



Genomics for the South African Beef industry

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Establishing genomic selection for the South African beef industry

Industry Sector: Cattle And Small Stock

Focus Area: Livestock Production With Global Competitiveness (2)

Research Institute: Department Of Animal & Wildlife Sciences, University Of Pretoria (UP) And SA Studbook Association

Researcher: Prof Este Van Marle-Köster PhD

Research Team:

Title	Initials	Surname	Highest Qualification
Dr	Japie	van der Westhuizen	PhD

Final Report Approved: 2016

Aims Of The Project

- To use high throughput SNP technology to establish reference populations for the SA beef industry.

Executive Summary

The project titled “Establishing genomic selection for the South African beef industry” was conducted at the University of Pretoria, Department of Animal & Wildlife Sciences in collaboration with South African Stud Book and Animal Improvement Association.

The overall aim was to use high throughput SNP technology to establish reference populations for the SA beef industry. To attain this goal, a process for the identification of high impact animals was established, guidelines for sample collection were compiled and genotyping were performed with the available funding using both 80K SNP and 150K SNP GeneSeek (GeneSeek GGP HD) bead chips at GeneSeek (USA). Population structure analyses were performed and parameters for genetic diversity and inbreeding were calculated.

Results has shown that breeds such as the Bonsmara and SA Hereford formed separate clusters while the other indigenous breeds such as the Tuli, Afrikaner and Drakensberger showed a closer relationship. These results are important for future across-breed analyses. The commercial chips also tended to be less informative for the indigenous breeds with regard to the number of SNPs available for analyses, but still had sufficient numbers for application in genomic selection. A substantial number of genotypes have been generated for Bonsmara cattle that have also been phenotypically recorded for the traits of interest.

In this project, the Bonsmara genotypes are currently being applied as a training set for estimation of Genomic Breeding Values (GEBV's). After GEBVs have been estimated for these animals, validation will commence followed by the roll-out of routine GEBV estimation. This genomic information will provide breeders with an additional, accurate tool for selection of superior stock.

Popular Article

Genomic Selection: A New Tool For Genetic Improvement Of SA Livestock

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Introduction

Over the past two decades major discoveries and technological developments in the field of molecular genetics opened up new opportunities for genetic improvement in farm animals that were previously beyond the reach of animal breeders. The bovine genome has been mapped and sequenced and several DNA-marker types were discovered. The discovery of Single Nucleotide Polymorphism (SNP) markers and the concurrent development of appropriate high through-put technology gave rise to commercial SNP chips available for generating genomic information.

SNP markers and genomic selection

The DNA markers used for generating genomic information for genomic selection are single nucleotide polymorphisms (SNP) commonly referred to as "SNIPS". Each of these markers has two alleles and they occur very frequently across the genome. The *Bos Taurus* genome has an estimated total of nearly 4 million SNPs. It is currently estimated that a trait of economic importance (i.e. weaning weight, carcass weight, feed conversion ratio etc.) is governed by between 100 and 300 genes. Each of these genes contributes only a small amount to the phenotype that is expressed. In the past, individual genes and markers associated with genes were identified and thus only a very small portion of the phenotypic variation could be explained. By using a very dense SNP panel to genotype animals with, it is assumed that each individual SNP will be associated with at least one gene contributing to the trait of interest. When all the SNP effects are added, they should thus explain the total phenotypic variance that is expressed.

If a number of animals of a specific breed have been genotyped, and their phenotypic records are available, it is possible to draw a correlation between a SNP combination and the level of performance associated with it. This correlation is commonly referred to as the "prediction equation" or "SNP key". Genomic selection is therefore based upon the basic principle of using the information of many DNA markers and accurate and complete phenotypic records. In practical breeding, the genotypic information (Direct Genomic Value) will be included in the Estimated Breeding Value (EBV) of an animal. In this way, genomic data will be included as an additional source of information together with pedigree and performance records used in routine quantitative analyses. This process is referred to as blending and will result in providing a genomic estimated breeding value (GEBV) for each individual.

Prerequisites for implementation

The implementation of genomic selection is not a simple process and each phase requires careful planning to ensure that the end result will be accurate, useful and cost effective. The first step is the selection of the bulls to form the reference or training population. These bulls should represent the specific breed and include bulls with low, medium and high breeding values with accuracies above 60%. It is important that the traits recorded on these bulls will be the traits that breeders would like to include in selection programs and which form part of the breeding objectives for the breed. A biological sample of these animals should be available and this could be a hair, blood, semen or tissue sample for extraction of DNA.

Once the DNA is available the samples will be analyzed using an appropriate high density commercial chip. In this step the SNP effects based on high density chips and their correlation with the animals' known performance (EBV values) are established, in order to calculate the prediction equation.

Application Of SNP Technology

There is no doubt that genomic selection has significant advantages for improvement of farm animal genetics. Dairy cattle thus far have led the way and have experienced some of the advantages of having an added source of information. GEBVs can be obtained in a relative short period after birth compared to a 6-7 year period of progeny testing before a progeny-based EBV becomes available. GEBVs have distinct advantages for dairy cattle with regard to reducing costs on progeny testing and decreasing the generation interval. Genomic technology has been well received by dairy cattle breeders in the USA and Canada and indications are that genomic evaluations will replace traditional evaluations in these countries. The use of genomic selection in selection programs holds the most potential for sex-limited traits, traits that are expressed late in life and traits with low heritability.

In South Africa we are fortunate to have a long history of animal recording for a large number of cattle breeds. This data has routinely been used for EBV calculations and are widely used by South African stud breeders. The current challenge is to ensure the banking of biological samples of animals with desired traits and phenotypes, in order to obtain both molecular and phenotypic records from individuals. Application of GS globally in both the dairy and beef industries has become inevitable and smaller countries with fewer resources, like South Africa, will have to collaborate and carefully plan genetic programs to remain part of the international arena.

If you have any queries, please contact the researcher Prof Este van Marle-Köster PhD on Este.vanMarle-Koster@up.ac.za

📁 Cattle and Small Stock, Livestock Production, with global competitiveness

📅 2016, Paper, UP

< Agri Benchmark beef and sheep

> Heterosis effects on beef sensory and leather quality traits

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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

< 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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