

PCR-SSCP Polymorphism of BMP4 Gene (Intron II) in Goats in Damana and Thirukkivil Veterinary Service Divisions in the Ampara District of Sri Lanka

L.G.S. Lokugallappatti^{1,*}, H.R. Wijesena², D.M.S. Munasinghe¹, D.C.A. Gunawardena¹ and H.B.S. Ariyaratne¹

¹*Department of Basic Veterinary Sciences, Faculty of Veterinary Medicine and Animal Science, University of Peradeniya*

²*Faculty of Animal Science and Export Agriculture, Uva Wellasa University of Sri Lanka*

Application of molecular genetic approaches for screening of economically important quantitative traits (i.e. growth and reproduction) in goats is an effective way of increasing their productivity through improved selection based on genetic markers. Single Strand Confirmation Polymorphism (SSCP) analysis is one such powerful genetic screening method to identify the sequence variation in Polymerase Chain Reaction (PCR) amplified DNA. In the present preliminary study, we investigated genetic variation in the second intron of bone morphogenetic protein 4 (BMP4) gene, by PCR-SSCP, in local indigenous (LI) and Jamnapari crossbred (JC) goats in Damana and Thirukkivil Veterinary Service (VS) divisions in the Ampara district.

Genomic DNA was extracted from a total of 103 samples (49 LI and 54 JC) collected from 15 farms located in the two VS divisions and subjected to PCR-SSCP analysis. Polymorphism was detected in both LI and JC goats of the study area and five different conformational patterns were identified (A through E). Three conformational patterns (A, B and C) were found in both LI and JC animals. Patterns D and E were unique to LI animals, indicating the benefit of searching for more genetic markers. Calculated total frequencies of patterns A, B, C, D and E as revealed by PCR-SSCP were 58.25%, 14.56%, 5.83%, 11.65% and 9.71% respectively. In general, pattern A was predominantly found in both LI (40.43%) and JC (73.21%) whereas pattern C was found to be at lowest frequency in both groups. Pattern D observed in LI goats may have some association with phenotype and growth of the animals as we observed similar external characters in all the animals possessing pattern D. Gene sequencing of the five conformational patterns observed are being pursued to identify the genotypes and the alleles present.

Financial assistance by University of Peradeniya, Research Grants RG/2009/44/V is acknowledged.