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A Marker- and Runs of Homozygosity-Based Assessment of the Inbreeding Status of South African Beef Cattle Populations

SIMON LASHMAR, ESTE VAN MARLE-KÖSTER

University of Pretoria, Department of Animal Science, South Africa

Abstract

Various factors including directional, within-breed selection practices may lead to a reduction in the genetic diversity (and subsequently, an increase in the autozygosity) of indigenous beef cattle populations. These local breeds form an integral part of the South African (SA) beef-producing industry, and contribute to commercial, communal and small-holder production systems. The loss in genetic diversity may have a detrimental impact on their ability to adapt to the stressors that will accompany expected changes in their environment. It is therefore crucial to monitor and manage the level of inbreeding, and consanguineous mating. The aim of this study was to perform a genomic characterisation and quantification of the inbreeding and runs of homozygosity (ROH) in four SA breeds, namely the SA Boran (n=270), Drakensberger (n=299), Nguni (n=291), and Tuli (n=155). Single nucleotide polymorphism (SNP) genotypes, generated using the Illumina® Bovine 150K panel, were subjected to standard call rate (0.05), MAF (0.02) and Hardy-Weinberg Equilibrium ($p < 0.001$) quality control procedures and a subset of 130,475 autosomal SNPs were retained for marker- and ROH-wise inbreeding estimation as well as the profiling of genome-wide ROH segments. The analysis identified 20,015 ROH segments in total, with mean population-wide numbers ranging from 3,235 for the Nguni to 4,723 for the SA Boran. The mean across-population ROH length was 6.24Mb, and the highest frequency of ROH were observed in the shortest length category (<4Mb), corresponding to more a more distant introduction of inbreeding, for all populations. Across all breeds the F_{IS} and F_{ROH} estimates were small and positive, which is indicative of low levels of inbreeding; the F_{IS} values ranged from -0.05 for the SA Boran to 0.026 for the Nguni, whilst the F_{ROH} values were 0.002, 0.003, 0.002 and 0.003 for the SA Boran, Drakensberger, Nguni and Tuli breeds, respectively. Overall, the degree of inbreeding was found to be at an acceptable and manageable level, posing no imminent threat to the genetic diversity, which is important to sustain the breeds' adaptive capabilities. The frequency and lengths of the ROH identified furthermore corresponded to the individual breed histories and the selection pressures to which each breed is exposed.

Keywords: Autozygosity, cattle, indigenous, single nucleotide polymorphism