Genetics and Molecular Research

Genetic polymorphisms in β-defensin II gene in Amazon sheep from Brazil

B.B. Souza[1], E.M. Barbosa[2], J.S.N. Azevedo[3], J.E.G. Campelo[4], L.F.S. Rodrigues[3], L.M.L. Pinheiro[5], S.C.B Silva[7], A.S. Schierholt[3], P.H. Souza[3], E.C. Gonçalves[5] and E. Silva Filho[3]

[1]Curso de Zootecnia, Universidade Federal Rural da Amazônia, Belém, PA, Brasil
[2]Curso de Pós-graduação em Ciência Animal da Universidade Federal do Pará, Belém, PA, Brasil
[3]Centro de Pesquisa de Caprinos e Ovinos do Pará, Universidade Federal Rural da Amazônia, Belém, PA, Brasil
[4]Departamento de Zootecnia, Universidade Federal do Piauí, Teresina, PI, Brasil
[5]Departamento de Ciências Naturais, Universidade Federal do Pará, Breves, PA, Brasil
[6]Instituto de Ciências Biológicas, Universidade Federal do Pará, Belém, PA, Brasil
[7]Departamento de Medicina Veterinária, Universidade Estadual de Santa Cruz, Ilhéus, BA, Brasil

Corresponding author: E. Silva Filho
E-mail: silva.filho@ufra.edu.br

Genet. Mol. Res. 14 (4): 12805-12810 (2015)
Received May 14, 2015
Accepted August 20, 2015
Published October 19, 2015
DOI http://dx.doi.org/10.4238/2015.October.19.24

ABSTRACT. The northern region of Brazil produces a large number of sheep, with Pará being the largest sheep breeding state in the region. In the Amazon region, livestock production is a challenge due to the high diversity of pathogens affecting humans and animals. Defensins are antimicrobial peptides acting as a first barrier against micro-organisms and present high variation in different organisms. The objective of this study was to detect polymorphisms in exon II in β-defensin II in Amazon sheep. The gene was amplified by PCR from DNA extracted from 47 sheep blood samples from the Santa Inês breed. Products were sequenced, aligned and analyzed.

Three single nucleotide polymorphism (SNP) positions were observed with transition substitutions (A↔G) at positions 1643, 1659, and 1750. The 1643 and 1750 SNPs showed a low variability and significant deviations from Hardy-Weinberg equilibrium (HWE) ($P < 0.05$) meanwhile the SNP 1659 showed moderate absence of genetic variability and deviation from HWE ($P > 0.05$). Polymorphisms at 1643 and 1659 were predicted to modify amino acids in the peptide chain (isoleucine to valine and arginine to lysine, respectively) with no effects on protein function. Results from this study suggest that SNPs are important markers for β-defensin II efficiency studies on the immune system of sheep in the Brazilian Amazon.

Key words: Sheep beta defensin-2; Innate immunity; Sheep; Single nucleotide polymorphism; Antimicrobial peptides

