



# Genetic diversity of landrace cattle breeds

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## Genetic diversity and relationships among seven South African landrace and exotic cattle breeds

Industry Sector: Cattle And Small Stock

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

Research Institute: Agricultural Research Council Animal Production (ARC-AP)

Year Of Completion : 2019

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The Research Team

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## Executive Summary

### Introduction

An existing 11 microsatellite marker database that resulted from parentage verification, was used to assess genetic diversity among nine breeds of cattle. These breeds were drawn from *Bos indicus* (Boran and Brahman), *B. taurus* (Angus and Simmental) and *B. taurus africanus* (Afrikaner, Bonsmara, Drakensberger, Nguni and Tuli). Due to the cost of genotyping, genetic variability and population structure studies using single nucleotide polymorphisms (SNPs) rely on relatively low numbers of animals to represent each of the breeds. However, large numbers of animals have been genotyped for parentage verification using microsatellite markers and this microsatellite information on large numbers of animals have the potential to provide more accurate estimates of genomic variability than SNPs.

The breeds in this study were characterized by unbiased heterozygosity, effective number of alleles and inbreeding. Ranges in estimates of these parameters were 0.569–0.741, 8.818–11.455 and -0.001–0.050, respectively. The analysis of population structure revealed descent from taurine, indicine, and Sanga types with  $K=3$  and from unique progenitor populations with  $K=9$ . There are notable similarities between the results observed using a limited number of genetic markers and large numbers of animals with microsatellite markers.

The study revealed the southern African Sanga and exotic cattle breeds that are found in South Africa, are genetically distinct from each other. Therefore, using the Sanga and Sanga derived breeds in crossbreeding programs should be done with caution to ensure the conservation of genetic resources of these breeds. Furthermore, comparable genetic variability and inbreeding levels found in the present study demonstrate the genetic sturdiness of the Sanga and Sanga derived breeds. However, there is a notable similarity between the results observed in this study (using a limited number of genetic markers and large numbers of animals), with the results of studies with similar objectives which used substantial greater numbers of markers but much fewer animals.

The analyses revealed that the southern African, British and European breeds as well as the tropically adapted breed clustered separately. Therefore, exotic breeds in South Africa is expected to benefit from favourable heteroses effects due to crossing with Landrace breeds.

## Objective Statement

The present study used existing microsatellite marker databases (provided by Breeders' Societies) to estimate levels of heterozygosity and inbreeding of several southern African Sanga and exotic breeds, and quantify the genetic relationships between the breeds. To these ends, obtaining data from historical parentage databases allowed for use of substantially larger numbers of animals per breed to be studied than in previous investigations.

## Project Aims

1. To determine the level of genetic variation of each breed, therefore identifying the remaining resources of heterozygosity within the four South African landrace cattle breeds.
2. To compare the level of genetic variation between the four landrace breeds.
3. To determine the inbreeding for the breeds as whole.
4. To determine the relation (genetic un-relatedness) between South Africa's landrace breeds and Zebu, British and European breeds.

## Results

From a genetic diversity perspective, all breeds had large numbers of alleles at each locus and high frequencies of heterozygous genotypes; and thus each locus had substantial polymorphic information content. The number of alleles per locus and frequency of heterozygotes found in the present study were both toward the lower ends of the corresponding ranges for the same loci that were previously observed in a substantially larger sample of Afrikaner cattle. Inbreeding is not currently at a sufficient level so as to be problematic in the South African segments of these breeds. From the present study, the number of Clusters found with the highest probability of membership, required to describe the between-breed genetic relationships, were two ( $K=2$ ) and noticeably grouped the two taurine breeds separate from the Sanga and indicine (Afrikaner, Brahman, Boran, Nguni and Tuli) breeds. The second highest probability showed a total of three genetic Clusters ( $K=3$ ) and grouped the taurine, indicine and Sanga breeds separately. When  $K=9$  is used, breed individuality and admixture were clearly defined. Here, the Nguni was shown to be the most admixed with 31 % of membership belonging to the other eight Clusters. The Nguni is followed by Bonsmara and Drakensberger showing admixture from other Clusters up to 24 %. These results are in accordance with Makina *et al.* (2016), with the latter authors suggesting that the admixture within Nguni and Drakensberger have been involuntary, however, the admixture recognized within the Bonsmara was intentional given the breed history. Moreover, Angus showed to be the least admixed with significant membership within this Cluster with probability of 90 %. To demonstrate the genetic distances between the breeds, an NJ tree was generated. The tree illustrated the discrepancy between the three groups of cattle, with the southern African Sanga breeds grouping separately from the indicine and taurine cattle, but sharing a closer genetic background with the two indicine breeds. The NJ tree also supported the multi-locus clustering algorithm when  $K=2$  is used with reference to Bonsmara and Drakensberger and again highlights the discrepancy between the present study and the results of Makina *et al.* (2016).

## Discussion

From a genetic diversity perspective, all breeds had large numbers of alleles at each locus and high frequencies of heterozygous genotypes; and thus each locus had substantial polymorphic information content. The number of alleles per locus and frequency of heterozygotes found in the present study were both toward the lower ends of the corresponding ranges for the same loci that were previously observed in a substantially larger sample of Afrikaner cattle. Inbreeding is not currently at a sufficient level so as to be problematic in the South African segments of these breeds. From the present study, the number of

Clusters found with the highest probability of membership, required to describe the between-breed genetic relationships, were two ( $K=2$ ) and noticeably grouped the two taurine breeds separate from the Sanga and indicine (Afrikaner, Brahman, Boran, Nguni and Tuli) breeds. The second highest probability showed a total of three genetic Clusters ( $K=3$ ) and grouped the taurine, indicine and Sanga breeds separately. When  $K=9$  is used, breed individuality and admixture were clearly defined. Here, the Nguni was shown to be the most admixed with 31 % of membership belonging to the other eight Clusters. The Nguni is followed by Bonsmara and Drakensberger showing admixture from other Clusters up to 24 %. These results are in accordance with Makina *et al.* (2016), with the latter authors suggesting that the admixture within Nguni and Drakensberger have been involuntary, however, the admixture recognized within the Bonsmara was intentional given the breed history. Moreover, Angus showed to be the least admixed with significant membership within this Cluster with probability of 90 %. To demonstrate the genetic distances between the breeds, an NJ tree was generated. The tree illustrated the discrepancy between the three groups of cattle, with the southern African Sanga breeds grouping separately from the indicine and taurine cattle, but sharing a closer genetic background with the two indicine breeds. The NJ tree also supported the multi-locus clustering algorithm when  $K=2$  is used with reference to Bonsmara and Drakensberger and again highlights the discrepancy between the present study and the results of Makina *et al.* (2016).

## Conclusion

The study revealed the southern African Sanga and exotic cattle breeds that are found in South Africa, are genetically distinct from each other. Therefore, using the Sanga and Sanga derived breeds in crossbreeding programs should be done with caution to ensure the conservation of genetic resources of these breeds. Furthermore, comparable genetic variability and inbreeding levels found in the present study and Makina *et al.* (2014) demonstrate the genetic sturdiness of the Sanga and Sanga derived breeds. However, there is a notable similarity between the results observed in this study (using a limited number of genetic markers and large numbers of animals), with the results of studies with similar objectives which used substantial greater numbers of markers but much fewer animals. Thus, opportunities that arise to explore genetic diversity in both the livestock and wildlife industries in Southern Africa, may capitalize on microsatellite marker databases which remain cost-effective and accessible due to their continued use for parentage verification.

Both analyses revealed the southern African, British and European breeds as well as the tropically adapted breed clustered separately. Therefore, exotic breeds in South Africa is expected to benefit from favourable heterosis effects due to crossing with Landrace breeds. Opportunities that arise to explore genetic diversity in both the livestock- and wildlife industries may capitalize on microsatellite marker databases which remain cost-effective and accessible due to their continued use for parentage verification.

## Popular Article

### Genetic Diversity And Relationships Among Seven South African Landrace And Exotic Cattle Breeds

Genetic variability or genetic diversity is required for populations to be able to adapt to different environmental pressures. It can also be defined as the variation of alleles and genotypes present in a breed. This provides the basis for adaptive and evolutionary processes. The current level of diversity in livestock has been created by the combined forces of both natural- and artificial selection. These forces can be described as mutations, adaptations, segregation, selective breeding and genetic drift. Furthermore, genetic diversity in livestock species is essential for the adaptive responses needed in ever-changing farming conditions and ultimately to respond to the challenges created by climate change. Additionally, diversity also provides a reservoir for genetic variation to ensure that future market demands can be met through selection.

The indigenous cattle breeds of Southern Africa include the Sanga and Sanga derived cattle. Sanga cattle, especially those indigenous to southern Africa, are classified as *Bos taurus africanus*. The indigenous Sanga cattle of South Africa includes the Afrikaner, Nguni and Drakensberger, whereas the Tuli and Hugenoot are considered to be the Landrace breeds of Southern Africa. The Bonsmara is a Sanga derived composite breed. These breeds are extremely well adapted to the harsh climatic and other environmental conditions encountered under extensive ranching in South Africa. This will become even more important in the era of climate change.

Research has suggested that Sanga cattle, compared to European breeds are favourable with regard to meat tenderness. There has been speculation that the Landrace breeds may be closely related to other

tropically adapted breeds (*B. indicus*) such as the Brahman due to their morphological similarities. However, several genetic studies have demonstrated a closer relationship between Sanga and *B. taurus* breeds.

In the early 1900's there was a perception in South Africa that the indigenous breeds were inferior and this led to the promulgation of an Act in 1934 in which indigenous breeds and types were regarded as 'scrub' (non-descript). Inspectors were appointed to inspect the bulls in communal areas and to castrate them if regarded as inferior. Fortunately, this Act was applied effectively for only a few years, since it was very unpopular. However, the effect of this on especially the "purity" of the Nguni was never established. In addition, the Bonsmara is supposed to be 5/8 Afrikaner: 3/8 British composition. Through selection and subsequent upgrading, this composition may have shifted significantly. It is therefore important to also establish the relationship between the Landrace, Zebu, British and European breeds.

The Southern African landrace breeds are relatively poorly characterized at the genomic level in comparison to many taurine and indicine breeds. Using genotypes derived from microsatellite loci, several research projects have characterized contemporary populations of Bonsmara, Afrikaner, Nguni and the Tuli from Zimbabwe. Due to the cost of genotyping, substantially fewer animals (i.e.,  $\leq 50$ ) have been characterized by single nucleotide polymorphism (SNP) arrays using approximately 50 000 DNA markers to estimate the diversity of Afrikaner, Bonsmara, Drakensberger, and Nguni cattle and to evaluate their relationship to other breeds worldwide. Bi-allelic markers such as single nucleotide polymorphisms (SNPs) are currently the subject of interest globally. However, in Southern Africa, microsatellite markers have been used routinely and are more cost-effective in the livestock, wildlife and aquaculture industries. Microsatellite markers have multiple alleles and are generally more informative than SNPs. However, the latter statement is largely dependent on sample size. Microsatellites have also been used over the years for relationship studies, inbreeding levels and breed differentiation.

The aim of this study was to use microsatellite marker databases (provided by Breeders' Societies) to estimate levels of heterozygosity and inbreeding of nine Southern African Sanga and exotic breeds, and quantify the genetic relationships between the breeds. This allowed the use of substantially larger numbers of animals per breed to be studied than in previous investigations.

The breeds used in this study were Afrikaner, Angus, Bonsmara, Boran, Brahman, Drakensberger, Nguni, Simmental and Tuli. Animals were genotyped in response to requests from industry for parentage verification. At least 300 animals were randomly chosen to represent each breed,

All breeds had large numbers of alleles at each locus and high frequencies of heterozygous genotypes. Inbreeding was found not to be at a level where it will be problematic in the South African segments of these breeds. While the present study used microsatellite data, another study, using SNP data, showed similar findings regarding the genetic variability and inbreeding levels of southern African Sanga cattle.

When provision was made for two ancestral populations ( $K=2$ ), the two taurine (Angus and Simmental) breeds were separated from the Sanga and indicine (Afrikaner, Bonsmara, Brahman, Boran, Drakensberger, Nguni and Tuli) breeds. It was however noted that both Bonsmara and Drakensberger also showed some admixture of at least 30 % with the cluster belonging to Angus and Simmental. These results are consistent with the development of the Bonsmara breed with the *B. taurus* influence (5/8 Afrikaner, 3/16 Shorthorn, and 3/16 Hereford) and some uncertain or undefined breed origin of the Drakensberger.

When provision was made for three ancestral populations ( $K=3$ ), it grouped the taurine (Angus and Simmental), indicine (Brahman and Boran) and Sanga (Afrikaner, Bonsmara, Drakensberger, Nguni and Tuli) breeds separately. When  $K=9$  was used, breed individuality and admixture between the breeds could be clearly defined.

The study revealed the Southern African Sanga and exotic cattle breeds found in South Africa are genetically distinct from each other. Furthermore, comparable genetic variability and inbreeding levels found in the present- and other studies, demonstrated the genetic sturdiness of the Sanga and Sanga derived breeds.

There is a notable similarity between the results observed in this study (using a limited number of DNA markers and large numbers of animals), with the results of other studies, with similar objectives, which used substantial greater numbers of DNA markers but much fewer animals.

Both analyses revealed the southern African Sanga breeds, British and European breeds, as well as the tropically adapted Zebu breeds clustered separately. Therefore, exotic breeds in South Africa is expected

to benefit from favourable heterosis effects, when crossed with Landrace breeds. Finally, the results from this study indicate that genetic diversity in both the livestock- and wildlife industries may capitalize on microsatellite marker databases which remain cost-effective and accessible due to their use for parentage verification.

## Footer And Tags And Categorisation

**Please contact the Primary Researcher if you need a copy of the comprehensive report of this project.** Lene van der Westhuizen [lenevdwest@gmail.com](mailto:lenevdwest@gmail.com)

- Breeding, Cattle and Small Stock, Livestock Production, physiology and management
- ◆ 2019, ARC, ARC-API, CSS, Online, Westhuizen
- < Genotype imputation for indigenous beef cattle
- > Gene expression: Nguni and Bonsmara

## 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

## COMMITTEE MEETINGS for 2021

RMRDSA CSS Planning - TBC

Project Committee - TBC

Pork Planning - TBC



## Calendar

< <span style="color: red;">Apr 2021</span> >						
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**

