

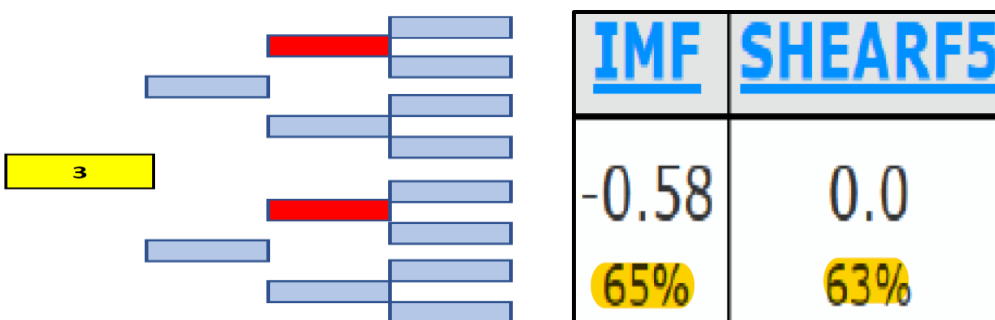
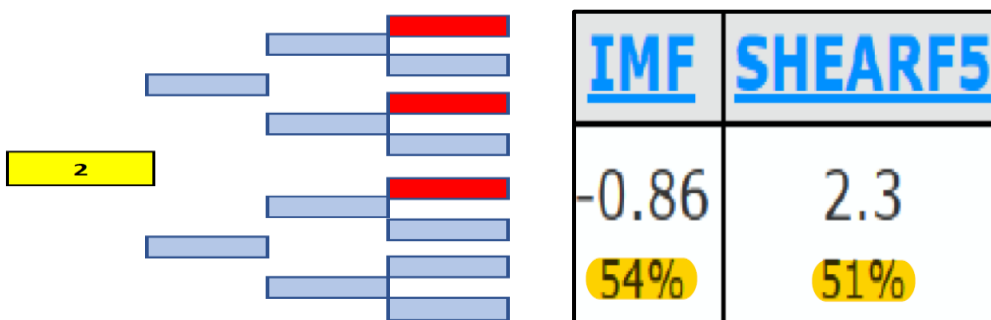
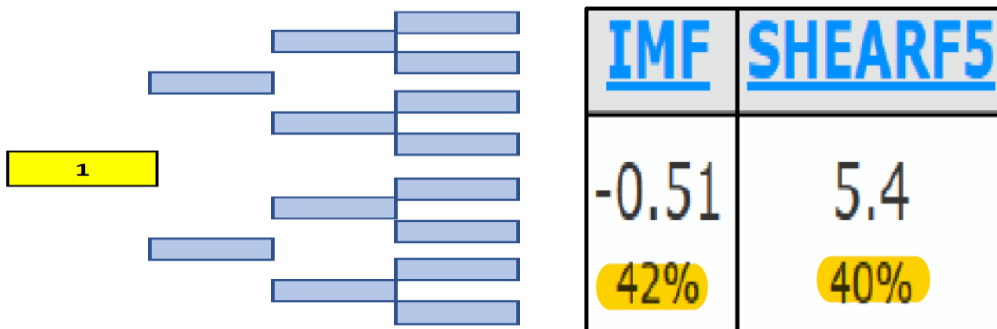
AWSA Satellite Flock Feb 2021

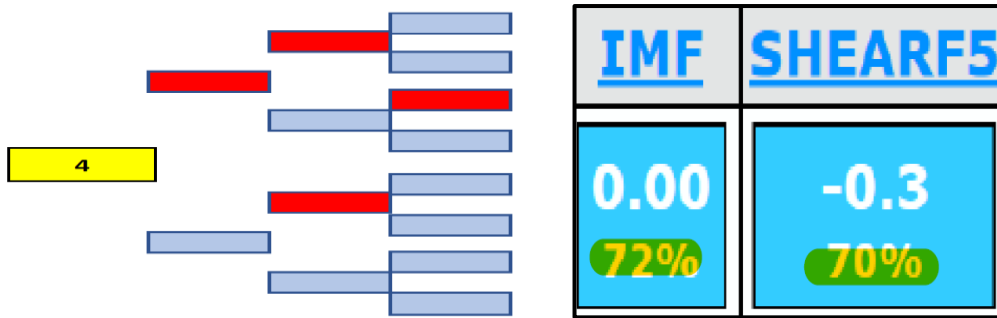
The AWSA has established an MLA backed “satellite flock” for the 2021 joining to help improve the accuracy of genomic predictions, especially for eating quality traits.

For some time, the lamb industry has been using genomics technology to predict hard to measure traits like those associated with eating quality. These genomic predictions depend on how closely a candidate animal is related to animals that have had both phenotypic (actual carcass measurements on lambs) and genomic information collected.

Apart from a few small trials such as the Superwhites group trial in 2017/18, the major source of phenotypic information with regard to eating quality traits and related genomic testing, has been the “Sheep CRC Information Nucleus Flock” – now called the “MLA Resource Flock”.

The figures below show the increase in accuracy of the ASBVs for Intramuscular Fat (IMF) and Shear Force (SF5) as the candidate animals (Yellow 1,2,3 & 4) are more closely related to those highlighted in red. The “Red” animals are sires which have been used in the MLA Resource Flock and have progeny slaughtered and measured for these traits. These examples of four animals from the same flock demonstrate the value of an improved relationship to measured animals with an increase in accuracy of Eating Quality ASBVs. (The accuracies are highlighted in orange)





These improvements in accuracy allow breeders to make more reliable decisions when selecting animals for these EQ traits.

Since the inception of the Information Nucleus/Resource Flock, a number of White Suffolk sires have had progeny tested for numerous traits, including eating quality. These flocks have relied on the nomination of sires by Breeders and this has to some degree limited the footprint of the genomic/phenotypic relationship across the White Suffolk breed.

The AWSA satellite flock project will broaden the footprint of phenotypic/genomic information within the White Suffolk breed. To do this, sires that don't currently have a close relationship with the MLA Resource Flock are being used. This will increase the number of animals across the breed that have a good relationship with those that have been phenotypically tested and improve the accuracy of genomic predictions. It will also give an increase in accuracy of EQ ASBVs calculated for related, but untested, animals through the single step analysis.

Sires were selected by the steering committee based on a list compiled from,

- A "search" of the animals in the Sheep Genetics database that had progeny in more than one flock and they or their sire and sire of dam had **not** been used in the Resource flock and had semen available for the project (23 rams)
- Sires nominated by members (11 rams)
- The unsuccessful White Suffolk nominations for the 2021 MLA Resource Flock (28 rams)

From this list of 62 rams a relationship program run by AGBU was then utilized to rank the nominated sires with the least relationship to the MLA Resource Flock. This list was further reviewed to ascertain whether semen was available and the number of flocks each sire had been used in.

Sires were selected based on the greatest diversity of bloodlines, sires used in the most number of White Suffolk flocks, and sires with the least relationship to the MLA Resource Flock.

The 15 sires selected for the project are,

Link Sire - Somerset 160067, Baringa 16W300, Yonga Downs 170386, Kurralea 160231, Warburn 140512, Bundara Downs 179821, Koonawarra 140259, Aylesbury Farm 177408, Anden 150277, Wheetlande 148159, Langley Heights 160054, Fairburn 180567, Mertex 170575, Booloola 170093 and Gemini 170171.

In early January 2021, 295 Merino ewes were AI'd to the selected 15 White Suffolk sires at Seriston SA. The aim was to AI 300 ewes but only 295 of the 312 ewes programmed were suitable to AI. 10 sires were AI'd to 20 ewes and 5 sires were AI'd to 19 ewes over 2 days. As ewes were AI'd, they were tagged with an additional visual tag that was linked to their EID tag and details recorded of which sire they were joined to.



Insert CIDRs



Tag ewes and record EID and Sire



AI "crew"

The ewes will be pregnancy scanned and separated into management groups based on litter size. This will determine the birth type of the lambs. At marking, lambs will be tagged with an EID tag as well as a visual tag and TSU samples taken. Birth type and sex will also be recorded. DNA/Genomic tests on the lambs will determine Sire parentage. Rear type will be determined by the survival of lambs at weaning. Lambs will be weighed at weaning and early post weaning and fat and muscle scanned prior to slaughter. The lamb carcasses will be measured in the abattoir and meat samples tested in the laboratory for IMF and SF5 as well as other eating quality traits.

All data including Genomic and eating quality measurements will be submitted to Sheep Genetics under a research Flock code and information will contribute to the Sires ASBVs as it is submitted. An analysis will be undertaken once the project is completed of the changes/benefits to the accuracy of ASBVs as data is submitted during the course of the project.

Thanks must go to all members who nominated sires, members who generously donated the semen to this project, sponsorship by Shearwell for the EID and VID tags, members who have provided labour and assistance to the project and Anthony Hurst "Seriston" who has provided the ewes, location and farm resources for this project.

Debbie Milne
Richmond Hill Agribusiness Pty Ltd
Project Manager
16/2/21