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Genetic parameters and QTL detection for milking speed in dairy Alpine and Saanen goats

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ABSTRACT: The aim of this study was to estimate genetic parameters and identify QTL regions for milking speed in French Alpine and Saanen goats. Heritabilities ranged from 0.38 to 0.60 depending on the milking speed traits. Relationships with milk traits and udder type traits were generally low (from -0.23 to 0.24) whereas lactation somatic cell score and milking speed was positively and strongly correlated, more particularly in Alpine breed. Linkage and association analyses were performed on data from a daughter design. A few promising regions were detected.

Keywords: dairy goat; milking speed; genetic parameter; QTL detection

Introduction

Improving the milking ability is a major issue for French goat breeders. The constant increase of both average herd size and productivity per goat has been contributing to the extent of milking time. Ilahi et al. 1999, have shown that the quantity of collected milk during the first minute of milking is an appropriate trait for selection purpose. For this trait, genetic factors explained a large part of the phenotypic variance ($h^2=0.65$ according to Ilahi et al. 2000). Moreover, the presence of a major gene affecting the milking speed was assessed by segregation analyses (Ricordeau et al. 1990, Ilahi et al. 2000). In 2011, the release of a 50K SNP goat chip (Tosser-Klopp et al. 2014) gave the opportunity to carry out the first large scale QTL detection design for many traits in goats (including milking speed). The objective of this work was (i) to assess the impact of the current selection on milking speed, and (ii) to identify QTL regions affecting milking speed, for Alpine and Saanen goat breeds.

Materials and Methods

Data. A first data set was used for genetic parameter estimation. It included 4,497 and 4,906 first lactations from Saanen and Alpine breeds, respectively, measured in 56 herds involved in official milk recording. Milking speed data were measured by a portable electronic milk meter (LactoCorder, WMB AG, Balgach, Switzerland). Four traits were investigated in this study: the quantity of collected milk during the first minute of milking (MF1), the average milk flow during the principal milking time (AMF), the maximum milk flow per minute (MMFm), the maximum milk flow during 8 measurement intervals (MMF). A mean lactation was computed from morning records between 8 and 360 days in milk and animals with at least two milkings. Milk production and somatic cell count traits were those considered for official

genetic evaluation: 250-d lactation for milk yield (MY), fat (FY) and protein (PY) yields, fat (FC) and protein (PC) contents, lactation somatic cell score (LSCS). Udder type traits were scored by official classifiers of the French goat breeding organization CAPGENES. Nine traits were measured by linear scores from 1 to 9: fore udder (FU), udder profile (UP), udder floor position (UFP), rear udder (RU), rear udder attachment (RUA), teat length (TL), teat form (TF), teat angle (TA), teat orientation (TO) (Manfredi et al, 2001). The subset of data with udder type traits included 1,979 and 3,248 goats in Saanen and Alpine breeds, respectively.

A second data set from a daughter design consisting of 20 Alpine and Saanen sires, with 40 daughters, on average, in first or second lactation was analysed. All the animals were genotyped with the 50K SNP Illumina goat chip. Phenotypic traits were test day MF1, collected during morning or evening milkings.

Statistical analyses

Genetic parameter estimation. Animal models were used to compute variance estimates of each trait, and genetic and environmental correlations of milking speed traits with other traits. Estimations were performed with the REML software WOMBAT (Meyer, 2007). The model included the fixed effects currently used in the genetic evaluation and the random effect of animal. For pedigree information, after five generations of ancestors traced back, each file included about 15,000 animals.

QTL detection. After quality control, 49,647 SNP were kept for the study. Phenotypes were yield deviations (YD). An average of elementary YD was computed for each goat having at least 3 measures. Linkage and association analyses were performed with the QTLMap software (Elsen et al. 1999, Legarra et al., 2009). Both breeds were analyzed together. A 5% chromosome-wise significance threshold was estimated by permutations ($n=500$) for linkage analysis and simulations ($n=1000$) for association analysis.

Results and Discussion

Means and heritabilities of milking speed traits. Averages of MF1, measured during morning milking of primiparous goats, were around 0.75 kg/min (Table 1). Whatever the trait, milking speed tended to be higher in the Alpine breed compared to the Saanen breed. Heritability estimates were moderate, significantly higher in Alpine breed than in Saanen breed, and similar depending on the trait (Table 1). Heritability for MF1 was close to

the estimate reported by Ilahi et al. 2000 for the Alpine breed (0.65). Our results were also in the range of heritabilities of milking speed traits in dairy sheep (between 0.30 and 0.54, Marie-Etancelin et al. 2006) and in dairy cattle (0.28 to 0.48 Kramer et al. 2013, Ilahi et al. 2004, Samore et al. 2010).

Table 1. Mean, standard deviation (SD) and heritability (h^2) for milking speed traits in Alpine (ALP) and Saanen (SAA) breeds.

	Mean \pm SD		h^2 ¹	
	SAA	ALP	SAA	ALP
MF1, kg	0.72 \pm 0.27	0.82 \pm 0.27	0.42	0.60
AMF, kg/min	0.66 \pm 0.23	0.75 \pm 0.22	0.38	0.56
MMFm, kg/min	0.83 \pm 0.29	0.95 \pm 0.29	0.38	0.53
MMF, kg/min	0.91 \pm 0.34	1.05 \pm 0.34	0.42	0.59

¹SE = 0.05 for all heritability estimates

Genetic correlations between MF1 and production and somatic cell count traits. Only genetic correlations with MF1 are reported here. Very similar results were found for the four milking speed traits (genetic correlations between them ranged from 0.992 to 0.999). Heritabilities ranged from 0.22 to 0.51 for milk production traits, and were estimated to 0.31 and 0.19 for LSCS in Saanen and Alpine breeds, respectively (results not shown). These values are consistent with those found in previous study in the same breeds Rupp et al. 2011. Genetic correlations between MF1 and milk production traits were generally low (Table 2), in agreement with Ilahi et al. 2000, and significantly different from zero only in the Saanen breed for MY, FC and PC. These results suggest that, in goats, milk yield is genetically independent of milking speed, conversely to ewes (r_g =0.45 for maximum milk flow in Casu et al. 2008 and r_g =0.46 in Marie-Etancelin et al. 2006) and cows (r_g =0.30 for average milk flow in Samore et al. 2010 and r_g =0.69 in Berry et al. 2013). Lactation SCS was positively and strongly correlated with MF1, especially in Alpine breed (Table 2). This result suggests higher susceptibility to inflammation, even infection, in fast milking goats. In cattle, however, although the correlation between LSCS and milking speed is equivalent (0.44 and 0.46 in Rupp et al. 1999 and Samore et al. 2010, respectively), no genetic relationship was observed between fast milking cows and clinical mastitis incidence (Rupp et al. 1999).

Table 2. Mean and standard deviation (SD) of production and somatic cell count traits, and genetic correlation (r_g) with MF1 in Alpine (ALP) and Saanen (SAA) breeds.

	Mean \pm SD		r_g with MF1 ²	
	ALP	SAA	ALP	SAA
MY, kg	1012 \pm 212	994 \pm 237	-0.03	0.14
PY, kg	32.9 \pm 6.6	30.6 \pm 7.2	0.07	0.07
FY, kg	38.5 \pm 8.4	35.6 \pm 9.6	-0.02	0.01
PC, g/kg	32.7 \pm 2.5	30.9 \pm 2.2	0.09	-0.17
FC, g/kg	38.3 \pm 4.4	35.9 \pm 5.2	-0.06	-0.18
LSCS	5.2 \pm 1.6	5.4 \pm 1.4	0.63	0.39

²SE between 0.07 and 0.10

Genetic correlations between MF1 and udder type traits. Heritabilities of udder type traits are not presented here but estimates were close to those reported earlier (Manfredi et al., 2001, Rupp et al., 2011) ranging between 0.15 (for TA in Alpine breed) and 0.43 (for RUA in Saanen breed). MF1 showed low correlations with udder type traits (Table 3). Regarding the traits included in the total merit index (FU, UFP, UP, RUA, TO), the patterns seems to be opposite between breeds: the positive and highest values for these traits in Alpine breed suggest an indirect slight improvement of milking speed by the current selection on udder type traits whereas, for the Saanen breed, it would be slightly deteriorating. In comparison with cows (Samore et al. 2010), the strong and positive association between udder size and milking speed was not found, partly explained by the weak association between milk yield and milking speed. The internal teat conformation is an important regulator of milking speed in small ruminants (Marnet et al. 2001). Further work would be necessary to evaluate the link between anatomical characteristics of the teat and milking speed kinetics, in relationship with mastitis resistance.

Table 3. Mean and standard deviation (SD) of udder type traits, and genetic correlation (r_g) with MF1 in Alpine (ALP) and Saanen (SAA) breeds.

	Mean (\pm SD)		r_g with MF1 ³	
	ALP	SAA	ALP	SAA
FU	3.0 \pm 1.0	3.1 \pm 1.1	0.16	-0.13
RU	6.2 \pm 1.1	5.8 \pm 1.2	0.22	0.16
UFP	6.5 \pm 0.9	6.4 \pm 1.1	0.16	-0.12
UP	5.9 \pm 1.4	6.3 \pm 1.4	-0.05	-0.05
RUA	4.1 \pm 1.5	4.2 \pm 1.7	0.20	-0.23
TL	5.4 \pm 1.3	5.8 \pm 1.5	0.15	0.03
TF	5.2 \pm 1.4	5.3 \pm 1.5	-0.14	-0.02
TA	4.7 \pm 0.8	4.8 \pm 0.7	0.24	0.10
TO	3.4 \pm 1.0	3.9 \pm 1.0	0.08	-0.23

³SE between 0.10 and 0.13 in ALP, and between 0.12 and 0.16 in SAA

QTL detection. With the linkage analyses, two QTL were found at the 5% chromosome-wise significance threshold. The most significant is presented in Figure 1 (chromosome number not given for confidential reasons). The results of the association analyses were shown in Figure 2. Significant haplotypes were found on all chromosomes, with highest significance level found on chromosome 10, 12 and 19. Both linkage and association analyses gave a set of promising regions, potentially including the major gene previously detected (Ricordeau et al. 1990, Ilahi et al. 2000). Further analyses, however, are needed to fine map those QTL, estimate the magnitude of their effect and their interaction. In cattle, about 20 QTL regions affecting milking speed were found, each of them having moderate effect (Gray et al. 2012, Boichard et al. 2003, Schrooten et al. 2004), but no major gene was highlighted (Ilahi et al. 2004).

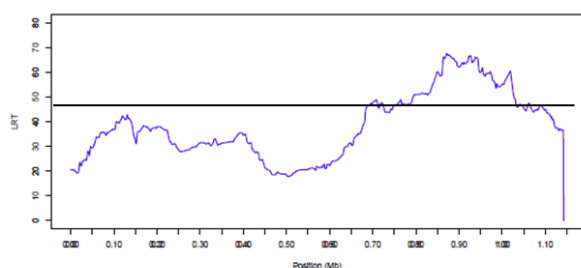


Figure 1. Likelihood ratio test (LRT) from linkage analysis along the chromosome with the most significant QTL for MF1. The horizontal line corresponds to a 5% chromosome wise significant threshold.

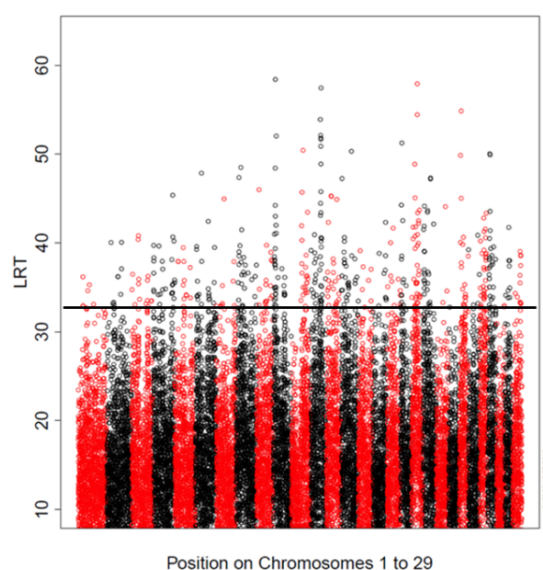


Figure 2. Manhattan plot of the likelihood ratio test (LRT) values from the association analysis on MF1. Each plot corresponds to a haplotype of 4 consecutive SNP. Each color change corresponds to a chromosome from 1 to 29.

Conclusion

Genetic parameters of milking speed suggest that the implementation of a selection in favor of these traits in Alpine and Saanen goats is possible. This implementation would be facilitated by the weak relationship between milking speed and the other current selected traits, except LSCS. The first QTL detection for milking speed traits in goats showed several promising regions that need to be further characterized. It could improve selection efficiency, especially to free from the unfavorable correlation between milking speed and LSCS, and, for instance, by culling animals carrying two “normal” alleles (low milking speed). However, the selection strategy at the population level was not obvious. The expected increase of the frequency at the major gene needs to be optimized in order to evaluate the most efficient way to improve, at the end, the milking conditions for breeders.

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