Data available for this study included all insemination and calving events, both for artificial insemination (Al) and natural service (NS) of Italian Holstein cows heifers collected from January 1996 until December 2002. Insemination data set consisted of 13,600,000 records with the following information: animal ID, date of service, service sire (SS), herd, service code (Al, NS, DN = donor, RE = recipient) and sampling bull code (NP = national proven bull, FP = foreign proven bull, YP = sampling bull). The calving data set consisted of 5,100,000 records including: animal ID, date of calving, date of birth, sire and herd. A detailed description of the data editing and of the validation procedure can be found in Biffani et al. (2003). After editing the data set consisted of 3,200,000 records and included the following traits: days to first service (DTPS), interval between two successive calving dates (CI), number of services per conception (NSC) and non-return rate at 56 and 90 days (NRR56/NRR90).

*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. The model included the following fixed effects: the interaction of year by month of calving (insemination), the herd-year-season interaction and the age of the cow in classes (> 18 mo and < 260 mo). In addition, a permanent environmental effect was fitted as additional random effect to account for multiple records. Binary traits (NRR56 and NRR90) were coded as 1 for success and -1 otherwise.

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. Statistics from sampling are presented in table 1.

Table 1. - STATISTICS FROM THE 8 SAMPLED DATA SET

| Trait | Records | Cows | Mean | Se |
|---|---|---|---|---|
| CI (days) | 40103 | 23785 | 413,5 | 5,4 |
| DTFS (days) | 65110 | 35390 | 85,7 | 2.2 |
| NSC | 64932 | 35353 | 1,7 | 0,1 |
| NRRS6 (%) | 62738 | 34396 | 62,5 | 2,3 |
| NRR90 (%) | 62738 | 34396 | 49,6 | 2,4 |

Heritabilities and correlations were also estimated by treating DTPS and CI in different lactations as if they were different traits. Only females in parity 1, 2 and 3 were considered. Because of the large size of the population only 2 datasets were used, one for each trait, sampling among farms with at least 150 records. The model used was the same as that described previously but without permanent environmental effects. Characteristics of the two datasets are presented in the table 2.

Table 2. - CHARACTERISTICS OF THE DATA SETS IN PARITY 1, 2 AND 3

| Trait | Parity | cows | mean | Std |
|---|---|---|---|---|
| DTFS (days) | 1 | 7931 | 88.6 | 40.7 |
| | 2 | 2730 | 83.8 | 35.3 |
| | 3 | 1360 | 81.0 | 33.5 |
| CI (days) | 1 | 10857 | 412.0 | 82.0 |
| | 2 | 4390 | 412.5 | 76.3 |
| | 3 | 2106 | 409.1 | 71.2 |

*Results*

*Multiple trait repeatability animal model.* Heritabilities, permanent environmental effects, their relative standard errors and repeatibilities from multiple trait analysis are given in table 3. Heritabilities for the five fertility traits were low ranging from 0,014 for NRR90 to 0,065 for a. Estimates of $c^2$ for score traits (NSC, NRR56 and NRR90) ranged from 0,010 to 0,025 and were lower than those for CI and DTPS. Standard errors ranged from 0,001 to 0,004 for $h^2$ and from 0,002 to 0,010 for CI. Genetic and phenotypic correlations $(r_s$ and $r_p$, respectively), are given in table 4. Residual $(r_e)$ and environmental correlations $(r_{pe})$ are presented in table 5. CI was genetically well correlated with DTPS and NS *(> .60)*, moderately correlated with NRR56 (0,30) and, surprisingly, showed no correlations with NRR90 (0,057). Absolute $r_s$ between DTPS and score traits were low, ranging from 0,094 to 0,256; estimates of $r_s$ between NSC and binary traits were low and negative. Genetic correlation between NRR56 and NRR90 was high but not as much as could be expected. Absolute $r_p$ was higher than .50 between CI and NSC (.684) and between NRR56 and NRR90 (0,757). DTPS was phenotipically correlated only with CI (0.442). Residual correlations were positive and high between CI and

NSC (0,70) and between NRR56 and NRR90 (0.759). Estimates of $r_e$ between CI and DTPS was moderate and positive (0.39) while $r_e$ between the other traits was near to zero or negative. Estimates of $r_{pe}$ were generally higher than estimates of $r_p$ even if the correlations between the group of trait related to time period (CI, DTPS) and the two binary traits (NRR56 NRR90 ) were of different sign and magnitude. *Estimates of genetic parameters between lactations,* Heritability, genetic and phenotypic correlations for DTPS and CI between parities are presented in table 6 and 7. Heritability increased from parity 1 to parity 3, ranging from 0.059 to 0.099 for DTPS and from 0,082 to 0,013 for CI. Genetic correlations were positive and high, ranging between 0,846 and 0,896 (DTPS) and between 0,817 and 0,871 (CI). Estimates of phenotypic correlations were positive and moderate both for DTSF and CI. Standard errors of estimates, calculated with the method related by Roots et al. (1994a, 1994b), were higher than 0,03.

Table 3. - HERITABILITIES (h2), PERMANENT ENVIRONMENTAL EFFECTS (c2) AND REPEATABILITY ($r=h^2 + c^2$) FOR FERTILITY TRAILS

| Trait | $h^1$ | $c^2$ | r |
|---|---|---|---|
| CI | 0,065 (0,004) | 0,089  (0,010) | 0,154 |
| DTFS | 0,057 (0,003) | 0,044  (0,006) | 0,101 |
| NSC | 0,027  (0,001) | 0,010 (0,002) | 0,037 |
| NRRS6 | 0,016  (0,001) | 0,025 (0,003) | 0,041 |
| NRR90 | 0,014  (0,001) | 0,024   (0.003) | 0,038 |

Table 4. - GENETIC (ABOVE THE DIAGONAL) AND PHENOTYPIC CORRELATIONS (BELOW THE DIAGONAL) BETWEEN FERTILITY TRAITS. STANDARD ERRORS IN PARENTHESIS

| Trait | ci | dtfs | ns | nrr56 | nrr90 |
|---|---|---|---|---|---|
| CI |  | 0,679 (0,023) | 0,610 (0,020) | 0,300 (0,032) | 0,057 (0,037) |
| DTFS | 0,442 (0,016) |  | 0,122 (0,038) | 0,256 (0,016) | 0,094 (0,030) |
| NSC | 0,684 (0,010) | -0,078 (0,004) |  | -0,064 (0,047) | -0,164 (0,036) |
| NRR56 | -0,045 (0,008) | 0,007 (0,006) | -0,338 (0,007) |  | 0,584 (0,020) |
| NRR90 | -0,178 (0,010) | 0,009 (0,005) | -0,417 (0,008) | 0,757 (0,006) |  |

Table 5. - RESIDUAL (ABOVE THE DIAGONAL) AND PERMANENT ENVIRONMENTAL CORRELATIONS (BELOW THE DIAGONAL) BETWEEN FERTILITY TRAITS. STANDARD ERRORS IN PARENTHESIS

| Trait | ci | dtfs | ns | nrr56 | nrr90 |
|---|---|---|---|---|---|
| ci | | 0,392 | 0,704 | -0,067 | -0,189 |
| | | (0,017) | (0,009) | (0,008) | (0,010) |
| dlfs | 0,826 | | -0,099 | -0,011 | 0,008 |
| | (0,025) | | (0,005) | (0,007) | (0,004) |
| ns | 0,521 | 0,192 | | -0,341 | -0,418 |
| | (0,038) | (0,023) | | (0,006) | (0,008) |
| nrr56 | 0,149 | 0,194 | -0,419 | | 0,759 |
| | (0,074) | (0,040) | (0,083) | | (0,006) |
| nrr90 | -0,128 | -0,003 | -0,559 | 0,762 | |
| | (0,070) | (0,047) | (0,072) | (0,039) | |

Table 6. - HERITABILITY (CM), GENETIC (ABOVE) AND PHENOTYPIC (BELOW THE DIAGONAL) CORRELATIONS FOR DAYS TO FIRST SERVICE BETWEEN PARITIES. STANDARD ERRORS IN PARENTHESIS

| DTFS | Parity 1 | Parity 2 | Parity 3 |
|---|---|---|---|
| Parity 1 | 0.059 | 0,896 | 0,847 |
| | ( 0.048) | (0,081) | (0,010) |
| Parity 2 | 0,168 | 0.081 | 0,846 |
| | (-) | (0.034) | (0,072) |
| Parity 3 | 0,270 | 0,188 | 0.099 |
| | (-) | (-) | (0.031) |

Table 7. - HERITABILITY (ON), GENETIC (ABOVE) AND PHENOTYPIC (BELOW THE DIAGONAL) CORRELATIONS FOR CALVING INTERVAL BETWEEN PARITIES. STANDARD ERRORS IN PARENTHESIS

| CI | Parity 1 | Parity 2 | Parity 3 |
|---|---|---|---|
| Parity 1 | 0.082 | 0,871 | 0,815 |
| | (0.033) | (0,055) | (0,069) |
| Parity 2 | 0,137 | 0.105 | 0,817 |
| | (-) | (0.028) | (0,056) |
| Parity 3 | 0,106 | 0,162 | 0.136 |
| | (-) | (-) | (0.029) |

*Discussion and conclusions*

*Multiple trait repeatability animal model.* This study provides genetic parameter estimates which generally confirm the literature data: fertility traits present low heritability (< .8), although some differences do exist between traits related to time period (CI, DTPS) and score traits (NSC, NRR56, NRR90). Time period related traits estimates from present study are higher than those reported by Bagnato and Oltenacu (1993) Kadarmideen et al. (2000, 2003) and Pryce et al. (1997, 1998) and similar to those reported by Schnyder and Strieker (2002). Those result could be the consequence of the data validation procedure which produced a more reliable data set and confirm the hypothesis of Pryce et al. (1998) that higher estimates might be expected from more accurate data sets. Nevertheless genetic parameters for score traits remain low, probably because they were analyzed by means of a linear model. Kadarmideen et al. (2000) showed that threshold models allow higher estimates of heritability for binary traits and such a conclusion should be tested on the data used in the present study. Genetic correlation were high between traits related to time period but were moderate between those traits and score traits, with the exception of the correlation between CI and NSC which approached 0,61. Genetic correlations between NRR56 and NRR90 was high but did not approach unity as could be expected. Weigel and Rekaya (2000) reported a correlation of 0.97 between NRR56 and NRR90, supporting the hypothesis that these two traits are nearly equivalent. The low genetic correlation obtained in the present study suggests the hypothesis that NRR90 contained errors due to unreported (repeat) matings, but the editing procedure should have been able to delete them. Further analyses are needed to check these results.

*Estimates of genetic parameters between parities.* Heritabilities of interval traits (CI, DTPS) vary over parities, with some indication that higher parities show higher estimates. Those results confirm previous findings by Jansen et al. (1987), Weller (1989) and Pryce et al. (1998). Besides biological aspects, heritability estimates can be inflated by other non genetic effects, such as preferential treatment. As stressed by Kadarmideen (2003), a multiple-trait analysis with milk yield would be more appropriate in order to reduce the bias in fertility observations caused by the selection on production. Supposedly third parity cows are expected to be the animals with high milk yield and which receive preferential treatment. Our results in terms of genetic correlations confirmed the high relationships with interval traits between parities found by Jansen et al. (1987) and Bagnato and Oltenacu (1994), although not equal

to 1, Phenotypic correlations of the same trait between different parities were low and as expected approached the repeatability estimate obtained by the multiple trait repeatibility animal model.

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**PROCJENA GENETSKIH PARAMETARA ZA OSOBINE PLODNOSTI TALIJANSKOG HOLSTEIN-FRIZIJSKOG GOVEDA**

**Sažetak**

Podaci o teljenju i osjemenjivanju talijanskih Holstein krava i junica, sakupljeni od siječnja 1996. do prosinca 2002., korišteni su za procjenu fenotipskog i genetskog parametra nekih osobina plodnosti. Primijenjen je postupak neospornosti podataka na temelju dužine gestacije i informacije o servisnom biku. Prema tom postupku u Italiji 75,9% teljenja povezano je sa servisom ili osjemenjivanjem. Glavne analizirane osobine bile su dani do prvog servisa (DTFS), interval teljenja (CI), broj servisa po koncepciji (NSC) i stopa bez rezultata u 90 dana (NRR90). Djelovanje mjeseca i godine teljenja (ili inseminacije), uzimanje šifre bika, dobi krave i stado-godina-sezona teljenja bili su značajni za sve analizirane osobine. Smanjenje djelotvornosti u plodnosti krava zapaženo je u zadnjih 5 godina, s više dana do prvog intervala servisa i veći omjer ponovo pripuštenih krava nakon 90 dana. Postepeno su određene skupine različitih podataka prema analogiji radi vrednovanja hipoteze da razne paritete treba smatrati kao različite osobine. Nasljednosti za pet osobina plodnosti bile su male u rasponu od 0.014 za NRR90 do 0.065 za CI. Procjena c2 za osobine skora (NSC, NRR56 i NRR90) kretale su se od 0.010 do 0.025 i bile su niže od onih za CI i DTFS. Genetske korelacije bile su visoke između osobina u vezi s vremenskim razdobljem ali su bile umjerene između tih osobina i osobina skora. Nasljednosti osobina intervala (CI, DTFS) variraju nad paritetom s nekim naznakama da viši pariteti pokazuju više procjene. Rezultati u smislu genetskih korelacija potvrdili su visoku povezanost s osobinama intervala među paritetima.