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Landscape genomics in South Africa

10/10/2018

Genomic technologies for the improvement of South African beef cattle

Industry Sector: Cattle And Small Stock

Research Focus Area: Livestock Production With Global Competitiveness: Breeding, Physiology And Management

Research Institute: Agriculture Research Institute – OVI

Researcher: Dr. Pranisha Omduth Soma

The Research Team

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Year Of Completion : 2018

Aims Of The Project

- To estimate linkage disequilibrium within South African beef cattle
- To perform a genome wide scan for signatures of selection in beef cattle
- To sequence genomic regions targeted by selection in order to identify possible polymorphisms

Executive Summary

South African indigenous and locally developed cattle breeds possess adaptive traits that are usually associated with tolerance to various diseases, extreme temperatures and humidity, and to change in feed availability. These breeds are also adapted to low-input management systems and have shown the ability to survive, produce and reproduce under harsh environments. Thus, these breeds hold potential in the changing South African production environments. However, little is known about the nature or extent of the genetic variation underlying these breeds.

The aim of this study was to conduct a genome wide scan for signatures of selection among Afrikaner, Nguni, Drakensberger, Bonsmara, Angus and Holstein cattle breeds of South Africa using data generated from the Bovine SNP50k BeadChip. The Angus and Holstein breeds were included as reference breeds since they have been extensively characterized using similar tools.

Therefore, in this project, the Bovine SNP50 BeadChip was used to characterize the genetic diversity and population structure of SA cattle breeds, determine the linkage disequilibrium and conduct a genome wide scan for signatures of selection among the Afrikaner (n=44), Nguni (n=54), Drakensberger (n=47) and Bonsmara (n=46)., using the Angus (n=31) and Holstein (n=29) cattle reference groups.

The first experiment performed included the evaluation of the Bovine SNP50 BeadChip to determine its utility for genome wide studies of South African cattle. Results of this experiment revealed that over 50 % of the SNPs were polymorphic (eg. Nguni = 35 843), indicating that the Bovine SNP50 assay would be useful for genome wide studies among South African cattle breeds.

Information about genetic diversity and population structure among cattle breeds is essential for genetic improvement, understanding of environmental adaptation as well as utilization and conservation of cattle breeds. Genetic diversity within the cattle breeds was analyzed using three measures of genetic diversity namely allelic richness, expected heterozygosity and inbreeding coefficient. The genetic diversity and population structure analyses indicated that the Afrikaner cattle had the lowest level of genetic diversity (He=0.24) while the Drakensberger cattle (He=0.30) had the highest among indigenous and locally-developed breeds. As expected, the average genetic distance was the greatest between indigenous breeds and *Bos Taurus* breeds but the lowest among indigenous and locally-developed breeds. Model-based clustering revealed some level of admixture among indigenous and locally-developed breeds and supported the clustering of the breeds according to their history of origin. Clear genetic divergence between South African (indigenous and locally-developed cattle breeds) and *Bos Taurus* cattle breeds was observed which suggested distinct genetic resources in South African cattle breeds which should be conserved in order to cope with unpredictable environments.

The extent of linkage disequilibrium (LD) is important for determining the minimum distance between markers for effective genome coverage for genome wide association studies. It can also provide insight into the evolutionary history of a population. The analyses of the extent of linkage disequilibrium (LD) showed that Afrikaner, Angus and Holstein had higher LD compared to Nguni, Drakensberger and Bonsmara cattle at all tested genomic distances. The higher LD within the Afrikaner cattle suggested that this breed has experienced considerable selection forces in contrast to what is expected of indigenous breeds and would require lower marker (50 000) density relative to what will be required for the Nguni, Drakensberger (150 000) and Bonsmara (75 000) cattle for genome wide studies. New breeding strategies may be required for the Afrikaner cattle breed to ensure future fitness of the breed. The effective population size for the Nguni, Drakensberger and Bonsmara were above the FAO recommended level.

The detection of selection signatures among cattle breeds may assist in locating regions of the genome that are, or have been, functionally important and targeted by selection. In this study, two approaches were employed. The first was based on the detection of genomic regions for which haplotypes have been driven towards complete

Fixation within breeds. The second approach identified regions of the genome exhibiting elevated population differentiation (Fst). A total of 47 genomic regions were identified as harboring potential signatures of selection using both methods. Thirty three of these regions were successfully annotated to identify candidate genes. Among these, were keratin genes (KRT222, KRT24, KRT25, KRT26 and KRT27) and one heat shock protein (HSPB9) on chromosome 19 (BTA) at 41,447,971-41,926,734 bp in the Nguni that have been previously associated with adaptation to tropical environments in Zebu cattle.

Furthermore, a number of genes associated with nervous system (WNT5B, FMOD, PRELP, ATP2B), immune response (CYM, CDC6, CDK10), production (MTPN, IGFBP4, TGFBI, AJAPI) and reproductive (ADIPOR2, OVOS2, RBBP8) performances were detected to be under selection in this study.

Target probes for enrichment were designed from exome and 5' and 3' untranslated regions of the cattle genome. Many SNP's were identified in regulatory regions, leading to conformational changes in factor-binding sites. Gene ontology enrichment and clustering, resulted in the enrichment of gene ontology terms involved in fertility-related categories. Taking advantage of the availability of the fully sequenced bovine genome, the South African beef breeds were sequenced to detect genetic variants, in particular, large-scale SNP's, which may contribute to the beef cattle genomics in South Africa.

The results presented in this study, forms the basis for effective management of South African cattle breeds and provides a useful foundation for the detection of mutations underlying genetic variation in traits of economic importance in South African cattle breeds.

This study produced one PhD thesis, 12 peer reviewed scientific articles and one popular article.

Popular Article

Genomic Technology For South African Beef Cattle

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South African (SA) indigenous and locally developed cattle breeds possess adaptive traits that are usually associated with tolerance to various diseases, extreme temperatures and humidity and to change in the availability to feed. These breeds are also adapted to low-input management systems and have shown the ability to survive, produce and reproduce under harsh environments. Thus, these breeds hold potential in the changing South African production environments. Despite their large numbers and not endangered status, their adaptive traits are of importance and there is a worldwide drive for the effective management of indigenous genetic resources, as they could be most valuable in selection and breeding programs in times of biological stress such as famine, drought or disease epidemics.

The recent development in molecular genetics and bioinformatics has enabled the development of genome wide SNP DNA arrays for livestock species including cattle. These chips present opportunities to study South African cattle breeds in order to unravel population structure as well as the genetic potential of these breeds.

The Bovine SNP50 BeadChip was used to genetically characterize these breeds. The study populations comprised the Afrikaner, Nguni, Drakensberger and Bonsmara cattle breeds with the Angus and Holstein cattle as reference groups. Results of this study demonstrated that the genomic information generated from the BovineSNP50 has potential for application in South African cattle populations and allow for the unravelling of their genetic potential with regard to production, reproduction, disease resistance and adaptation.

There was a clear genetic divergence between South African (indigenous and locally-developed cattle breeds) and Bos taurus cattle breeds which suggested distinct genetic resources in South African cattle breeds that should be properly utilized in order to cope with unpredictable future environments. The level of inbreeding was relatively low across the study populations although the assessment of the inbreeding level should be done every five years to determine any unfavourable change in inbreeding levels, so that appropriate steps can be taken. The population structure analysis in the study revealed some signals of admixture and genetic relationship between Afrikaner, Nguni, Drakensberger and Bonsmara. Nguni cattle shared some genetic links with the Afrikaner cattle, with about 8% of its genome derived from the Afrikaner cattle.   This result may reflect co-ancestry regarding the origin of these breeds as both these came from the same migration route into Southern Africa (Scholtz, 2011).

On the other hand, the Bonsmara cattle shared limited genetic links (0.5%) with Afrikaner cattle, which was unexpected. This low relationship may be attributed to genetic drift or a small sample size. Information generated from this study forms the basis for future management of these cattle breeds. The effective population size appeared to have decreased in all the study breeds in recent generations. The lower effective population sizes for the Afrikaner, Angus and Holstein breeds compared to those of Nguni, Bonsmara and Drakensberger at more recent generations, could be due to intense selection, inbreeding and probably wide spread use of artificial insemination in South Africa and the use of relatively few elite sires after 1970 (Hayes et al., 1990). In order to maximise the net response in genetic gain, Food and Agricultural Organisation (FAO) (FAO 1998) recommended an effective population size of 50 per generation. The Afrikaner, Angus and Holstein were below the FAO recommended number.

This suggested that these breeds are endangered and close to critical stage therefore pointing out the need for implementation of appropriate conservation programs as well as new selection and breeding strategies to ensure long-term fitness of these breeds. These could include increasing the number of

animals contributing offspring to each generation by increasing the cow populations. It is critical for food security and rural development because it allows farmers to select stock or develop new breeds in response to changing conditions, including climate change, new or resurgent disease threats, new knowledge of human nutritional requirements, and changing market conditions or societal needs (FAO, 2010).

A total of 47 genomic regions were identified including genes associated with immune response, reproductive performances, coat colour, tropical adaptation and nervous system were identified. For example, the keratin family and one heat shock protein in the Nguni cattle were associated with tropical adaptation. In addition to the role that the keratin genes play during epidermis development, they also play a role in the formation of the hair shaft (Wu et al., 2008). Skin colour and the thickness of hair directly influence the thermos-resistance of cattle living in the tropics. Nguni cattle have smoother and shinier hair coats compared to European cattle breeds. These characteristics provide Nguni cattle with a greater ability to regulate body temperature and to more efficiently maintain cellular function during heat as well as the ability to resist tick infestation (Marufu et al., 2009).

Several candidate genes directly or indirectly involved in reproductive pathways including oestrus process, ovulation rate, testis development and prostaglandin were found. The fact that the Afrikaner, Nguni, Drakensberger and Bonsmara cattle have the ability to produce and reproduce under harsh environment conditions and are considered excellent dam lines for crossbreeding (Scholtz, 2010), supports the strong selection on reproductive loci that is likely to have occurred in their adaptation to South African conditions. Genes involved in muscle organ development and skeleton development were also identified as being under selection in the Bonsmara and Afrikaner cattle populations. The results presented in the study forms the basis for effective management of South African cattle breeds. Furthermore, a genomic understanding of how and where natural selection has shaped the pattern of genetic variation among cattle breeds in SA was unveiled by identifying loci that are important to the development of SA cattle breeds.

Future studies should focus on expanding the breed level analysis through the inclusion of all major African cattle breeds (Gautier et al., 2009) together with cattle breeds of the world. This could further provide insight with regard to the genetic relationship shared among South African cattle breeds and cattle breeds of the world and shed more light on the genomic requirement for survival in African environments.

Please contact the Primary Researcher if you need a copy of the comprehensive report of this project – Pranisha Soma on *pranisha@arc.agric.za*

📁 Breeding, Cattle and Small Stock, Livestock Production, physiology and management, with global competitiveness

🏷 2018, ARC, ARC-OVI, CSS, Online, Soma

‹ Chilling and electrical stimulation of beef carcasses

› Crossbreeding Afrikaner, Bonsmara and Nguni cows

DEADLINES for RESEARCHERS 2021

Proposals for 2021: TBC
Progress reports: 28 Jan 21
Final reports: 29 Jan 21 Final includes comprehensive report and popular article

COMMITEE MEETINGS for 2021

RMRDSA CSS Planning - TBC
Project Committee - TBC
Pork Planning - TBC

Calendar

			Apr 2021			
<						>
Sun	**Mon**	**Tue**	**Wed**	**Tur**	**Fri**	**Sat**
				1	2	3
4	5	6	7	8	9	10
11	12	13	14	15	16	17
18	19	20	21	22	23	24
25	26	27	28	29	30	

PORK Priority Areas

Cattle & Small Stock Programmes

1 Sustainable natural resource utilisation

2 Improvement of Livestock production and forage

3 Management of agricultural risk to create a resilient Red Meat sector

4 Sustainable health and welfare for the Red Meat sector

5 Enhancement of production and processing of Animal Products

6 Consumer and market development of the Red Meat sector

7 Commercialisation of the emerging sector

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