GENETIC RELATEDNESS OF THE SA MERINO POPULATION

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Introduction

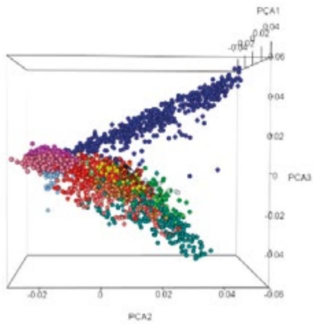
Genomics in livestock has made tremendous advances in recent years. The ability to capture an animal's unique DNA sequence has become a cornerstone of stud breeding in the local and international community. Over 60 000 DNA markers, called single nucleotide polymorphisms (SNPs), are analysed on a genomic chip (genotype) and is sometimes referred to as an "All in One" DNA test. The use of genomic information in small stock genetic evaluations has a large impact on increasing the prediction accuracy of production and fertility traits that are lowly heritable, sex-limited and are only measured later in life (Berry et al., 2014; Van Marle-Köster & Visser, 2018). Although this aspect of genomics may be limited to breed societies with routine genetic evaluations, there are other vital use cases that should not be overlooked by commercial and informal livestock breeders.

Genebox

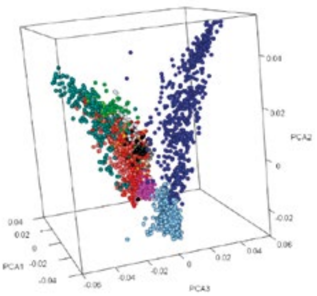
A three-dimensional Genebox can reveal the true depth of genetic variation between animals within the same breed, and the corresponding flock to which they belong to. Each dot is representative of a single animals' genotype, with animals from the same flocks clustering together. A larger cluster indicates a larger amount of genetic variation while flocks that cluster closer together have shared ancestry. It must be noted that the Genebox and genetic spread of the animals is determined by the number of animals placed in the analysis, the number of genetically different flocks, as well as the type of animals within the SA Merino population, e.g. strong wool vs fine wool selection practices.

Whole Genomic Population

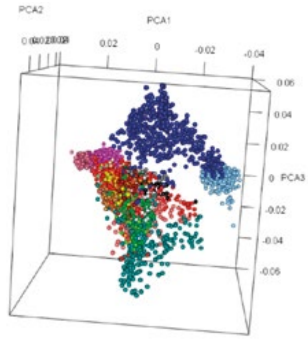
The following Genebox includes the total SA Merino genomic population comprising of around 3 250 animals from over 30 different flocks. The Grootfontein Strong-Wool Flock (dark blue) shows a distinct separation from the Industry Flocks (multiple colours), indicating that these are genetically different from the animals genotyped from Industry Flocks (Picture 1). The tight clustering of the Industry Flocks points to the fact that these breeders are selecting for similar types of genetics.



As the Genebox is 3-dimensional, rotating it allows for different perspectives of the genetic spread these animals have. Picture 2 shows the Grootfontein Fine-Wool Flock (light blue) to be rooted at the bottom of the box, with a clear separation between the industry animals and the Grootfontein Strong-Wool Flock.



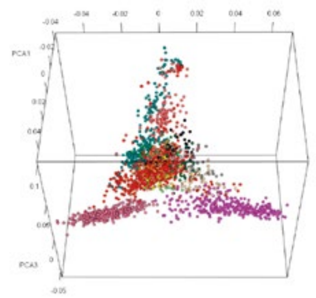
Picture 3 indicates an overlapping of genetics between the industry animals, which is expected due to breeders buying rams from other flocks and showcases the true genetic linkages between these flocks. Two flocks (Purple and Metallic Purple) show a tighter clustering in comparison to the other industry flocks, and it is known that these are closed flocks, using rams bred within their flocks as future breeding stock. This tight clustering is an indication of high genetic similarity within the flock and that they are genetically distinct from each other, as well as the total population at large.



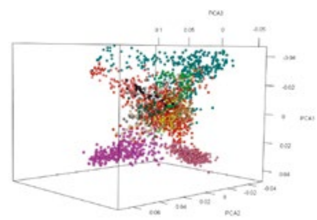
Industry Genomic Population

The two Grootfontein flocks (strong-wool and fine-wool) were removed from the analysis to allow for a more detailed analysis at an industry level. Keep in mind that when the number of animals changes within the analysis, it will create a totally different Genebox, which is representative of the genetic diversity present.

Picture 4, using the same colours for each flock as the Whole Genomic Population, paints a slightly different picture than what we initially saw. The two tightly clustered flocks have opened up, although the fact they still distinctly cluster together and are not intertwined with the rest of the industry population, supports the closed flock hypothesis. The rest of the population shows an admixed cluster, meaning that animals from different flocks show genetic similarity between these SA Merino's.



When rotating the Industry Genebox, one can see that the Industry animals are wedged in between the two closed flocks and the greenish blue (aquamarine) indicating those flocks are genetically different, while the majority of the population falls in between these flocks.



Future applications

As research constantly innovates, genomics can assist in revealing the true underlying genetic mechanisms that influence adaptability and fertility traits. Genomics will allow for the detection of gene regions that influence adaptation and resistance to certain diseases, assisting farmers with selecting and breeding animals suitable for seasonal changes in environment and disease presence. A common misconception widely stated is that "Genomics is the future", when in fact genomics is already available in South Africa with current and relevant applications.