ANIMAL BIOTECHNOLOGY

COMPARATIVE GENOMICS OF GROWTH-ASSOCIATED *MSTN* GENE EXONS 1 AND 3 AMONG NIGERIAN GOAT BREEDS AND SELECTED ANIMAL SPECIES

M.T. Sanni[1]*, M. Okpeku[2], G.O. Onasanya[3], B.O. Oluwatosin[4], C.O.N. Ikeobi[1], O.A. Adebambo[1]

[1]*Department of Animal Breeding and Genetics, Federal University of Agriculture, Abeokuta, Nigeria*

[2]*Department of Animal Science, Niger Delta University, Wilberforce Island, Amasomma, Bayelsa State, Nigeria*

[3]*Department of Animal Science, Federal University, Dutse, Nigeria*

[4]*Department of Animal Production and Health, Federal University of Agriculture, Abeokuta, Nigeria*

***Corresponding Author:** sannitim4real@yahoo.com*

Abstract

To better understand the homology and evolution of the myostatin (MSTN) gene and its exonic regions in goat, we amplified and sequenced the exons 1 and 3 regions of MSTN gene from the blood of Nigerian West African dwarf (WAD), Sahel (SH), Red Sokoto (RS) goats by using polymerase chain reaction. The sequences of WAD, SH, RS goats were compared with those of other selected animal species available in GenBank. The sequence homology of the exon 1 region of MSTN gene of Nigerian goat with published species ranged from 88 - 100% in ruminants and 78 - 92% in monogastric and nonruminants. The percent amino acid sequence similarity of the Nigerian caprine sequence at the exon 3 region of MSTN gene ranged from 95 - 100% in ruminants and with little variation from 97 - 98% in other nonruminants. Phylogeny analyses showed sequences from within the same species having close relationships and clustering together. The homology of the MSTN in the evolution of Nigerian goat breeds and the selected species used for the study is highly conservative.

Key Words: Comparative genomics, myostatin, *MSTN*, goats, Nigeria

Introduction

Myostatin gene is an important candidate gene for growth and development of domestic animals due to its key role in muscle growth and its potential applications in goat breeding (Alakilli *et al.*, 2012). The *MSTN* gene belonging to the Transforming Growth Factor β (TGF-β) superfamily of secreted growth factors and differentiation factors is responsible for embryonic and adult skeletal muscle development (Baron *et al.*, 2011). This superfamily encompasses a large number of growth and differentiation factors that play pivotal roles in regulating embryonic development and maintaining tissue homeostasis in adult animals (Hickford *et al.*, 2010). This superfamily is known to block haematogenesis, myogenesis, and enhance chondrogenesis as well as epithelial cell differentiation *in vitro* (Dehnavi *et al.*, 2012). *MSTN*, like most other TGF-β factors, is highly conserved across species, with evidence of a high level of diversity within species (Grobet *et al.*, 1998). Exons of genes contain the genetic information that is transcribed and translated to the protein product that produces, directly or indirectly, observed phenotypes of traits (Singh *et al.*, 2012). Sequencing of the myostatin locus from farm animals is important to produce genomic resources for understanding the structure, function, and evolution of the gene. The focus of this study is to comparatively analyse the *MSTN* gene among Nigerian goat breeds and other selected animal species with particular emphasis on the exons 1 and 3 regions of *MSTN* gene.

Materials and Methods

Blood samples were collected through the jugular vein from randomly-selected **WAD** (45), **SH** (44) **and RS** (55) goat samples of Nigeria from institutional farm, farmers' herds, and local markets in Abeokuta, Ogun State, Nigeria. Genomic DNA was isolated at the Animal Breeding and Genetics Laboratory, Federal University of Agriculture, Abeokuta, Nigeria using *Quick-gDNA*™ MiniPrep Genomic DNA Purification Kit (Zymo Research, USA). The PCR primer pairs used to amplify the exons 1 and 3 regions of *MSTN* gene were designed from the exon-intron boundaries using web interface of Primer3 (http://frodo.wi.mit.edu/). The primer pair sequences were: exon 1, 1F: AGGCATTAACGTTTGGCTTG, 1R: ACACTAGAACAGCAGTCAGCAGA and exon 3, 3F: TCTTTAATAATGACTCCCTGCG and 3R: GAACACCCACAGCGATCTACT. Standard reagent and protocols were from Qiagen. The amplification reaction for exon 1 consists of 35 cycles of 95°C for 30 sec, 56°C for 1 min and 72°C