

**Expression of Interest: Terms of Reference****MLA Resource Flock: Satellite flocks for eating quality and carcass traits – Round 2**

**Date:** 24<sup>th</sup> September 2021

**MLA Program:** Livestock Genetics

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**1. Purpose:**

Meat & Livestock Australia (MLA) are seeking breeders to collaborate and co-invest with the MLA Resource Flock project and contribute to the industry's reference population by collecting additional measures of carcass and eating quality traits from industry animals as a satellite flock to the MLA Resource Flock.

**2. Relevant and necessary background:**

The MLA Resource Flock collects reference data (phenotypes) for use in genomic testing, as well as providing a resource for additional R&D projects. The data collected is used for the purpose of generating Australian Sheep Breeding Values (ASBV's) and other genetic and genomic information, for delivery to sheep breeders through Sheep Genetics.

Collecting more data will improve the accuracy of selection for traits that are either too expensive to measure routinely, are hard-to measure or can only be measured late-in-life. These traits include lean meat yield, eating quality, disease resistance, animal welfare, fertility, methane production and net feed intake.

A key component of the Resource Flock project is to seek additional co-investment from industry into the collection of genotypes matched to hard-to measure phenotypes on progeny from commercial (non-research) flocks known as satellite flocks. These satellite flocks will need to demonstrate an ability to meet selection criteria for items such as additional co-investment through in-kind resources and the ability to meet data quality standards.

**3. Objective**

The project aims to increase the number of animals in the reference population for eating quality carcass phenotypes. Preference will be given, but not limited to, breeds that currently have a limited reference population size.

The eating quality and carcass phenotypes recorded will include;

- On-farm pre-slaughter live weight (PSWT); Pre-slaughter live weight before going to abattoir with a 6-hour fast
- Hot carcass weight (HCWT); weight of hot carcass immediately following slaughter
- Carcass fat depth measured at the GR (GRFAT) and C-Site (mm) (CFAT)
- Carcass eye muscle depth (mm, CEMD) and width (mm, CEMW) between 12<sup>th</sup> and 13<sup>th</sup> ribs

- pH decline (PHD), left hand portion of the m. Longissimus thoracis et lumborum (LL) LL pH decline (when temperature reaches 18)
- Intramuscular fat (IMF), intramuscular fat measured on frozen sample caudal end of LL
- Shear force (SF5), shear force on loin muscle – day 5
- Where possible additional traits or devices may be used for research and development purposes such as DEXA or hyperspectral imaging.

#### 4. Terms of Reference: Scope

The project is looking for partners to collect the data and DNA samples for lambs born and slaughtered **prior to June 2023**. Individual breeders and/or breeder groups are invited to submit an EOI if they meet the following requirements and information recorded on-farm. To participate you will need to effectively manage and co-ordinate all the on-farm components of the project and organise with a processor to consign the lambs. Please note that resource flock project staff will contact the processor after successful applicants have been notified. *NOTE: PLEASE DO NOT CONTACT PROCESSORS. THIS WILL BE LIASED ON YOUR BEHALF PENDING THE SUCCESS OF YOUR APPLICATION*

Slaughtered animals must be:

- Slaughtered before June 2023 with an estimated carcase weight between 18kg and 32kg, and fitting the current lamb dentition definition
- Lambs from a structured progeny test where all lambs from the test will be slaughtered. It does not include surplus or cull animals.
- From large contemporary group cohorts where;
  - A minimum of 5 sires represented within each cohort and at least 5 progeny per sire. Preference will be given to cohorts with more animals and sires represented.
  - A minimum of 100 project lambs in the consignment and killed as one cohort. Preference will be given to applications with greater numbers of progeny in the slaughter cohort.
  - Lambs have been born within a 5-week period of each other
  - Lambs have been managed in the same mob until slaughter
- An industry representation of breeds, in particular minor breeds. A breed or sire line within a breed not heavily represented in the resource flock to date may be given preference.

Recommendations for trial design and sire selection:

- Preference will be given to expressions of interest that can provide information for the greatest number of the following fixed effects: date of birth, birth type, rear type, age of dam, flock of birth.
  - If using commercial ewes, use ewes of the same age group
  - AI is preferable to natural mating as the lambing spread is much more condensed allowing for a more uniform age and live weight of progeny at the time of slaughter

- If natural joining over an extended period, the minimum requirement to estimate date of birth to the nearest week of birth.
- It is recommended that both male and female progeny are slaughtered from each sire
- Applicants do not need to submit a full list of sires, however the genetic diversity of the sire candidates proposed will be a contributing factor to the evaluation of successful proposals
  - Sires nominated should be influential in future generations
  - Consideration of a linkage sire is important. This is a sire that already has (or will have) progeny in the resource flock that have been recorded for eating quality traits.
  - Appropriate linkage sires improve the accuracy of the ASBVs which is important to the breeders of sires contributed.
- For minor breeds, you could consider nominating a sire for the current intake of the resource flock to provide your sire candidate list with a link sire

Information captured on-farm that will be submitted by the collaborator to MLA for the Sheep Genetics Evaluation and for further research and development. The data must adhere to the [Sheep Genetics Breeders Quality Assurance Manual](#) and include:

- Information on sire and dam breeds
- Accurate management groups
- Base Traits: BWT (optional), WWT and live weight at ultrasound scanning for eye muscle depth (EMD) and fat depth (FAT).
- Pre-slaughter liveweight (PSWT)
- Satellite flock data stored and submitted through one of the Sheep Genetics accepted software programs
- Collection of DNA using TSU's (resource flock project to provide TSU's and further information)

### **Desirable criteria**

Applications will be preferred from proposed satellite flock/s with;

- Cross bred animals (in particular Merino or Maternal cross)
- Cohorts with larger sire representation i.e. progeny from more sires
- Representation of genes within industry that are not been previously represented in the MLA Resource Flock and will be of value to the future of the sheep industry

### **Outputs and Outcomes**

Successful EOI applicants will meet agreed milestones, which will identify progress in achieving the objectives and outcomes identified in this Terms of Reference (ToR) to result in the impact of improved annual rates of genetic gain in the Australian sheep industry.

Outputs specific to the enhanced carcase phenotypes EOI will include;

- Records, data and information that will contribute to industry through 'Breeding Value Services' and any 'National Genetics Data Platform'

Outcomes specific to the enhanced carcase phenotypes EOI will include;

- Increased accuracy for lean meat yield, eating quality and carcase ASBV's for industry flocks directly contributing genes into the satellite flock/s
- Reference populations for eating quality traits for a wider population of the Australian Sheep Industry
- Increased accessibility of genomic tools and technologies in the Australian Sheep Industry
- Improved productivity and profitability of sheepmeat breeding enterprises that contribute to industry targets

## 5. Confidentiality and Intellectual property

Successful EOI's will be funded with sheepmeat levies and required to enter into a standard agreement with the University of New England (UNE) as a sub-contractor to the MLA Resource Flock project. Project funding from UNE and MLA will include;

- genotyping of satellite flock animals (this includes TSU and the type of test will be dependent on representation of genes in the current reference population), and
- half the cost of the collection of carcase and meat science traits which has an approximate cost of \$150 per animal so the funding will equate to \$75 per animal.

While the satellite flock/s costs will include:

- the animals for slaughter sold to a collaborating processor on a commercial basis
- management and travel costs associated with collecting DNA samples, on-farm pre-slaughter traits and preparing the satellite flock for slaughter
- Information captured on-farm including pedigree, fixed effects and base traits
- half the cost of the collection of the carcase and meat science traits (approximately \$75 per animal)
- Satellite flocks will receive payment from the processor for the carcasses less the cost of the loins taken for collection

Failure to meet requirements and timelines set by the resource flock staff including but not limited to TSU return deadlines, number requirements and data submission may result in additional costs for the applicant or exclusion from the project.

All data and cited references will be acknowledged in the MLA Resource Flock milestone/s and final report. Any data/information collected under the satellite flock will be managed by MLA and may be used for research and development by MLA, as well as being incorporated and used in the 'Breeding Values Services' and any 'National Genetics Data Platforms', defined as below.

Raw carcase data can be made available for the own internal purposes of participants under the caveat that it is not to be published broadly and is to be used solely for educational purposes and not for the marketing of individual animals. Participants will also get improved ASBV accuracy for the sires used in their trial.

**Breeding Values Services** means any service which involves estimation of genetic or genomic breeding values for cattle, goat and sheep, including without limitation the service offered which uses the analytical software currently known as BREEDPLAN and OVIS software;

**National Genetics Data Platform** means database or network of databases and analytics infrastructure established to store, process and enable access to, in accordance with defined IP rights, data, IP, products and tools relevant to livestock genetics;

### Submissions

Breeders and/or breeder groups should submit the Expression of Interest Template to [livestockgenetics@mla.com.au](mailto:livestockgenetics@mla.com.au) by COB on 17th October 2021.

Meat & Livestock Australia will acknowledge receipt of each application. Applicants will be advised in writing of the outcome of their expression of interest by 22<sup>nd</sup> October.

**Further information**

For any enquiries about your eligibility or for further details on the EOI, please email Resource Flock Project Coordinator, Elise Bowen at [sheepdatamanagement@gmail.com](mailto:sheepdatamanagement@gmail.com).