

Genetics of milk traits including lactose and somatic cell score in Italian Jersey cows

C. Roveglia¹, A. Costa¹, M. Penasa¹, R. Finocchiaro², M. Marusi², N. Lopez-Villalobos³, M. Cassandro¹

¹ *Università degli Studi di Padova, Dipartimento di Agronomia Animali Alimenti Risorse Naturali e Ambiente (DAFNAE), Viale dell'Università 16, 35020 Legnaro, Italy.*

Corresponding Author: chiara.roveglia@phd.unipd.it

² *Associazione Nazionale Allevatori Frisona Italiana, via Bergamo 292, 26100 Cremona, Italy.*

³ *Massey University, Institute of Veterinary, Animal and Biomedical Sciences, Private Bag 11222, 4442 Palmerston North, New Zealand.*

Summary

The objective of this study was to estimate phenotypic and genetic parameters for milk traits including lactose and somatic cell score (SCS) over lactation of Italian Jersey dairy cattle. A total of 38,831 test-day records from 1,902 cows were collected from 2005 to 2016 in 20 dairy herds located in Italy. Days in milk were between 5 and 480 and thirteen classes of days in milk were defined. Analysis of variance was performed with a mixed linear model that included the fixed effects of herd-test day ($n = 920$), parity (5 classes), stage of lactation, calving season and interaction between parity and stage of lactation, and the random effects of animal and cow permanent environment. Heritabilities were estimated using a single-trait repeatability animal model, and genetic correlations were assessed through bivariate analyses. Mean milk yield was 18.76 kg/d, containing 5.29% fat, 4.09% protein, 3.20% casein, 4.80% lactose and 3.02 units of SCS. During lactation solids content and SCS increased, while solids yield decreased. Heritability estimates were 0.14, 0.21, 0.26, 0.24, 0.20 and 0.10 for milk yield, fat, protein, casein, lactose percentage and SCS, respectively. Genetic correlations between SCS and solids yield were negative, with the strongest estimate with lactose percentage (-0.30). Results of the present study emphasize quality of milk yield and composition of Italian Jersey cows and the possibility to develop new selective strategies for this breed.

Keywords: genetic parameter, milk yield, milk composition, somatic cell count, Jersey breed

Introduction

Jersey dairy cows were introduced in Italy in the early 1980's and in 1991 the Italian Jersey herd book was established. Since then, number of registered cows has more than doubled and nowadays there are more than 7,000 registered cows in 751 herds. The Italian Holstein Association (ANAFI) is in charge of Jersey cattle genetic evaluation and of maintaining the herd book. Until now, the Jersey breed has been appreciated by Italian breeders for the efficiency and high quality of milk yield (ANAFI, 2016). As a result of the growing interest of the breeders for Jersey cows, a national genetic breeding value estimation and a selection index named IQJ (Jersey Quality Index) were developed. The introduction of the IQJ is a first tool for Italian Jersey breeders aiming to select for protein and fat yields and contents (Biffani *et al.*, 2003). The current model used to analyse data from Italian Jersey breed is a lactation model, whereas a novel aspect of the present study is to propose a test-day model.

Estimates of genetic and phenotypic parameters are necessary to determine the degree of

variation due to genetics and environment, and also to predict genetic associations between two or more variables. These parameters are commonly required to construct selection indexes and predict correlated responses and to perform more efficient genetic evaluations (Rincòn *et al.*, 2015). Milk quality traits play an important role in genetic selection programs due to their economic impact on the dairy industry (Miglior *et al.*, 2005). Additionally, somatic cell score (SCS) and lactose are considered as variables of milk quality, also considered as indicators of subclinical mastitis, which is one of the most common and costly disease in dairy cattle population (Petzer *et al.*, 2017).

The aim of this study was to estimate genetic parameters for milk yields, SCS and milk composition traits in the Italian Jersey cattle population.

Material and methods

Data editing and analysis of variance

In the present study, 38,831 test-day records from 1,902 cows collected between 2005 and 2016 in 20 dairy herds were available for investigation. Data were provided by the Italian Holstein Association (ANAFI). Herd-tests between 5 and 480 days in milk and from cows of parity 1 to 6 were retained in the dataset. Somatic cell count (SCC, cells/mL) was converted to somatic cell score (SCS) by applying the equation of Wiggans and Shook (1987): $SCS = 3 + \log_2(SCC/100,000)$. Values of milk yield, fat, protein, casein, and lactose percentages, and SCS outside mean ± 3 standard deviations (SD) were treated as missing data. Fat, protein, casein and lactose yields were calculated by multiplying milk yield by the respective content (%). Only cows with at least 3 test-day records within lactation and with known sire and dam were retained. Also, the minimum number of cows per herd-test day (HTD) was set to 3.

Analysis of variance were performed using SAS version 9.4 (SAS Institute Inc., Cary, NC, USA) with a mixed linear model that included fixed effects of HTD ($n = 920$), parity (5 classes; first, second, third, fourth, and fifth and six parities), stage of lactation (13 classes of 30 d each, except for the first class, which was between 5 and 30 d, and the last four which were classes of 40, 40, 50, 80 d, respectively), calving season [4 classes: winter (December to February), spring (March to May), summer (June to August) and autumn (September to November)], and first-order interaction between parity and stage of lactation. Cow effect was considered as random.

Genetic parameters

A repeatability animal model was used to estimate variance and covariance components for each of the traits considered in this study using the package VCE version 6 (Groeneveld *et al.*, 2010), with a linear mixed model that considered the fixed effects of HTD, parity, stage of lactation, season of calving, interaction between parity and stage of lactation, and the random effects of additive genetic animal, cow permanent environment and residual. The pedigree ($n = 6,300$; 6 generations) was provided by ANAFI. Heritability (h^2) and repeatability (rep) were defined according to the ratios:

and ,

where σ^2_g , σ^2_p and σ^2_e are the additive genetic, cow permanent environmental and residual variances, respectively. Genetic correlations between traits were estimated through bivariate repeatability animal models considering the same fixed and random effects described for the single-trait analysis.

Results and Discussion

Descriptive statistics

Milk yield, fat percentage and protein percentage averaged 18.76 kg/d, 5.29% and 4.09%, respectively (Table 1). These means were similar to the values reported by Sneddon *et al.* (2012) in a New Zealand Jersey herd under grazing conditions. Lactose percentage of this study was 4.80%, which is higher than 4.45% in Brazilian (Ramos Garcia *et al.*, 2015), but lower than 5.09% in New Zealand (Sneddon *et al.*, 2012) Jersey cows.

The mean of SCS in this study was 3.02, which is lower than the value reported in Brazil (Ramos Garcia *et al.*, 2015). Comparison of SCS with the New Zealand Jersey study (Sneddon *et al.*, 2012) is not possible because the transformation from SCC to SCS was not the same. Least squares means of milk and solids yield, solids content, and SCS over the lactation of Italian Jersey cows are shown in Figure 1. Lactation curves of these traits were similar to the lactation curves of first-lactation Jersey cows in New Zealand (Sneddon *et al.*, 2016).

Heritability

The estimate of heritability for milk yield in this study was 0.14 (Table 1), which agrees with the values reported by Rincón *et al.* (2015) in Holstein Friesian (0.16) and Jersey (0.15) in Colombia. However, estimates vary from 0.19 (Sneddon *et al.*, 2015) to 0.50 (Sneddon *et al.*, 2012) in the New Zealand Jersey population, suggesting an important influence of environmental factors and sample size.

The estimates of heritabilities for yields of milk components were generally low, but comparable to those reported by Sneddon *et al.* (2015), who showed the same estimate of heritability for fat yield (0.12). Heritabilities for contents of milk components were slightly lower than those reported by Sneddon *et al.* (2015). Heritability of SCS was low (0.10) but similar to the value (0.08) reported by Sneddon *et al.* (2015), suggesting that this trait is more affected by environmental rather than genetic factors. This trait is associated with udder health, which also is not highly inheritable.

Correlations

The estimates of genetic correlations between SCS and yields of milk components were slightly negative (-0.25, -0.25, -0.27, -0.26 between SCS and milk yield, fat yield, protein yield and lactose yield, respectively; Table 2). Furthermore, as confirmed by New Zealand studies (Sneddon *et al.*, 2012; Sneddon *et al.*, 2015) the genetic and phenotypic correlations between lactose yield and milk yield was almost 1, and between lactose yield and protein yield was strong and positive (Table 2), which indicates that an increase in milk yield will be accompanied with an increase in lactose yield. Selection for increased yields may decrease SCS as the estimated genetic correlation between yields and SCS were negative. However, selection for increased concentration of milk components may increase the SCS in cows due to positive estimated genetic correlations between concentrations and SCS (Sneddon *et al.*, 2012). The estimated phenotypic correlations were generally weak, which agree with estimates reported in the literature (Rincón *et al.*, 2015). However, the estimates of these correlations are very variable, according to the environment where they were estimated, so that it is common to find higher values in highly controlled production conditions.

Conclusion

The estimates of phenotypic and genetic parameters obtained in this study are within the ranges previously reported in other Jersey dairy cattle populations. These estimates of genetic parameters can be used in simulation studies to evaluate the genetic responses for individual traits of alternative selection indices and breeding objective that may be implemented in the Italian Jersey population,

that ensure genetic in the right magnitude and direction.

Table 1. Mean, standard deviation (SD), heritability (standard errors within parentheses), and repeatability of studied traits in Italian Jersey cows.

Trait	Mean	SD	Heritability	Repeatability
Solids yield, kg/d				
Milk	18.76	6.96	0.14 (0.02)	0.37
Fat	0.98	0.38	0.12 (0.08)	0.26
Protein	0.76	0.28	0.14 (0.02)	0.33
Casein	0.59	0.24	0.08 (0.02)	0.26
Lactose	0.91	0.35	0.13 (0.03)	0.37
Solids content, %				
Fat	5.29	1.04	0.21 (0.01)	0.28
Protein	4.09	0.48	0.26 (0.03)	0.39
Casein	3.20	0.39	0.24 (0.03)	0.33
Lactose	4.80	0.21	0.20 (0.02)	0.35
SCS ¹ , units	3.02	1.69	0.10 (0.02)	0.31

¹ SCS = somatic cell score, calculated as $3 + \log_2(\text{SCC}/100,000)$, where SCC is somatic cell count.

Table 2. Genetic (below the diagonal) and phenotypic (above the diagonal) correlations¹ between studied traits in Italian Jersey cows.

Trait ²	MY	FP	PP	CP	LP	FY	PY	CY	LY	SCS
MY		-0.21	-0.20	-0.13	0.21	0.84	0.94	0.94	0.99	-0.24
FP	-0.37		0.50	0.52	-0.29	0.29	-0.06	-0.03	-0.24	0.04
PP	-0.43	0.82		0.98	-0.33	0.05	0.10	0.14	-0.20	0.11
CP	-0.43	0.82	0.99		-0.34	0.12	0.16	0.16	-0.14	0.09
LP	-0.02	-0.28	-0.21	-0.22		0.05	0.11	0.05	0.31	-0.38
FY	0.72	0.36	0.16	0.14	-0.14		0.88	0.89	0.82	-0.22
PY	0.91	-0.03	-0.04	-0.01	-0.07	0.88		0.99	0.93	-0.21
CY	0.91	-0.02	-0.06	-0.02	0.01	0.83	0.99		0.93	0.20
LY	0.99	-0.42	-0.43	-0.43	0.17	0.67	0.88	0.89		-0.25
SCS	-0.25	0.11	0.18	0.29	-0.30	-0.25	-0.27	-0.13	-0.26	

¹ Standard errors of genetic correlations ranged from 0.001 to 0.17.

² MY = milk yield; FP = fat percentage; PP = protein percentage; CP = casein percentage; LP = lactose percentage; FY = fat yield; PY = protein yield; CY = casein yield; LY = lactose yield; SCS = somatic cell score calculated as $3 + \log_2(\text{SCC}/100,000)$, where SCC is somatic cell count.

Figure 1. Least squares means of milk and solids yield, solids content, and somatic cell score (SCS) over the lactation in Italian Jersey cows.

Mi
lk
yie
ld
(kg
/d)

References

ANAFI, 2016. <http://www.anafi.it/Jersey/Jersey/LaJerseyItaliana.htm>

- Biffani, S., A.B. Sarmorè & F. Canavesi, 2003. Breeding strategies for the Italian Jersey. *Italian J. Anim. Sci.* 2 (suppl.1): 79-81.
- Groeneveld, E., M. Kovač and N. Mielenz, 2010. VCE User's Guide and Reference Manual, version 6.0. Institute of Farm Animal Genetics; Neustadt, Germany.
- Miglior, F., B.L. Muir & B.J. Van Doormaal, 2005. Selection indices in Holstein cattle of various countries. *J. Dairy Sci.* 88: 1255-1263.
- Petzer, I.M., J. Karzis, E.F. Donkin, E.C. Webb & E.M.C. Etter, 2017. Validity of somatic cell count as indicator of pathogen-specific intramammary infections. *J. South Afr. Vet. Assoc.* 88: 1-10.
- Ramos Garcia, R., V. Bufon Maion, K. Molin de Almeida, E. H. Walter de Santana, M. Rezende Costa, R. Fagnani & A. Ludovico, 2015. Relationship between somatic cell counts and milk production and composition in Jersey cows. *Rev Salud Anim.* 37:137-142.
- Rincón, F., A. Zambrano & J. Echeverri, 2015. Estimation of genetic and phenotypic parameters for production traits in Holstein and Jersey from Colombia. *Revista MVZ Córdoba.* 20: 4962-4973.
- Sneddon, N. W., N. Lopez-Villalobos, S.R. Davis, R.E Hickson, L. Shalloo & D.J. Garrick, 2016. Supply curves for yields of dairy products from first-lactation Holstein Friesian, Jersey and Holstein Friesian-Jersey crossbred cows accounting for seasonality of milk composition and production. *Proc. N.Z. Soc. Anim. Prod.* 76: 139-143.
- Sneddon, N.W., N. Lopez-Villalobos, S.R. Davis, R.E. Hickson & L. Shalloo, 2015. Genetic parameters for milk components including lactose from test day records in the New Zealand dairy herd. *N. Z. J. Agric. Res.* 58: 97-107.
- Sneddon, N.W., N. Lopez-Villalobos, R.E. Hickson & L. Shalloo, 2012. Genetic parameters for lactose and its relationship with concentrations and ratios of other milk components. *Proc. N.Z. Soc. Anim. Prod.* 72: 76–80.
- Wiggans, G.R. & G.E. Shook, 1987. A lactation measure of somatic cell count. *J. Dairy Sci.* 70: 2666-2672.