Genetic study on wet carcass syndrome

10/08/2018 by admin

Detection of quantitative trait loci affecting wet carcass syndrome in sheep

Industry Sector: Cattle And Small Stock

Research Focus Area: Animal Products, Quality And Value-Adding

Research Institute: Agricultural Research Council – Animal Production Institute

Researcher: Lené Van Der Westhuizen

The Research Team

Title	Initials	Surname	Highest Qualification
Prof	MM	Scholtz	D.Sc.
Prof	MD	MacNeil	Ph.D.
Prof	FWC	Neser	Ph.D.
Prof	A	Maiwashe	Ph.D.
Mrs	A	Theunissen	M.Sc.
Ms	M	le Roux	M.Sc.

Final Report Approved: **23 August 2018**

Aims Of The Project

- To map quantitative trait loci affecting wet carcass syndrome.
- To identify specific loci affecting the predisposition to wet carcass syndrome (detection of a major gene).
- To develop a diagnostic test for the genetic predisposition to wet carcass syndrome (if a candidate gene can be identified as the cause).
- If a major gene is not responsible for wet carcass syndrome the second phase of the project will have the aim to develop a polygenic prediction equation for the predisposition of sheep to wet carcass syndrome.

Executive Summary

Wet carcass syndrome (WCS) is a condition predominantly found in sheep, which negatively affects the quality of their carcasses. During the pre-slaughter period, the animal appears to be clinically normal, showing no symptoms of an abnormality. However, after the removal of the skin during the slaughter process the carcass appears to be "wet". When the description and results of prior research are taken into account, no physiological, environmental or management system was conclusively identified as the causative agent of WCS. Previous research has also not considered a potential genetic basis for WCS or the potential for an interaction of genotype with the environment (stress). Furthermore, the tentative breed-specificity, i.e. Dorper sheep breed, of the condition lends some credence to a potential genetic basis for it. The current study employed the Ovine Infinium® HD SNP BeadChip and a genome-wide association analysis approach to scan the genomes of both afflicted- and unafflicted sheep in search of putative quantitative trait loci associated with the WCS phenotype. This study was not only one of the first in Southern Africa to make use of this specific BeadChip but also the first to investigate the role of genetics as a causative factor of WCS. Muscle samples from sheep carcasses (33 afflicted and 36 unafflicted) were collected from three different abattoirs.

Using a candidate gene approach it was possible to map genetic loci, *RYR1* (Chromosome 14) and *PRKAG3* (*RN*$^{-}$; Chromosome two) causative of phenotypically similar conditions such as porcine stress syndrome and red, soft and exudative meat to the ovine genome, respectively. The positions of these loci mapped to the ovine genome were not in accordance with the loci showing significant association with the WCS phenotype; and no relationship was found between single nucleotide polymorphisms located within these genes and WCS. Furthermore, along with the latter approach, the test of runs of homozygosity presented similar results as well as providing plausible evidence that WCS is not a recessive inherited condition. To test for an association between the phenotype (WCS) and a genetic marker(s) i.e. SNPs, a case-control study design was implemented. Given the relatively small sample size of the current study, the results obtained from the GWAS attested strong evidence of at least two loci, oar3_OARX_29903534 and oar3_OARX_113973214 positioned within the non-homologous region of the X chromosome for WCS carcasses. All afflicted animals, both males and females, carried at least one allele for marker oar3_OARX_113973214, which was shown to be related to the WCS phenotype. On the contrary, some of the unafflicted animals also carried this specific allele. Given the apparent influence of stress on WCS, these unafflicted males and females in all likelihood did not experience adequate levels of stress to manifest the condition post-slaughter. The results of the current study also indicated that WCS may possibly be a rare X-linked inherited condition, provided only female individuals are considered. Finally, two possible major loci involving two major genes, *HTR2C* and *DMD*, positioned on the non-homologous region of the X chromosome have been identified as novel positional and functional candidate genes for WCS in sheep.

Please contact the Primary Researcher if you need a copy of the comprehensive report of this project – Lené van der Westhuizen on PienaarL@arc.agric.za