GENETIC PARAMETERS ESTIMATION FOR MILKABILITY TRAITS RECORDED WITH FLOWMETERS IN ITALIAN BROWN SWISS

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SUMMARY

Data on milkability of dairy cows have been collected with two different methods in Brown Swiss cows in Italy: the first producing a data set consisting of 13,177 observations, one for each cows collected with a milking machine separating milk produced in each quarter, while 1,918 observations, two for each cow, were collected with flowmeters. REML estimates of genetic parameters for comparable milkability traits are consistent for the two data sets. All the estimates calculated on flowmeter data are affected by high standard errors due to small size of sample. If further analysis on a larger data set will confirm estimates found, flowmeters will be a new tool available for genetic improvement.

Keywords: Dairy cattle, milking speed, flowmeter.

INTRODUCTION

Milking speed is one of the most important functional trait in dairy cattle. Is well known that in practice cows slow to be milked are not desirable, and genetic selection against this characteristic would be appreciated by farmers. In operating a selection schemes for milking speed a basic moment is the phenotypic measurement. Milking speed can be measure as a threshold traits classifying cows in categories, or alternatively recording duration in time for each cow during routine test day. Different approaches are described in literature (Banos and Burnside 1992; Beard 1993; Canavesi and Santus 1996).

The flowmeter, an instrument widely applied in other fields, can represent a break through in milk recording system: it can easily record the amount of milk produced together with milking speed and parameters describing milk release characteristics of each cow. Flowmeter is not an expensive instrument and can be easily adapted on different milking machine.

Aim of this study is to estimate genetic parameters for some variable recorded with the flowmeter in the Italian Brown dairy cattle breed as a first screening of possible new traits to be considered in breeding strategies for the population.

MATERIALS AND METHODS

Two different data set were used in the analysis.

Data set 1) Data were collected by technicians of the National Association of Brown Swiss Breeders in Italy (ANARB) from 1972 to 1996. Cows were milked morning and evening with a milking machine separating milk produced in each quarter. Milk produced by each quarter and total time of milking were collected. Daily observations have been processed by cow, computing the total amount of milk produced (1MY-kg) in 2 milkings (morning and evening), average milk flow (1AMF-kg/min.) as total milk produced divided by total time of milking, and percentage of milk from the fore quarters (1FQM-%) as ratio of milk produced by the fore udder and total milk produced in 2 milkings. A total of 13,117 records were available, reduced to 10,668 out of 2,037 sires after edits. Only cows with at least four other paternal half sibs have been kept reducing the data set to 8,165 observations out of 387 sires. A REML multiple trait analysis has been performed using the following model:

$$y_{ijklmng} = \mu_g + h_{ig} + st_{jg} + p_{kg} + s_{lg} + t_{mg} + e_{ijklmng}$$

where: μ_g = overall mean for trait g; h_{ig} = effect of the herd i on trait g; s_{ig} = effect of stage of lactation j on trait g; p_{kg} = effect of parity l on trait g; s_{ig} = random effect of sire l on trait g; t_{mg} = effect of technician m in trait g; $e_{ijlkmng}$ = random error. Stage of lactation was defined as months from calving and had 10 levels while parity had 8 different levels where parities greater than 7 were grouped in the 8th class.

Data set 2) Data were collected by technicians of ANARB and Provincial Breeder Association of Bozen using a flowmeter (Lactocorder by Foss Electric). For each milking the following variables were stored: milk yield (kg), maximum milk flow (kg/min.), lag time to a milk flow of .5 kg/min. (min.), total milking time (min.), time, in min., of stable flow (plateau) time of decreasing flow (min.), average milk flow (kg/min.), stripping time (min.), milk yield during stripping (kg), milk flow during stripping (kg/min.), code to identify two milking peaks, and code to identify not regular recording (air in flowmeter). A total of 1,918 observations on Brown Swiss cows in Italy have been recorded. Morning and evening observations have been averaged by cow resulting in a total of 959 observation, one per each animal, out of 270 different sires. Data set has been reduced to cows with at least two other paternal half sibs. This procedure yielded a final set to be analyzed of 724 observations out of 88 sires. Data collection is still in progress averaging 100 cows per week. Only 5 variables were further analyzed: average milk flow (2AMF), milk yield (2MY), maximum milk flow (2MMF), total milking time (2TMT) and time of plateau (2TP). A REML multiple trait analysis has been performed in order to estimate the genetic parameters of these five variables using DFREML algorithm (Meyer 1985). Same model of data set one was used excluding the effect of technician. Stage of lactation has been defined in 3 periods of two months from calving: between calving and 90 days stage 1, from 91 d. to 180 d. stage 2 and over 270 days stage 3. Parity effect has been defined as primiparous cows versus pluriparous. Relationship matrix among sires has been used.

RESULTS AND DISCUSSION

In Table 1 and in Table 2 are shown descriptive statistics for the variable considered in the two data sets. Differences in values are probably due to reduced size of data set 2 being not completely representative of the population. In Figure 1 and 2 are shown milking curves of two different cows. Great variability exists among milking curves in terms of milking time and milk releasing flow. Milking curve result to be like a fingerprint of each cow.

The least square estimates for fixed effects included in the model used for data set 1 are

reported in Figures 3, and 4. Standard errors of the estimates for the fixed effects are reasonably small (i.e. 3-5% of the estimates) for parity and stage of lactation lower than 7. In table 3 correlation matrix of the traits considered in the analysis of data set 1 is presented.

Table 1. Descriptive statistics data set 1 (N=8165).

	Mean	S.D.	C.V.	Min	Max
1MY	19.8	5.64	28.4	4.9	46.9
1AMF	2.5	0.83	33.1	0.6	5.6
1FQM	44.8	6.43	14.4	19.0	92.
Flow [kg/min]					

Table 2. Descriptive statistics data set 2(N=724).

	mean	S.D.	C.V.	Min	Max
2AMF	1.9	0.59	29.8	0.68	5.24
2MY	10.8	3.23	29.9	2.20	22.9
2MMF	2.9	0.97	32.4	0.83	9.31
2TMT	5.4	1.77	33.0	1.53	10.9
2TP	2.4	1.55	64.3	0.03	10.0



Figure 1. Milking curve. Bold line morning milking.

Figure 2. Milking curves. Bold line morning milking.

In table 4 the correlation matrix of the traits considered in the analysis of data 2 set is shown. The estimations of genetic parameters of same traits id data set 1 and 2 yielded comparable results with differences in the magnitude of the standard errors: heritability of 1AMF results .22 (.04) and that of 2AMF .23 (.12) while heritability for 1MY and 2MY are .22 (.04) and .16 (.09) respectively. This values are lower of those found by Duda (1996) for German Simmental, but similar to those found in other German Breeds for average milking flow (Inerbull 1996). The estimate of heritability for 1FQM is .41 (.09). The ratio of production in fore udder is genetically negatively correlated with overall production (-.14) even if the standard error in this case is quite high. From the estimates of genetic parameters for type it is known that significant differences are present among sires in the shape and volume of the rear udder: higher and wider rear udders are correlated with higher productions. Results of this study suggest that difference in overall production among cows is mainly due to greater genetic influence on rear udder production. Further results from the analysis of the 2nd data set are often difficult to interpreter because large standard errors. The genetic correlation between 2AMF and 2MY is quite large (.51) and is similar to the correlation between 2MMF and 2MY (.50) suggesting that good producing cows are faster at milking. Higher milk flow is negatively correlated with 2TP (-.65), indicating that peak in milking is normally followed by rapid decrease in milk release as in Figure 1.





Table 3. Data set 1: heritabilities (diagonal)geneticcorrelations (lower triangle)phenotypiccorrelations (upper triangle).Std. errors within brackets.

	1MY	1AMF	1FQM
1MY	.22(.04)	.37(.01)	02(.01)
1AMF	.36(.12)	.22 (.04)	0.00(.01)
1FQM	14(.12)	11(.12)	.41(.06)



Figure 4. Least square estimates for the parity effect for the three variables 1MY, 1AMF,1FQM.

Trait 2TP, 2MMF, and 2AMF have an higher correlation with milk yield than total milking time (2TMT) suggesting their consideration in further studies aim to estimate relationships with production. In order to better clarify the relationships among variables it is necessary to substantially increase the size of the sample. Genetic evaluation for milking speed is

Table 4. Data set 2: heritabilities (diagonal), geneticcorrelations (lower triangle), phenotypic correlations (uppertriangle). Sta. errors within brackets.

	2AMF	2MY	2MMF	2TMT	2TP
2AMF	.23(.12)	.49(.03)	.86(.01)	45(.03)	27(.04)
2MY	.51(.30)	.16 (.09)	.38(.03)	.49(.03)	.39(.03)
2MMF	.99(.01)	.50(.31)	.21 (.10)	43(.03)	50(.03)
2TMT	86(.16)	01(.45)	.86(.15)	.13 (.09)	.72(.02)
2TP	65(.28)	.24(.40)	65(.27)	.92(.10)	.14(.09)

routinely performed for the Brown Swiss population based on 1st data set; the estimation of breeding values from data collected with a flowmeter will be possible only when more observations will be recorded. Further investigation is needed to check

the correlation among different milking emission shapes and total milk yield. If strong correlation will be found flowmeters will be a new tool available for genetic improvement.

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