Genetic analysis on South African Santa Gertrudis: the way forward

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INTRODUCTION

Since the development and/or introduction of composite breeds, including the Santa Gertrudis, into the South African beef industry, composite breeds have played an increasing role in local beef production. The proven performance of composite breeds renders them ideal cattle genetic resources for the challenges presented by climate change and to contribute to future sustainable beef production. The outstanding reproductive (fertility) and productive (above-average feed conversion, growth, and beef quality) performance, as well as adaptive traits, are all beneficial attributes of the Santa Gertudis breed.

Despite their local relevance and importance, composite breeds (including the Santa Gertrudis) have received limited research focus relating to their current population demographics and the genetic progress achieved to date. The potential of introduced genomics-based technologies has also not been explored for smaller composite breeds (apart from the most populous Bonsmara breed).

The Animal Breeding & Genetics research group at the University of Pretoria has, therefore, designed a research project that aimed to comprehensively characterize the current genetic status of three South African composite breeds, including the Santa Gertrudis. This study was undertaken by a Masters's student Philippine Sithole under the supervision of Dr. Simon Lashmar and Prof Este Van Marle-Köster.

The primary objective was to use available pedigree data to profile these breeds in terms of their population demographics and parameters and investigate genetic trends based on available estimated breeding values (EBVs). In addition, the available single nucleotide polymorphism (SNP) genetic marker information was used to perform a genome-level characterization of the breed's diversity and inbreeding levels. We here share some of the highlights of the outcomes of the research.

PEDIGREE BASED PARAMETERS

The data required for the study which included, pedigrees, EBVs, and genotypic data were obtained from the Livestock Registering Federation (LRF) with the consent of the breeders' society. For the first objective, there were 346 671 pedigree records available since the start of the breeders' society in 1974. Using a software program called PopReport, the pedigree completeness (i.e. for how many animals, their complete pedigrees – parents, grandparents, great-grandparents, etc. – are available or known) of the Santa Gertrudis breed was estimated at 93.4% for animals born within one generation ago. Considering the generation interval estimated by the same software, one generation equals 5.9 years. For animals born six generations ago, the pedigree completeness was 21.5% lower, indicating that animal (and more specifically, pedigree-) recording for the breed has improved over the years. This is an important aspect for the breed as improved pedigree completeness accompanied by performance records for the traits of interest drives genetic progress. Research has confirmed that pedigree completeness should also be complemented with regular parentage testing to ensure high-quality pedigree information for genetic evaluations.

Effective population size (referred to as Ne) is a genetic diversity indicator that, in simplified terms, relates to the number of breeding individuals in the population (or breed). For two breeds with the same census population size (or the total number of animals), for example, the breed with the lower *effective* populations size would have fewer animals that are genetic contributors to the breed – this in turn would imply that more animals within the breed share similar genetics, and this improves the chances of inbreeding. The Food and Agriculture Organization (FAO) of the United Nations (UN) has proposed certain guidelines for genetic diversity and has recommended a minimum effective population size of 50 animals to maintain inbreeding rates below 1% and to guarantee a breed's continued survival. Based on the pedigree data, the effective population size of the Santa Gertrudis was estimated as 152 animals. This supports the very low genomics-based inbreeding calculated in this study (please see later), and implies that the Santa Gertrudis breed still has a sufficient degree of within-breed genetic diversity to achieve genetic progress and respond to future trends and "shocks". The breed is not currently at risk of inbreeding-related effects.

GENETIC TRENDS

Genetic trends were compiled based on the available EBV data and overall indicated a positive trend for all the traits included. In Table 1, the change in EBVs between the years 2000 and 2020 is summarized for a few growth and reproduction traits. In Figures 1 and 2, furthermore, positive trends are also shown for carcass traits namely carcass weight and eye muscle area (EMA).

Table 1 Estimated rate of change in EBVs for Santa Gertrudis between 2000 and 2020

Trait	Ave. change in EBV
Birth weight (kg/year)	+0.017
Weaning weight (kg/year)	+0.190
Yearling weight (kg/year)	+0.220
Final weight (kg/year)	+0.342
Mature cow weight (kg/year)	+0.436
Scrotal size (cm^2)	+0.017

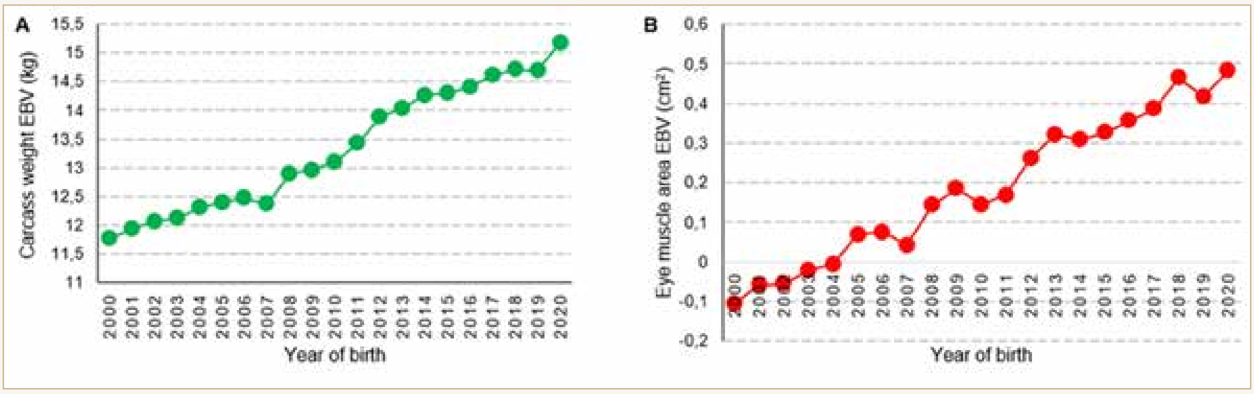

Figure 1 Genetic trends of carcass weight (A) and eye muscle area (B) for the Santa Gertrudis breed

These trends relate to the progress in the breed and may seem slight, but are moving in the desired direction for the relevant traits. The genetic trends are useful to the breed in consideration of their overall breeding objectives for moving the breed forward.

GENOMIC CHARACTERIZATION

For the genomics part of the study, 432 SNP profiles were available for the Santa Gertrudis breed. The animals were genotyped on a 100K "SNP Chip" (i.e. a genotyping tool containing more or less 100 000 SNP genetic markers spread across the entire animal's DNA). There were also 69 animals genotyped on a smaller panel (containing approximately 7 000 SNPs), however, genetic diversity analyses were performed using the 100K panel (for diversity studies, more – animals and markers – are better!). From this data, the genetic diversity was negligibly smaller than expected – the expected heterozygosity (a measure of genetic variation) was 0.396, whilst the observed heterozygosity was 0.395 (almost the same). The genomic inbreeding coefficient was furthermore 0.002 (translating to *only* 0.2% inbreeding within the breed). This shows that inbreeding levels are still very low, and presents no risk to the breed at the moment – breeding practices should, however, still be managed properly and the over usage of "high-impact" bulls prevented in the future. Inbreeding can be detrimental to performance (called "inbreeding depression") and may introduce several defects.

Compared to the other composite breeds included in the study, the Santa Gertrudis was genetically unique. In Figure 2, a principal component analysis (PCA) is shown – this analysis shows, based on the markers, how closely related animals are (without considering their known breed). The PCA clustered all the Santa Gertrudis animals in one cluster, separate from the other breeds.

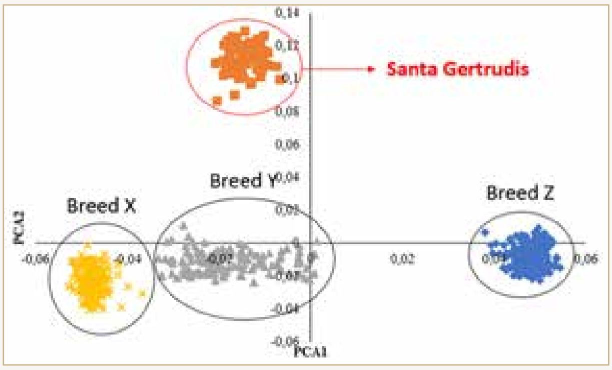

Figure 2 Principal component analysis (PCA)

The ADMIXTURE results (Figure 3) supported the results shown in Figure 2 and demonstrate the Santa Gertrudis as a breed with limited shared ancestry with the other breeds displayed – in the Figure, each colour represents a different ancestor. With genomic diversity studies, it should be remembered that the results are, in this instance, based on 432 animals' (of the entire breed) genotypes, and are compared to breeds that had even fewer available genotypes. To get a more complete picture, more (in terms of numbers and diversity) animals should be genotyped.

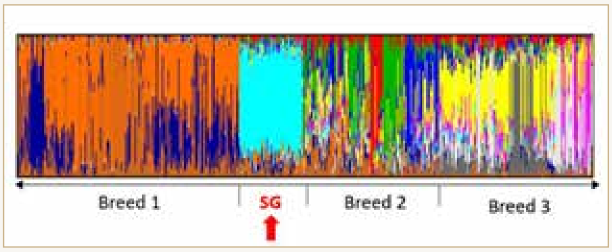

Figure 3 Population structure of the Santa Gertrudis

The results are promising and adding more genotypes will result in a training population for the breed which could be applied in the estimation of genomic enhanced breeding values (GEBVs) for genomic selection. Research has shown that training populations should represent the genetics of the whole breed, including the "good", the "bad" and the "ugly". Genetic linkage among herds is also beneficial when selecting animals for a training population. To fully reap the benefits of genomic selection for the Santa Gertrudis would require strategic sampling and genotyping efforts. These initial results have shown that the breed is in a good "space" in terms of its genetic diversity status – this diversity should now be optimally utilized towards genomics-based selection and management of the Santa Gertrudis.

CONCLUSION

The Santa Gertrudis is a well-established beef breed in South Africa. The results of the study indicated that animal recording has benefited the breed and continuous participation will enhance EBV accuracies and genetic progress. The next step for the breed would be to add sufficient genotypes for adding genomic information to the genetic evaluation for genomic selection.