

## **DESIGN AND PURPOSE OF THE MERINO LIFETIME PRODUCTIVITY PROJECT**

**A.M.M. Ramsay<sup>1</sup>, A.A. Swan<sup>2</sup>, and B.C. Swain<sup>1</sup>**

<sup>1</sup>Australian Merino Sire Evaluation Association, 1534 Prairies Rd, Gunnedah, NSW, 2380

<sup>2</sup>Animal Genetics & Breeding Unit\*, University of New England, Armidale, NSW, 2351 Australia

### **SUMMARY**

The Merino Lifetime Productivity project is a major research initiative undertaken by industry with funding support from Australian Wool Innovation, aiming to develop Merino breeding and selection strategies that will maximise the lifetime productivity of Merino ewe enterprises. The project involves mating 134 diverse industry sires across five sites around Australia to generate up to 5,500 Merino ewe progeny that will be annually evaluated through life for a wide range of wool, growth, carcase, reproduction and disease resistance traits. It is planned that all ewe progeny will be genotyped and will add to the genomic reference population for the Merino industry.

### **INTRODUCTION**

The Merino Lifetime Productivity (MLP) project was established in 2015 to generate a unique Merino database that will enable the enhancement and validation of existing Merino ewe breeding and selection approaches in order to increase the long-term productivity of Australian woolgrowers. The project is a ten-year partnership between Australian Wool Innovation, the Australian Merino Sire Evaluation Association, Merino ram breeders, RD&E organisations, and five sire evaluation sites and their hosts around Australia.

The project was largely initiated to answer a range of industry questions relating to lifetime productivity in the Merino ewe enterprise. The practice of selecting animals at increasingly younger ages had raised concerns that industry was selecting for animals that performed well in their early years to the detriment of their lifetime productivity. Further, the diversification of the Merino ewe enterprise to include carcase traits, disease resistance attributes, reproduction along with wool production, led to concerns that current selection approaches might not adequately account for lifetime relationships between all these production elements.

The MLP dataset will be of significant value to the Merino industry for longer term phenotypic, genetic and economic analysis in order to answer a diverse range of commercial producer and ram breeder industry questions. Some of the short-term value of the project will be the submission of data to MERINOSELECT (Brown *et al.* 2007) and the resulting enhanced accuracy of Australian Sheep Breeding Values (ASBVs) for traits which are not routinely measured such as reproduction, body wrinkle and adult age assessments of key production traits.

### **OBJECTIVES**

The immediate objective of the project is to create an extensive dataset that captures the lifetime performance of 5,500 diverse F<sub>1</sub> Merino ewes across five environments. A range of research and development activities will be undertaken using the completed dataset. These will include the precise estimation of genetic parameters for lifetime production across traits and between ages that will help to address the range of industry questions that underpin the project.

Additional objectives include the identification of the best number of visual and quantitative assessments of wool, reproduction, disease resistance and carcase production required to maximise lifetime productivity, and to find the most cost-effective means to achieve flock breeding objectives

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

and lift rates of genetic gain.

The project aims to provide a major stimulus to the collection of reproduction data and to raise the profile and increase collection of adult growth, body composition and wool performance data.

**DESIGN AND IMPLEMENTATION**

**The sites and management.** The sites are operated by five sire evaluation groups affiliated with AMSEA and site hosts with details of these key parties outlined in Table 1. Each site has a specific set of protocols that are reinforced by standard sire evaluation requirements which include the management of ewe progeny of the sires (known as F<sub>1</sub> ewes) as much as possible as one management group. In the event that animals need to be split into smaller groups, ewes are stratified across these groups, the exception is the management of ewes during pregnancy whereby ewes are able to be run based on their pregnancy status from pregnancy scanning to lamb tagging as long as each group is genetically linked.

The sire evaluation sites were selected to represent geographically diverse environments and genetically different ewe bases (see further details in Table 1) to ensure that the outcomes of the project are relevant to all Merino breeders. Sites have strong local site committees to integrate industry into the project oversight and support. All sites were selected to have extensive experience in electronic identification, good sheep handling facilities, prior experience in sire evaluation, and proven sheep management skills.

**Table 1. MLP site name, number of industry sires joined, details of site hosts and site associations, ewe base details (microns and type), annual rainfall and rain fall distribution**

Site	Number of Sires	Host	Ewe Base	Rainfall
Balmoral, Harrow, Vic	50	Balmoral Breeders and Tuloona Pastoral	17.2um fine wool base	470mm winter
MerinoLink, Temora NSW	26	MerinoLink, Moses and Sons, Blue Chip Livestock	18um, previous sire evaluation progeny, and studs with ASBVs	500mm winter
Pingelly, WA	30	Yardstick Sire Evaluation Association, Murdoch University, the University of Western Australia	19.5um, meat focused Merino ewes	440mm winter
New England, Armidale, NSW	30	New England Merino Sire Evaluation Association, CSIRO	17um, ultra-fine flock	800mm summer
Macquarie, Trangie, NSW	32	Macquarie Sire Evaluation Association and NSW Department of Primary Industries	19-21um, two skin types	500mm even

**Ewe base joining.** The ewe base at each site was generally sourced from a single flock that had been inspected and approved as an even line of ewes by the site committee. There were two exceptions to this; at the MerinoLink site where the ewe base was derived from five performance recorded flocks (and ewe progeny from a previous sire evaluation), and the Macquarie site where the ewe base was made up of an equal split of ewes sourced from two studs that have differing approaches to selection and divergent skin wrinkle.

A total of 90 ewes were randomly allocated to each sire (stratified for age, ewe source, body weight and condition score) and mated via AI with the aim of generating 30 live ewe progeny per sire for

lifetime assessment. At several sites the AI program was split over two weeks to manage potential risk of climatic extremes on embryonic or neonatal loss (date of birth was recorded). The target of 30 progeny per sire was considered a balance between involving as many industry sires as possible whilst generating enough sire progeny to produce sufficiently accurate estimates of breeding value for lowly heritable traits such as reproduction. Each site joined to industry sires via AI for two years with the first AI program undertaken in March 2015 and the last in April 2018.

**F<sub>1</sub> ewes and wethers.** The core MLP sheep are the F<sub>1</sub> female progeny of industry sires that will be assessed throughout their life with ewes only removed for welfare purposes (e.g. severe injury, deformity or disease). The male F<sub>1</sub> progeny have been castrated and exited the core MLP project post weaning. In several instances these F<sub>1</sub> wethers have become the subject of separate projects. Lambs of the F<sub>1</sub> ewes, (F<sub>2</sub> progeny), leave the project following a DNA sample and weaning weight record.

**Sires and genetic linkage.** Across the five sites there were 166 sire joining groups, and after accounting for designed linkage across sites and years, a total of 134 unique sires from 95 different ram breeding flocks are represented in the project. All MLP sites are genetically linked by use of repeat sires and to the Australian national genetic evaluation service, MERINOSELECT. To achieve adequate linkage across MLP sites and years for traits with low heritability, approximately one in five sires provide linkage.

A sire selection protocol was developed to ensure that the project included sires that were both industry relevant and representative, and that offered extremes and combinations of performance that will help to explore the drivers of Merino lifetime productivity.

To achieve the sire selection goals the sires selected were a mixture of horn and poll, representative of different selection approaches and Merino strains, rams with progeny evaluated for production and without, rams from flocks who were and were not members of MERINOSELECT, a diverse range in performance, those that have been used extensively in industry or have made an industry impact (e.g. have sold sons for record prices or had exceptional show winning performance) and, those that were predicted to increase, decrease or maintain fleece value over time (based on performance information collected prior to the project).

**Assessments recorded.** A summary of the traits recorded on all F<sub>1</sub> ewes is given in Table 2. These traits are measured from birth through to 6-7 years of age, to capture performance over the productive life of Merino sheep. To complement the measurement program, it is planned that all F<sub>1</sub> ewes will be genotyped on a high-density SNP based chip platform, so that the project will be a valuable resource in adding to the genomic reference population for hard to measure Merino lifetime productivity traits.

**Pedigree, reproduction and early environmental effects.** Dam and sire pedigree of the F<sub>1</sub> progeny was allocated via DNA with exception of the New England site where daily lambing rounds were conducted to record date of birth, dam pedigree, and number of lambs born (sire pedigree was assumed from AI records). For the remaining four sites, the F<sub>1</sub> date of birth was estimated from the day of AI, birth type was inferred from pregnancy status estimated by ultrasound pregnancy scanning (at or between 40 and 70 days post AI), and rearing type was inferred based on the number of lambs at weaning.

The F<sub>1</sub> ewes are naturally joined as one group to a syndicate of Merino rams annually from 18 months of age, with the older drop of ewes at each site to be joined for 5 years and the younger drop to be joined for 4 years. Generally, each site is naturally joining for a period of five weeks using sires that have ASBVs available and have passed fitness and health requirements. The joining percentage at each site varies slightly from site to site based on local practices. Female reproduction traits on the F<sub>1</sub> ewes are derived from information recorded at joining, pregnancy scanning, in combination with DNA parentage tests on the F<sub>2</sub> lambs to identify maternal pedigree.

**Table 2. Visual and measured assessment program per year across all MLP sites**

Wool Measurements	Fleece weight, yield, fibre diameter (FD), FD standard deviation, FD coefficient of variation, staple strength, staple length, comfort factor and curvature
Growth and Carcase	Body weight, eye muscle, fat depth and adult ewe size
Health and Welfare	Worm egg count, faecal consistency, dag, urine stain, breech cover, crutch cover, breech wrinkle, and weaner and adult survival
Visual Wool Traits	Fleece rot, wool colour, wool character, dust penetration, staple weathering, staple structure, fibre and non-fibre pigmentation, recessive black, random spot
Visual Conformation Traits	Face cover, jaw, legs/feet, shoulder/back, body wrinkle
Classing	Two classings, flock classing (AMSEA), stud classing (Professional)
Reproduction	Sire and dam pedigree, pregnancy scanning, number of lambs weaned (conception, litter size, ewe rearing ability) body weight and condition score (at pre-joining, pregnancy scanning, pre lambing, weaning)

**Analysis.** During the sire evaluation phase each site produces an AMSEA accredited standard site report which includes progeny sire results presented within site and year of birth as average visual scores, classing grades, adjusted least square sire means, flock breeding values and indexes. In response to industry demand a separate MLP report is also produced that presents sire results within site within year and packaged as raw data, classing grades, visual scores, adjusted least square sire means, flock breeding values, research breeding values (for reproduction component traits) and indexes.

The details of future analyses are still in development and will include the estimation of genetic parameters for lifetime production across traits and between ages. An analysis to identify measurement and assessment strategies for recording of wool, reproduction, disease resistance and carcase production traits that are required to improve lifetime productivity, and achieve flock breeding objectives, is also planned.

A dedicated analysis committee will direct genetic and economic analysis priorities relevant to both the Merino ram breeder and ram buyer.

## **CONCLUSIONS**

The MLP project will provide a platform for Merino genetics research and development and extension through a range of analyses to test current selection tools across different genotypes and environments and refine and evolve these selection methodologies to deliver greater lifetime productivity.

## **ACKNOWLEDGEMENTS**

We gratefully acknowledge Australian Wool Innovation, nominating Merino breeders, site committees (Balmoral Breeders, MerinoLink, Yardstick Sire Evaluation, New England Merino Sire Evaluation Association, Macquarie Sire Evaluation Association) and site hosts (Tuloona Pastoral, Moses and Son, Murdoch University, the University of Western Australia, CSIRO and NSW Department of Primary Industries) for supporting and funding this work. A special acknowledgement is also made to the Australian Government who support research, development and marketing of Australian wool.

## **REFERENCE**

Brown D.J., Huisman A.E., Swan A.A., Graser H.U., Banks R.B., Ball A.J., Atkins, K.D. and Woolaston, R.R. (2007) *Proc. Assoc. Advmt. Anim. Breed. Genet* **17**: 187.