Breeders paper

IMPROVE YOUR SOCIAL LICENSE – BREED SHEEP FOR DISEASE RESISTANCE

S.F. Walkom[1] and K.L. Bunter[1]

[1] Animal Genetics Breeding Unit*, University of New England, Armidale, NSW, 2350 Australia

SUMMARY

Consumer interests in the health and welfare of animals has increased as production systems become more transparent. This brings about a need for cultural change around how the industry approaches the long-term management of disease traits. Genetic tools have been used by leading sheep breeders for decades to bring about genetic gain in production traits. The same approach can also be applied to breeding for good health and welfare. This paper provides a summary of the steps required to develop long-term solutions to diseases outbreaks allowing sheep producers to breed for disease resistance and improve the social license for the agricultural industry.

INTRODUCTION

The welfare of food-producing animals has become a contentious issue across the world. There is evidence of a disparity between what consumers think livestock production "should be" and what actually happens on farm (Buddle *et al.* 2021). Sheep producers have recognised that good farming practices are essential for not only animal health and welfare, but also benefit the profitability of their production systems. For example, mulesing to reduce flystrike incidence, and hoof bathing and trimming to address footrot. However, there are opportunities to further optimise animal welfare in these labour-intensive strategies. Therefore, alternative or complimentary strategies must be considered as long-term solutions, which also maintain a social license to produce wool and lamb.

In addition to veterinary strategies, genetic selection provides a long-term solution to health and welfare issues. There has been an increase in the research and application of genetic solutions. This has been due to a number of factors: a growing appreciation of the role that host genetics can play in disease control, an increase in the tools available to dissect host genetic variation in disease resistance, and growing pressures on breeders to select animals that are healthier and more resistant both to infectious and metabolic diseases (Bishop and Morris 2007). Consequently, as Australian sheep producers continue to farm within the social license provided by consumers there is a growing interest and desire to breed for disease resistant animals, in an attempt to both reduce the health and welfare impact on the flock and also remove the repeated costs associated with short term solutions.

Meat and Livestock Australia report that the top 10 biggest disease costs to the Australian sheep industry are internal parasites (National Cost; $369 million/year), flystrike ($280 m), lice ($123 m), perinatal mortality ($118 m), post-weaning mortality ($75 m), perinatal ryegrass toxicity ($63 m), bacterial enteritis ($29 m), arthritis ($26 m), footrot ($18 m), OJD ($4 m) and phalaris toxicity ($1.6 m) (Sackett *et al.* 2006). The majority of these diseases have been well studied and also shown to have some evidence of underlying genetic variation that could be exploited to improve the long-term health and welfare of the flock (Bishop and Morris 2007). However, the relative merits of implementing traits into breeding programs depends not only on the presence of genetic variation, but also the ability to accurately record meaningful data in a time frame that enables selection decisions to be made.

Any traits of interest can be bred for if there is genetic variation in the phenotypes recorded. However, disease resistance traits are difficult to capture because: 1) preventative treatments are

* A joint venture of NSW Department of Primary Industries and the University of New England

often delivered early and before the disease expresses itself; 2) environmental conditions often influence disease expression; 3) allowing the disease to progress to allow genetic variation to be expressed is a welfare issue; 4) identifying the desired phenotype can be difficult; 5) disease phenotypes can impact production phenotypes; 6) getting disease phenotypes on genetic selection candidates can be difficult, and 7) legislative constraints may exist, such that breeding stock are not able to experience health issues and therefore record phenotypes (eg restricted sale of rams due to footrot). However, overcoming these issues, whilst difficult, is not impossible. For some diseases, breeding values have become available in recent years. Some examples include most recently development of the footrot susceptibility Australian Sheep Breeding Value (ASBV) (Walkom *et al.* 2019) and the continued utilisation within breeding programs of the worm egg count ASBV (Brown and Fogarty 2017). This paper highlights learnings from previous research in developing genetic solutions to improve disease resistance. Industry could take these learnings to meet their social license to breed for fitter and healthier animals.

BREEDING FOR DISEASE RESISTENCE

Step 1. Understand the disease. Both disease incidence and disease management are important for industry and consumers, affecting performance, profitability and welfare standards, the latter of which also affects social license to produce by the general public. *The short and long-term costs associated with production losses and disease management are more easily estimable (Sackett et al. 2006). However, the cost of long-term change required to meet consumer perception of animal production systems and welfare standards can be difficult to model (Buddle et al. 2021).*

Step 2. Find your champions. To bring about change there needs to be people that are willing to invest in and back opportunities to develop genetic tools to help breed for disease resistance. Champions need to encourage others to participate in the idea and develop public and private investment of money and time. *Champions are needed throughout both the research community and industry because both time and finances are finite, and it is the continued desire to bring about change by the champions that will make sure progress is made. The success and rate of development of the footrot breeding value can be attributed to the "leg work" and "support" from New Zealand sheep breeders along with associated industry bodies, service providers and researchers, as highlighted in Walkom et al. (2019).*

Step 3. Research the biology. Significant research into disease aetiology, to inform researchers of the most appropriate phenotypes and challenge protocols for characterising variation amongst individuals is required. *Often the initial research into the biology of the disease occurs without good genetic design and focusses primarily on finding management solutions. The biology of footrot was first studied in 1941, with the current understanding of the biology developed in the late 1960's and the first studies of genetic variation in Australian sheep occurring 1990's (Raadsma and Egerton 2013).*

Step 4. Identify genetic variation. Selection for disease resistance is only achievable if the trait exhibits genetic variation. Investigations are required to examine alternative phenotypes and the most appropriate statistical models for analysis to estimate heritabilities. This often requires controlled challenge protocols and standardised recording. For most traits, this requires a central progeny test (CPT) / reference population, serial records to capture disease progression where possible, and accredited scorers. *Initially industry engagement and "buy in" to the footrot research occurred after a proof of genetic variation study (Ferguson et al. 2016) but it was the development of a CPT and the data that came from it that underpinned the ability to develop the genetic analysis for the Footrot Breeding Value (Walkom et al. 2018).*

Step 5. Understand genetic associations. Obtain correlations with other traits, to establish impacts of including new disease phenotypes into existing breeding programs, and to identify indirect selection criteria. This becomes problematic if animals recorded in Step 3 have no other

industry relevant data or are not sufficiently representative of the industry. Therefore, these data need to be connected with the wider performance data from industry flocks. Correlated traits can provide the opportunity to avoid the need to select on the disease phenotype. *In the case of flystrike the genetic associations between breech, wrinkle and dag traits (Brown et al. 2010) provide the opportunity to move away from the current short term management solutions with questionable welfare practices. The advantage here is that the prevalence of the disease can be reduced through breeding, without the need to capture the flystrike phenotype on the individual.*

Step 6. Build awareness within industry. Arguably this needs to occur throughout the process. Clear, honest and repetitive communications of the results is required to change mindsets from short term management decisions to long-term genetic change. *Extension of research through clear communication strategies, especially around proof of concept, are required to prompt breeders to bring about changes to their breeding decisions and achieve genetic gain (Collison et al. 2018). This is even more important for disease traits where management practices to suppress the expression of the disease phenotype will most likely need to change.*

Step 7. Genomic investment. Genomics presents a potential tool to extend accuracy outside central test populations, but it is still a case of 'suck it and see' to obtain estimates of the improvement in accuracy. Additional investment in genotype data will be required at the research stage with no guaranteed return to investment yet. *The polygenic nature of many disease traits (eg. footrot, Raadsma et al. 2018) often means that "silver bullet" genomic solutions are rarely available. However, genomics remains valuable through linking the reference population with animals of interest and increased accuracy.*

Step 8. Expanding disease recording into industry flocks. The genetic information base can be expanded considerably with the expansion of recording, with defined protocols, to broader industry (non-research flocks). This includes breeders being willing to admit to disease presence and to follow the necessary recording protocols, and therefore training in correct procedures and data delivery. Investment of genotyping in industry flocks is also required to keep the reference population up to date. This genotyping cannot be solely confined to the best animals, so breeders will wear additional recording and genotyping costs for the sake of their industry clients. *The transition from a research study to an industry recorded phenotype database in the footrot study was possible due to clearly defined protocols around identifying a sufficient disease challenge and scoring standards, combined with an analysis robust enough to account for the greater variability in genetic makeup and disease expression across challenges (Walkom et al. 2018).*

Step 9. Automation of phenotype submission pathways. Development of automated inclusion of data and analyses into the national genetic evaluation systems, such as provided by Sheep Genetics. This requires data pipelines and software development, as well as approval by independent committees (technical and industry advisory). There needs to be sufficient push from industry for public funding. *Incorporation into the national genetic evaluation system enabled footrot breeding values to reach a much larger number of breeders and increase the number of people interacting with the genetic tool (Walkom et al. 2019).*

Step 10. Building up accuracy of ASBVs within flock. Sufficient data is required for individual animals to have accuracies of breeding values that enable their publication. *The accuracy of an individual's breeding value is directly related to the individual's genetic relationship with the informative phenotype. Thus, as more phenotypes are recorded on individuals closely related to the selection candidates the greater the accuracy of breeding values and the greater the ability to identify the superior candidates (Walkom et al. 2018).*

Step 11. Incorporate EBVs in breeding objective. Breeders need to use the resulting breeding values for selection decisions, or no informed genetic trend will occur. *Now that the footrot breeding value is available, breeders are using it in their breeding objective and as a marketing tool to distinguish themselves from other breeders.*

Step 12. Continued monitoring and development. Constant monitoring of progress is required as selection progresses, as low disease incidence will eventually cause redundancy and ineffective data collection. This is of course great on one hand, because it means that disease incidence is low and welfare and productivity are improved. *The footrot phenotype has a base line standard around the minimum disease expression required to score the disease challenge (Walkom et al. 2018). However, as the individuals become less susceptible the ability to meet these standards becomes harder, meaning flocks with low susceptibility will become reliant on external progeny tests or genomic based breeding values, where accuracy will be influenced by the size of the reference population.*

CHANGING PERSPECTIVES

Ultimately, the question is "*can we afford not to do something?*" The success of the production system is driven by the ability to meet the demands of the consumer. Genetics has provided us with the opportunity to make real-life improvements through genetic gain in both the quantity and quality of meat and wool (Collison *et al.* 2018), and has also been shown to be a solution to many diseases that impact global sheep production systems (Bishop and Morris 2007). Unfortunately, discussing the presence of diseases is difficult. Thus, the ability to change management practices and implement genetic solutions has been slow at the industry level. However, where attitudes are more progressive and social stigmas are broken down, producers can achieve long-term change in the impact of diseases as evidenced by the development of the footrot breeding value (Walkom *et al.* 2019). The ability to lead social change and influence the industry also has the potential to improve market access and address discerning consumer demands around health and welfare standards.

CONCLUSIONS

Sheep breeders have been able to utilise quantitative genetic tools to improve the productivity of their wool and lamb meat enterprises. These tools are also available to help bring about long-term change in the expression and impact of disease. The biggest limitation to the industry is not the availability of these tools but the need for cultural change in the management of diseases that are currently limiting productivity and potentially threatening the social licence to breed sheep in Australia and beyond.

REFERENCES

Bishop S.C. and Morris C.A. (2007) *Small Rum. Res.* **70:** 48.

Brown D.J. and Fogarty N.M. (2017) *Ani. Prod. Sci.* **57:** 209.

Brown D.J., Swan A.A. and Gill J.S. (2010) *Ani. Prod. Sci.* **50:** 1060.

Buddle E.A., Bray H.J. and Ankeny R.A. (2021) *J. Rural Stud.* **83:** 50.

Collison C.E., Brown D.J, Gill J.S., Chandler H.R., Apps R., Swan A.A. and Banks R.G. (2018) *Proc. Wld. Congress Gene. App. Livestock Prod*. **11**: 661

Ferguson M.B., Scobie D.R., Kearney G.A, Walkom S.F and Raadsma H.W. (2016), Available at https://static1.squarespace.com/static/57479299e32140c00f38405e/t/5876f13e5016e15c3137b779/1484190018748/Best+Foot+Forward.pdf [Accessed 17/09/2019].

Raadsma H.W., Walkom S.F., Sharland B., Esquivelzeta-Rabel C., Brown D.J., Bunter K.L. and Ferguson M.B., (2018). *Proc. Wld. Congress Gene. App. Livestock Prod*. **11**: 335.

Raadsma H.W. and Egerton J R. (2013) *Livest. Sci.* **156:** 106.

Sackett D., Holmes P., Abbott K., Jephcott S. and Barber M. (2006) MLA Report: AHW.087

Walkom S.F., Bunter K.L., Raadsma H.W., Brown D.J., Gibson W., Swan A.A., Borner V. and Ferguson M.B. (2018) *Proc. Wld. Congress Gene. App. Livestock Prod*. **11**: 261.

Walkom S.F., Bunter K.L., Raadsma H.W., Brown D.J. and Ferguson M.B. (2019) *Proc. Assoc. Adv. Anim. Breed. Genet.* **23:**556.