

Reference Population for South African Bonsmara Cattle

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ABSTRACT: The Bonsmara breed is the largest beef cattle breed in South Africa with complete phenotypic animal recording on traits of economic importance. In order to make use of genomic selection as an additional tool for improvement of the breed a reference population is required. The aim of the study is to report on the establishment of a reference population for the Bonsmara breed and present the first results for 187 animals using the 80K GGP. The call rate was above 95% with a MAF of 0.27. After quality control 70880 usable SNP remained in the data.

Keywords: genomic selection; Bonsmara; beef cattle

Introduction

The Bonsmara is a composite beef cattle breed that was scientifically developed in South Africa to be adapted to sub-tropical areas. It was originally bred from the indigenous Afrikaner, Hereford and Milk Shorthorn breeds during the late fifties in South Africa (Bonsma (1980)). Since the formal establishment of the breed 50 years ago, the Bonsmara population has grown to currently 150 000 live animals. It is the largest beef cattle breed in South Africa and, apart from populations in other African countries like Namibia and Zambia, has been exported to South American countries such as Brazil, Argentina and Columbia, as well as Australia and the USA. Animal recording has been compulsory for Bonsmara breeders and the breed therefore also has a large complete data base containing phenotypic records on growth, fitness and production traits, as well as feed efficiency traits such as feed intake and feedlot growth. For genetic evaluation, 1.6 million pedigree records and 1 million animals with weaning weights are available. Measured traits for which EBVs (Estimated Breeding Values) are estimated include Birth Weight (Direct and Maternal), Weaning Weight (Direct and Maternal), Post Wean Weight, Mature Weight, Scrotal Circumference, Age At First Calving And Inter-Calving Period. Bulls are tested in intensive and extensive growth tests after weaning. EBVs for traits measured during growth tests on bulls include Height, Length, Intake, Average Daily Gain, Feed Conversion Ratio and RTU carcass traits. Feed intake is measured in intensive growth tests and 18 000 individual intake measurements are available. EBVs are combined into the following selection indices: Cow Value, Growth Value and Production Value.

The development and commercial availability of different SNP bead chips (Wiggans et al (2013)) for genotyping large numbers of animals have provided cattle breeders with an additional tool to increase selection accuracy and to accelerate genetic improvement. Genomic selection holds the largest potential for traits with low heritability, that are difficult to measure or are measured late in life (Dekkers & Hospital (2002)) such as fertility, milk production and adaptive traits. In beef cattle, genomic selection will increase the accuracy of genetic predictions for growth, carcass, reproduction, and health traits (Kuehn et al (2011); Montaldo et al (2012)). These traits are most important for breeds such as the Bonsmara farmed in extensive production systems. Due to available DNA repositories dairy cattle has taken the lead in establishment of reference populations and using genomic information for estimation of GEBV's (Wiggans et al (2011)). Beef cattle breeds in North and South American countries such as the Angus and Hereford have reference populations available with more than 3000 bulls genotyped for application in genomic selection (Garrick (2011)).

In order for the Bonsmara breed to engage in genomic selection a reference population is required that will include at least a 1000 reference animals with recorded phenotypes for the desired traits. Research has shown that within the major international breeds, reference or training populations were required for the specific populations to capture the polymorphisms to be applied in GS (Saatchi et al (2013)). The aim of this paper is to report on the establishment of a reference population and present results on the validation of the high density 80KGGP Illumina bead chip in the Bonsmara cattle breed in South Africa.

Material and Methods

For the establishment of the reference population the existing database were searched for suitable animals. Up to 5 high accuracy (>60%) sires per sire family of calves born within the last 3 years were identified. Hair samples were collected for these animals and are stored at SA Stud Book in Bloemfontein, South Africa. All biological samples are linked to the animals recorded in the Logix (Livestock Operational and Genetic Information Exchange) database (www.logix.org.za). Genotyping is planned in phases according to the available budget. For the purpose of this study 187 hair samples representing 186 bulls and one cow was sent for genotyping. The samples were prepared according the protocols for exporting

samples to the USA and sent via UNISTEL (Suite 13, Private Bag X22, Tygervalley, 7536, South Africa) to the GeneSeek laboratory (Lansing, MI, USA). Genotyping was performed using the 80K GGP bead chip from Illumina (www.illumina.com) containing 76 883 SNP. Results files were provided for analyses. Files were merged and a ped (Pedigree file) and Map (SNP panel file) file compiled for further analyses. Plink open software (Purcell (2007); Shaun Purcell, GNU General Public License, 2009 v2) was used to calculate descriptive genotype statistics for each marker, including call rate, minor allele frequency (MAF), HWE, allele and genotype counts. The criteria for quality control were set to remove all SNPs with less than 95 % call rate and SNPs with less than 0.05 minor allele frequency (MAF). Samples with more than 10% missing genotypes were removed from the study.

Phenotypes used in the study will be the EBVs for measured traits and selection indices with an accuracy of >60%. Genotypes and phenotypes will be combined according to the method described in vanRaden (2008) when at least 500 animals have been genotyped.

Results and Discussion

Genotyping was successful for all animals with an average call rate of above 95%. 2 805 SNP was not in HWE and 3012 SNP had a MAF < 0.02 (2%). These SNP's were removed and 70880 usable SNP remained in the data set.

The call rate obtained for the study complied with the expected average call rates of 99.7 % by the manufacturer (Illumina Inc., San Diego, CA) and to average call rates of 97.9 % reported by Makutumalli et al. (2009) across 21 different cattle breeds.

An average minor allele frequency of 0.27 was observed. In a study with smaller sample sizes including SA Angus and Nguni the MAF varied between 0.22 and 0.19. The MAF for Bonsmara was higher compared to Nguni cattle (Qwabe et al (2013)). In other African breeds such as the African N'Dama and Sheko breeds lower SNP were reported by Matukumalli et al. (2009). Although the Bonsmara breed is recognized as a local breed in South Africa, the genetic variation can be expected to be higher than other African breeds due to the original breed composition and practicing an open herd system where base animals are allowed for upgrading.

This study presents the first data for the Bonsmara reference population in South Africa and it is envisaged that another 800 animals will be genotyped within the next two years to provide the breed with a comprehensive population for application of genomic selection.

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