

Preserving Unique Genetic Resources of Nguni Cattle for Sustainable Production in Changing Environments



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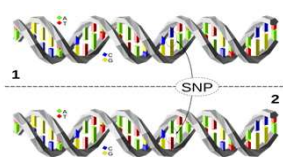
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Introduction

- Indigenous livestock have important functions of provision of food and income to socio-economic, cultural and ecological roles.
- They also have adaptive traits ranging from drought tolerant, resistance to ticks and tick borne diseases, heat tolerance and resistance to trypanosomosis, traits needed for changing environments.
- Indigenous cattle breeds of South Africa, Afrikaner, Bonsmara, Drakensberger, Nguni and Tuli, provide a valuable genetic resource that supports communities with reasonable products such as meat, milk, leather, as well as various socio-cultural functions.
- These breeds provide reliable resources for climate changes.
- Genomic improvement on these breeds is very important in maintaining their diversity and sustainable production for food security.
- The aim of this study was to perform functional annotation on selective sweep regions identified on Nguni cattle genome-wide

South African Nguni



Methods

Selective sweeps data and functional annotation

- Selective sweep regions used in this study was obtained from the study of Zwane et al., (2019).
- These regions were identified using the Z-transformed pooled heterozygosity (Zhp) scores computed using a 50% overlapping sliding window approach with 150 kb windows of SNP distribution.
- A total of 264 candidate selective sweep regions (Zhp Z-scores ≤ -4) were identified in Nguni cattle, and these were the regions used for gene annotation.
- Animal QTLdb was used to retrieve quantitative trait loci (QTL) within the putative selective sweep regions.
- Gene ID lists were converted to gene names and symbols using the Database for Annotation, Visualization, and Integrated Discovery (DAVID) (Kanehisa and GOTO)
- Gene enrichment in molecular functional categories (KEGG pathways) were then examined using DAVID.
- The top-listed gene ontology terms associated with phenotypic characteristics and with statistical significance ($p < 0.05$) were selected.

Results

Table 1: List of DAVID's top 10 genes within genomic location (strand) and their phenotypic annotation

Gene Name	Genomic location (strand)	Phenotype
CRHR2	4:66002072-66006203	Increased insulin sensitivity
NOD2	18:19157447-19166134	decreased tumour necrosis factor secretion
YWHAZ	14:65584487-65617329	abnormal skin morphology
IRAK3	5:47796256-47839675	decreased body size
IL21R	25:25233186-25268874	decreased T cell proliferation
CRHR2	4:66002072-66006203	increased insulin sensitivity
RGS4	3:6287012-6292402	decreased systemic arterial diastolic blood pressure
PRKAA1	20:33688291-33716677	None found
RGS5	3:6228349-6426528	decreased systemic arterial diastolic blood pressure
SP1	5:26753574-26759487	None found

Results

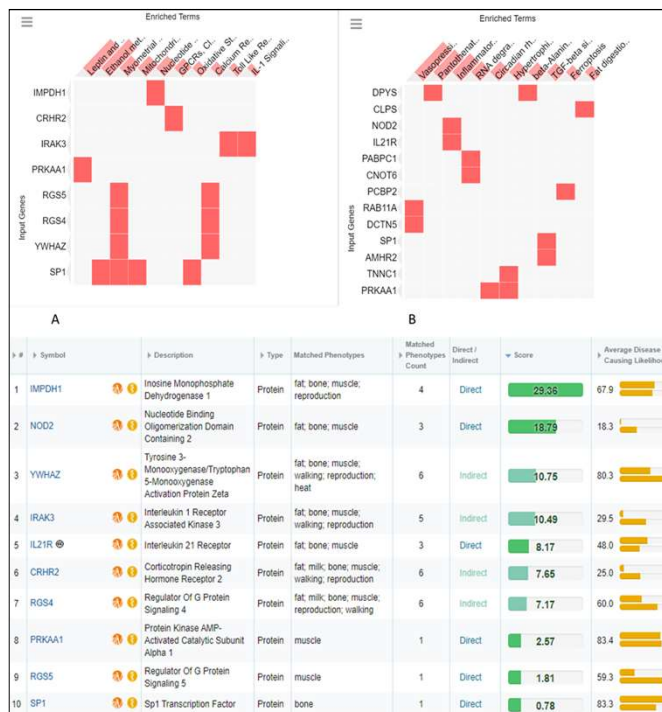


Figure 1: Genes associated with cattle phenotypes

Discussion and conclusion

- Gene annotation and enrichment analysis of selective sweeps in Nguni cattle identified about 58 genes that were associated to eight randomly chosen phenotypes queries (fat, milk production, walking ability, heat tolerance, meat production, reproduction, bone and muscle development).
- Four genes were found to be associated with Myometrial Relaxation and Contraction Pathways in Nguni cattle (SP1, YWHAZ, RGS4 and RGS5).
- These genes have been previously reported to be associated with fat digestion, bone and muscle development, reproduction and walking ability in cattle.
- This is in line with the observable phenotypes in Nguni cattle such as walking ability reported by Matjuda et al., (2012).
- Genes NOD2 and IL21R were associated with inflammatory bowel diseases (IBDs).
- The CLPS gene have been found to be associated with fat content in cattle.
- These genes serve as useful genetic tools for genetic variation presence in Nguni cattle, and can be important for their conservation and improvement together with other South African indigenous cattle breeds
- More annotations are needed to determine functional genes on non-synonymous and other important regions in these breeds, for enhanced production.



Acknowledgement

