

Abstract

The Genetic Analysis of the Barbados Blackbelly Sheep and Other Caribbean Hair Sheep at Microsatellite Loci

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This dissertation examines the genetic analysis of the Barbados Blackbelly (BBB) sheep and other Caribbean hair sheep breeds at 19 polymorphic microsatellite loci. The study examines the usefulness of a panel of 19 *ovine*, *bovine* and *caprine* microsatellites in the identification of breeds of sheep and the genetic similarities within and between populations of a particular breed. Through the construction of phylogenetic neighbour joining trees based on allele frequencies it is possible to determine the population structure and differentiate breeds of Caribbean hair sheep. Analysis of molecular variance (AMOVA) confirms that the Barbados population of Barbados Blackbelly sheep is genetically distinguishable from other populations of Barbados Blackbelly sheep and that it is possible to use the methodology to assign individual sheep to the correct population of the Barbados Blackbelly sheep. All of the populations of Caribbean hair sheep were found to be inbred. The Virgin Island White sheep was least inbred with an inbreeding coefficient (F) value of 0.22 as compared to values of 0.42 for the Barbados Blackbelly and 0.44 for the St. Elizabeth sheep. This level of inbreeding is reflected in the loss of heterozygosity in the populations that were investigated ($R^2=0.680$, $p<0.001$) and reflected in the fixation at locus *MAF214* the Barbados population of Barbados Blackbelly sheep with an inbreeding coefficient of 1. The methodology confirms that the calculation of Wright's F_{ST} can determine the genetic variation within and between the populations. Each individual in the study was correctly assigned to a population with $\geq 95\%$ confidence at $p < 0.005$.

KEY WORDS: Leroy McClean; Barbados Blackbelly sheep; Caribbean Hair sheep; Microsatellite polymorphism; Heterozygosity, Inbreeding coefficient; Phylogenetic trees; Wright's F_{ST} .