

Structure of cattle, sheep, goat and buffalo populations using single nucleotide polymorphisms in genes affecting lipid metabolism

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ABSTRACT

Single nucleotide polymorphism (SNPs) have the potential to become the genetic marker of choice in studies on the ecology and the conservation of natural populations because of their high frequency across the genome. Being biallelic markers, SNPs are intrinsically less variable than microsatellites, so individual locus information content is low. However, in population studies, this can be compensated for by the use of many more SNPs to obtain a suitable statistical power. SNPs in candidate genes could reveal chromosomal regions subject to natural or artificial selection directly or by linkage disequilibrium. In this study we used 69 SNPs, identified in 20 candidate genes involved in milk fat composition, to assess the genetic diversity within and across four ruminant species (cattle, sheep, goat and buffalo). SNPs were characterised and genotyped on 459 individuals belonging to 15 breeds and the allelic frequencies of the 2 alleles were calculated both at species and breed level. Individuals were clustered applying a parametric genetic mixture analysis implemented in the Structure 2.0 software. The number of genetic clusters (K) was tested using the no admixture model, a burning period of 100,000 followed by 200,000 MCMC repeats and considering SNPs frequencies correlated. The likelihood values and the variance of the bootstrap samples so obtained were plotted against K (ranging from 2 to 20, a number higher of the true number of breeds) in order to estimate the optimal K value. The method resolved 10 populations, being able to correctly identify breeds of cows, sheep and buffalo. Goat breeds remained unresolved, demonstrating the lower diversity found in this species in comparison to the other species. These findings are in agreement with other studies that used neutral markers like microsatellites.