

# 2020 FLYSTRIKE PREVENTION RD&E PROGRAM PROJECT SUMMARY REPORT

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## GENOTYPING OF BREECH FLYSTRIKE RESOURCE FLOCK

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### SUMMARY

Breech flystrike is a costly trait to measure. Australian Wool Innovation's investment into genetic solutions for breech flystrike has resulted in the availability of estimated breeding values for indicator traits, such as breech wrinkle, breech cover and dag through SheepGenetics to enable genetic and permanent improvement in breech flystrike through selection. However, because selection is still based on indicator traits rather than breech flystrike itself, genetic gains are not at their maximum yet. Genomic information provides approaches that could help fast-track genetic gains in the trait of breech flystrike resistance itself.

The data and materials collected on the Breech Flystrike Resource flocks in NSW and WA form an exceptional and unique resource to explore genomic approaches. The data set in this study forms the largest reference population for breech flystrike resistance to date. It was investigated whether genomic approaches based on genes of major influence exist and enable approaches such as marker assisted selection, whether genomic selection based on genomic breeding value estimated from all available genomic information or whether a combination of the two would be the most efficient application of genomic information for selection for breech flystrike resistance.

The project demonstrated that genomic selection based on genomic breeding values will be the most efficient approach to create benefit to industry within the next 5 years. Based on the approaches evaluated in this project it is concluded that the existing genomic breech flystrike data resource provides a basis for industry to create reliable selection tools that provide the fastest genetic progress in five years' time.

### PROJECT REPORT

#### DATA

The data comprised ~1,500 animals of the WA and NSW Breech Flystrike Resource flocks that had phenotypes and genomic information on 600K genetic DNA markers available. Traits analysed included breech flystrike (STRIKE), coded as "struck" or "not struck", and breech cover (BCOV), dag score (DAG) and wrinkle score (WRK), all categorised as low, medium, or high. A genome wide association study was conducted for each of the traits to establish if any single or small number of markers could be detected with major effect on any of the traits. In addition, genomic breeding values were estimated using the information of all genetic markers.

#### RESULTS AND DISCUSSION

Genomic analyses point at the most efficient approaches for the application of genomic information in breeding programs. These include methods that are based on major genes, such as marker assisted selection, or based on genomic breeding values that draw on the information of all genetic markers.

As a first step it was explored if genetic markers with significant associations with STRIKE, BCOV, WRK or DAG exist. Overall, none of the genetic markers showed a large enough effect on any of the traits to be useful for marker assisted selection approaches. Although two regions were in proximity to interesting genes for STRIKE and DAG, they were not large enough to indicate that the region would harbour a gene with major effects on these traits. Further investigation might be warranted because it is possible that the data structure masks major genes. Difference in phenotype and genetic background between NSW and WA might warrant splitting the data by site or choosing extreme animals (e.g. based on lifetime strike) for potential further analyses. The results of this analysis did not support marker assisted selection as an approach for enhanced genetic gains for breech strike resistance.

The current genomic resource of the Breech Flystrike Resource flocks is an excellent start for a reference population and provided the data for the estimation of genomic breeding values. The project demonstrated that genomic breeding values can be estimated, but the current accuracy is not sufficient yet to select animals reliably for breech strike resistance. However, higher accuracies can be achieved with an increase of the number of animals with phenotypes and genotypes in the reference population. In order to build on the current reference population other aspects have to be taken into consideration. Breech flystrike remains expensive to measure, therefore it would be costly and impractical to run a specific reference population for this trait, although, the resource could be used for genomic predictions of other traits as well. A dispersed reference population, that includes data from various sources, would be advantageous based on opportunistic sampling in flocks of key breeders, Merino Lifetime Productivity flocks, sire evaluation flocks - any flock with reliable records. However, in order to include phenotypes from different sources in a reference population, the effect of different management procedures on breech flystrike needs to be established, e.g. does breech flystrike in sheep that have been chemically treated for flystrike, correlate well with flystrike in untreated sheep. Other options of adding more phenotypes could be explored, such as the collection of “pooled” phenotypes from commercial wool production operations.

It is recommended that a future reference population should have at least 7,500 phenotypes to achieve sufficient accuracy, which would require the collection of a further 6,000 phenotypes in addition to the Breech Flystrike resource. It is suggested that a time frame of 5 years would be a maximum time frame to build a dispersed reference population.

## **CONCLUSIONS AND RECOMMENDATIONS**

Genomic selection can provide substantial benefit to wool focussed Merino breeding programs. The project demonstrated that the Breech Flystrike Resource Flock from WA and NSW are a great resource that will have impact on the wool industry in the short and long term. In this study genomic breeding values were estimated for breech flystrike resistance, but they do not yet have the accuracy to be used as reliable selection tools in industry. The addition of the genomic data of the Breech Flystrike Resource flocks to the current genomic resource will provide an increase in accuracy for existing genomic breeding values for wool production traits in the short term and for breech strike resistance in the long-term.

Within the next five years, a much larger dispersed reference population could be built that increases the accuracy of genomic breeding values to a level that allows accurate selection directly on breech flystrike resistance and fast-track genetic improvement for this trait.

For a detailed description of the outcomes from this project, please see the [project final report](#), available at [www.wool.com/flystrikelatest](http://www.wool.com/flystrikelatest).

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