# DAVIES LIVESTOCK RESEARCH CENTRE

## 2019 Annual Report

adelaide.edu.au/davies-research-centre

# PARTNER ORGANISATIONS

Centre for
Nanoscale
BioPhotonics
ARC CENTRE OF EXCELLENCE

mla
MEAT & LIVESTOCK AUSTRALIA

Government
of South Australia
Primary Industries
and Regions SA

SARDI
R&D
SOUTH AUSTRALIAN
RESEARCH AND
DEVELOPMENT
INSTITUTE

Australian Government
Department of Agriculture
and Water Resources

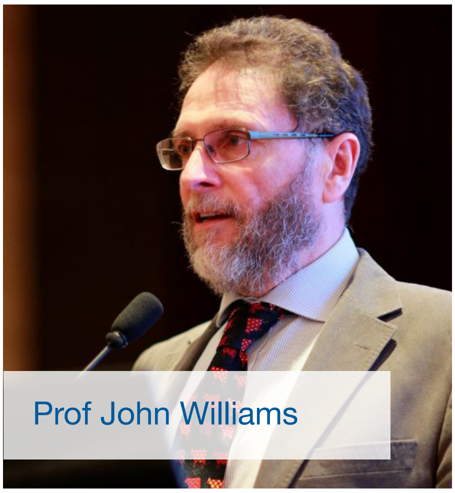
awi
Australian Wool
Innovation Limited

# CONTENTS

# DIRECTOR’S REPORT

Thank you for taking the time to read about our Centre. I have been with The University of Adelaide since 1992 and began as Director of the Davies Livestock Research Centre when John Williams stepped down in November 2019. I would like to use this Annual Report as an opportunity to honour the legacy of others and to outline a strategy for the future.

John S Davies was a respected grazier who generously bequeathed properties to the University. The proceeds from the sale of these properties have been invested and an annual disbursement underpins the operations of the Davies Livestock Research Centre.


Prof John Williams

Prof John Williams was appointed Davies Fellow in 2015 with the Davies Centre launched in November 2016. John initiated the work on Gene Editing, Genome Assembly and PCR based diagnostics, all with international collaborators. He initiated work with multiple companies, and MEQ Probe and Weatherbys Scientific are profiled herein. He was also a strong supporter of aligning activities to SA Sheep and Beef industry priorities which continues to provide fruit. Many of the projects in this report were initiated and/or supported by John.

Prof Stefan Hiendleder was appointed Davies Fellow in 2005 and established the Davies Epigenetic project which has also been an outstanding biological resource for training postgraduate students and high quality research publications.

Prof Cindy Bottema was appointed Davies Fellow in 1991 and together we established the Davies Gene Mapping project upon which formed the foundation for other grants, training of many postgraduate students and research publications. The Gene Mapping project resulted in a commercial test for the F94L myostatin mutation utilised by Limousin breeders, increased biological understanding genetics control of feed efficiency, carcass and meat quality traits. The technology of the time led to genomic selection programs now utilised in leading livestock breeding programs. Cindy retired in 2016 and continues to contribute to the Centre in an honorary capacity.

As a Centre we have an outstanding legacy of funding, research output and resources, and staff as a foundation. I believe we have a responsibility to our livestock industries and the University to broaden our areas of work. When assessing investment opportunities we measure them against developing good teams, excellent science, good stewards of money and outcomes for industry.

Our focus areas are developing Livestock Wellbeing in collaboration with colleagues from the Centre for Nanoscale Biophotonics; and ongoing work in genetics, genomics and breeding; reproductive productivity; assisted reproductive technologies; meat and wool science; and nutrition and metabolism.

> “As the child feeds the cow, so the cow feeds the child”


Prof Wayne Pitchford

In 2019 we had $1.85M Bequest funding, 83% of which was spent on salaries. We attracted $2.10M of external income and were involved in projects with funding to partner organisations of $1.44M, a total of $5.39M of research activity. The leverage of money to the University and the Bequest was 1.1:1. We are aiming to grow external income to 4:1 by 2025.

Throughout the report you will see a picture which is significant to me. It was drawn by Ebony Ackland, a former student with a passion for developmental agriculture. I would caption it “As the child feeds the cow, so the cow feeds the child” which reflects our focus on developing people and livestock. An additional saying that reflects our modus operandi is “Doing well by doing good” which is taken from the title of a book by Derek Tribe.

I hope you enjoy the information herein about a selection of our people and projects, and invite you to join us in growing our research programs.

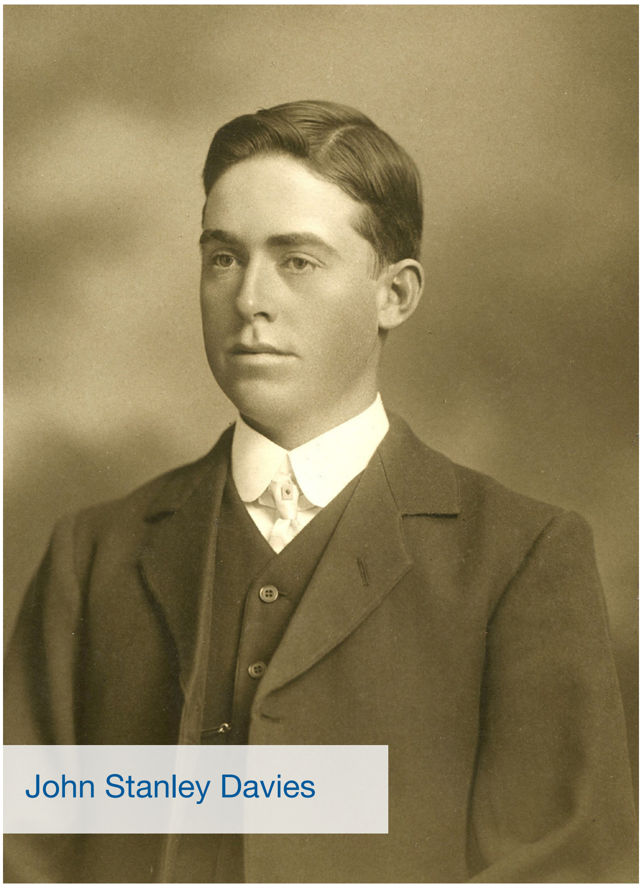
# JS DAVIES

The John Stanley Davies bequest to the University of Adelaide was one of the most significant in its long history.

Edward Davies arrived in South Australia from Wales in 1850. He carted copper from Burra until 1853 when he married and settled on a small farm near Mintaro. In 1869, he bought the first 2,000 acres of land a few miles from the town of Spalding which would eventually grow into the 18,500 acre Munduney (which means 'beautiful waters') property. Edward's son John took over in 1889, and was followed by his eldest son, John Stanley, who inherited the property after his father's death in 1948.

John Stanley Davies never married and spent his working life developing excellence in the strains of beef cattle. By the judicious introduction of imported animals, he made his stock some of the best available in the land and raised the standard of cattle in many parts of Australia.

Mr Davies passed away on Christmas Day 1968, and Prince Alfred College and the University of Adelaide learned soon after that the two institutions had been bequeathed the $2 million estate on a 1/5 to 4/5 share. It included both Munduney and the 450 square mile pastoral property Moralana, near Hawker.



John Stanley Davies

> …the income used to promote research into improving the quality of cattle, especially beef-producing animals

## The Munduney Homestead

The Will directed that the properties be carried on for 20 years and the income used to promote research into improving the quality of cattle, especially beef-producing animals. It also specified that the properties could be sold in 1989, or continued on. Under management of Martindale Holdings, the properties continued to operate until their sale which was undertaken in order to reinvest the proceeds into world-class research facilities for animal science.

In 2009, the University announced the sale of the Munduney and Moralana properties that had been bequeathed to it in 1968 by pastoralist, John Stanley Davies. Upon sale, the Certificates of Title for the properties were released for processing by the National Australia Bank. The eight titles, dating from 1910 to 1950, were returned to the University Archives for preservation along with other historic legal documents contained in Series 654.

Records, photographs, artworks, furniture and artefacts from the Munduney homestead have been retained by the University. Over time, these will be accessioned and added to its archival and heritage collections in order to preserve the memory of one of South Australia's most generous benefactors, John Stanley Davies.

# BOS TAURUS INDICUS

## Essential Resources: A globally unique bovine embryo and fetus collection

Major cattle breeds contribute significantly to global food supply and belong to either of two subspecies, which were domesticated independently more than 10,000 years ago: The European taurine (Bos taurus) cattle known for their superior carcase and meat quality, and Asian zebu (Bos indicus) cattle superior in parasite and draught tolerance. The harsh Australian environment and a changing climate require the combination of traits from both subspecies to secure national and global meat and milk production.

The combination of traits from both subspecies has been achieved to some extent in tropical composite breeds such as the Australian Droughtmaster. However, state of the art marker assisted selection programmes that are increasingly used in livestock production to achieve more efficient outcomes, require a much more detailed knowledge of the underlying trait biology, and their genetic and epigenetic basis, to harness and fully utilise the potential locked into (epi)genetic variation of both subspecies.

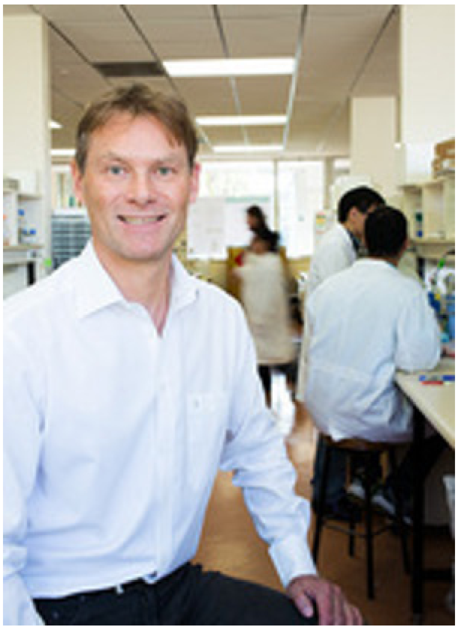
Immediately after his arrival at the University of Adelaide's Roseworthy Campus as JS Davies Professorial Fellow in 2005, Prof Stefan Hiendleder created a globally unique embryo and fetus collection to fill major gaps in our understanding of how Bos taurus and Bos indicus cattle, and breeds with a combination of both subspecies (epi) genetics, (i) differ in development and phenotype, and (ii) how endocrine, clinico-chemical and (iii) (epi)genetic parameters interact.

Prenatal developmental stages were chosen because of the understanding in 2005 emerging, and more than a decade later commonly accepted, paradigm that prenatal programming of interacting epigenetic and genetic factors determine postnatal phenotype, including crucial livestock performance parameters that affect health and productivity.

After three years of field work the resource comprised 60 conceptuses at the embryo stage, and 100 conceptuses at the fetal stage, with clearly defined age and (epi)genetic status. Completed and ongoing studies and theses based on this unique resource range from analyses of prenatal phenotype, crucial hormones and biomarkers in the circulation and in fetal fluids, gene expression, and genomics work.

Importantly, the most complete Bos taurus and Bos indicus cattle reference genomes to date were assembled using one of the fetuses of the resource in an international collaboration with NIH and USDA in a novel approach for genome assembly in general (see Genome Assembly case study page 9). Furthermore, extensive transcriptome data that provide fundamental insights into mammalian development and the (epi) genetic differences of the two subspecies are currently being finalised for publication.

The collaborative research environment, strong interactions, and collaborations, with Roseworthy colleagues and the Research Centre for Reproductive Health, which later grew into the Robinson Research Institute at the University of Adelaide, and membership of Davies group members in both institutions, provided the fertile ground for a several collaborative national and international research projects. These enabled a significant number of Honours, PhD, DVM and other student projects that contribute to a significantly improved understanding of the biological basis of the phenotypic variation in Bos taurus and Bos indicus cattle. Most importantly, this resource will deliver important insights for many years to come.



Prof Stefan Hiendleder, JS Davies Fellow, with PhD students in the laboratory

# SEX & PARENTAL GENOME EFFECTS ON BOVINE FETAL DEVELOPMENT

Lifelong development is largely programmed prenatally and is affected by many genetic and epigenetic factors. During fetal development, the process of forming organs and tissues is mediated by tissue-specific patterns of gene expression. Therefore, determining the patterns of expression and mechanisms of gene regulation at key fetal stages will provide information about normal development. Studying qualitative and quantitative changes in the transcriptome and understanding the mechanisms that regulate gene expression and the association with specific phenotypes in bovine fetal development will help us to explore both the sex effect and breeds effect. To carry out this work, we sequenced fetal samples of purebred and reciprocal cross individuals of the two cattle sub-species, (Bos taurus indicus and Bos taurus taurus). One hundred and twenty samples (60 males and 60 females) were collected from tissues derived from all three germ layers of the embryo, including brain, liver and lung, skeletal muscle and placenta. Sequencing data were mapped to the Brahman and Angus cattle reference genomes which is created from a genome assembly project that is lead by local scientists at the Davies Centre.

For sex effect, a remarkably small set of XY genes (gametologues) was identified that differentiate males and females across all tissues. Expression levels of paired gametologues in males and females are unbalanced and explain 18% - 96% of the phenotypic variance in organ weights attributed to the sex effect.  Considering the significant programming events at the embryo-fetal stage, we propose that early differences in gametologues expression between females and males is the fundamental driver of phenotypic differences between the sexes. Further studies on how these ancestral X-Y gametologues regulate gene activity using ATAC-seq and Methylation-seq will contribute to our understanding of the sexual dimorphism in health and diseases.

For breeds effect, there were a large number of genes that showed a significant breed difference in expression in each tissue. These genes were found to participate in pathways related to tissue-specific function. Genes that were differentially expressed between pure Angus and pure Brahman in all tissues were found to relate to functions such as immune response and stress response.

The differentially expressed genes (DEG) between the purebred groups and in the reciprocal crosses showed an additive expression pattern, where both paternal and maternal genomes contributed to the gene expression levels. Only 5% of DEGs in each tissue showed a parent of origin driven expression, Angus or Brahman, and showed both maternal and paternal dominant effects. Exploring these further would require long read Iso-seq data to resolve haplotype specific expression. The data provide a basis for future research on parental genome effects underlying phenotypic differences in cattle fetal development. Taking these factors into account may improve the welfare and productivity of cross-bred cattle in tropical environments.

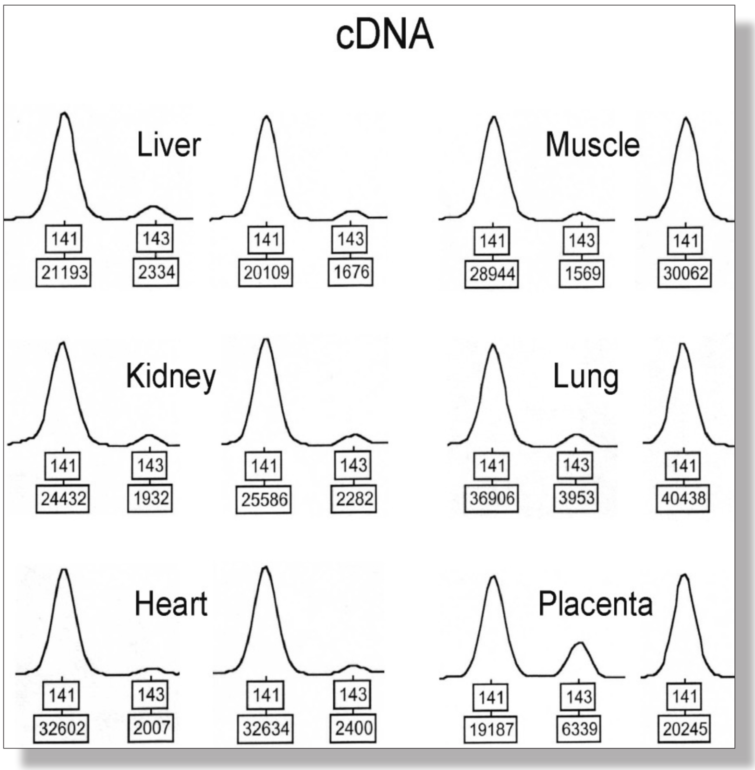
Dr Ben Rosen & Dr Georg Liu, USDA, Dr Lloyd Low & Cynthia Liu, Davies Centre

# DAVIES EPIGENOME PROJECT

## The global bovine epigenome

Hard wired genetics, i.e., the genetic code as the blueprint for phenotype and genetic mutation as the basis for phenotypic variation, is fundamental to our understanding of variation in important livestock traits. However, the last three decades have revealed another, additional layer of information across a broad range of organisms. This epigenetic (literally, “on top of genetics”) information has its own epigenetic code, in particular cytosine methylation and histone modification.

Combined with the classic genetic code, the epigenetic code provides a much more complete picture of the factors that determine and shape complex phenotypes in an ever changing environment.



The majority of the epigenetic layer of genomic information is erased in each generation and reset in the embryo and the developing germ cells. The epigenome can therefore confer phenotypic plasticity, i.e., enable the development of more than one phenotype from a given genotype, as the genome in a developing animal responds to environmental cues. As the environment may be different for each generation, epigenetic reprogramming thus ensures survival and genetic fitness through short term adaptation.

Although the epigenome is generally transiently heritable, there is increasing evidence that some environmentally induced epigenetic information may be transmitted across generations. Furthermore, genetic differences in components of the epigenetic machinery could potentially affect the epigenome of phenotypically diverse breeds and subspecies.

Epigenetic mechanisms such as RNA interference and genomic imprinting account for significant amounts of variation in animal phenotypes that is currently insufficiently captured by standard quantitative genetic models used in combination with genomic marker assisted selection. This is due to a lack of understanding of such mechanisms and their effects.

The Bos taurus and Bos indicus cattle studied here differ significantly in phenotype and genome. Although we have studied epigenetic mechanisms such as imprinting and micro RNA interference in our embryo-fetal resource collection previously, these were targeted approaches and thus limited in scope.

The current global methylome project will for the first time deliver a complete picture of the methylomes of Bos taurus (Angus) and Bos indicus (Brahman) cattle and their hybrids. The combination of the methylome data with existing transcriptome data and recently published novel genome sequences for both breeds will significantly boost our understanding of (i) how the epigenome in both types of cattle differ, (ii) interact with their respective genomes, and (iii) affect gene expression and thus phenotype.

Prof Stefan Hiendleder is gathering this data in collaboration with Dr Bastien Llamas, Australian Centre for Ancient DNA, The University of Adelaide.
The resulting information will assist development of genomic breeding tools by incorporating epigenomic information into existing technology platforms.

# GENOME ASSEMBLY: BRAHMAN & ANGUS

An international team of scientists led by the University of Adelaide Davies Livestock Research Centre has shown that it is possible to disentangle the DNA sequences of the chromosomes inherited from the mother and the father, to create true diploid genomes from a single individual.


Dr Lloyd Low

## True diploid genomes using an innovative trio sequencing approach

In a research article published in Nature Communications, the researchers showed that genomes of two important modern-day cattle breeds, Angus (Bos taurus taurus) and Brahman (Bos taurus indicus), can be completely decoded from a single hybrid individual carrying the genetics of both breeds, using an innovative genome assembly strategy. As a proof of principle, the work was done using cattle, but the assembly method is applicable to other diploid organisms including human.

Dr Lloyd Low from the Davies Centre says the technique, called trio binning, gives the true genome sequence of each chromosome in an individual. Obtaining a full genome from an organism that inherits half the chromosomes from the mother and the other half from the father is difficult due high similarity between the parental chromosomes.

“Back in 2018 we were able to demonstrate that with this method it was possible to identify large sections of the DNA from the parents. Now in 2020 we have used the same concept to create the sequence of full chromosomes,” Low said.

Disentangling maternal and paternal genomes is very difficult, but we have now been able to do this and create the best genome assemblies available for any livestock. These high quality genome sequences will make it easier to more accurately study the genetics of cattle to improve production and welfare traits.

Brahman and Angus cattle subspecies were domesticated separately thousands of years ago and have been subjected to very different selection pressures since then: pest and drought environments in the case of the Brahman cattle and beef production in Angus cattle. These different characteristics and histories are reflected in their genomes, which makes them ideal test subjects.

Brahman cattle are better able to cope with hot and humid environments and are routinely crossed with European breeds such as Angus to combine tropical adaptation with growth, reproduction and meat quality. Considering the large differences in production and adaptation traits between taurine and indicine cattle, comparing the genomes helps us understand how the animals adapt to their environment, which is of substantial scientific and economic interest.

One notable example of genetic differences between Brahman and Angus is an indicus-specific extra copy of fatty acid enzyme, which may be important for the regulation of the metabolism related to heat tolerance.

# ANALYSIS OF HONG KONG FERAL CATTLE REVEALS ANCIENT ORIGINS

Although Hong Kong is one of the most densely populated regions in the world, it is mainly forest, and in that forest is a remnant cattle population of uncertain origin.

We carried out an analysis of genotypes from 21 of these Hong Kong Feral (HFK) cattle, along with those from 703 individuals of 36 cattle populations of European, African taurine, and Asian origin, and 3 other cattle species The starting dataset contained ~50k genotypes but because of ascertainment bias – the genotype chip was designed for taurine cattle and did not capture the other animals well – was eventually reduced to ~4k genotypes.

The HKF separate out from taurine and indicine cattle very early, along with the other species (Fig. 1, K = 3). At K = 4, HKF had ~30% wild Asian ancestry, with the remainder a combination of European taurine and Asian indicine ancestry. Ultimately, we assigned HKF ancestry as ~60% European taurine, ~20% indicine, ~10% gaur and ~10% banteng, the latter 2 being other species of cattle. The taurine component comes from European Holstein dairy cattle.

Our interpretation of this pattern of ancestry is that wild Hong Kong cattle were interbred with Holstein dairy cattle in Hong Kong, hence the high level of Holstein ancestry. The presence of indicine and such high levels of other species in HKF suggests that the non-taurine progenitors of HKF were from a local indicine population, along with introgression from the other species.

However, we cannot rule out that the non-taurine component actually reflects a different domestic cattle domestication event in Southern China, preceded or followed by introgression from other species. The genotype data is too sparse and too biased toward taurine cattle to address this question, so we have now fully sequenced 30 HKF genomes and have begun a deeper analysis to address this question.

By working on projects like the Hong Kong Feral, we develop staff, build collaboration and grow our understanding of cattle genomes. This increased understanding will provide insights into productivity and adaption in terms of impacts of specific genomic regions and overall heterozygousity, both of which complement our other research and commercial programs.

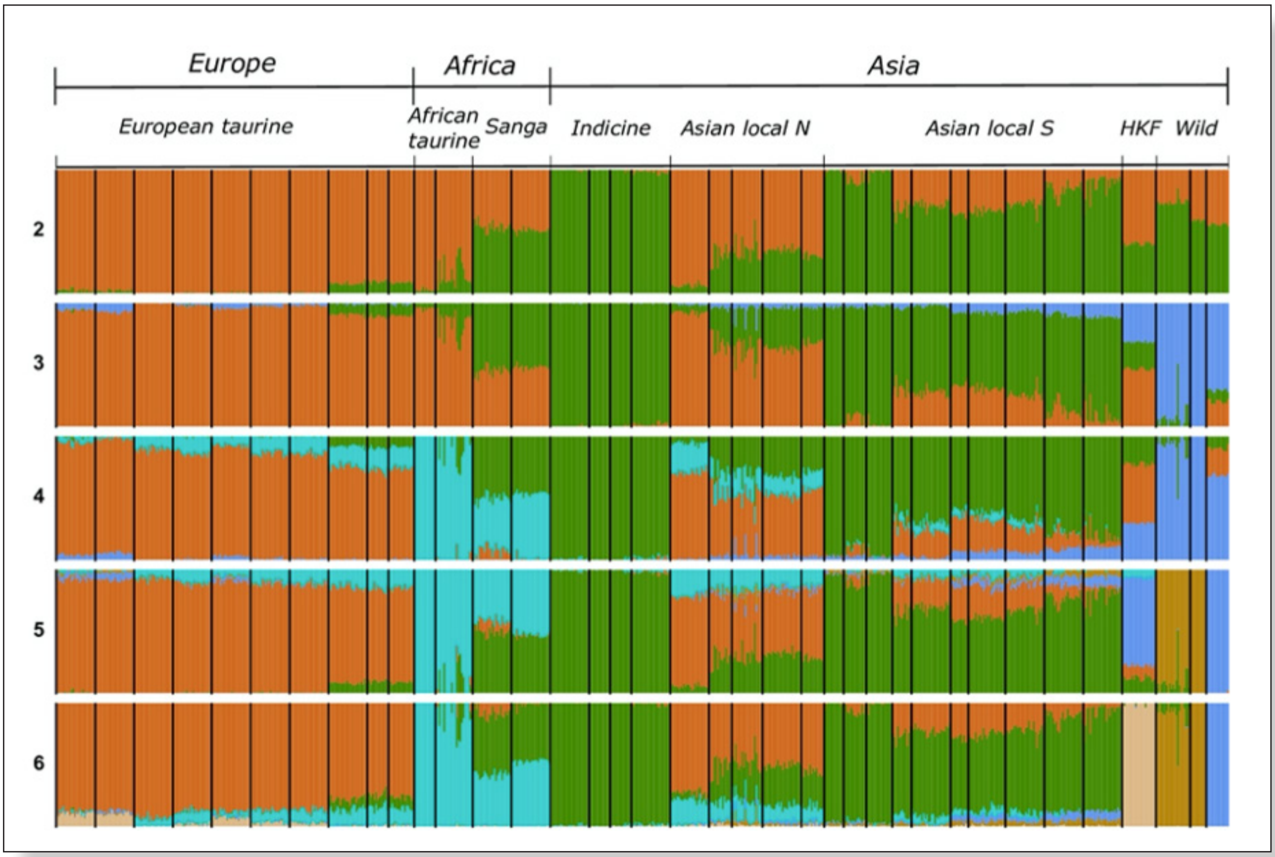


Fig 1. Admixture analysis of the first 10 K solutions for the 37 cattle populations. Hong Kong cattle are labelled HKF.

# STUDY OF CATTLE HORN DEVELOPMENT

In dairy and beef production, there is pressure towards breeding for hornless, or polled, cattle because there are concerns for the welfare of horned animals. Producers routinely disbud or de-horn horned calves to stop horns from growing because they are a danger to the animals and their handlers. While this procedure does improve the safety of herd-mates and handlers, it impacts the welfare of animals.

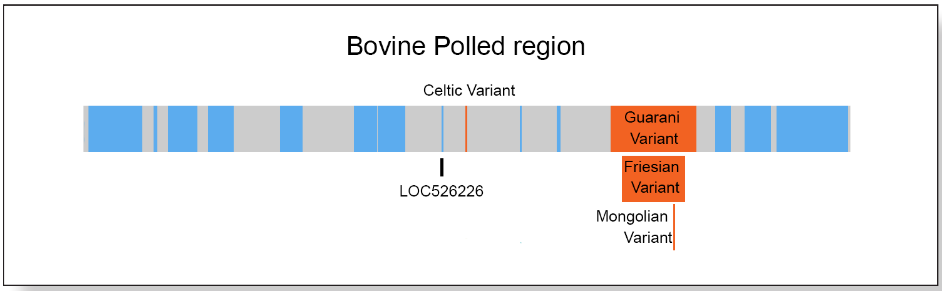


Fig 1. Location of polled gene LOC526226 in cattle

Hornless, or polled, cattle are also naturally occurring. Polledness in cattle is associated with four genetic variants that all occur in the same region of chromosome 1. Johanna Aldersey, a PhD candidate at the University of Adelaide, is studying the molecular pathway(s) that cause horns to grow in cattle. "The variants are not located within any genes, so we don't know which pathways are being affected," said Johanna, "We think the variants change the expression of nearby genes." Although the gene order of this region is well conserved across horned and hornless species, one gene in this region, LOC526226, is unique to cattle (Fig. 1).

An RNA sequencing experiment was conducted to investigate this hypothesis, in which gene expression in the horn bud growing regions is being compared between horned and polled bovine foetuses. Early studies reported that the horn bud was visible at 60 days of development. "We wanted to study gene expression just before the horn bud formation, so we chose to study 58 day old foetuses for our experiment. We found that the horn bud is already formed at 58 days, and the horn bud appears as a ring of depressed skin," said Johanna, "This is not seen on the 58-day old polled foetuses that have smooth skin at this site."

Jo Aldersey

Histological analysis of the horned foetuses showed that the epidermis of the horn bud is six to eight layers thick, whereas the surrounding tissue only has one or two layers. There also appears to be an aggregation of cells within the dermis that is not seen in polled foetuses.

"Given these differences, comparing the gene expression of horned and polled foetuses will be useful in uncovering the genes and pathways that are important for the formation of the horn bud," said Johanna.

The RNAseq data is currently being analysed and Johanna is excited, "This is the earliest gestational age that gene expression has been studied to understand horn development in cattle."

This study was initiated by Professor John Williams and will contribute to the understanding of how horns develop and how the genetic variants affect normal development. Horns are a unique characteristic of Bovidae, and this research in cattle could potentially translate to other important related domestic species such as sheep and goats.

# SHEEP LICE DIAGNOSTIC ASSAY

Sheep lice cost the Australian sheep industry over $120M annually. Lousy sheep not only produce about 10% less wool, but also further decrease about 10% wool quality value plus the costs of chemical treatment. Infestation of the flock with sheep lice is an ongoing significant health management issue for sheep in Australia. Moreover, lousy sheep are more susceptible to flystrike, and have an increased risk of infection from dipping sheep causing high mortality.

Wide spread current practice is for wool producers to treat sheep directly after shearing whether the sheep are known to have lice or not. This incurs both a treatment and labour cost, results in unnecessary use of chemical treatments risking the development of resistance, and impacts wool production. “A test that can accurately, quickly and cost effectively determine presence of lice before or at shearing would allow wool producers to make informed decisions about immediate post-shearing treatment”, said Dr Tong Chen, Laboratory Manager, Davies Centre. Given the importance of the wool sector to SA agriculture the search for a cost effective and practical lice detection test was supported by Primary Industries and Regions SA.

The pen side louse detection project addressed the development of a test based on presence of sheep lice (Bovicola ovis) DNA on shearing hand pieces, with the aim of delivering results in under 60 minutes.

We designed three PCR primer sets that target specific sheep louse mitochondria DNA regions in three genes COX1, rrnL and NAD5. These primers were tested on louse DNA experimentally added to wool and were shown to be specific, with detection limits as low as a few nano-grams of DNA. These assays were also tested on grease collected from shearing sets following routine shearing of a small commercial flock, infested with lice. The PCR test has proven robust to contaminants present in the grease. Therefore we addressed the challenge of delivering results rapidly in the field.

Prof John Williams initiated the project which included MatMaCorp Inc., from Nebraska, to migrate the laboratory-based test to a pen-side assay. The rapid DNA extraction kit based on the Magictip protocol was develop for various louse sample types, and specifically the grease from shearing hand-sets. The test involved taking samples using a thin plastic rod which is transferred to a tube containing extraction buffer. This is incubated in the portable Solas 8™ instrument for about 20 minutes. An aliquot of the lysate is then transferred to the assay tubes containing assay buffer. MatMacorp used the based PCR primers and target sequences to develop “padlock” probes and assays for use on the Solas 8™ instrument that is portable and has the potential to be used in the sheep shed or on the back of a ute. The Solas 8™ assays that detect COX1 and rrnL specific regions gave promising results in tests of grease samples collected from shearing heads used for lice infested and non-infested sheep.

The next challenge is to develop current test into a viable pen-side, on farm, assay. The current diagnostic assay using portable Solas 8™instrument takes about 2 hours in laboratory and this needs to be reduced to below 1 hour. We also need to develop protocols to decontaminate shearing combs to ensure that there is no carry-over of material that will test positive in a subsequent run.


Dr Tong Chen

Tong concluded that, “The MatMacorp assay has an advantage compared with the enzyme-linked immuno-sorbent assay developed in 2009 in so far as samples do not need to be sent to a laboratory for testing. However, the novel assay system still needs to be validated under field conditions”.

# MICRO-RNA AS BIOMARKERS OF EMOTION IN PIGS

Critical to understanding animal welfare is the ability to assess the affective (emotional) state of an animal. Current methods to measure the affective state of an animal are either unable to distinguish between positive and negative affective states or are unsuitable for a production environment. There is a need to develop novel biological markers, or biomarkers for positive welfare states, e.g. reward and contentment, and negative welfare states, e.g. pain, anxiety, and fear.

Laura Marsh - PhD candidate from the Davies Centre, completed her bachelor of Animal science with honours at the University of Adelaide. Currently in her final year of PhD, Laura's research focusses on developing novel biomarkers of pig welfare. Supervised by Dr Alexandra Whittaker, Prof Stefan Hiendleder, and Prof Paul Verma, she incorporates epigenetics, neurophysiology, endocrinology, stress physiology and behaviour in order to better understand the biological processes involved in animal emotion.

"My project proposes to identify novel molecular biomarkers, specifically small microRNA (miRNA) for positive and negative affective states in order to improve the welfare of pigs, and improve the assessment of welfare in pigs."

MicroRNA are small single stranded non-coding RNA molecules (approximately 22-24 nucleotides long) that are involved in the regulation of many biological processes and have the ability to modulate or inhibit expression of multiple genes post-transcriptionally. These molecules are ubiquitous throughout the body, including the brain, and are released into circulation where they can then be measured.

"We expect specific microRNA to be produced in response to different emotional states, and that these specific miRNAs can then be measured in the blood of pigs, thus providing a proxy marker of the emotional state of the animal"

So far Laura's research has successfully been able to identify differentially expressed microRNA as biomarkers for negative emotional state in pigs including pain. It is expected that further analysis of results, will lead to the identification of microRNA biomarkers of positive emotional state such as reward.

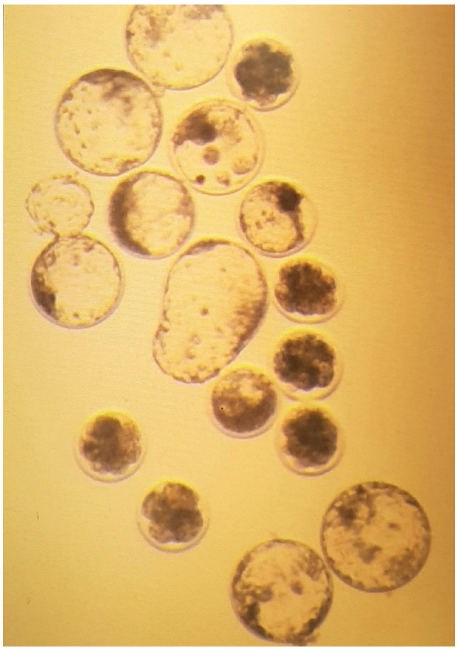
Laura concluded that, "The outcomes of this research will be to provide industry with a suite of novel biomarkers that can accurately assess both positive and negative emotional states in pigs, where this assessment is essential to enable the continued improvement to animal welfare."


Laura Marsh

"The initial findings of this research are really exciting and relevant to the pig industry. There are changing expectations from consumers about appropriate animal welfare standards within farming systems, where the Australian pig industry is expected to provide not only minimization of harm and exposure to adverse conditions, but provide opportunity for positive experiences in their animals"

# ANTI-MÜLLERIAN HORMONE AS A PREDICTIVE MARKER OF FERTILITY IN CATTLE & SHEEP

Variation in cow and ewe fertility profoundly influences reproductive efficiency of herds/flocks and success of embryo collection and transfer programs. Circulating anti-Müllerian hormone (AMH) is a predictive marker of the ovarian response to, and embryo production following, multiple ovulation protocols in cattle.



Sheep embryos varying in quality as indicated by stage of development

Previously, we have demonstrated that circulating AMH levels predict the number, and quality of embryos produced by Merino lambs in a JIVET program. Jamee Daly is currently completing a PhD focussing on utilising circulating AMH as a predictive marker of ewe fertility within commercial flocks and in vitro embryo collection programs. This is a collaboration between the School of Animal and Veterinary Sciences (Dr's Will van Wettere and Karen Kind) and SARDI (Dr Jen Kelly), and involves data collected at SARDI's Turretfield Research Station, Roseworthy Campus and two commercial NSW farms. Alongside this, a collaborative project between the Davies Centre and Holbrook Vet Centre was conducted to determine the relationship between circulating AMH levels and embryo production for mixed age, Bos taurus (Wagyu) cows used as donors in repeated multiple ovulation embryo transfer (MOET) cycles.

## Outcomes of sheep studies

Jamee's work has found plasma AMH concentrations at 5 months of age were higher ($P<0.05$) for singleton and twin-bearing ewes compared with non-lambing ewes (2.74± 0.23 and 3.34± 0.81 vs 1.26± 0.48 ng/ml, respectively). A large scale trial is currently being undertaken to confirm this relationship within two large commercial flocks in New South Wales. From Jamee's PhD, distinct AMH profile and ovarian maturity differences between Merino and Suffolk ewe lambs have been identified. Understanding these differences may lead to breed specific cut off values and selection recommendations for the Australian sheep industry.

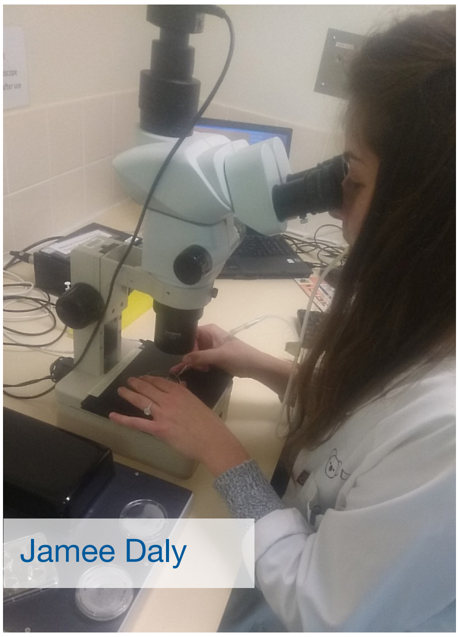
The in vitro aspects of Jamee's PhD are ongoing, with juvenile and mature in vitro fertilisation and embryo transfer (JIVET and MIVET, respectively) technologies being employed to understand whether AMH correlates with oocyte and embryo quality. Preliminary in vitro studies determined ewes retrospectively classified as having high follicular AMH (17.9 – 19.25 ng/ml) produced more blastocysts from cleaved oocytes than lambs with low (0.5-10.8 ng/ml) or medium (10.81-17.89 ng/ml) follicular AMH.

## Outcomes of cattle studies

Retrospectively, AMH concentrations collected at oestrus synchronisation for 182 mixed age Waygu cattle, were divided into three groups: LOW, <416pg/ml; MED, 416- 831.4 pg/ml; and, HIGH, >831.4 pg/ml and correlated to embryo flush data. There was a positive relationship ($P < 0.001$) between plasma AMH and average embryos / flush; with 1 pg/ml increases in AMH resulting in additional 0.00125 ± 0.003 embryos per flush. The mean number of embryos / flush was higher ($P < 0.05$) for cows with HIGH compared with LOW AMH (3.07 ± 0.46 versus 2.03 ± 0.31), with MED cows intermediate (2.82 ± 0.30). The maximum number of embryos produced in a single flush was also higher ($P < 0.05$) for HIGH versus LOW cows (8.13 ± 1.24 versus 5.18 ± 0.79), with MED cows intermediate (7.09 ± 0.74).

## Summary

Jamee's PhD has demonstrated AMH levels at weaning are predictive of ewe fertility following their first mating, with ongoing in vitro studies designed to understand the predictive value of AMH. Even though the bovine study used retrospective data, a single AMH measure may be sufficient to select or discard potential donors in MOET programs, improving efficiency and cost-effectiveness.



Jamee Daly

# IMPROVING CATTLE CLONING TECHNOLOGIES

Cloning has the potential to improve cattle breeding. However only a few per cent of cloned embryos produced using skin cells from live animals produce calves, which limits its use commercially. Instead of using skin cells we can make stem cells from embryos which we are using to increase cloning efficiencies.

Assoc Prof Mark Nottle (Robinson Research Institute) and Dr Karen Kind (Davies Centre) aim to demonstrate that a new stem cell type isolated by us can be used to improve cloning efficiencies in cattle.

Current cattle cloning efficiencies are relatively low compared with other breeding technologies such as embryo transfer, which limits its use commercially. Cloning involves the insertion of a skin cell (fibroblast) into an unfertilised egg or oocyte, which has had its genetic material removed. However only around 2% of embryos are sufficiently reprogrammed to allow them to develop to term. Previous work in mice has suggested that the use of embryonic stem cells can increase cloning efficiencies by up to 10 fold.

Embryonic stem cells are isolated from embryos and require less reprogramming than fibroblasts. However ESCs are yet to be isolated for any of the livestock species preventing the use of this approach for improving cloning. In a breakthrough we have isolated a new type of embryonic stem cell in pigs, cattle and mice (inner cell mass stem cells) . In other work we have shown that these cells can also be isolated from cloned embryos produced using skin cells taken from live males or females. The aim of the present study is to determine whether these cells can be used to improve cloning efficiencies in cattle as shown in Fig. 2. These cells will also be useful for other applications including gene discovery using gene editing.

1. Three porcine lines have been isolated and characterised (we are using pigs as a model initially because of a temporary lack of cattle oocytes).

2. Currently we are determining the best way to fuse these cells to oocytes as well as activate these embryos. Several approaches have are being examined including injecting cells into oocytes.

3. As part of work we have also demonstrated that addition of Granulocyte Macrophage Colony Stimulating Factor (GM-CSF) a cytokine found in the ovary, to our embryo culture media increases the proportion of embryos that produce stem cell lines. It is hypothesized that this is due to its effect in increasing the number of cells in the embryo that give rise to the fetus. As such we are also examining whether GM-CSF can be used to in vitro embryo production (IVP) success rates in a separate project aimed at raising awareness and adoption of this technology by breeders.

Having optimised methods for fusing and activating these cells, the next step is to demonstrate that inner cell mass stem cells increase cloning efficiencies by examining embryo development and then birth rates. The study will also examine differences in gene expression between cloned embryos produced using or stem cell type and fibroblasts as a measure of reprogramming success. Ultimately we aim to determine what are the factors in the oocyte that reprogram the donor nucleus so that these can be used to reprogram skin cells in vitro before using them for cloning.

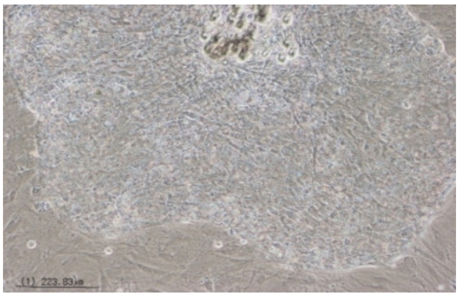


Fig 1. Cattle inner cell mass stem cells

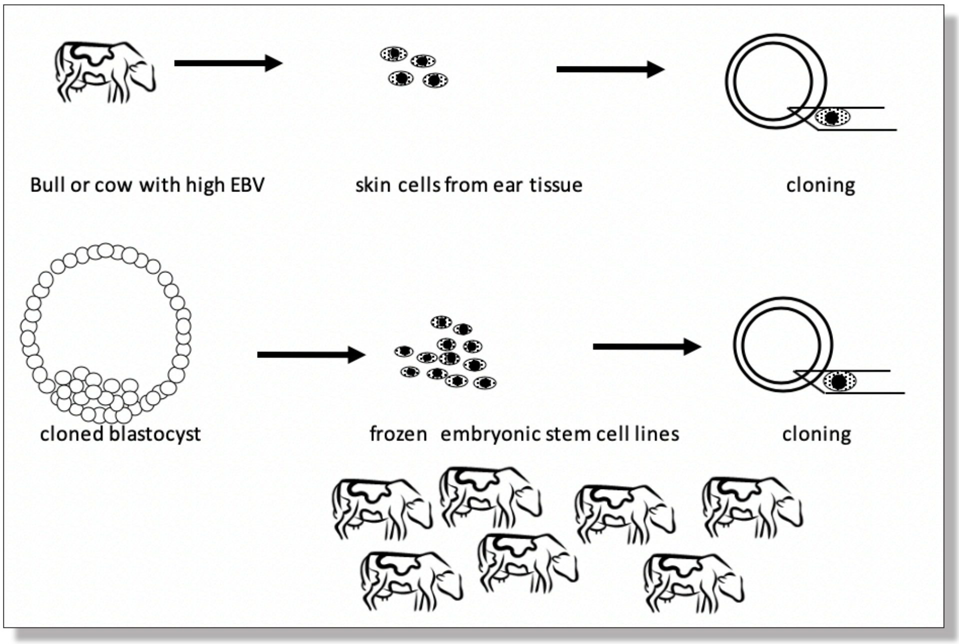


Fig 2. Improving current cattle cloning efficiencies using embryonic stem cells. Skin cells isolated from the ear tissue of live animals are used to produce cell lines which are then frozen. Fibroblasts are then used for cloning to produce embryos from which embryonic stem cells are then isolated and frozen. These are then used for cloning to increase efficiencies.

# HEAT STRESS LIMITS SHEEP PRODUCTIVITY

The thermal environment is the largest single stressor affecting the efficiency of sheep production, especially those managed in the pasture and pastoral based systems typical of Australia.

## The problem

The thermoregulatory mechanisms of sheep are seriously challenged when temperatures rise above 25 to 31°C, and the physiological and behavioural adaptations that allow sheep to maintain homeothermy negatively impact growth, welfare and reproduction. From late spring to early autumn (November to March), cycling and pregnant ewes, as well as working rams, are commonly exposed to ambient temperatures which challenge homeothermy, wellbeing and reproductive function. Based primarily on observed and projected increases in temperature associated with climate change, exposure of the Australian sheep flock to thermal stress will occur more frequently and for longer periods.

## The exercise

The vulnerability of the Australian sheep industry to the impacts of heat stress stimulated Meat and Livestock Australia to call for tenders for a review of the impacts of heat stress, and climate change scenarios on the reproductive performance of the Australian sheep flock. This review was conducted as a collaboration involving scientists from a range of disciplines within the University of Adelaide and SARDI. Contributors from the University of Adelaide were: Dr's Will van Wettere, Alyce Swinbourne, Stephan Leu, Stephen Lee and Karen Kind (School of Animal and Veterinary Sciences); Assoc Prof Kathy Gatford (Research Centre for Reproductive Health); and, Dr Sam Culley and Proft Seth Westra (Faculty of Engineering, Computer and Mathematical Sciences). Contributors from SARDI were: Dr's Dave Kleemann, Alice Weaver, Jen Kelly, Simon Walker, Dane Coleman and Peter Hayman.

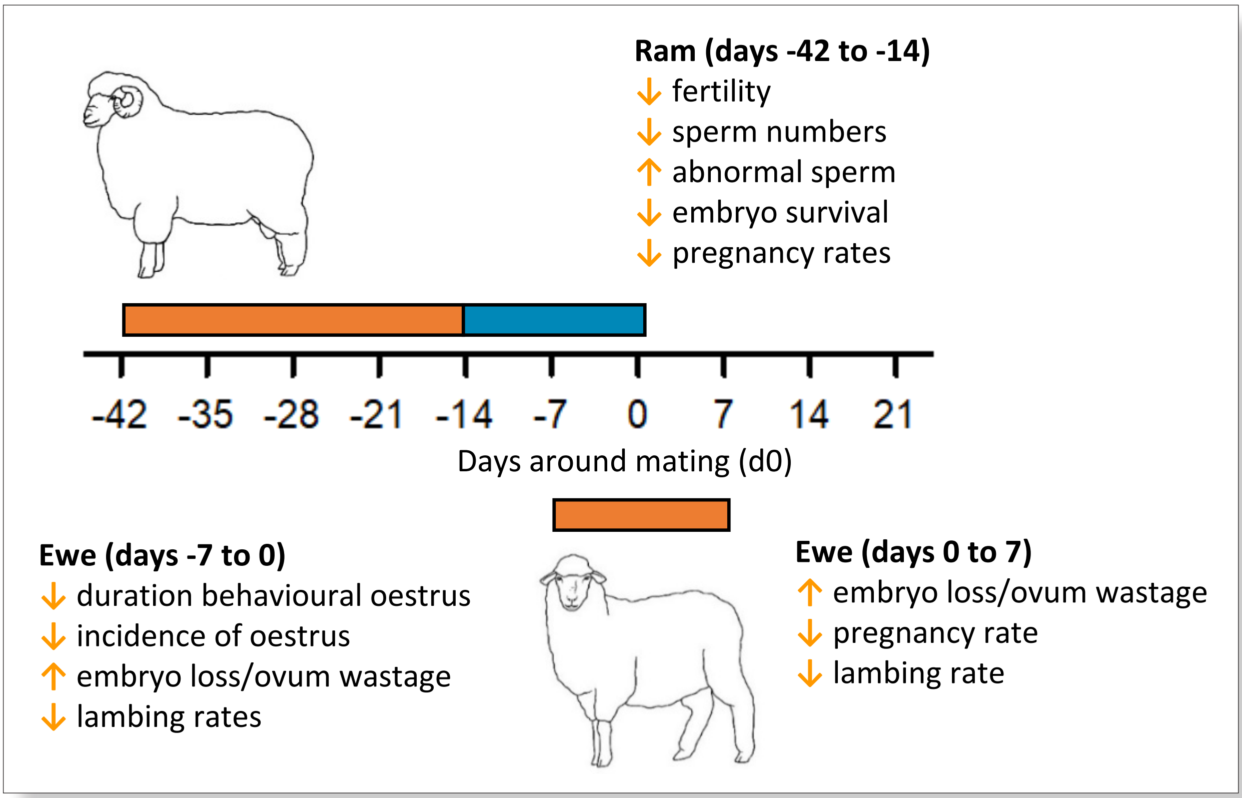


Fig 1. Effect of heat stress around mating on ewe and ram fertility.

# The Outcomes

## Part One: Heat stress and reproductive function

Ewes experiencing heat stress during the 6 to 10 days around the timing of joining experience reductions in oocyte quality, fertilisation and embryo survival, resulting in a reduction in the number of lambs born and the number of ewes lambing. Ram fertility is reduced during the 14 to 50 days following a heat stress incident. Heat stress during pregnancy reduces lamb birthweight by 0.6 – 1.4 kg, decreases the proportion of lambs born alive by 30% and causes approximately 25% more lambs to die after birth (These effects are summarised in Fig. 1 and 2).

## Part Two: Impact of heat stress on the Australian Sheep Flock

Based on the sites investigated and their current seasonal joining patterns, it is estimated that 2.1 million potential lambs are lost due to heat stress under the current climate, with this number likely to increase to 2.5 and 3.3 million should a 1 °C or 3 °C increase in Australian temperatures occur.

The current national cost of heat stress is estimated to be $97 million annually (based on lambs not born / mated ewe) or $168m when the impacts of low birthweight on lamb survival were also considered (lamb price $6/kg), which increases up to $166 million or $278 million annually in a climate scenario +3 °C.

## Part Three: Research priorities to protect the sheep industry from heat stress

1) Establishing mitigation strategies which promote homeothermy and reproductive function of ewes and rams under thermal strain (i.e. nutrition, shade, wool cover, mating protocols)

2) Understanding the impact of ambient conditions on the behaviour, resource use and fertility of sheep under typical production systems, and identify differences between individuals (behavioural, physiological, molecular) in their ability to thermoregulate and maintain reproduction under thermal strain.

3) Modifying the environment to reduce the severity of thermal strain (use of shade, establishing cooler micro-climates, establishing Temperature Humidity Index thresholds, adoption of containment housing systems)

4) Selection for physiological and behavioural adaptions which promote heat resilience without impairing productivity.

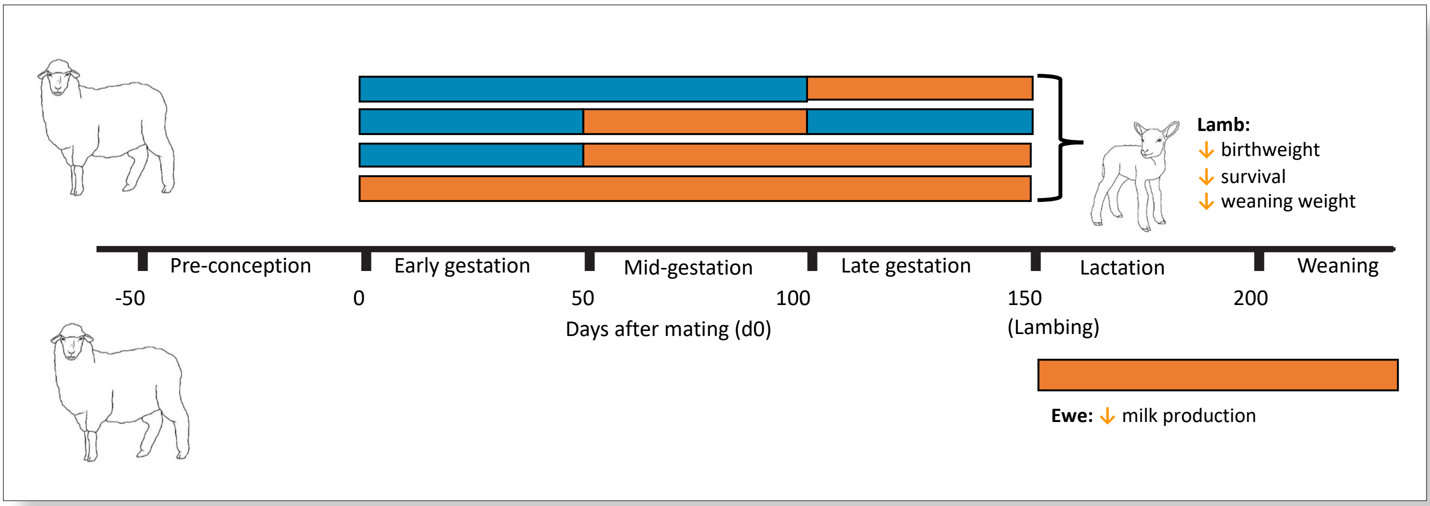


Fig 2. Effect of heat stress during pregnancy on ewe and lamb reproduction.

# IMPROVING THE RELIABILITY OF FEMALE FOCUSED LIVESTOCK ARTIFICIAL BREEDING

Lead by Prof Jeremy Thompson and in partnership with the MLA Donor Company, Holbrook Vet Centre and Quantitative, the Davies Livestock Research Centre has adapted an approach, first used in human reproductive medicine, to determine whether embryos would successfully establish a pregnancy using specialist images collected prior to transfer.

The benefits of this research will be higher confidence of predicting successful pregnancy in livestock artificial breeding programs.

Uptake of female focused advanced artificial reproduction (ART) in bull breeding herds remains low which limits the rate of genetic gain. Our aim is to improve efficiency and thus reduce costs per calf making advanced breeding methods more attractive. This is expected to lead to significantly greater adoption of female ART within bull breeding herds. The major interlinked limitations to the use of embryo transfer technologies by bull breeders stem from the modest but variable pregnancy success rate of transferred embryos which for Multiple Ovulation and Embryo Transfer (MOET) currently averages approximately 60% and for In vitro Fertilization (IVF) technology, pregnancy rates are in the order of 40% for mature cows and lower and very variable for juvenile animals (JIVET). This low success rate means a large numbers of recipient cows need to be managed, and hence there is a significant on-farm logistics challenge and high overall cost per live calf born.

Traditionally an embryologist has assessed an embryo and determined whether it is suitable for transfer or not. The current method recommended by the International Embryo Technology Society (IETS) grades embryos based on morphological classification as 1. Excellent or Good, 2. Regular, 3. Poor. This embryo grading approach is subjective and operator dependent. Embryos classified as 1, (excellent or good) have higher successful pregnancy outcomes than regular embryos. However, there remains considerable scope for improvement in the assessment. Improving objective assessment of embryos by analysis of digital images is an ideal approach as it is non-invasive, objective, with high reproducibility, and can be carried out in "real time" thus facilitating the selection of freshly produced embryos for immediate transfer, or freezing.

Some 476 high resolution images of day 7 embryos were collected on properties across southern Australia from a range of breed types including Angus, Poll Hereford, Wagyu and Composite cattle with pregnancy outcomes also collected. A machine learning approach was used to assess the predictive capacity for pregnancy establishment from imaging of routinely selected transferable cattle embryos prior to transfer. Outstanding results were achieved with the probability of an accurate prediction for MOET embryos of 88% and for JIVET embryos of 96% (a probability over 95% is considered a highly predictive assay).

In a follow up study, positive predictive value and negative predictive value were determined in a new data set. Positive predictive value (PPV) is the probability that embryos with a positive screening test truly are going to lead to pregnancy. Negative predictive value (NPV) is the probability that embryos with a negative screening test truly are not going to lead to pregnancy. For the cattle industry, it is paramount that embryos that test positive, are indeed truly positive otherwise the cow would be given an impaired embryo. If we predict a positive but the classifier is wrong it's a critical problem since inserting a poor embryo could waste time and money. Hence a very high positive predictive value will ensure the likelihood that we choose a truly good embryo leading to pregnancy. Now consider if the classifier predicts a negative, then we will not use this embryo, if it turns out that the classifier was wrong (in which case the embryo was a good one) we have wasted an otherwise perfectly good embryo. Positive prediction values of over 95% were achieved such that a recipient cow would only ever poorly implanted one in twenty times.

Davies Centre is now working with Holbrook Vet Centre and clients to undertake a prospective study whereby the pregnancy prediction results from image analysis will be generated prior to pregnancy testing occurring. If the exceptional predictive performance from the initial studies is maintained we look forward to equipping service providers with the tools to reliability increase artificial breeding program performance.

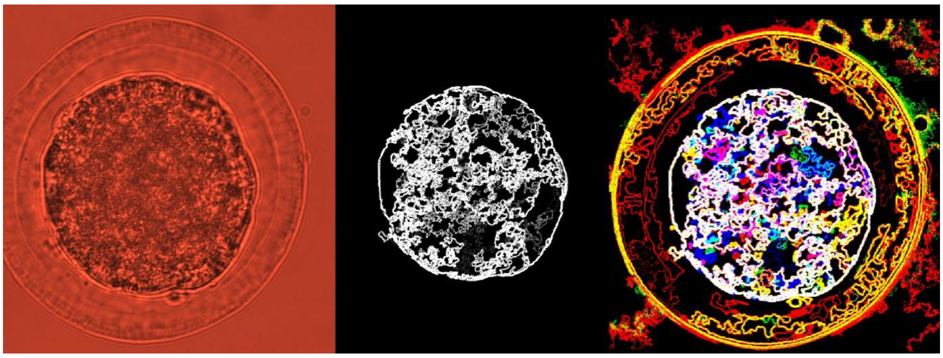


Fig 1. Grey scale and colour adjusted imagery of embryos.

# MEATING THE CHALLENGE TO OPTIMISE LAMB

When profit margins are small, businesses look to innovate to find the one-percenters that can make the difference between success and failure. In the red meat processing industry innovation opportunities are emerging with a new generation of carcase measurement technology that significantly increases the precision and accuracy of yield prediction of lamb carcases.

With this information at hand, lamb processors can now turn to the power of mathematics and employ optimisation methodologies to guide them to make the most from each carcase.

In a multi-disciplinary collaboration led by Davies Livestock Centre's Director and Program Leader of the Advanced Livestock Measurement Technologies project (ALMTech), Prof Wayne Pitchford, the University's Teletraffic Research Centre, researchers from Murdoch University, and commercial partners Agbiz Solutions and Gundagai Meat Processors (GMP), the development of a Lamb Carcase Optimisation Tool has been a journey of discovery.

For ALMTech Research Fellow, Dr Sean Miller, bringing all involved in the project together to develop an understanding of the problem at the outset has been a critical success factor. "Everyone from the meat science research team to the mathematicians and red meat processing partners has had to share and learn each other's language to enable the platform to be built. Without this basic understanding of how lamb processing works, and how the mechanics of meat fabrication can be coded mathematically, it would have been unachievable to develop a tool that is credible to industry."

For lamb processing company GMP's Client Research Adviser, Dr Michelle Henry, "the objective of optimisation is to select the right carcase for the right cut." Using the ALMTech Lamb Carcase Optimisation Tool, GMP can begin to compare the impact on the profitability of the business of fabricating lamb carcases to a range of different specifications, and empower them with the ability to improve the decision they make on a day to day basis.

Dr Andre Costa, Director of the University's Teletraffic Research Centre, believes that it was "important that we took a systematic approach; starting simple and validating our understanding of the outputs at each step." This has been helping the team develop an appreciation of the variability associated with predictions of profit as carcase fabrication decisions are changed, and the scale of improved profit, both positive and negative, that may result. And like all involved in the project, Andre sums it up best when he says "We are very keen to see this succeed"!

# MEQ PROBE: CHEWING THE FAT

Intramuscular Fat (IMF) has a large impact on the juiciness, tenderness, flavour and overall consumer satisfaction of meat. The Australian Red Meat Industry is valued at over $25 Billion. The industry is searching for objective ways to measure the IMF to be able to guarantee an enjoyable, consistent experience for consumers around the world.

## Who?

MEQ Probe is an AgTech StartUp building an objective measurement solution of IMF for the global meat industry. MEQ uses lasers and machine learning to deliver IMF data in real time on a hot carcass.

MEQ is a spin-out from the Centre for Nanoscale Biophotonics on North Terrace Campus and their meat scientists are co-located in the Davies Centre meat laboratory.

## How?

The MEQ Probe is inserted into a carcass, where lasers are used to obtain a biofluorescent signature for each individual carcass. Machine learning algorithms are applied to this signature to be able to measure the IMF content of the meat. This provides the IMF data to the processor in real time, and on a hot carcass, which is a critical time point in the production process, enabling key production decisions to be made.

## Big Data

Machine learning often requires very large datasets to generate the desired algorithm performance. This has led to MEQ running large-scale IMF data collection trials at abattoirs around Australia. Thousands of animals have been tested to calibrate the MEQ Probe tool in both beef and lamb.

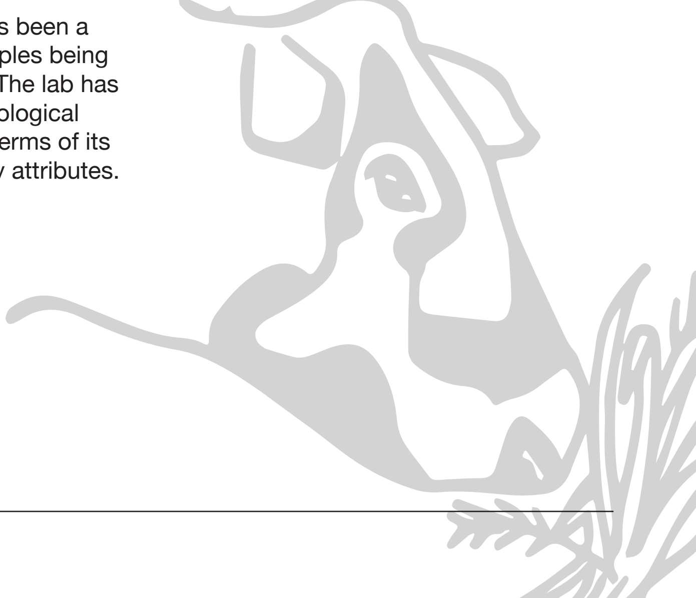
## MEQ Meat Lab

This data collection requires MEQ taking teams of people into the abattoirs to probe carcasses, and subsequently collect meat samples for calibration of the tool. In the past 12 months, MEQ has on-boarded more than 20 students from the University of Adelaide and around Australia to perform the data collection. This work includes collecting samples within an abattoir and the processing of samples in the meat laboratory, where the IMF is determined. This work is a great opportunity for students to broaden their understanding of meat science and learn practical skills that are useful for potential careers in the meat industry.

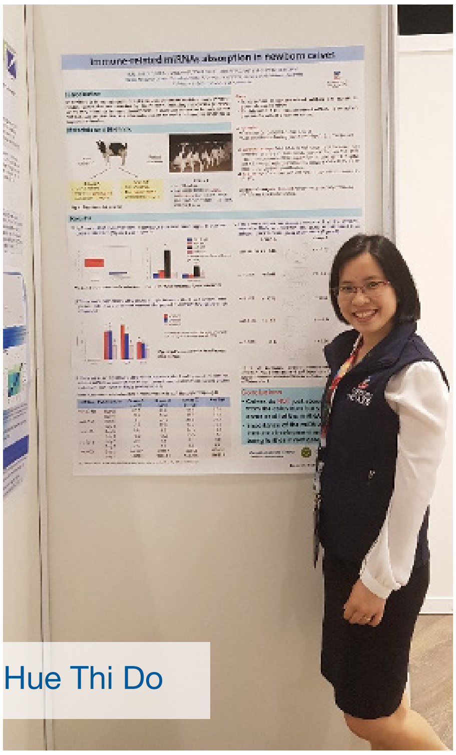
The Davies/MEQ Meat Lab has been a central point for the meat samples being collected around the country. The lab has been used to gain a greater biological understanding of the meat in terms of its composition and eating quality attributes.

## Looking Forward

The successful commercialisation and adoption of the MEQ Probe technology will be pivotal for the Australian Red Meat Industry, providing an objective way to underpin the eating experience of Australian meat products. For the lamb industry, this will be a world first opportunity.



# UNDERSTANDING COLOSTRUM IMMUNOLOGY



Hue Thi Do

> “There is now a huge demand for milk and colostrum products in Vietnam, and the Vietnamese government is developing a national cattle herd, with an emphasis on dairy cattle and their products. All the techniques and knowledge from my colostrum studies here in Australia will certainly help me contribute to the new dairy cattle industry in Vietnam”

Colostrum plays an important role in providing passive immunity to newborn mammals. This is especially true for neonate calves because the ruminant placenta prevents the transfer of immunoglobulins to the foetus during pregnancy. However, surprisingly little is known about the absorption of other factors, besides immunoglobulins, in the colostrum by calves and this is the focus of the PhD research project of Hue Thi Do. “Investigating different immune components in colostrum and their absorption by the neonate calf will help producers manage calf health and their production in the longer term “, Hue said.

“I have enjoyed the research and learned many new techniques from my lab work and field trips associated with my colostrum project”.

Before becoming a PhD student at the Davies Centre, Hue was working as a lecturer and researcher at the Department of Animal Breeding and Genetics, Faculty of Animal Science, Vietnam National University of Agriculture.

In Vietnam, Hue and her team investigated the biological characteristics, performance and product quality of different native chicken breeds, such as Dong Tao and Ho. She also measured the semen quality and the effects of different semen diluents on hatching rate using artificial insemination on these chicken breeds. In addition, Hue worked with the important livestock species in Vietnam, pigs, trying to improve their welfare and find molecular markers to improve their reproductive performance.

In 2017, Hue received a scholarship sponsored by the Vietnamese government to enrol at The University of Adelaide as a PhD candidate. “Luckily, I became in the colostrum project under the supervision of Assoc Prof Cynthia Bottema, Prof John Williams and Assoc Prof Kiro Petrovski”, Hue said. “I would like to give my thanks and sincerest gratitude to my supervisors who have supported me with their knowledge, patience, motivation, and engagement throughout my study as well as my life as an international student”.

“Research on bovine colostrum is very interesting and the most exciting field that I have ever studied because colostrum immune components are not only important to calf health but also contribute to improve human health as well”, Hue commented. “The importance of immunoglobulins has been well studied, but other immune components such as immune-related miRNAs, immune cells, or microbiome need to be further investigated”.

Hue’s research has revealed that while some factors, such as IgG, must be transferred from the colostrum to the neonate calves, other factors such are microRNAs are actually synthesized by the calves themselves. Her research also suggests that calves given the same colostrum will absorb the nutrients in that colostrum equally well. However, the results hint that components in the colostrum from the calf’s own dam are better absorbed by the calf than if those components are from colostrum provided by a foster dam or pooled from multiple dams. Hue said, “If absorption varies between colostrum sources, then the management of dairy calves may be improved by allowing the neonate calf to suckle from their own dam for 12 – 24 hours.”

# COLOSTRUM EFFECTS ON DAIRY COW PRODUCTIVITY

"I was lucky enough to spend my childhood in some of South Australia's most beautiful rural regions and by the age of 14, I had decided on a career as a vet. I studied Veterinary Science at Murdoch University and graduated in 2001 with BSc. and BVMS with academic honours", Rebel Skirving, Honours student.


Rebel Skirving

Over the next decade, I established my career as a mixed practice vet and started a family with my husband (also a vet). When I was pregnant with our second child, we bought a vet clinic from our retiring bosses and during maternity leave, I completed a Diploma in Business Management. Shortly after having our third child, I studied Certificate 4 in Teaching and Education and began some part-time lecturing with TAFE, while still working in, and managing our practice.

In 2018, I enrolled with University of Adelaide as an Honours student. My project was to determine if there were any benefits of calves receiving colostrum from their biological dams, compared with colostrum from a single foster dam, or "pooled" colostrum (from multiple dams). It involved collecting new-born calves before they had a chance to suckle from their mothers, then allocating calves to each of the 'treatment' groups and measuring their progress. We measured the calves adequacy of passive transfer of immunity, weight, height and health status. I hand-raised all 38 calves from birth to 6 months of age and continued to follow their progress (weight, height, blood parameters and fertility) until they were over 2 years old.

The main findings from the project were that calves performed just as well with foster colostrum as they did with maternal colostrum. We also found 'pooled' colostrum was generally poorer quality than maternal or foster colostrum, but even so, given adequate amounts of 'poor' colostrum at the correct time, it could still confer adequate transfer of passive immunity to most of the calves in that cohort. Given that a lot of commercial dairy farms use 'pooled' colostrum for their calves, it was important to identify that the colostrum was likely to be poorer quality BUT, if given in sufficient amounts, at the right time, it could still confer adequate transfer of passive immunity to the calves.

I was initially apprehensive about managing the Honours study load amidst my other commitments, but the external program offered by the University of Adelaide allowed me to do most of my study from home, at times that worked around my other engagements. The online teaching facilities were well delivered and my supervisors were amazing in their support for the entire 18 months. We conducted some fun and successful field trials locally and on occasions, I travelled to the Roseworthy campus for a few days at a time, to deliver samples to the laboratory, to meet with my support team face to face, and to do seminars and intensive tutorials.

It was the perfect combination of work and study and in December 2019, I was awarded the Honours Degree for Bachelor of Science (Animal Science), with first class honours! But that's not the end of my story... In May this year, I commenced my candidature for PhD with an estimated finish date of 2026.

# WEATHERBYS SCIENTIFIC AUSTRALIA

Weatherbys Scientific was founded in 1985 as a subsidiary of the Weatherbys Ltd Group based in Ireland.

Weatherbys Scientific supplies Genotyping and Genetic services to several industries in the northern hemisphere as well as food traceability services to the food processing industry.

Weatherbys Scientific Australia, founded in 2018 is a supplier of animal genomic services to the ANZ market and has a primary focus on Bovine and Ovine Genotyping.

A strategic partnership with the Davies Livestock Research Centre based at the University of Adelaide's Roseworthy Campus has allowed Weatherbys to kick start its expansion into Australia. Joint and collaborative projects have and do include industry research and commercial operations and services.

The further analysis of data and bioinformatics performed by the team within the Davies Livestock Research Centre is complimentary to the raw genotyping files and services offered by Weatherbys. By partnering together, the collective offering to commercial parties is wholistic and when applied can have considerable impacts on business profitability and ROI.

Current Genotyping Chips for both Bovine and Ovine will be updated to include new and novel data points of interest and further increase the inclusion of SNP data specific to Australian customers. With assistance from the Davies Livestock Research Centre Weatherbys Scientific is hoping to create and release the most market applicable genotyping chips available whilst using internal business volumes and purchasing arrangements to maintain and control costs for the Australian consumers.

As the Weatherbys Scientific Australia business grows more species will be included in the commercial offering and in time the intention is for expansion into Asia Pacific.

Weatherbys Scientific Australia is a proud collaborator of the Davies Livestock Research Centre and is committed to furthering and strengthening the existing relationship.

WEATHERBYS
SCIENTIFIC AUSTRALIA

# MEATING THE FUTURE


Farrah Preston

For the past seven years, the second week of July has been marked out for meat judging in Farrah Preston's diary. What started out as an interest to learn more about production beyond the farm gate quickly turned in to the foundations for an exciting career.

Farrah first attended the Australian Intercollegiate Meat Judging (ICMJ) Association's conference in 2014 during the final year of her Animal Science degree. The five-day conference and competition was enlightening and sparked her enthusiasm for meat science, although not successful in the competition herself.

"I did terribly in the competition when I competed. But that didn't matter, the most important part of that week was the experience and being involved, and the doors it has opened since"

Every year, 150 students and 40 coaches from twelve Australian and four international universities descend on Wagga Wagga, NSW. The week-long ICMJ program includes guest lectures from industry leaders, practical skill-building sessions, a careers expo, and sponsored networking dinners. The program culminates with the competition and a celebratory awards dinner.

Inspired by the ICMJ program, Farrah pursued an Honour's project investigating abattoir factors related to dark cutting beef where she had the opportunity to work closely with Teys Australia. This study provided exciting results and grew into a PhD project supervised by Professor Wayne Pitchford, Dr Peter M$^{c}$Gilchrist (UNE) and Dr Michael Wilkes (Thomas Elder Institute). Farrah is currently completing her final year.

Whilst continuing postgraduate study, Farrah has remained involved in the ICMJ program as coach of the University of Adelaide team. This has also included coaching students from Bogor Agricultural University, Indonesia.

"Each year we host five Indonesian students and it's such a fantastic opportunity for everyone involved. We get to show them Australia and they compete at ICMJ with us, then they return the favour by hosting us in Indonesia later in the year. There have been some great friendships formed through this program."

Coaching the team, which includes final year Animal, Agricultural, and Veterinary Science students, has included many early mornings spent layered up in cold chillers.

"I really enjoy being able to provide students the same experience I had and see them get so excited about the meat industry."

Farrah's dedication to coaching and mentoring for the past five years was rewarded when she received the Dr Tom Carr Award for Coaching Excellence and the Cattle Council Australia Industry Scholarship at ICMJ's 30th Anniversary event in 2019. Encouraging students and being involved in the ICMJ program remains set in Farrah's plans for the foreseeable future.

"Meat judging provides invaluable skills and experience to students, regardless of where they see themselves working in industry: stud managers, livestock buyers, nutritionists, geneticists, consultants; not just meat processing. Almost every part of an animals life – from pre-conception to post-slaughter - ultimately contributes to meat production and quality. It's important we send students into jobs with this breadth of knowledge so they can provide good lifetime management advice and make decisions with the end goal in sight."

Farrah has coached 125 students from Adelaide and Bogor through the meat judging training and said "I couldn't be more proud of the success they're having in their careers, many of which have been shaped by participating in ICMJ".

# BEEFING UP YOUR DEGREE

Following on from the competing in the 2018 Intercollegiate Meat Judging Competition and the 2018 Indonesian/Cambodia Study Tour, Jamie Jones knew she wanted to work in the meat science field. The fascination and endless possibilities with the Australian red meat industry became a huge drawcard in Jamie undertaking further study after her Animal Science degree.


Jamie Jones

In 2014 a trial began in Tasmania using Hereford and Angus sires over Angus dam's to produce either a purebred Angus calf or a Hereford cross Angus calf, otherwise known as a Black Baldy. Carcase and scanning data was collected over three consecutive years for three cohorts of steers. In 2019, the data from this study was offered as an honours project. Jamie quickly jumped at the opportunity to closely study the effects of crossbreeding on beef carcasses and how this affects farm profitability. With the Australian beef industry worth in excess of AUS$10billion she understood the importance for Australian producers to be able to adapt to continually changing markets conditions. Her Honours project was supervised by Prof Wayne Pitchford, Dr Michelle Hebart and Dr Judith Pitchford.

The aim of the study was to determine if Hereford cross Angus cattle have heavier carcasses at slaughter than purebred Angus cattle, and also to determine if Hereford cross Angus cattle are more valuable to the producer. Two pricing scenarios were calculated using a pricing scheme 1) that only used lean meat yield and 2) that used both lean meat yield and eating quality.

The key findings for the breed differences were that Hereford sired steers have larger carcass weights, larger eye muscle areas and more P8 fat, whereas the Angus sired steers have more marbling and more rib fat. Value differences favoured the Hereford sired steers in both pricing scenarios, with overall carcass value highly correlated with carcass weight.

Whilst undertaking her honours project, Jamie also volunteered to coach The University of Adelaide's 2019 ICMJ team.

"Not only was I excited at the opportunity to network with industry leaders again, I wanted to expand the students minds into the study of meat science and multitude of career options that are not otherwise apparent."

A big part of the ICMJ competition is the careers expo, and even coaches are allowed to attend. Whilst networking at the event, Jamie was introduced to a representative from Hancock Agriculture, the parent company of S Kidman & Co.

The two discussed a role that S Kidman & co were currently advertising for, Data Analytical clerk. A resume was sent off the next day and an interview set for two days later. A week after getting back from the ICMJ competition, Jamie had a full time job with one of the biggest Agricultural companies in Australia.

A large part of Jamie's role at S Kidman & Co as Data Analytical clerk involves data management and reporting for feedlots that the company own or custom feed at. She works very closely with the Kidman finance team, feedlot managers, abattoirs and various other industry personnel. More recently she has had the opportunity to get involved with the pasture fed side of the business through herd modelling. Jamie enjoys the constant challenges and opportunities that S Kidman & Co have provided her over the last year and is excited to assist the future growth of the business.

# FINANCIAL REPORT

The 2019 Davies Bequest funding to the Davies Livestock Research Centre was $1,851,560, of which 83% was spent on salaries. The remaining $310,639 was spent on projects which, where possible, were to leverage funds to form bigger partnerships and projects.

In total, $2,100,299 was brought into the Centre for projects funded by Meat and Livestock Australia, Australian Wool Innovation, SA Sheep Industry Fund, Primary Industries and Resources SA, and the Federal Government's Rural Research and Development for Profit and Innovation Connection Programs.

University funding leverage against the bequest was $2,100,299 relative to $1,851,560, a ratio of 1.1:1 which we aim to grow to 4:1 by 2025.

Davies Centre staff collaborate widely and are part of projects worth an additional $1,438,531 of research and development activity to our partner organisations and businesses.

The total project income including partners for 2019 was $5,390,390

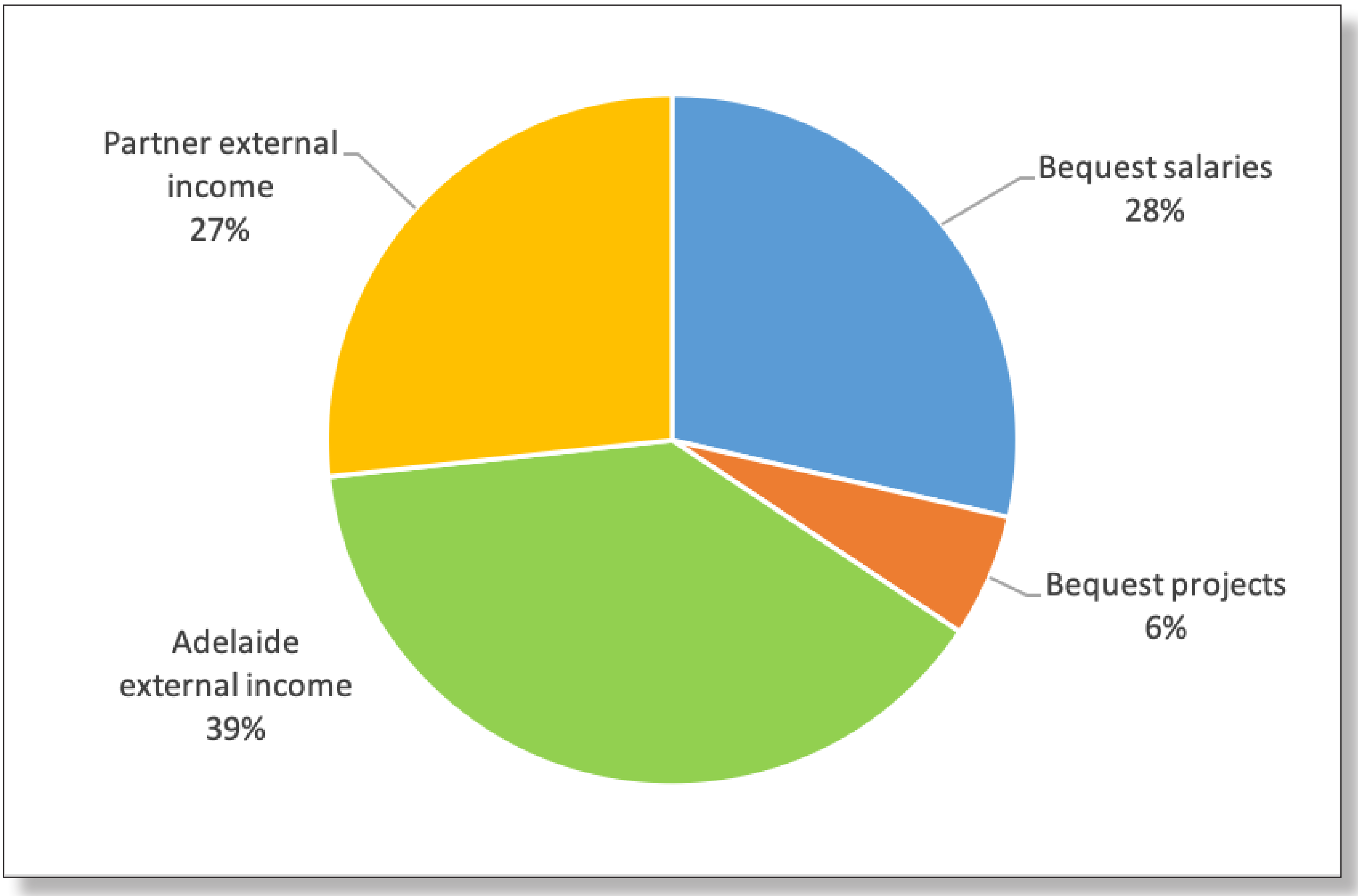


Fig 1. Distribution of $5.39M to Davies Centre including partner projects.

# PROJECTS

Improved ruminant health and productivity through neonatal microbiome manipulation

Future Livestock Consultants 2

Reducing the financial impact of endemic conditions in sheep - a value chain approach

Accelerating genetic gain through integrating genomics and high value MSA carcass traits in genetic evaluation to aid selection

Corriedale eating quality genomics

Rate of Genetic Gain in Reducing Breech Flystrike

Improving productivity of commercial cattle through utilising superior sires within and across breeds

New approaches to increase the weaning rate of the national sheep-flock

Longitudinal analysis of antimicrobial resistance of grain-fed beef cattle

Antimicrobial Resistance Surveillance of Bovine Respiratory Disease Pathogens

Reducing foetal and lamb losses in young ewes

Optimising heifer development and management to increase whole herd profit

MLPAO Evaluating the ability of anti-mullerian hormone to predict ewe reproductive rate

Optimizing temperate cow herd efficiency - a Trans-Tasman collaboration

Increasing lambing percentages through better use of pregnancy scanning technology

Advanced measurement technologies for globally competitive Australian meat value chains

Portable real time test for the detection of sheep lice

Development of Single Nucleotide Polymorphism tests for Genomic Evaluation of Japanese Black (Wagyu) Cattle.

Genomic Studies of Major and Novel Economic Traits of Tropical Composite Beef Genetics

Genetic Evaluation and Genome Wide Association Studies of Japanese Black (Wagyu) Cattle in a Data Driven Breeding Program.

Genomic Study of Phenotypic Traits, Heterozygosity and Unfavourable Recessive Inherited Conditions in a Temperate Beef Composite Cattle Population.

A review of the impact of heat stress on reproductive performance in sheep.

Genomic Studies of Major and Novel Economic Traits of Tropical Composite Beef Genetics

Meat and Livestock Australia Supplementary Scholarship - Aldersey
Sponsor: Meat and Livestock Australia Grant Scheme

Genetic Evaluation and Genome Wide Association Studies of Japanese Black (Wagyu) Cattle in a Data Driven Breeding Program.

A novel amino acid approach to lamb survival

Establishment and importance of the microbiome in the neonate calf

Biomarkers for the detection of failure of passive immune transfer in neonate dairy calves

Development of an improved cattle cloning technology platform for animal breeding and gene editing

DNA methylome of purebred and reciprocal cross concepti with Bt.taurus and B.t. indicus genetics

Evaluating anti-mullerian hormone (AMH) for use in selection of donor cows to embryo production programs

Refurbishment of the embryology lab at Roseworthy campus

Breath biomarker for measurement of volatile fatty acids in ruminants

Transcriptome Iso-Sequencing study

Automated assessment of intramuscular fat in lamb

# PERSONNEL

## Staff

Alexandra Whittaker
Alyce Swinbourne
Anne Peaston
Anne-Lise Chaber
Bec Forder
Bryden Quirk
Chantal Barrass
Charles Caraguel
Colin Trengove
Cynthia Bottema
Dario Mendoza
Darren Koopman
Darren Trott
Eleonora Dal Grande
Eman Taher
Emma Greenwood
Farhid Hemmatzadeh
Forbes Brien
Hayley McGrice
Ian Nuberg
James Pitchford
Jim Franklin-McEvoy
Jeremy Thompson
John Williams
Judith Pitchford
Kapil Chousalkar
Karen Kind
Kiro Petrovski
Lloyd Low
Madeline Batsiokis
Mandi Carr
Mariana Caetano
Mark Hutchinson
Mark Nottle
Michelle Hebart
Milton McAllister
Nicky-Lee Willson
Rachel Withers
Rick Tearle
Rob McLaughlin
Rob Paterson
Roy Kirkwood
Robin Terry
Ryan O'Handley
Sasha Lanyon
Sean Miller
Sharon Siva Subramaniam
Stefan Hiendleder
Stephan Leu
Stephen Lee
Susan Hazel
Tong Chen
Torben Nielsen
Wayne Boardman
Wayne Hein
Wayne Pitchford
William van Wettere

| Collaborators | Organisation |
|---|---|
| Joe Grose | 3D Genetics |
| Chris Smith | AgBiz Solutions |
| Paul Dalby | AIML |
| Javen Shi | AIML |
| Michelle Henry | Gundagai Meat Processors (GMP) |
| Danny Meehan | Meehan AgriBusiness Solutions |
| Bruce Hancock | Rural Solutions |
| Greg Popplewell | Popplewell Composites |
| Kathy Gatford | Robinson Research Institute |
| Alan Humphries | SARDI |
| Emma Winslow | SARDI |
| Jen Kelly | SARDI |
| Dave Kleemann | SARDI |
| Alice Weaver | SARDI |
| Simon Bawden | SARDI |
| Clive McLaughlan | SARDI |
| Jim Cox | SARDI |
| Andre Costa | Teletraffic Research Centre |
| Vince Wang | Teletraffic Research Centre |
| Joshua Philp | Waite Research Institute |
| Julian Taylor | Waite Research Institute |
| Matthew Denton | Waite Research Institute |
| Olena Kravchuk | Waite Research Institute |
| Helena Oakey | Waite Research Institute |

## PhD Students

- Bianca Agenbag
- Billie Jaye Brougham
- Cynthia Liu
- Farrah Preston
- Hanh Nguyen
- Hue Do
- Jamee Daly
- Johanna Aldersey
- Laura Latimer-Marsh
- Niki McCarthy
- Rudi McEwin
- Sarah Weaver
- Tom Flinn
- Megan Tscharke
- Laura Marsh

## Honours Students

- Bobbie Baida
- Cassandra Woods
- Gemma Balog
- Jackie Chapman
- Jamie Jones
- Kellie Wenham
- Leesa Flanagan
- Pia Riddel
- Rebel Skirving
- Sarah Welsh
- Solyn Bao

## Students

- Matilde Passamonti
- Junpeng Yao

# PUBLICATIONS

Aldridge, M.N, **Pitchford, W.S** and Brown, D.J. (2019) Current Progress On Developing A Selection Index For Australian Meat, GoatsProc. Assoc. Advmt. Anim. Breed. Genet. 23:51-54

**Brien FD**, Walkom SF, Swan AA, Brown DJ. (2019). Breeding for reduced breech flystrike as part of multi-trait selection. Proceedings of the Association for the Advancement of Animal Breeding and Genetics 23, 528-31.

**Caetano, M,** Wilkes, MJ, **Pitchford, WS, Lee, SJ,** Hynd, PI (2019) Effect of ensiled crimped grape marc on energy intake, performance and gas emissions of beef cattle. Animal Feed Science and Technology 247, 166-172.

**Caetano, M.,** Goulart, R. S., Rizzo, P. M., Silva, S. D. L., Drouillard, J. S., Leme, P. R., & Lanna, D. P. D. (2019). Impact of flint corn processing method and dietary starch concentration on finishing performance of Nellore bulls. Animal Feed Science and Technology, 251, 166-175. doi:10.1016/j.anifeedsci.2019.03.006

**Caraguel, C.** (n.d.). Diagnostic test accuracy when screening for haliotid herpesvirus 1 (AbHV) in apparently healthy populations of Australian abalone Haliotis spp.. doi:10.25909/5c416aaf948cf

Clark, N., **Caraguel, C.** G., Heller, J., & Magalhaes, R. (2019). Australia's drought could be increasing Q fever risk, but there are ways we can protect ourselves. Retrieved from https://theconversation.com/australias-drought-could-be-increasing-q-fever-risk-but-there-are-ways-we-can-protect-ourselves-112297

Ebrahimi, M., Mohammadi-Dehcheshmeh, M., Ebrahimie, E., & **Petrovski, K.** (2019). Comprehensive analysis of machine learning models for prediction of sub-clinical mastitis: Deep Learning and Gradient-Boosted Trees outperform other models. Computers in Biology and Medicine, 114, 9 pages. doi:10.1016/j.compbiomed.2019.103456

**Greenwood, EC,** van Dissel, J, Rayner, J, Hughes, PE, **van Wettere, W** (2019) Mixing Sows into Alternative Lactation Housing Affects Sow Aggression at Mixing, Future Reproduction and Piglet Injury, with Marked Differences between Multisuckle and Sow Separation Systems. Animals 9, 20.

**Greenwood, EC, van Wettere, W,** Rayner, J, Hughes, PE, Plush, KJ (2019) Provision Point-Source Materials Stimulates Play in Sows but Does Not Affect Aggression at Regrouping. Animals 9, 16.

**Greenwood, E.,** Dickson, C., & **van Wettere, W.** (2019). Feeding strategies before and at mixing: The effect on sow aggression and behavior. Animals, 9(1), 17 pages. doi:10.3390/ani9010023

**Hutchinson, M.,** & **Terry, R.** (2019). Review: What innovations in pain measurement and control might be possible if we could quantify the neuroimmune synapse?. Animal, 13(12), 3000-3008. doi:10.1017/S1751731119001885

James, P, **Brien, FD** and Anderson, A. (2019). A Review of Predisposing Factors for Breech Flystrike - Final Report to Australian Wool Innovation for Project ON-00510.DOI: 10.13140/RG.2.2.17330.56001

Kronenberg, Z.N., Rhie, A., Koren, S., Concepcion, G.T., Peluso, P., Munson, K.M., **Hiendleder, S.,** Fedrigo, O., Jarvis, E.D., Phillippy, A. M., Eichler, E.E., **Williams, J.L.,** Smith, T.P.L., Hall, R.J., Sullivan, S.T. and Kingan, S.B. (2019) Extended haplotype phasing of de novo genome assemblies with FALCON-Phase. bioRxiv doi.org/10.1101/327064.

Ledda, S., **Kelly, J.,** Nieddu, S., Bebbere, D., Ariu, F., Bogliolo, L. et al. (2019). High in vitro survival rate of sheep in vitro produced blastocysts vitrified with a new method and device. Journal of Animal Science and Biotechnology, 10(1). doi:10.1186/s40104-019-0390-1

**Lee, S.J, Hebart, M.L.** and **Pitchford, W.S** (2019) Investigating relationship between traits associated with eating quality and market end point, Proc. Assoc. Advmt. Anim. Breed. Genet. 23:322-325

Li, WL, Bickhart, DM, Ramunno, L, Iamartino, D, **Williams, JL,** Liu, GE (2019) Comparative sequence alignment reveals River Buffalo genomic structural differences compared with cattle. Genomics 111, 418-425.

Lim, M., Brown, H., **Kind, K.,** Breen, J., Anastasi, M., Ritter, L., Tregoweth, E., Dinh, D., **Thomspon. J.,** Dunning, K. (2019). Haemoglobin expression in in vivo murine preimplantation embryos suggests a role in oxygen-regulated gene expression. Reproduction, Fertility and Development, 31(4), 724-734. doi:10.1071/RD17321

Liu, R, **Low, WY, Tearle, R,** Koren, S, Ghurye, J, Rhie, A, Phillippy, AM, Rosen, BD, Bickhart, DM, Smith, TPL, **Hiendleder, S, Williams, JL** (2019) New insights into mammalian sex chromosome structure and evolution using high-quality sequences from bovine X and Y chromosomes. Bmc Genomics 20,

Liu, SL, Kang, XL, Catacchio, CR, Liu, M, Fang, LZ, Schroeder, SG, Li, WL, Rosen, BD, Iamartino, D, Iannuzzi, L, Sonstegard, TS, Van Tassell, CP, Ventura, M, **Low, WY, Williams, JL,** Bickhart, DM, Liu, GE (2019) Computational detection and experimental validation of segmental duplications and associated copy number variations in water buffalo (Bubalus bubalis). Functional & Integrative Genomics 19, 409-419.

Liu, YW, Ong, JS, Gan, CY, Khoo, BY, Yahaya, S, Choi, SB, **Low, WY,** Tsai, YC, Liong, MT (2019) Lactobacillus fermentum PS150 showed psychotropic properties by altering serotonergic pathway during stress. Journal of Functional Foods 59, 352-361.

**Low, WY, Tearle, R,** Bickhart, DM, Rosen, BD, Kingan, SB, Swale, T, Thibaud-Nissen, F, Murphy, TD, Young, R, Lefevre, L, Hume, DA, Collins, A, Ajmone-Marsan, P, Smith, TPL, **Williams, JL** (2019) Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. Nature Communications 10,

**Low W-Y., Tearle, R.,** Liu, R., Sergey Koren, S., Arang Rhie, A., Bickhart, D.M., Rosen, B.D., Kronenberg, Z.N., Kingan, S.B., Tseng, E., Thibaud-Nissen, F., Martin, F.J., Billis, K., Ghurye, J., Hastie, A.R., Lee, J., Pang, A.W.C., Heaton, M.P., Phillippy, A.M., **Hiendleder, S.,** Smith, T.P.L. and **Williams. J.L.** (2019). Haplotype-Resolved Cattle Genomes Provide Insights Into Structural Variation and Adaptation. bioRxiv: http://dx.doi.org/10.1101/720797.

**McEwin, R.A, Hebart, M.L, Oakey, H, Tearle, R, Grose, J, Popplewell, G.I, Pitchford, W.S** (2019) Selection of refence candidates for whole genome sequencing in an Australian Wagyu Population, Proc. Assoc. Advmt. Anim. Breed. Genet. 23:286-289

**McGrice, H., Kelly, J. M., Kleemann, D. O.,** Kind, K. L., Hampton, A. J., Hannemann, P., Walker, S.K., **van Wettere, W. H.** (2019). Plasma anti-Müllerian hormone concentration as a predictive endocrine marker for selection of donor lambs to improve success in juvenile invitro embryo transfer programs.. Reproduction, fertility, and development, 32(4), 383-391. doi:10.1071/rd18498

Mokhber, M, Shahrbabak, MM, Sadeghi, M, Shahrbabak, HM, Stella, A, Nicolzzi, E, **Williams, JL** (2019) Study of whole genome linkage disequilibrium patterns of Iranian water buffalo breeds using the Axiom Buffalo Genotyping 90K Array. Plos One 14,

Nowland, TL, **van Wettere, W,** Plush, KJ (2019) Allowing sows to farrow unconfined has positive implications for sow and piglet welfare. Applied Animal Behaviour Science 221,

Nowland, T., & **Kirkwood, R.** (2020). Faecal microbiota transplantation: Is it the future for pig production?. Microbiology Australia, 41(2), 91-94. doi:10.1071/MA20023

Nowland, T. L., Plush, K. J., Barton, M., & **Kirkwood, R. N.** (2019). Development and function of the intestinal microbiome and potential implications for pig production. Animals, 9(3), 76-1-76-15. doi:10.3390/ani9030076

Ong, C., Kwong, Q., Ong, A., Heng, H., & **Low, W.** (2019). Pipeline of High Throughput Sequencing. In S. Ranganathan, M. Gribskov, K. Nakai, & C. Schönbach (Eds.), Encyclopedia of Bioinformatics and Computational Biology (Vol. 3, pp. 144-151). doi:10.1016/B978-0-12-809633-8.20091-5

**Popplewell, G.I, Tearle, R.G, McEwin, R.A,** Facy, M.L and **Pitchford, W.S** (2019), Popplewell Composites: Adding bale to our customers' tropical beef supply chains though genomic evaluation and selection.

Subarmaniam, NS, **Bawden, CS,** Rudiger, SR, Yazbeck, R, Faull, RLM, Snell, RG, Howarth, GS (2019) Development of a novel C-13-labelled methionine breath test protocol for potential assessment of hepatic mitochondrial function in sheep using isotope-ratio mass spectrometry. International Journal of Mass Spectrometry 442, 102-108.

Szyda, J, Mielczarek, M, Fraszczak, M, Minozzi, G, **Williams, JL,** Wojdak-Maksymiec, K (2019) The genetic background of clinical mastitis in Holstein-Friesian cattle. Animal 13, 2156-2163.

Taggart, P., Stevenson, M., Firestone, S., **McAllister, M.,** & **Caraguel, C. G.** (2019). A spatial analysis of risk factors for sarcocystosis in South Australian sheep flocks, 2007-2017. Poster session presented at the meeting of GeoVet 2019. Davis, USA.Taggart, PL, Stevenson, MA, Firestone, SM, **McAllister, MM,** Caraguel, CGB (2019) Spatial Analysis of a Cat-Borne Disease Reveals That Soil pH and Clay Content Are Risk Factors for Sarcocystosis in Sheep. Frontiers in Veterinary Science 6, 9.

Taggart, P., Fancourt, B., Peacock, D., **Caraguel, C.,** & **McAllister, M.** (2019). Variation in Toxoplasma gondii seroprevalence: effects of site, sex, species and behaviour between insular and mainland macropods. Wildlife Research. doi:10.1071/WR19041

Taggart, P., Fancourt, B., Bengsen, A., Peacock, D., Hodgens, P., Read, J, **McAllister, M.,** & **Caraguel, C.** (2019). Evidence of significantly higher island feral cat abundance compared to the adjacent mainland. Wildlife Research, 46(5), 378-385. doi:10.1071/WR18118

Taggart, P., Fancourt, B., Fabijan, J., Peacock, D., Speight, K., **Caraguel, C.,** & **McAllister, M.** (2019). No evidence of toxoplasma gondii exposure in South Australian Koalas (phascolarctos cinereus). Journal of Parasitology, 105(4), 638-641. doi:10.1645/19-40

Taggart, P., Stevenson, M., Firestone, S., **McAllister, M.,** & **Caraguel, C.** (2019). Spatial analysis of a cat-borne disease reveals that soil pH and clay content are risk factors for sarcocystosis in sheep. Frontiers in Veterinary Science, 6(APR), 127-1-127-9. doi:10.3389/fvets.2019.00127

van Lingen, H., Niu, M., Kebreab, E., Valadares Filho, S., Rooke, J., Duthie, C., Schwarm, A., Kreuzer, M., Hynd,P., **Caetano, M.,** et al. (2019). Prediction of enteric methane production, yield and intensity of beef cattle using an intercontinental database. Agriculture, Ecosystems and Environment, 283, 18 pages. doi:10.1016/j.agee.2019.106575

Wallace, RJ, Sasson, G, Garnsworthy, PC, Tapio, I, Gregson, E, Bani, P, Huhtanen, P, Bayat, AR, Strozzi, F, Section, FB, Snelling, TJ, Saunders, N, Potterton, SL, Craigon, J, Minuti, A, Trevisi, E, Callegari, ML, Cappelli, FP, Cabezas-Garcia, EH, Vilkki, J, Pinares-Patino, C, Fliegerova, KO, Mrazek, J, Sechovcova, H, Kopecny, J, Bonin, A, Boyer, F, Taberlet, P, Kokou, F, Halperin, E, **Williams, JL,** Shingfield, KJ, Mizrahi, I (2019) A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. Science Advances 5,

**Whittaker, A.,** & **Marsh, L.** (2019). The role of behavioural assessment in determining 'positive' affective states in animals. CAB Reviews: Perspectives in Agriculture, Veterinary Science, Nutrition and Natural Resources, 14. doi:10.1079/PAVSNNR201914010

Young, R, Lefevre, L, Bush, SJ, Joshi, A, Singh, SH, Jadhav, SK, Dhanikachalam, V, Lisowski, ZM, Iamartino, D, Summers, KM, **Williams, JL,** Archibald, AL, Gokhale, S, Kumar, S, Hume, DA (2019) A Gene Expression Atlas of the Domestic Water Buffalo (Bubalus bubalis). Frontiers in Genetics 10,

Zhou, SJ, **Tearle, R,** Jozani, RJ, Winra, B, Schaaf, O, Nicholson, A, **Peaston, A** (2019) Genetic cause for congenital methemoglobinemia in an Australian Pomeranian dog. Journal of Veterinary Internal Medicine 33, 868-873.