Genome-wide association study of conformation and milk yield in mixed-breed dairy goats

**Sebastian Mucha,*† Raphael Mrode,† Mike Coffey,† Mehmet Kizilaslan,†‡ Suzanne Desire,†[1]
and Joanne Conington†**
*Poznan University of Life Sciences, 33 Wolynska, 60-637 Poznan, Poland
†Animal and Veterinary Sciences, Scotland's Rural College, Easter Bush, Midlothian EH25 9RG, United Kingdom
‡International Center for Livestock Research and Training, Breeding and Genetics Department, 06852, Ankara, Turkey

ABSTRACT

Identification of genetic markers that affect economically important traits is of high value from a biological point of view, enabling the targeting of candidate genes and providing practical benefits for the industry such as wide-scale genomic selection. This study is one of the first to investigate the genetic background of economically important traits in dairy goats using the caprine 50K single nucleotide polymorphism (SNP) chip. The aim of the project was to perform a genome-wide association study for milk yield and conformation of udder, teat, and feet and legs. A total of 137,235 milk yield records on 4,563 goats each scored for 10 conformation traits were available. Out of these, 2,381 goats were genotyped with the Illumina Caprine 50K BeadChip (Illumina Inc., San Diego, CA). A range of pseudo-phenotypes were used including deregressed breeding values and pseudo-estimated breeding values. Genome-wide association studies were performed using the multi-locus mixed model (MLMM) algorithm implemented in SNP & Variation Suite v7.7.8 (Golden Helix Inc., Bozeman, MT). A genome-wise significant $[-\log_{10}(P\text{-value}) > 5.95]$ SNP for milk yield was identified on chromosome 19, with additional chromosome-wise significant $(-\log_{10}(P\text{-value}) > 4.46]$ SNP on chromosomes 4, 8, 14, and 29. Three genome-wise significant SNP for conformation of udder attachment, udder depth, and front legs were identified on chromosome 19, and chromosome-wise SNP were found on chromosomes 4, 5, 6, 10, 11, 12, 13, 14, 15, 16, 17, 18, 21, 23, and 27. The proportion of variance explained by the significant SNP was between 0.4 and 7.0% for milk yield and between 0.1 and 13.8% for conformation traits. This study is the first attempt to identify SNP associated with milk yield and conformation in dairy goats. Two genome-wise significant SNP for milk yield and 3 SNP for conformation of udder attachment, udder depth, and front legs were found. Our results suggest that conformation traits have a polygenic background because, for most of them, we did not identify any quantitative trait loci with major effect.

Key words: genome-wide association study (GWAS), dairy goat, conformation, quantitative trait loci (QTL)

INTRODUCTION

Conventional goat breeding schemes are often hampered by the cost of measuring phenotypes and maintaining accurate pedigree and data recording. Many goat breeders do not perform routine data recording or do so on a very basic level. Identification of genetic markers and candidate genes that affect economically important traits is therefore of high value from a biological point of view, as well as providing practical benefits to industry. Compared with that in cattle and sheep, the number of QTL studies in goats is limited; however, at present, goat QTL are not included in Animal QTLdb database (http://www.animalgenome.org/cgi-bin/QTLdb/index), which makes it difficult to judge the exact number of studies in this species (for review, see Amills, 2014).

Quantitative trait loci for traits such as birth and weaning weight (Mohammad Abadi et al., 2009; Visser et al., 2013), hair fiber characteristics (Cano et al., 2007; Visser et al., 2011), growth (Mohammad Abadi et al., 2009), body conformation (Marrube et al., 2007), parasite resistance (Bolormaa et al., 2010; De La Chevrotière et al., 2012), milk traits (Roldán et al., 2008), and α_{S1}-casein (Sacchi et al., 2005; Hayes et al., 2006; Dagnachew et al., 2011) have been identified in goats using microsatellite markers. With the availability of the Illumina Caprine 50K BeadChip (Illumina Inc., San Diego, CA; Tosser-Klopp et al., 2012, 2014), it is now possible to perform genome-wide scans in goats

with much greater resolution. To date, the chip has been utilized to find QTL associated with milk and type traits (Maroteau et al., 2013; Martin et al., 2017), polledness (Kijas et al., 2013), milking speed (Palhière et al., 2014), coat color (Becker et al., 2015; Martin et al., 2016a), wattles (Reber et al., 2015), and supernumerary teats (Martin et al., 2016b). In addition, due to the application of sequencing and whole-genome optical mapping, information on gene annotation for goats has become available (Dong et al., 2013). The goat genome assembly has been refined and updated using dense radiation hybrid mapping (Du et al., 2014).

In cattle, feet and leg conformation has been genetically linked to claw disorders (van der Waaij et al., 2005), although there is evidence that animals with good udder conformation are less sensitive to high yields than those with poor udder conformation (Philipsson and Lindhé, 2003). In dairy goats, there is evidence of genetic correlations with production traits such as milk yield (McLaren et al., 2016) and productive life, as well as functional productive life (Castañeda-Bustos et al., 2017). Udder and teat conformation have also been linked with elevated SCC and clinical mastitis (Rupp and Boichard, 1999; Rupp et al., 2011; Huntley et al., 2012) as well as milking speed (Sewalem et al., 2011). Conformation traits are therefore important from both a health and welfare perspective and a production perspective; however, these traits are costly to phenotype. Identifying SNP associated with QTL that significantly affect a trait would allow for marker-assisted selection, saving time and money on phenotyping adult animals. The main objective of this study was to perform genome-wide association studies (**GWAS**) to identify SNP associated with conformation of udder, teat, legs and feet, as well as milk yield. This study is one of the first to investigate genetic background of economically important traits in dairy goats using the caprine 50K SNP chip.

MATERIALS AND METHODS

Data

A total of 5,026 first-lactation goats were scored for 10 conformation traits. Goats were a composite breed of Saanen, Toggenburg, and Alpine. A more detailed description of breed composition investigated with a principal component analysis is given in Mucha et al. (2015). Scoring was performed on 2 farms owned by the same farming business, over 2 yr (2013 and 2014) by the same scorer. All goats in their first lactation were scored once on both participating farms. Animals were ranked on a linear scale (1–9), similar to the scoring

system developed by the French dairy goat breeders' association (CAPGENES) and used by Manfredi et al. (2001) and Rupp et al. (2011). A detailed description of the scoring system can be found in McLaren et al. (2016). The data contained information for udder traits (udder furrow, udder depth, udder attachment), teat traits (teat shape, teat angle, teat placement), and traits relating to legs and feet (front legs, back legs, front feet, back feet). A total of 137,235 milk yield records were available for 4,563 of the scored animals. The pedigree contained 34,391 individuals over 15 generations, with a total of 296 and 12,468 registered sires and dams, respectively.

Genotyping

Initially, 1,960 animals were selected for genotyping to build a reference population for implementation of genomic selection. All of the available sires (150 individuals) were sampled, and this set was subsequently supplemented by females. Details on the structure of the genotyped population and selection method are given in Mucha et al. (2015). Subsequently, all female animals selected as replacements and all males used in the population were genotyped. In total, 2,381 goats with milk yield data and 402 of the conformation-scored goats were genotyped. Selection of animals for genotyping was done purely based on milk production, because this was the main breeding objective on the participating farms. That is why only 402 of the genotyped goats had conformation data. Animals were genotyped commercially with the Illumina Caprine 50K BeadChip (Illumina Inc.; Tosser-Klopp et al., 2012) at Edinburgh Genomics (Edinburgh, UK). Single nucleotide polymorphisms were removed from further analyses if they were not in Hardy-Weinberg equilibrium, had minor allele frequency <0.05, were monomorphic, had a call rate of <0.95, or if the Illumina GenCall (GC score) was below 0.6. Missing genotypes (0.2% of all genotyped SNP) were imputed as homozygous for the major allele. Three animals were removed because they had call rate <0.90. This resulted in a data set with 2,378 goats with milk yield data and 402 conformation-scored goats genotyped for 44,798 SNP from 29 chromosomes (the X chromosome was excluded from the analysis).

Calculation of Deregressed Breeding Values

Basic statistics describing the data were estimated using R (R Development Core Team, 2011). Appropriate statistical models for conformation traits and milk yield were developed in previous studies on the same population (Mucha et al., 2014; McLaren et al., 2016).