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Genetic analysis of coagulation properties, curd firming modeling, milk yield, composition, and acidity in Sarda dairy sheep

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ABSTRACT

Sheep milk is an important source of food, especially in Mediterranean countries, and is used in large part for cheese production. Milk technological traits are important for the sheep dairy industry, but research is lacking into the genetic variation of such traits. Therefore the aim of this study was to estimate the heritability of traditional milk coagulation properties and curd firmness modeled on time t (CF_t) parameters, and their genetic relationships with test-day milk yield, composition (fat, protein, and casein content), and acidity in Sarda dairy sheep. Milk samples from 1,121 Sarda ewes from 23 flocks were analyzed for 5 traditional coagulation properties by lactodynamographic tests conducted for up to 60 min: rennet coagulation time (min), curd-firming time (k_{20}, min), and 3 measures of curd firmness (a_{30}, a_{45}, and a_{60}, mm). The 240 curd firmness observations (1 every 15 s) from each milk sample were recorded, and 4 parameters for each individual sample equation were estimated: rennet coagulation time estimated from the equation (RCT_{eq}), the asymptotic potential curd firmness (CF_P), the curd firming instant rate constant (k_{CF}), and the syneresis instant rate constant (k_{SR}). Two other derived traits were also calculated (CF_{max}, the maximum curd firmness value; and t_{max}, the attainment time). Multivariate analyses using Bayesian methodology were performed to estimate the genetic relationships of milk coagulation properties and CF_t with the other traits; statistical inference was based on the marginal posterior distributions of the parameters of concern. The marginal posterior distribution of heritability estimates of milk yield (0.16 ± 0.07) and composition (0.21 ± 0.11 to 0.28 ± 0.10) of Sarda ewes was similar to those often obtained for bovine species. The heritability of rennet coagulation time as a single point trait was also similar to that frequently obtained for cow milk (0.19 ± 0.09), whereas the same trait calculated as an individual equation parameter exhibited larger genetic variation and a higher heritability estimate (0.32 ± 0.11). The other curd firming and syneresis traits, whether as traditional single point observations or as individual equation parameters and derived traits, were characterized by heritability estimates lower than for coagulation time and for the corresponding bovine milk traits (0.06 to 0.14). Phenotypic and additive genetic correlations among the 11 technological traits contribute to describing the interdependencies and meanings of different traits. The additive genetic relationships of these technological traits with the single test-day milk yield and composition were variable and showed milk yield to have unfavorable effects on all measures of curd firmness (a_{30}, a_{45}, a_{60}, CF_P, and CF_{max}) and t_{max}, but favorable effects on both instant rate constants (k_{CF} and k_{SR}). Milk fat content had a positive effect on curd firmness traits, especially on those obtained from CF_t equations, whereas the negative effects on both coagulation time traits were attributed to the milk protein and casein contents. Finally, in view of the estimated heritabilities and additive genetic correlations, enhancement of technological traits of sheep milk through selective breeding could be feasible in this population.

Key words: heritability, sheep milk, milk coagulation properties, curd-firming modeling, cheese-making

INTRODUCTION

The ovine species contributes significantly to overall milk production, especially in countries of the Mediterranean Basin, Central and Eastern Europe, and the Middle East, with an estimated economic value of approximately $5,600 million US (FAOSTAT, 2014). The island of Sardinia is the region of the Mediterranean basin with the highest concentration of dairy sheep (about 3 million head on 24,090 km^2), and the Sarda sheep breed, now also reared in other Italian regions

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and other countries, is the most numerous specialized dairy sheep breed found there (Astruc et al., 2008).

Selective breeding of dairy sheep populations is not carried out as with the bovine species because, although the cost of milk recording and analysis, flock-book organization, and breeding value estimation is similar to the major species, individual milk yield and economic value are much smaller, making the income/cost ratio much less favorable. Selection of dairy sheep breeds is often carried out through pyramidal management of populations, with nucleus flocks enrolled in flock-books at the top, performing milk recording, practicing artificial or controlled natural mating, and using estimated breeding values as selection criteria (Macciotta et al., 2005). This nucleus provides semen and rams for spreading genetic improvement in commercial flocks, as reviewed by Carta et al. (2009), according to whom current genetic improvement in dairy sheep populations is generally aimed at increasing milk yield and, especially in the case of French breeds, milk fat and protein yields or percentages (or both). In a few cases, SCC and udder traits are included in the selection indices (Carta et al., 2009; de la Fuente et al., 2011).

The heritability of milk yield of dairy ewes is well known (Pollott and Gootwine, 2001; Gutiérrez et al., 2007), as are the genetic parameters of somatic cell content (el-Saied et al., 1999; Riggio et al., 2010). Milk components, such as fat and protein, and their daily yield are far less frequently studied (Baro et al., 1994) than milk yield. As sheep milk is especially used for the production of cheese, the ovine cheese industry would benefit from an improvement in cheese-making traits (milk coagulation traits, curd firming and syneresis, milk nutrient recovery in curd, and cheese yield). The difficulty of measuring these phenotypes in a large population coupled with their cost limits the number of available studies. In fact, only one study has been carried out to estimate the genetic parameters of cheese yield in ovine species (Othmane et al., 2002a,b), and only one in the bovine species (Bittante et al., 2013a). In the case of milk coagulation and curd firming properties, the situation is different in the 2 species: several studies on genetic parameters have been carried out with dairy cattle, as reviewed by Bittante et al. (2012), whereas no genetic information is available for the small ruminant species.

The traditional single point traits regarding milk coagulation properties (**MCP**) were set up for the classification of bovine milk and are not particularly suitable for evaluating ovine milk due to its very rapid coagulation and curd firming after rennet addition (Bencini, 2002; Park et al., 2007). New modeling techniques aimed at better describing milk coagulation, curd firming, and syneresis using all the information recorded during a lactodynamographic test have recently proved to be able to better describe the cheese-making ability of sheep milk with respect to traditional traits (Bittante et al., 2014). These new curd firming and syneresis model parameters have been comprehensively studied from a phenotypic point of view by Vacca et al. (2015), but, to our knowledge, the literature contains a dearth of studies investigating the genetic variation of such traits.

Therefore the aims of the present study were to estimate (1) the genetic parameters of milk yield and composition in the Sarda sheep breed; (2) the genetic parameters of traditional single point coagulation properties; (3) the genetic parameters of the new milk coagulation, curd firming, and syneresis model parameters and derived traits; and (4) the phenotypic and genetic correlations among all the aforementioned traits.

MATERIALS AND METHODS

Animals and Milk Sampling

The animals and the milk sampling procedures adopted in the present study have been described in detail in a previous study on phenotypic variation in traditional MCP by Pazzola et al. (2014). Briefly, a total of 1,121 ewes enrolled in the flock-book of the Sarda breed and reared on 23 commercial farms were used. Genetic connectedness was taken into consideration in selecting the farms (i.e., the use of AI of the ewes or the exchange of rams and ewes with other farms, or both). Within flocks, ewes were selected to include all the animals genetically connecting the flock with the other selected flocks (daughters of AI or exchanged rams, exchanged ewes), whereas ewes sired by rams with less than 3 or more than 40 daughters in the database of sampled ewes were excluded. Ewes with clinical signs of disease were also excluded.

The farms were evenly distributed over the island of Sardinia, Italy, representing its different environmental conditions and sheep dairy systems. Lactating ewes were pasture fed and received a commercial concentrate supplement during milking and were generally managed following the common semi-extensive and semi-intensive methods as described by Carta et al. (2009). Flock classification was based on flock size (Pazzola et al., 2014). The ewes sampled (32 to 82 per flock) were milked by manually operated milking machines twice a day (usually at 0600 and at 1600 h) and were sampled once at 140 ± 42 DIM. The descriptive statistics of milk yield are shown in Table 1. Pedigree information was supplied by the Flock Book Society of Italian sheep and goat breeders (Associazione Nazionale della Pastorizia) and included ewes with phenotypic records for