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Genetic diversity of South African dairy goats for genetic management and improvement

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ABSTRACT

The dairy goat industry is a small, but important role player in the South African agricultural sector. The limited number of animals representing the three main breeds (Saanen, British Alpine and Toggenburg) has raised concerns over the genetic diversity of these animals and the impact on their genetic management. In this study, 240 dairy goats representing three breeds were genotyped with 25 microsatellite markers. Sufficient levels of genetic diversity were observed in all the breeds, with observed heterozygosity values exceeding 60%. A slight population differentiation was indicated by the low F_{ST} values across and within the populations. This was confirmed by the AMOVA analyses with most of the variation shown within populations (91.7%). Negative F_{IS} values in the three breeds indicated limited inbreeding. Population structure analyses revealed six distinct groups, with the Saanen population clustering into three sub-groups. The Toggenburg and British Alpine breeds formed their own separate cluster, with a last cluster formed by animals from all three pure-bred populations, indicating high levels of admixture. These results caution farmers against uncontrolled crossbreeding practices and recommend routine evaluation of genetic diversity.

1. Introduction

Dairy goats were introduced to South Africa at the turn of the 20th century, originating primarily from Switzerland and the United Kingdom. Originally four breeds were officially recognised in South Africa, namely the Saanen, Toggenburg, British Alpine and an Anglo-Nubian Swiss composite (Muller, 2005). Current dairy goat production systems include purebred Saanen, Toggenburg and British Alpine goats as well as crosses between these breeds.

The total goat population in South Africa is estimated at 6.2 million animals of which 63% are unimproved types (FAO, 2012). The dairy goat sector is however small with only approximately 4000 goats (Directorate: Animal Production, 2007). Despite this relatively small population size, a niche market is served with production of fresh milk and specialty cheeses (Directorate: Animal Production, 2007). Marketing of these products occur mostly in an informal way, such as by selling directly to consumers via on-farm sales, or at fresh food, organic or farmer's markets. Limited quantities of local goat's milk products are sold through retailers and supermarket chains, therefore no official milk production figures are available, but unofficial estimates gauge South African goat milk production around 1.4 million tonnes per annum (Directorate: Animal Production, 2007).

The continuous supply of goat milk is hampered by the seasonality of production seen in the commercial herds, where around 82% of the does kid in the spring (Muller, 2005), resulting in a couple of months in a year when no fresh goats' milk is produced. The total volume of milk produced is insufficient to warrant investment in large scale freezing facilities to ensure year-round supply (Directorate: Animal Production, 2007).

The dairy goat population in South Africa originates from a small number of foundation animals that were imported from Germany, Switzerland, Italy, France and the United Kingdom during the early 1900s (Muller, 2005). Despite limited additional imports over the past few decades, the South African population has been isolated from the rest of the world's goat production centres largely due to logistical difficulties. There is a growing interest in keeping dairy goats and concerned breeders are questioning whether there is sufficient genetic variation within the

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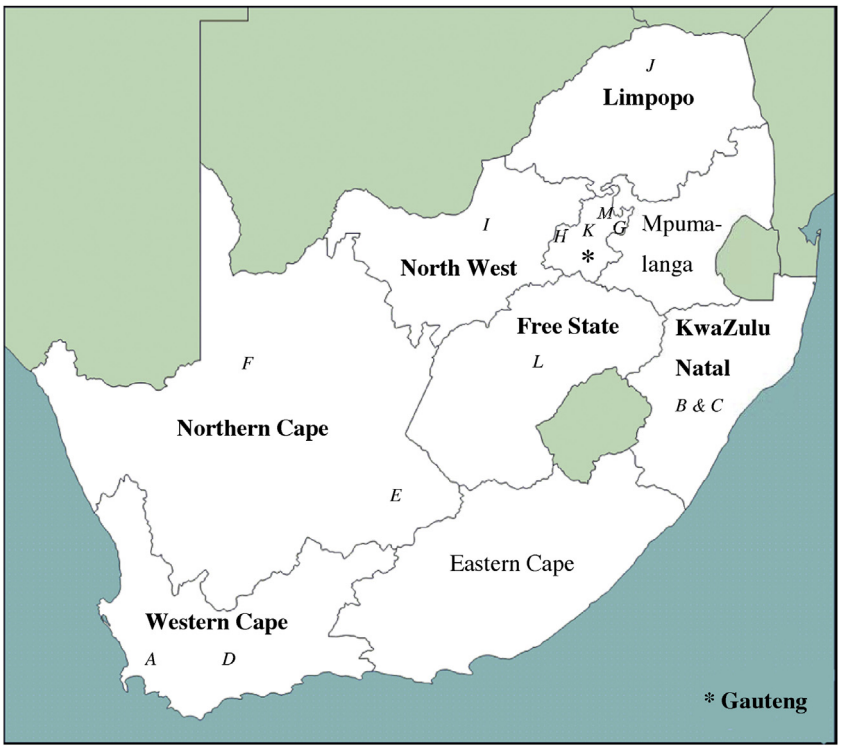

Fig. 1. Sampling locations with the sampled provinces printed in bold, the closest town shown in italics (A: Paarl; B and C: Nottingham Road; D: Montague; E: De Aar; F: Middelpos; G: Bronkhorstspruit; H: Hekpoort; I: Delareyville; J: Louis Trichardt; K: Pretoria; L: Brandfort; M: Rayton).

population to support the growing industry. Microsatellite markers have been widely used to assess genetic diversity in livestock species, including goats (Saitbekova et al., 1999). In this study a panel of microsatellite markers was used to assess the genetic diversity of the South African commercial dairy goat population to guide decision making for genetic management and improvement.

2. Materials and methods

2.1. Sample collection and DNA extraction

A total of 240 dairy goats were sampled for the study with consent of the individual farmers and breeders. Ethical approval (EC088-12) for the study was obtained from the University of Pretoria Animal Use and Care Committee in the Faculty of Natural and Agricultural Sciences. Blood was collected from 240 dairy goats (130 Saanen, 51 Toggenburg and 59 British Alpine) from 13 dairy goat farms representing seven provinces in South Africa (Fig. 1). Six of these farms specialised in only one of the breeds (five in Saanen and one in Toggenburg), while the remainder had two or more of these breeds in their herds. Both registered and grade animals were sampled from these herds, and pedigree records were used to ensure unrelated sampling. In instances where on-farm records were unavailable, random sampling based on differences in age and production status were performed to prevent sampling related animals.

5 ml blood was collected from the jugular vein of mature goats using EDTA tubes. The blood samples were transferred into screw-top tubes, which was duplicated for each sample, and stored at −40 °C until DNA extraction. DNA was extracted using a Qiagen DNeasy® Blood and Tissue kit (Qiagen, Hilden, Germany), according to the standard protocol prescribed by the manufacturer in the Animal Breeding and Genetics Laboratory of the Department of Animal and Wildlife Sciences at the University of Pretoria.

2.2. Genotyping and statistical analysis

Twenty-five microsatellites were used for this study, consisting of 16 markers from the FAO/ISAG panel recommended for diversity studies in goats (FAO, 2011). Three additional markers from studies by Glowatzki-Mullis et al. (2008), Barrera-Saldaña et al. (2010) and Bruno-de-Sousa et al. (2011), as well as six markers from Visser et al. (2011) were respectively added based on the polymorphic nature reported in these studies.

The microsatellites were fluorescently labelled, and PCR amplification was carried out using a GeneAmp® PCR System 9700 thermocycler (Applied Biosystems, Foster City, USA). Successful amplicons were genotyped using an ABI PRISM® 3500XL DNA Genetic Analyser (Applied Biosystems, Foster City, USA) at the FABI (Forestry and Agricultural Biotechnology Institute) sequencing laboratory of the University of Pretoria. Raw genotyping results were processed with the GeneMarker™ software (www.softgenetics.com/GeneMarker.html) to determine the fragment sizes for each locus for further analysis. Excel Microsatellite Toolkit (Park, 2001) was used to perform quality control and to determine polymorphic information content (PIC) values. Data conversion for use in other statistical software were performed with CONVERT 1.31 (Glaubitz, 2004) software. CONVERT and MSTookit (Park, 2001) were used to calculate allelic frequencies, mean number of alleles, observed and expected heterozygosity in the different populations. Private alleles within the populations were also identified using this software.

FSTAT version 2.9.3.2 (Goudet, 2001) was used to calculate Wright's *F*-statistics (F_{ST}, F_{IT}, F_{IS}) for each locus, both over the whole population, and for each breed separately. Calculations are based on the method by Weir and Cockerham (1984) (Goudet, 2001). The analysis of molecular variance (AMOVA) and the deviation from Hardy Weinberg Equilibrium (HWE) were conducted using ARLEQUIN version 3.5.1.2 (Excoffier and Lischer, 2010).

The analysis of the population structure was performed with the software STRUCTURE 2.3.4 (Pritchard et al., 2000; Falush et al., 2003) to determine the true number of populations (K), by using Bayesian-based assignment principles. The model used for the simulation assumes admixture in the ancestry, and therefore assumes correlated allele frequencies. The model assumed the probability of the number of populations (Ln Pr ($X|K$)) to be $2 \leq K \leq 9$. Five independent runs were performed for each K, and the probability value for each K was averaged over the runs. The runs were carried out with a burn-in period of 100,000 steps, followed by 500,000 Markov chain Monte Carlo (MCMC) iterations.