7th International Symposium on Animal Functional Genomics
&
Functional Annotation of Animal Genomes Workshop 2018

Adelaide, South Australia

CONFERENCE PROCEEDINGS

12-15 November, 2018

International Symposium on Animal Functional Genomics — Adelaide 2018

FAANG Functional Annotation of Animal Genomes

Organised by

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7th ISAFG & FAANG Workshop 2018: Program At-A-Glance

	Monday, 12th Nov	Tuesday, 13th Nov	Wednesday, 14th Nov	Thursday, 15th Nov
7:30 AM	Registration	Registration	Registration	Registration
	Plenary Session 1 (Chair: Stefan Hiendleder)	Plenary Session 2 (Chair: Dave Burt)	Joint ISAFG - FAANG Plenary (Chair: Paolo Ajmone-Marsan)	FAANG Workshop: breakout sessions
8:30 AM Plenary	David Gorkin: *"Navigating the genome with epigenome maps: insights from the systematic mapping of chromatin state and accessibility across mouse fetal development"*	Peter Dearden: *"The architecture of a plastic trait"*	Christine Wells: "*Cell identity in the era of single cell profiling*" (Sponsored by Illumina)	Data: transcriptomes (Nathan Watson-Haigh) Wet lab: histone modification (Stephanie McKay + Brenda Murdoch)
9:15 AM Plenary	Michael Skinner: *"Environmentally induced epigenetic transgenerational inheritance of health and disease: ancestral ghosts in your genome"*	Sue Lamont: *"Some like it hot: functional genomics of response to heat stress in poultry"*	Brian Dalrymple: *"Genetics and genomics pathways to form and function: point and counterpoint"*	Data: genomes (Lloyd Low) Wet lab: transcriptomics (miRNA, RNA, IsoSeq: Brenda Murdoch + Stephanie McKay)
10:00 AM	Morning tea	Morning tea	Morning tea	Morning tea
10:30 AM	Session 1: Disease & immunity (Chair: Paul Coussens)	Session 4: Gene regulation (Chair: Steve Moore)	Joint ISAFG - FAANG Session: New technology applications (Chair: Ben Hayes)	FAANG WORKSHOP: plenary discussions (Chair: Chris Tuggle)
Keynote	David MacHugh: *"Functional and integrative genomics of bovine and human tuberculosis: a One Health perspective"*	Amanda Chamberlain: *"Identification of regulatory variation in dairy cattle with RNA sequence data"*	Tim Smith: "*Advances in genome technology*"	Summary of breakout sessions
11:15 AM	Laura Miller: "*e-PIG-enetics: porcine sncRNA response to highly pathogenic PRRSV* "	Stephanie McKay: "*A neuroepigenomic investigation of DNA methylation in cattle with extreme measures of docility* "	Tad Sonstegard: *"Discovery and editing of adaptive traits in livestock"* (sponsored by Recombinetics Inc)	Recommendations for FAANG
11:45 AM	Lunch	Lunch	Lunch	CLOSE
12:30 PM	Poster Session (even numbers)	Neogen Australasia Sponsor Session: Russell Lyons "*Neogen Agrigenomics: Global Innovation | Local service* "; Kylie Munyard "*Shades of alpaca grey: the causative mutation for grey in alpacas* "; Iona MacLeod "*Ovine sequencing and functional annotation: the future for genomic selection in sheep* "; George Sofronidis "*Meet the Laboratorydoodle, a genetically innovative breed* "	Weatherbys Scientific Australia Sponsor Session: Delivering animal genomics to drive research and profitability in livestock production, Romy Morrin-O'Donnell "*Welcome and Introduction to Weatherbys Scientific: our contribution to the Irish cattle industry and beyond* "; Wayne Pitchford "*Incorporating functional genomics into the selection of tropically adapted beef cattle* "	
1:30 PM	Session 2: Reproduction & fertility (Chair: Brenda Murdoch)	Session 5: Functional genomics (Chair: Clare Gill)	FAANG Workshop (Chair: Chris Tuggle)	SHORT COURSES:
Keynote	Claire Wade: *"Evolution of reproductive behaviour in the dog"*	James Kijas: *"Functional genomics in atlantic salmon: a trait specific investigation generating multiple FAANG datatypes"*	FAANG overview: Chris Tuggle	Venue @ North Terrace Campus, University of Adelaide
2:15 PM	Marina Fortes: *"The landscape of bovine retrotransposon polymorphisms and its association with fertility and production traits in Australian tropical beef cattle* "	Chris Tuggle: "*An improved functional annotation of the domestic pig genome* "	FAANG project updates: Chris Tuggle, Colin Kern, Brenda Murdoch, David MacHugh, Amanda Chamberlain, Ben Hayes	
2:45 PM	Vanmathy Kasimanickam: "*Serum miRNA profiling in pregnant and non-pregnant beef heifers* "	Terry Bertozzi: "*Functional genomics without a genome: the phototransduction pathway of blind beetles* "	Open Discussion/ Q & A on FAANG Future	Introduction to R (Thursday 1:00 - 5:00 pm)
3:15 PM	Afternoon tea	Afternoon tea	Afternoon tea	
3:45 PM	Session 3: Environmental interactions (Chair: Carl Schmidt)	Session 6: Quick fire poster talks (Chair: Cindy Bottema)	FAANG Workshop: breakout sessions	Gene annotation with R (Friday, 9:00 am - 5:00 pm)
Keynote	Yanfang Wang: *"Genetic regulation of cold-induced WAT browning in pigs"*	5 x 15' talks: Adetula Abiola Adeyinka, Thomas Hall, Min Wang, Luciana Regitano, Tomasz Sadkowski	Data: retrieval (Carl Schmidt + Peter Harrison) Wet lab: methylation (Bastien Llamas)	
4:30 PM	Daniela Lourenco: *"How genomics can help to identify resilient animals under environmental stress conditions"*		Data: submission (Peter Harrison + Carl Schmidt) Wet lab: chromatin structure (HiC,ATACseq; Monique Rijnkels)	
5:00 PM	Raluca Mateescu: "*Current insights into genomics of thermotolerance in beef cattle* "	CLOSE	CLOSE	
5:30 PM	Poster Session (odd numbers)			
6:00 PM	Welcome Reception (6:00 - 7:30 pm):			
6:30 PM	National Wine Centre Concourse	Conference dinner (6:30 - 11:00 pm):		
7:00 PM		Adelaide Zoo - please meet at entrance by 6:25 pm		

7th INTERNATIONAL SYMPOSIUM ON ANIMAL FUNCTIONAL GENOMICS

&

FUNCTIONAL ANNOTATION OF ANIMAL GENOMES WORKSHOP 2018

NOVEMBER 12 – 15, 2018, ADELAIDE, AUSTRALIA

CONFERENCE PROGRAM

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WELCOME TO THE 7TH INTERNATIONAL SYMPOSIUM ON ANIMAL FUNCTIONAL GENOMICS

&

2018 FUNCTIONAL ANNOTATION OF ANIMAL GENOMES WORKSHOP

ADELAIDE, AUSTRALIA NOVEMBER 12 – 15, 2018

G'day!

It is with great pleasure that the ISAFG 2018 Organising Committee welcomes you to Adelaide, Australia. We trust that you will enjoy the wonderful hospitality of the Aussies, delight in the beautiful sights of this land down under, and have a fantastic scientific conference. The hospitality and the natural delights will take care of themselves, but delivering the science would not be possible without three important groups – our sponsors, our speakers and our FAANG session chairs. So we are deeply indebted to them for their contributions to making this a great conference.

Molecular tools are being applied as never before, and as a consequence, genetics as a discipline is evolving with amazing speed. How genomics can be implemented is of interest from an animal production standpoint in all countries. From the scientific standpoint, the opportunities are equally tremendous as genomics helps unravel the mysteries of epigenetics, microRNA, and gene expression. These developments are recurrent theme of the conference. Thus, we trust that everyone will find the conference interesting, diverse, exciting and most of all, inspiring.

We know that many of you will have traveled great distances to join us. Adelaide is renowned for its excellent food, wine, parklands, and beaches. Adelaide is also the gateway to the South Australian wine regions and national parks. So we hope that your schedule will allow you to absorb some science as well as have some fun.

Cheers,

Cindy Bottema, Rick Tearle and John Williams
ISAFG 2018 Organising Committee

FAANG Workshop Chairs

We would like to thank our FAANG Workshop Chairs for their assistance with the FAANG session. In particular, we would like to acknowledge Chris Tuggle for his dedication to making the FAANG Workshop 2018 a success!

Sessions	Chair
FAANG overview + updates	Chris Tuggle
Data: retrieval	Carl Schmidt, Peter Harrison
Wet lab: methylation	Bastien Llamas
Data: submission	Peter Harrison, Carl Schmidt
Wet lab: chromatin structure (HiC, ATACseq)	Monique Rijnkels
Data: transcriptomes	Nathan Watson-Haigh
Wet lab: histone modifications	Stephanie McKay, Brenda Murdoch
Date: genomes	Lloyd Low
Wet lab: transcriptomics (miRNA, RNA, IsoSeq)	Brenda Murdoch, Stephanie McKay
FAANG plenary discussions	Chris Tuggle

ISAFG & FAANG 2018 SPONSORS

We are particularly grateful to our following sponsors without whom this conference would not have been possible. Please take the opportunity to visit with those exhibiting on the Concourse (see page 50).

Hosts	
University of Adelaide	Supporting partner
Davies Research Centre	Support partner

Sponsor	**Level**
Neogen Australasia	Gold
Weatherbys Scientific Australia	Gold
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Recombinetics	Silver
Thermo Fisher Scientific	Silver
MatMaCorp	Bronze
Millennium Science	Bronze
Zoetis	Bronze
Dovetail	Other
PacBio	Other

GENERAL INFORMATION

Venue

Welcome to the 7th International Symposium on Animal Functional Genomics and Functional Annotation of Animal Genomes Workshop 2018 in Adelaide, Australia. The conference venue is the National Wine Centre of Australia, located on North Terrace just northeast of the business district and adjacent to the Adelaide Botanic Gardens. It is within a 10-15 minute walk of many hotels and restaurants. The new city tramline stop and the City Loop bus stop are a 5 minute walk. The City Loop bus and tram within the central business district are free. Public car parking is available within a 3-5 minute walk on Hackney Road for a maximum of 4 hours ($2.60 per hour) or Plane Tree Drive for a maximum of 10 hours ($2.60 per hour).

All scientific sessions and the Welcome Reception will be held at the National Wine Centre (see floor plan on page 50). The registration desk will be located on the Concourse at the main entrance. Note that wireless internet is available throughout the National Wine Centre.

All ISAFG oral sessions will be in the Hickinbotham Hall. The ISAFG poster sessions will be in the Ferguson & Broughton Rooms. The FAANG workshop breakout sessions will be in the Hickinbotham Hall and Broughton Room. Sponsor exhibits will be located on the Concourse.

Lunches and morning and afternoon teas will be served in Hickinbotham Hall and on the Concourse with the exhibits and posters at the scheduled times. Do not forget to take the opportunity to visit the exhibitors and posters during these breaks! If the weather permits, there will be access to the outside terrace. In addition, a small cafe (Wined Bar) within the Centre will be open throughout the conference, where coffee and food can be purchased. [Note: If you have specific dietary requirements, please make yourself known to the catering staff as we have made special arrangements to match your needs.]

Registration desk
The registration desk will be open from 7:30 pm to 5:00 pm on Monday (November 12th), Tuesday (November 13th), and Wednesday (November 14th). On Thursday (November 15th), the registration desk will be open from 8:00 am until and 12:00 pm.

If you have any problems or questions, please visit the registration desk and we will do our best to assist you.

PRESENTATION INFORMATION

Oral presentation instructions
For the oral presentations, Powerpoint slides are preferred, and should be sized for wide screen (16:9). Please contact the organisers if you are using a different program for your slides or need to show a video.

Presenters must upload their slides no later than 30 minutes prior to their session (see Scientific Program). Please see the technician in the Hickinbotham Hall. Presenters will **NOT** be able to use their own computers. So please bring the presentation on a USB flash drive.

Please arrive at your session at least 15 minutes before the scheduled start time and make yourself known to the chair. You will be given instructions regarding the operation of equipment at that time.

Quick fire poster talk instructions
Presenters giving a Quick Fire poster talk are requested to prepare their oral presentation as above and their poster as below.

Poster presentation instructions
As instructed on the website, the posters should be in portrait orientation A0 in size (that is, 841 x 1189 mm or 33.1 x 46.8 inches for width x height). Posters that do **not** conform to these specifications may be rejected if they encroach on neighbouring poster space.

Posters should be mounted in the Ferguson/Broughton Rooms by 8:30 am on Monday, November 12th. Velcro and poster numbers will be provided upon arrival. Please arrive by 7:30 am on Monday morning to ensure that your poster is mounted **before** the start of the first plenary session. Posters should **remain** mounted until after 5:00 pm on Tuesday afternoon. Posters not removed by 6:00 pm on Tuesday will be stored by the organisers and can be retrieved from the registration desk on Wednesday. Posters will not be kept thereafter.

There will be 2 poster sessions on Monday in the Ferguson/Broughton Rooms (see National Wine Centre floor plan inside back cover). Those with even numbered posters will present after lunch (12:30 to 1:30 pm) and those with odd numbered posters will present prior to the Welcome Reception (5:30 to 6:30 pm). Please be present near your posters during these times.

There will be 2 prizes for the best student posters. The poster prizes will be awarded at the Conference Dinner on Tuesday night.

Abstracts
Abstracts for the plenary sessions, invited talks and posters are available in these proceedings. These abstracts are also available on the ISAFG website.

BUSINESS MATTERS

Award Ceremonies

ISAFG strongly encourages the participation of students. To this end, funds have been provided for the heavily discounted student conference registration fees and travel bursaries. We will be awarding travel bursaries for the 7th ISAFG at the Conference Dinner on Tuesday evening.

In addition, ISAFG promotes excellence in students. To this end, there will be 2 awards for the best posters, So if you applied as student, please attend the Conference Dinner on Tuesday evening. You may have won a prize!!!

Business Meeting

The business meeting will be held just before the close of the conference on Thursday morning to discuss the future of ISAFG. Your participation is strongly encouraged.

SOCIAL EVENTS

One of the great aspects of ISAFG conferences is the opportunity to meet old friends and to make new ones. Please join us for the both the Welcome Reception and the Conference Dinner, which are included as part of your conference registration. These events have been specifically organised to encourage interaction amongst conference delegates.

Welcome Reception

The Welcome Reception is on Monday, November 12th on the National Wine Centre Concourse following the afternoon poster session with drinks and canapés from 6:00 pm to 7:30 pm.

Note for those wishing to dine after the Welcome Reception, Adelaide has many good restaurants, but on Monday nights after 8 pm the choices are limited! Near-by Rundle Street offers the best local options or you may stop by the registration desk for other suggestions.

Conference Dinner

The Conference Dinner will be held at the Adelaide Zoo Rotunda on Tuesday, November 13th from 6:25 pm to 11 pm. The Zoo is adjacent to the Botanic Gardens and easily reached on Frome Road or Plane Tree Drive. It takes approximately 15 minutes to walk to the Zoo from the National Wine Centre along Plane Tree Drive (see map on page 49). **Please note** that the Zoo closes at 5:00 pm and we will be escorted to the Rotunda. So you must arrive at the Zoo entrance no later than **6:25 pm!**

Dress is smart casual. However, with regards to your choice of clothing, be forewarned. This is not your traditional conference dinner. The dinner is in an outdoor rotunda with brick flooring and Adelaide can be chilly in the evening (14^0C/57^0C). So please dress accordingly.

There will be entertainment but we must depart the Zoo by 11:00 pm - something to do with animals needing their sleep. Those who wish to continue late into the night can do so at one of the several bars or pubs nearby (see ISAFG website for links). Just remember that we do have a plenary session at 8:30 am on Wednesday morning!

GENE ANNOTATION SHORT COURSES

Two short courses are being held directly after ISAFG and FAANG conference at the University of Adelaide. The first short course on Thursday afternoon (November 15th) is to provide new users with the basics of R in preparation for the second course on gene annotation using R on Friday (November 16th).

Introduction to R (Thursday, November 15th, 1:00 pm – 5 pm): *Braggs Building, Room 450 Dry Laboratory 4A, North Terrace Campus*

This half day course will introduce the fundamentals of working in R to new users. As most users migrate to R from Excel when they reach the limits of spreadsheet manipulation, we will focus on R data structures and processes that will help the user make that transition. The aim of the course is to prepare the user for the R annotation course to be held on Friday, November 16th. No prior knowledge is assumed, but any programming skills will be helpful. Users will be required to install R, RStudio and specific packages before they attend the course.

Topics will include:

- Data building blocks: data frames, matrices, lists and vectors
- Basic operations in R
- Basic data input and output
- Data visualisation

Genome Annotation with R (Friday, November 16th, 9:00 am – 5:00 pm); Kevin Marjoribanks Building (on corner of Pulteney & North Terrace with signs for ThincLab), Room 128 BankSA Teaching Suite

This one day course will introduce the user to: data structures that enable sophisticated manipulation of genomic data in R; online annotation databases that are tailor-made for importing into R; how to combine annotations with the user's data and extract useful information; and how to visualise genomic annotations. The aim of the course is to educate the users about the tools available and assumes that the user can carry out basic commands in R. Users will be required to install R, RStudio and specific packages before they attend the course.

Topics will include:

- The Bioconductor Project
- IRanges and GRanges
- biomaRt, AnnotationHub and TxDb
- RMySQL
- Genomic Data Visualisation

7th ISAFG & FAANG WORKSHOP 2018 CONFERENCE PROGRAM

Monday, November 12th

Registration (7:30 am – 5:30 pm), National Wine Centre of Australia Concourse

Opening Ceremony, Hickinbotham Hall

8:25 am
Prof John Williams (Director of Davies Research Centre, University of Adelaide), ISAFG 2018 Organising Committee Chair: *Welcome Address*

Plenary Session #1 (Chair: Stefan Hiendleder, University of Adelaide)

8:30 am
David Gorkin (University of California, San Diego; Abstract S06):
"Navigating the genome with epigenome maps: insights from the systematic mapping of chromatin state and accessibility across mouse fetal development"

9:15 am
Michael Skinner (Washington State University; Abstract S15)
"Environmentally induced epigenetic transgenerational inheritance of health and disease: ancestral ghosts in your genome"

MORNING TEA (10:00 am – 10:30 am), Hickinbotham Hall & Concourse

Session #1 Disease & immunity (Chair: Paul Coussens, Michigan State University)

10:30 am Keynote address
David MacHugh (University College Dublin; Abstract S11):
"Functional and integrative genomics of bovine and human tuberculosis: a One Health perspective"

11:15 am
Laura Miller (USDA; Abstract S14):
"e-PIG-enetics: porcine sncRNA response to highly pathogenic PRRSV"

LUNCH (11:45 pm – 12:30 pm), Hickinbotham Hall

Poster Session #1 (12:30 pm – 1:30 pm): Even numbered posters (Broughton & Ferguson Rooms)

Session #2 Reproduction & fertility (Chair: Brenda Murdoch, University of Idaho)

1:30 pm Keynote address
Claire Wade (University of Sydney; Abstract S19):
"Evolution of reproductive behaviour in the dog"

2:15 pm
Marina Fortes (University of Queensland; Abstract S05):
"The landscape of bovine retrotransposon polymorphisms and its association with fertility and production traits in Australian tropical beef cattle"

2:45 pm
Vanmathy Kasimanickam (Washington State University; Abstract S07):
"Serum miRNA profiling in pregnant and non-pregnant beef heifers"

Monday, November 12th ~ continued

AFTERNOON TEA (3:15 pm – 3:45 pm), Hickinbotham Hall & Concourse

Session #3: Environmental interactions (Chair: Carl Schmidt, University of Delaware)

3:45 pm – 4:30 pm Keynote
Yanfang Wang (Chinese Academy of Agricultural Sciences; Abstract S20):
"Genetic regulation of cold-induced WAT browning in pigs"

4:30 pm – 5:00 pm
Daniela Lourenco (University of Georgia; Abstract S10):
"How genomics can help to identify resilient animals under environmental stress conditions"

5:00 pm – 5:30 pm
Raluca Mateescu (University of Florida; Abstract S12):
"Current insights into genomics of thermotolerance in beef cattle"

Poster Session #2 (5:30 pm – 6:30 pm): Odd numbered posters (Broughton & Ferguson Rooms)

WELCOME RECEPTION (6:00 pm – 7:30 pm): National Wine Centre Concourse

Tuesday, November 13th

Plenary Session #2 (Chair: Dave Burt, University of Queensland)

8:30 am
Peter Dearden (University of Otago; Abstract S04):
"The architecture of a plastic trait"

9:15 am
Susan Lamont (Iowa State University; Abstract S09):
"Some like it hot: functional genomics of response to heat stress in poultry"

MORNING TEA (10:00 am – 10:30 am), Hickinbotham Hall & Concourse

Session #4 Gene regulation (Chair: Steve Moore, University of Queensland)

10:30 am Keynote address
Amanda Chamberlain (Agriculture Victoria; Abstract S02):
"Identification of regulatory variation in dairy cattle with RNA sequence data"

11:15 am
Stephanie McKay (University of Vermont; Abstract S13):
"A neuroepigenomic investigation of DNA methylation in cattle with extreme measures of docility"

Tuesday, November 13th ~ continued

LUNCH (11:45 pm – 12:30 pm), Hickinbotham Hall

Neogen Australasia Sponsor Session (12:30 pm – 1:30 pm)

Russell Lyons (Neogen Australasia): "Neogen Agrigenomics: Global Innovation | Local service"

Kylie Munyard (Curtin University): "Shades of alpaca grey: the causative mutation for grey in alpacas"

Iona MacLeod (Agriculture Victoria): "Ovine sequencing and functional annotation: the future for genomic selection in sheep"

George Sofronidis (Orivet Genetic Pet Care): "Meet the Laboratorydoodle, a genetically innovative breed"

Session #5: Functional Genomics (Chair: Clare Gill, Texas A&M University)

1:30 pm Keynote address
James Kijas (CSIRO Agriculture; Abstract S08):
"Functional genomics in Atlantic salmon: a trait specific investigation generating multiple FAANG datatypes"

2:15 pm
Chris Tuggle (Iowa State University; Abstract S18):
"An improved functional annotation of the domestic pig genome"

2:45 pm
Terry Bertozzi (University of Adelaide, South Australian Museum; Abstract S01):
"Functional genomics without a genome: the phototransduction pathway of blind beetles"

AFTERNOON TEA (3:15 pm – 3:45 pm), Hickinbotham Hall & Concourse

Session #6: Quick fire poster talks (Chair: Cindy Bottema, University of Adelaide)

3:45 pm – 5:00 pm
Adeyinka Abiola Adetula (Huazhong Agricutural University; Abstract P01): "*Transcriptome sequencing reveals key potential long non-coding RNAs related to duration of fertility trait in the uterovaginal junction of egg-laying hens"*

Thomas Hall (University College Dublin; Abstract P10): *"Initial host response to mycobacterial infection is orchestrated through H3K4 trimethylation at key immune genes"*

Min Wang (Agriculture Victoria/LaTrobe University; Abstract P33): "*Mammalian topological association domains and CTCF binding motifs regulate gene expression in the bovine genome"*

Luciana Regitano (Embrapa; Abstract P27): "*In silico identification of putative cis-eQTLs affecting allelic expression"*

Tomasz Sadkowski (Warsaw University of Life Science; Abstract P31): "*Expression of miRNA in semitendinosus muscle of cattle breeds with varying intramuscular fat deposition"*

CONFERENCE DINNER (6:30 pm – 11:00 pm): Adelaide Zoo (must be at entrance by 6:25 pm)

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Wednesday, November 14th

Joint ISAFG & FAANG Plenary Session (Chair: Paolo Ajmone-Marsan, Università Cattolica del Sacro Cuore)

8:30 am

Illumina Sponsored Speaker

Christine Wells: (University of Melbourne):
"Cell identity in the era of single cell profiling"

9:15 am

Brian Dalrymple (University of Western Australia; Abstract S03):
"Genetics and genomics pathways to form and function: point and counterpoint"

MORNING TEA (10:00 am – 10:30 am), Hickinbotham Hall & Concourse

Joint ISAFG & FAANG Session: New technology applications (Chair: Ben Hayes, University of Queensland)

10:30 am Keynote address

Tim Smith (USDA, MARC; Abstract S16):
"Advances in genome technology"

11:15 am

Recombinetics Inc Sponsored Speaker

Tad Sonstegard (Recombinetics Inc; Abstract S17):
"Discovery and editing of adaptive traits in livestock"

LUNCH (11:45 pm – 12:30 pm), Hickinbotham Hall

Weatherbys Scientific Australia Sponsor Session (12:30 pm – 1:30 pm): Delivering animal genomics to drive research and profitability in livestock production

Romy Morrin-O'Donnell (Weatherbys Scientific Australia): *"Welcome and introduction to Weatherbys Scientific: our contribution to the Irish cattle industry and beyond"*

Wayne Pitchford (University of Adelaide): *"Incorporating functional genomics into the selection of tropically adapted beef"*

FAANG WORKSHOP 2018 (Chair: Chris Tuggle, Iowa State University)

1:30 pm FAANG Overview

Chris Tuggle (Iowa State University): Introduction to FAANG

1:50 pm FAANG project updates

Colin Kern (University of California, Davis): FAANG projects at UC Davis
Brenda Murdoch (University of Idaho): Sheep FAANG
David MacHugh (University of College Dublin): FAANG in Ireland
Amanda Chamberlain (Agriculture Victoria): FAANG projects at AgVic Australia
Ben Hayes (University of Queensland): More FAANG in Australia
Chris Tuggle (Iowa State University): Additional FAANG projects

3:00 pm Open Discussion/ Q & A on FAANG Future

Wednesday, November 14th ~ continued

AFTERNOON TEA (3:15 pm – 3:45 pm), Hickinbotham Hall & Concourse

3:45 pm – 4:30 pm: FAANG breakout session #1
Data (Hickinbotham): retrieval (Chairs: Carl Schmidt University of Delaware & Peter Harrison, EMBL-EBI)
Wet lab (Broughton): methylation (Chair: Bastien Llamas, University of Adelaide)

4:30 pm – 5:15 pm: FAANG breakout session #2
Data (Hickinbotham): submission (Chairs: Peter Harrison, EMBL-EBI & Carl Schmidt, University of Delaware)
Wet lab (Broughton): chromatin structure (HiC,ATACseq) (Chair: Monique Rijnkels, Texas A&M University)

Thursday, November 15th

FAANG WORKSHOP 2018 BREAKOUT SESSIONS CONTINUED ~

8:30 am – 9:15 am: FAANG breakout session #3
Data (Hickinbotham): transcriptomes (Chair: Nathan Watson-Haigh, University of Adelaide)
Wet lab (Broughton): histone modification (Stephanie McKay, University of Vermont & Brenda Murdoch, University of Idaho)

9:15 am – 10:00 am: FAANG breakout session #4
Data (Hickinbotham): genomes (Chair: Lloyd Low, University of Adelaide)
Wet lab (Broughton): transcriptomics (miRNA, RNA, IsoSeq) (Chair: Brenda Murdoch, University of Idaho & Stephanie McKay, University of Vermont)

MORNING TEA (10:00 am – 10:30 am), Hickinbotham Hall

FAANG WORKSHOP Plenary Discussion, Hickinbotham Hall

10:30 am: Summary of breakout sessions (Chair: Chris Tuggle, Iowa State University)

11:00 am: Recommendations for FAANG & ISAFG (Chair: John Williams, University of Adelaide)

11:30 am: CLOSE OF CONFERENCE

Invited Speakers

Amanda Chamberlain
Research Scientist, Agriculture Victoria

Dr Amanda Chamberlain undertook her PhD at the University of Melbourne, under the supervision of Professor Michael Goddard on mapping QTL for milk production in dairy cattle and using them in marker assisted selection. She joined what is now known as Agriculture Victoria as a post-doctoral scientist where she has been involved in the implementation of genomic selection in the Australian dairy industry, the 1000 bull genomes consortium and more recently the Functional Annotation of Animal Genomes (FAANG) consortium. Dr Chamberlain is currently working on sequencing the bovine genome and identifying regions involved in regulating gene expression.

Brian Dalrymple
Adjunct Professor, The University of Western Australia, Australia

After more than thirty years at CSIRO Brian Dalrymple is now an Adjunct Professor at The University of Western Australia. Brian has undertaken a wide range of research projects that used molecular biology, genomics and bioinformatics methodologies to address problems in animal production and disease. In his early days at CSIRO Brian was involved in the development of a recombinant vaccine for sheep foot rot. As part of a large project to increase the digestion of low quality forages Brian developed recombinant rumen bacteria expressing novel fibre degrading enzymes. The application of bioinformatics to antibiotic development was his next target, leading to the development of a small spin-off company from CSIRO. Brian led the international teams that designed the first commercial single nucleotide polymorphism chip for sheep and delivered the first three assemblies of the sheep genome. He has also had a long term interest in gene expression as part of a systems biology approach to understanding the functional genomics of key biological processes in animal production. Brian has applied these approaches to the deposition of lipid as intramuscular fat and most recently to the functions of the gastrointestinal tract, in particular the rumen of sheep and cattle.

Peter Dearden
Professor, Biochemistry Department, University of Otago, New Zealand

Peter Dearden is a Professor in the Biochemistry Department, University of Otago, and Director of Genomics Aotearoa, a national network that aims to improve the use and value of genomics in New Zealand. He trained as an evolutionary developmental biologist focussing on the evolution of traits in insects. During his career he has worked on many species, but became fascinated by bees and their ability to produce different phenotypes in response to their environment.

Invited Speakers ~ continued

David Gorkin
Associate Director, UCSD Center for Epigenomics, USA

Dr. Gorkin is the Associate Director of Epigenomics at the UCSD Center for Epigenomics, where he directs a team of researchers in developing and applying epigenomic technologies to a answer a variety of questions related to basic and clinical research. Prior to joining the Center, Dr. Gorkin was the project manager for the San Diego ENCODE data production center led by Dr. Bing Ren, and remains an active contributor to the ENCODE and 4D Nucleome consortia. He was also an A.P. Giannini Foundation postdoctoral fellow in Dr. Ren's laboratory, where his research focused on the roles of histone modifications and 3D genome organization in the regulation of gene expression. Dr. Gorkin received his Ph.D. in Human Genetics and Molecular Biology from The Johns Hopkins University School of Medicine, where his work in Dr. Andrew McCallion's lab focused on the epigenomics of melanocytes (pigment cells), and their role in human pigmentation.

James Kijas
Research Group Leader, CSIRO Agriculture, Australia

Dr Kijas is a genome scientist who has developed an international reputation in the field of animal science. Following completion of his PhD in plant genetics (1996), James embarked on a research career focused on the genetics and genomics of domesticated animals. As a postdoctoral scientist guided by Prof. Leif Andersson (SLU, Sweden), he identified a collection of gene mutations responsible for inherited traits in pigs and dogs. He moved to Cornell University in 2000 under the guidance of Prof. Gus Aquirre and successfully identified the genetic basis of a number of inherited canine eye diseases, and was awarded his first research grants as a principal investigator. He joined the CSIRO Division of Livestock Industries in 2003 and has been instrumental in the development and delivery of a range of genomic tools for sheep. These have included pilot scale SNP arrays, the ovine SNP50 BeadChip and the reference genome assembly. Using these SNP arrays, he has completed studies into the population history and genetic diversity of sheep breeds as well as a sequence based analysis of wild bighorn sheep populations. In the last couple of years he has initiated a research program focussed on farmed Atlantic Salmon, studying sex determination, the functional biology of sexual maturation, genetic diversity and selection. He currently holds the role of Research Group Leader in CSIRO Agriculture and is based in Brisbane, Australia.

Sue Lamont
C.F. Curtiss Distinguished Professor, Department of Animal Science, Iowa State University, USA

Sue Lamont has been a faculty member in the department of Animal Science at Iowa State University for 35 years, and is currently a C.F. Curtiss Distinguished Professor. She leads an active research program with an emphasis on determining the molecular genetic control of important biological traits of poultry, especially those related to host response to stressors such as heat and pathogens. She enjoys extensive national and global research collaborations. Sue has published over 200 peer-reviewed journal papers. She has won numerous awards, including the Helene Cecil Leadership Award, the Embrex-Pfizer Fundamental Science Award and the Merck Award for Achievement from the Poultry Science Association. Sue is an elected Fellow of both the Poultry Science Association and of the International Society of Animal Genetics.

David MacHugh
Professor, School of Agriculture and Food Science, University College Dublin, Ireland

David MacHugh obtained a BA (Mod) degree in Genetics from Trinity College Dublin in 1988 and undertook PhD research in animal genomics at TCD. His postdoctoral work on livestock paleogenomics was funded by a Wellcome Trust Research Fellowship in Bioarchaeology. In 1999 he took up a lectureship in University College Dublin and was appointed Professor in 2009. He is currently the Associate Dean for Research, Innovation and Impact at the UCD School of Agriculture and Food Science. He is also a Conway Investigator (www.ucd.ie/conway), co-founder and Scientific Advisor to Equinome/Plusvital Ltd. (www.plusvital.com) and a co-founder and member of the Scientific Advisory Board of IdentiGEN Ltd. (www.identigen.com). David's research programme is focused on functional genomics of host-pathogen interactions for Mycobacterium bovis infection and development of novel disease biomarkers for bovine tuberculosis. Other research activities include livestock production genomics; population genomics of extinct and modern livestock populations; and in collaboration with Associate Professor Emmeline Hill, genomics of health and performance traits in Thoroughbred horses.

Michael K. Skinner
Eastlick Distinguished Professor, Center for Reproductive Biology, School of Biological Sciences, Washington State University

Dr. Michael Skinner is a professor in the School of Biological Sciences at Washington State University. He did his B.S. in chemistry at Reed College in Portland Oregon, his Ph.D, in biochemistry / chemistry at Washington State University and his Postdoctoral Fellowship at the C.H. Best Institute at the University of Toronto. He has been on the faculty of Vanderbilt University and the University of California at San Francisco. Dr. Skinner's current research has demonstrated the ability of environmental toxicants to promote the epigenetic transgenerational inheritance of disease phenotypes due to abnormal germ line epigenetic programming in gonadal development. Dr. Skinner has over 300 peer reviewed publications and has given over 288 invited symposia, plenary lectures and university seminars. He has founded several biotechnology companies.

Invited Speakers ~ continued

Tim Smith
USDA ARS Meat Animal Research Centre

Dr. Smith holds a B.S. degree in Microbiology from Montana State University and Ph.D. in Chemistry from the University of Oregon. He has been working in the field of livestock genomics since 1992, at the U.S. Meat Animal Research Center in Nebraska, a part of the USDA Agricultural Research Service. He was raised to "supergrade" status (roughly equivalent to Distinguished Professor) within the ARS system in 2010. His studies have identified genome variation underlying muscle hypertrophies and recessive disease, and provided DNA markers associated with a variety of production traits in cattle. Recently, he has been a leader in application of new technologies to create greatly improved reference genome assemblies for multiple species. He has led USDA efforts to develop systems approaches that integrate genomics and traditional genetics with microbiome and immune repertoire studies to examine respiratory disease, an important concern in beef cattle production in the U.S. Dr. Smith is a Writing Team Leader for both "Genomics Tools and Resources" and "Microbiome" sections of the "2018-2028 Genomes to Phenomes Blueprint" to guide investments of the National Institutes of Food and Agriculture grants programs, and the Agricultural Research Service Office of National Programs, through the next decade.

Tad Sonstegard
Chief Scientific Officer, Acceligen

Dr. Tad Sonstegard is currently Chief Scientific Officer of Acceligen, a Recombinetics company, where he leads both business development and research efforts dedicated to discovery and precision breeding of causative sequence variants in food animals. A main goal is to apply genome editing for livestock genetic improvement that promotes sustainability and animal welfare. Previously at the USDA-ARS Beltsville, he led a genomics research program developing applications in germplasm conservation and genetic improvement that included the first commercially successful, ag-based SNP tool. He also identified causative variation affecting fertility and thermo-tolerance in cattle and has led consortia to generate genome assemblies of the water buffalo, goat, Zebu cattle, and an expression atlas of cattle. Dr. Sonstegard received his undergraduate degree from Iowa State University and his Ph.D. from the University of Minnesota. His has published 193 peer-reviewed articles and has received award recognition for his work in genomic research for livestock genetic improvement.

Claire Wade
Chair of Computational Biology and Animal Genetics, The University of Sydney

Claire Wade began her career in quantitative genetics before making the leap to genomics in 2002 when she began a position with the Whitehead Institute for Biomedical Research at Massachusetts Institute of Technology. The genomics group at the Whitehead later became one of the founding groups of what is now the Broad Institute. While in the USA, Claire worked on several mammalian genome projects including the mouse, dog and horse (for which she was the lead researcher). Claire's research interests include unravelling the secrets of genome biology using next generation sequencing. In particular, she

studies the application of new genomic technologies to improve our understanding of diseases and behavioural traits in domestic animals and wildlife and our understanding of the links between DNA and phenotype in general. Projects currently underway are as diverse as studying the genetics of durability in Thoroughbred race horses, finding genes underlying canine separation anxiety and working dog performance, improving captive animal management using new genetic resources, and better understanding the genomics of behaviour. Other projects involve mapping genes causing congenital disorders in dogs including cleft palate and deafness using whole genome association analysis and genotyping by sequencing.

Yanfang Wang
Institute of Animal Science, Chinese Academy Agricultural Sciences

Dr. Yanfang Wang received her Ph.D. degree in animal genetics and breeding in 2004 in Huazhong Agriculture University, China. From 2005-2011, she worked as a postdoctoral researcher in field of animal functional genomics in United States. Then, she was appointed as a research assistant professor at University of Missouri at Columbia (2012-2014). In 2014, she was recruited as a full professor at the Institute of Animal Science, Chinese Academy Agricultural Sciences (CAAS) in Beijing. Dr. Wang's research interests are mainly focused on investigating molecular and cellular mechanisms of adipose formation and deposition using mice and pig models; discovering the agriculturally useful candidate genes that can impact important economic traits for potential pig breeding.

Christine Wells
Director, Centre for Stem Cell Systems, University of Melbourne, Australia
Deputy Program Lead, Stem Cells Australia
ARC Future Fellow
Chair, Stem Cell Systems, University of Melbourne
Honorary Fellow, Walter and Eliza Hall Institute
Emeritus Professor, The University of Queensland, Australia.

Professor Christine Wells is the Chair of Stem Cell Systems, an ARC Future Fellow and Founding Director of the University of Melbourne Centre for Stem Cell Systems. Christine is a genome biologist interested in tissue injury and repair. She leads a program of research across three pillars of impact and output: (1) collaboration platforms for data integration and visualization for the stem cell community; (2) bioinformatics method development; and (3) stem cell models of inflammation. Christine leads the Stemformatics.org stem cell collaboration resource which hosts the largest compendium of curated stem cell data with >300 public stem cell datasets consisting of ~10,000 stem cell samples, used to generate definitive signatures of stem cell subsets and their differentiated progeny.

Speaker Abstracts

S01 Functional genomics without a genome: the phototransduction pathway of blind beetles

BARBARA LANGILLE[1], TERRY BERTOZZI[1,2], SIMON TIERNEY[3], ANDREW AUSTIN[1], WILLIAM HUMPHREYS[4], STEVE COOPER[1,2]
[1]The University of Adelaide, Adelaide, Australia; [2]South Australian Museum, Adelaide, Australia.
[3]Western Sydney University, Sydney, Australia; [4]Western Australian Museum, Perth, Australia

Understanding how gene networks adapt to environmental changes is of fundamental importance to evolutionary biology and can help to uncover the relationship between an organism's genome and its phenotype. Independently evolved subterranean beetle (Dytiscidae) species of Western Australia have converged on eye loss, providing a powerful system to explore changes to the genome with respect to troglomorphic characters. Using next generation sequence data, we have begun to investigate key genes in the visual pathway of subterranean and surface dwelling species. We used RNAseq data from five beetle species to explore differences in the expression of phototransduction genes between subterranean and surface dwelling species and also to design baits for targeted enrichment of 60 gene targets from 31 subterranean and surface species. While the study is ongoing, we have already found evidence for a lack of transcription or pseudogenisation in subterranean species relative to surface species in a number of genes in the pathway.

S02 Identification of regulatory variation in dairy cattle with RNA sequence data

AMANDA J. CHAMBERLAIN[1], BENJAMIN J. HAYES[1,2], RUIDONG XIANG[3], CHRISTY J. VANDER JAGT[1], CORALIE M. REICH[1], IONA M. MACLEOD[1], CLAIRE P. PROWSE-WILKINS[1], BRETT A. MASON[1], HANS D. DAETWYLER[1,4], MICHAEL E. GODDARD[1,3]

[1]Agriculture Victoria, AgriBio, Centre for AgriBiosciences, Bundoora, Victoria 3083, Australia.; [2]Centre for Animal Science, The University of Queensland, St Lucia 4067, Queensland, Australia; [3]Faculty of Veterinary & Agricultural Science, The University of Melbourne, Parkville 3052, Victoria, Australia; [4]School of Applied Systems Biology, La Trobe University, Bundoora, Victoria 3083, Australia

Most of the significant variants from genome wide association studies for complex traits in dairy cattle using whole genome sequence data fall outside coding genes. These results lead to the hypothesis that many causal mutations affecting complex traits may be regulating the expression of genes. The identification of such causal regulatory variants could lead to increases in the accuracy and persistency of genomic breeding values. With the aim of identifying this type of variant, we performed expression QTL (eQTL), allele specific expression QTL (aseQTL) and splice variant QTL (sQTL) detection on RNA sequence data from milk and white blood cells collected from 141 lactating cows with imputed whole genome sequence data. Many variants were detected with significant eQTL, aseQTL and sQTL effects, with low false discovery rates. There was significant overlap in genes with significant eQTL, aseQTL and sQTL. eQTL with a large effect in white blood cells were likely to have a large effect, in the same direction, in milk cells as well. sQTL significant in both milk and white blood cells more often caused expression of the same isoform. There was a trend for the most significant variant to be < 100 kb from the transcription start site of the gene they were affecting for all three QTL types.

S03 Genetics and genomics pathways to form and function: point and counterpoint

BRIAN P. DALRYMPLE[1]
[1]Institute of Agriculture, The University of Western Australia, 35 Stirling Hwy, Perth, WA 6009, Australia

After almost 35 years as a livestock molecular biologist I will take a somewhat personal look at the past, present and future of functional animal genomics. Big improvements in livestock productivity etc. have been made with limited understanding of the molecular biology underlying the phenotypes. However, the law of diminishing returns tells us we need to invest more and learn more to keep making progress. The use of increasing numbers of genetic markers associated with variation in phenotypes has improved genetic prediction accuracy, albeit with limited impact on our understanding of the underlying biology. If we knew which variants actually cause differences in gene and protein expression and function a further increase in

prediction accuracy is expected, at the same time as increasing our understanding of the biology. To achieve this understanding, we cannot rely on just using species, let alone breed, specific datasets. We also have to develop innovative methodologies to compensate for sometimes barely adequate datasets. Fortunately, comparative genomics has shown us that the majority of genes are functionally conserved across all mammals and that regulatory signals are fairly well conserved, but that small differences in regulation to gene expression can lead to large differences in form and function. I will discuss some lessons from livestock transcriptomics studies, and our approach to using the large volumes of data generated by ENCODE, FANTOM and other projects to bootstrap a solution to the identification of putative causative SNPs in livestock to complement the generation of species specific data through FAANG.

S04 The architecture of a plastic trait

PETER K. DEARDEN
Genomics Aotearoa and Biochemistry Department, University of Otago. New Zealand

Understanding how a trait is built by an organism is a critical problem in developmental biology, which has implications in both artificial and natural selection. While advances in developmental biology have taught us much about how morphology is built in an embryo, we are only just beginning to determine how environment influences those processes. Using honeybees as our model system we have examined in detail how an environmentally responsive (plastic) trait is regulated, from the cell signalling events that trigger it, to the epigenetic changes that regulate it, to the final cellular events that maintain it. By understanding the architecture of a plastic trait, we hope to understand its evolution, the constraints it places on an organism and, more generally, the biological consequence of the way a plastic trait is built. Along the way we will touch on the remarkable genetics of bees, the role of epigenetics in developmental biology and the implementation of this data in a bee breeding programme.

S05 The landscape of bovine retrotransposon polymorphisms and its association with fertility and production traits in Australian tropical beef cattle

MARINA R S FORTES[1,2], ANTONIO REVERTER[3], LAERCIO R PORTO NETO[3], KYLE UPTON[1]
[1] *School of Chemistry and Molecular Biosciences, The University of Queensland, Australia.*
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[3] *CSIRO Agriculture, St Lucia, Australia.*

Retrotransposons are genomic regions with the ability to amplify themselves and are abundant in many organisms. Retrotransposon activity generates polymorphisms that may underpin the molecular mechanisms associated with phenotypes of economic interest in livestock species. In humans, retrotransposons insertion polymorphisms were associated with changes in gene expression and inflammatory conditions. Retrotransposons were also related to gametogenesis and therefore may influence fertility traits that are crucial for cattle production. In *Bos indicus* and *Bos taurus* 30 families of endogenous retroviruses have been proposed, with over 13 thousand elements described. Some of these elements are highly conserved among the bovidae family and others seemed to be under selective pressure. Having collected genomes from phenotyped bulls and with an improved reference genome released, it is timely to revise our knowledge of retrotransposons across the entire bovine genome. In this study, we aim to compare the genomes of 20 tropically adapted sires with the newly released reference bovine genome to map the landscape of retrotransposons in a breed that is relevant to the Australian beef industry. Retrotransposons polymorphisms were mapped and characterized with our Bioinformatics pipeline. We then compared retrotransposons location with GWAS hits for over 40 production and reproductive traits measured in Australian tropical cattle. Retrotransposons that map to regions associated with production and reproductive traits were further analyzed using PCR amplification. Further, we explored the expression of retrotransposons in testicular samples to further prove their link to male fertility traits in cattle.

S06 Navigating the genome with epigenome maps: Insights from the systematic mapping of chromatin state and accessibility across mouse fetal development

DAVID U. GORKIN[1,14]*, IROS BAROZZI[3]*, YUAN ZHAO[1,8]*, YANXIAO ZHANG[1]*, HUI HUANG[1,15]*, AH YOUNG LEE[1], BIN LI[1], JOSHUA CHIOU[15,16], ANDRE WILDBERG[2], BO DING[2], BO ZHANG[6], MENGCHI WANG[2], J. SETH STRATTAN[11], JEAN M. DAVIDSON[11], YUNJIANG QIU[1,8], VEENA AFZAL[3], JENNIFER A. AKIYAMA[3], INGRID PLAJZER-FRICK[3], CATHERINE S. NOVAK[3], MOMOE KATO[3], TYLER H. GARVIN[3], QUAN T. PHAM[3], ANNE N. HARRINGTON[3], BRANDON J. MANNION[3], ELIZABETH A. LEE[3], YOKO FUKUDA-YUZAWA[3], YUPENG HE[8,9], SEBASTIAN PREISSL[1,14], SORA CHEE[1], JEE YUN HAN[14], BRIAN A. WILLIAMS[12], DIANE TROUT[12], HENRY AMRHEIN[12], HONGBO YANG[6], J. MICHAEL CHERRY[11], YIN SHEN[7], JOSEPH R. ECKER[9,10], WEI WANG[2], KYLE GAULTON[16], DIANE E. DICKEL[3], AXEL VISEL[3,4,5], LEN A. PENNACCHIO[3,4,13], BING REN[1,2]

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** equal contribution*

Embryogenesis requires epigenetic information that allows each cell to respond appropriately to developmental cues. The state and accessibility of chromatin are core components of a cell's epigenome, modulating the function of the underlying genome sequence. Here, we systematically profile histone modifications by ChIP-seq, and chromatin accessibility by ATAC-seq, in a diverse panel of mouse tissues at eight developmental stages from 10.5 days post conception until birth. In total we performed 1,128 ChIP-seq assays and 132 ATAC-seq assays across 72 distinct tissue-stages. Through integrative analysis we develop a unified set of chromatin state annotations, identify dynamic enhancers, reveal key transcriptional regulators, and characterize the relationship between chromatin state and accessibility in developmental gene regulation. We also leverage these data to link enhancers to putative target genes, and uncover tissue-specific enrichments for human disease-associated sequence variation. Our study provides a compendium of resources for biomedical researchers and achieves the most comprehensive view of fetal chromatin dynamics to date.

S07 Serum miRNA profiling in pregnant and non-pregnant beef heifers

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MicroRNAs (miRNAs) are fine tuners of gene expression and regulate target genes at the post-transcriptional level. Their role in development, including pregnancy, has been widely recognized since their discovery. Pregnancy specific miRNAs in placenta, uterine tissue, and maternal circulation have been elucidated in humans and the molecular mechanisms by which miRNAs regulate pregnancy are being investigated. The placenta expresses numerous miRNAs with some being released in the maternal circulation. Conventional pregnancy diagnostics are not always accurate to determine early stages of pregnancy in cattle. To avoid feeding non-productive cattle, accurate detection of pregnancy is essential. Serum miRNAs may serve as precise biomarkers of pregnancy. The objective of this study was to identify differentially expressed serum miRNAs at 30 and 60 days of pregnancy compared to non-pregnancy in beef heifers. Out of 84 bovine-specific,

prioritized miRNAs analyzed, seven were upregulated and five were downregulated in 30 and 60 days of pregnancy compared to non-pregnancy ($p \leq 0.05$, Fold Regulation ≥ 2.0 magnitudes). One miRNA was downregulated in 30-day pregnancy and upregulated in 60-day pregnancy. Interestingly, ten miRNAs were only found in pregnant heifers proposing their pregnancy-specific roles whereas two miRNAs were only detected in non-pregnant serum, suggesting their irrelevancy of pregnancy. Pregnancy and stage specific expressions of miRNAs exist. Degree of expression of one miRNA differs at various stages. MiRNAs differently regulate the gene at various stages of pregnancy. The identification of pregnancy and stage specific miRNAs and their respective characterization will facilitate to use them as accurate biomarkers for pregnancy.

S08 Functional genomics in Atlantic salmon: a trait specific investigation generating multiple FAANG datatypes

JAMES KIJAS [1], ANTONIO REVERTER[1], HARRY KING[2], BRADLEY EVANS[3] and AMIN R. MOHAMED[1]
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Atlantic salmon is one of the first aquaculture species for which functional genomics is now possible. Development of the underpinning genomic tools and resources has been driven by the Atlantic salmon farming industry and their value as an ecological species of interest. To develop data standards and coordinate relevant data generation and analysis, the international community commissioned the Functional Annotation of All Salmonid Genomics (FAASG) consortium. While not yet available, a comprehensive functional annotation will be essential for understanding the biological basis of both life history and production traits. An important example for the Tasmanian salmon industry is the timing of sexual maturation, which in males has significant negative impacts on production. In response, we performed a GWAS using 2721 fish and a SNP50 chip to characterise the genetic architecture of two maturation traits. This revealed a polygenic basis and the absence of genes identified in other farmed populations with very large effect size. Next, we photoperiod manipulated an experimental population, before sampling relevant tissues across the period they committed to sexual maturation. RNA-seq data was used to identify clusters of tissue specific genes, before analysis sought to characterise the transcripts involved in the earliest triggers for maturation. In order to identify control elements in general, and those putatively relating to regulation of maturation, we subjected the same tissues to whole genome bisulphite sequencing. The collated datasets make a contribution to FAASG and provide insights into an important biological trait to the salmon industry.

S09 Some like it hot: functional genomics of response to heat stress in poultry

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High ambient temperature is an environmental stressor with major negative impacts on animal production and welfare. An integrative approach was used to elucidate the transcriptomic and physiologic responses to, as well as genetic control of, heat stress in chickens at the whole-animal, tissue and cellular levels. Biodiverse chicken populations representing modern broiler genetics, historical broiler genetics, historical layer genetics and non-commercial village-type chickens were used to model relative susceptibility versus resilience to heat stress. After exposure to acute or chronic heat episodes, RNA-seq and pathway analyses of multiple tissues characterized the many novel transcriptomic responses that differed between birds under thermoneutral versus heat-stress conditions, as well as amongst contrasts of the genetic lines. Genome-wide association study of an advanced intercross line between a heat-susceptible broiler line and a heat-resilient Fayoumi line identified genomic regions associated with productivity and other physiologic traits under heat stress. Assessing the impacts of heat stress alone or with the combined inflammatory stimulus of lipopolysaccharide exposure, on the whole animal tissue and in vitro cellular levels, revealed that distinct families of genes responded uniquely to either stressor or to their combination. These functional genomic studies have collectively identified candidate genes, genetic pathways and genomic mechanisms related to chickens' response to heat stress and may provide insight into approaches to mitigate the negative impacts of this common and important stressor.
Support: USDA-NIFA-AFRI Climate Change Award #2011-67003-30228.

S10 How genomics can help to identify resilient animals under environmental stress conditions

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[1]*University of Georgia, Dept. of Animal and Dairy Science, Athens, GA 30602*

Climate change and extreme weather can negatively impact animal production. When animals are under heat stress, growth, reproductive performance, and livability are affected. This may be a result of intensive selection for production traits, which reportedly compromises fitness and environmental flexibility. To mitigate the impact of heat stress in livestock, selection for resilient or robust animals can be applied, although there may be a trade-off with economically important traits. Identifying animals that are able to perform well, independent of the environmental condition, would require changing the definition of the traits, collecting phenotypes in a variety of environments, and developing new genetic evaluation models. Reaction norm models can account for the environmental gradient affecting performance for commonly recorded traits. As a result, breeding values can be obtained for the range of environmental conditions represented in the data, and resilient or robust animals can be identified. If genomic information is available, the best animals can be identified earlier in life and in a more accurate way. This leads to an increased genetic gain and a reduction in the generation interval, speeding up the genetic improvement process. Additionally, genomic information enables the search for genomic regions with major effect on traits recorded under regular conditions and under heat stress. In my talk, I will give an overview about how genomic selection combined with models that account for environmental changes can help to better identify resilient animals. I will also share my experience using this methodology to mitigate heat stress in pigs.

S11 Functional and integrative genomics of bovine and human tuberculosis: a One Health perspective

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Human tuberculosis, caused by *Mycobacterium tuberculosis*, is second only to HIV/AIDS as the greatest killer worldwide due to a single infectious agent. Bovine tuberculosis, caused by the closely related *Mycobacterium bovis* (99.95% sequence identity), is an economically-important disease affecting global cattle production, particularly in many developing countries where it also represents a significant zoonotic disease. We have taken a One Health approach to tuberculosis by using network- and pathway-based approaches to compare and integrate host transcriptome data from macrophages infected with *M. tuberculosis* and *M. bovis*, respectively. These analyses have shed light on host-pathogen interaction for human and bovine tuberculosis disease and have provided information that can also be used to prioritize genome-wide association data and enhance detection of genomic variants for susceptibility/resistance to mycobacterial infections in cattle and humans. In addition, we have used high-throughput epigenomics to functionally dissect transcriptional control of the bovine alveolar macrophage response to infection with *M. bovis*. Results from this work reveal mechanisms underlying mammalian macrophage M1/M2 polarisation in response to infection and provide a novel perspective on host-pathogen interaction and subversion of host innate immune processes by mycobacterial pathogens.

S12 Current insights into genomics of thermotolerance in beef cattle.

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Climatic stress is a major limiting factor of production efficiency in beef cattle in tropical and subtropical environments. More than half of the cattle in the world are maintained in hot and humid environments, including about 40% of beef cows in the US. Substantial differences in thermal tolerance exist among breeds and among animals within breeds indicative of opportunities for selective improvement. Vaginal temperature was measured at 5-min intervals for 5 days in 286 cows over two years (2015 and 2017) from the multibreed herd (ranging from 100% Angus to 100% Brahman) of the University of Florida. Ambient environmental conditions were monitored using HOBO data loggers, which continuously record temperature, humidity, solar radiation, black globe temperatures, and wind speed which were used to calculate a temperature humidity

index (THI). There was a breed effect on body temperature with Angus and 3/4 Angus cows had a vaginal temperature higher 39°C even during lower heat stress conditions while Brahman cattle were the only ones able to maintain a lower vaginal temperature throughout the 24h-day during high heat stress conditions. Heritabilities for all different vaginal temperature measures were low or medium and ranged from 0.11 to 0.27. The lowest heritability estimate is for vaginal temperature under high THI conditions (0.11), while heritability for vaginal temperature under low or average THI was slightly higher (0.25 and 0.20, respectively).

S13 A neuroepigenomic investigation of DNA methylation in cattle with extreme measures of docility

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DNA methylation has been shown in rodents and humans to promote variation in behavioural phenotypes. It is unknown if DNA methylation in the bovine brain contributes to phenotypic variation in docility. Initially, variation in global DNA methylation levels between tissues within the bovine brain was examined. Next, we examined methylation in the bovine brain at a single nucleotide resolution. Eight brains from cattle with extreme measures of docility (4 docile and 4 aggressive) were dissected for five functionally distinct regions of the brain. DNA was extracted for Whole Genome Bisulfite Sequencing with Illumina HiSeq, paired-end 150bp. Fastq sequencing files were trimmed with Trim Galore using a phred score of 20. Trimmed reads were aligned to a bovine reference index using BSseeker2 and the bowtie2 aligner. BSseeker2 was further used to call for methylation levels. Coverage statistics were determined in CGmap Tools. Differentially methylated regions between docility phenotypes were identified with RADmeth. An average alignment coverage of 15.9X was obtained across all samples. Average DNA CG methylation ranged between 70.91% to 72.67% in all cattle, 70.17% to 72.98% in docile cattle, and 71.57% to 73.3% in aggressive cattle between brain tissue types. No significant differences were found in average DNA CG methylation between aggressive and docile cattle for any tissue type ($P<0.05$). Further analysis of differentially methylated regions will allow for an understanding of genomic regions of interest for future research in the environmental impact on bovine behaviour.

S14 e-PIG-enetics: porcine sncRNA response to highly pathogenic PRRSV

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Porcine respiratory and reproductive syndrome virus (PRRSV) is a single stranded RNA virus that infects pigs and causes losses to the pork industry reaching upwards of a billion dollars in the USA annually. Recently the United States has begun to see an increase in type 2 PRRSV strains of higher virulence comparable to highly pathogenic PRRSV (HP-PRRSV) first described in China in 2006. The high pathogenicity of these strains drastically alters host immune responses indicating underlying changes in gene and regulatory element expression profiles. The actions of small non-coding regulatory RNAs (sncRNA), and how they influence host immunologic and metabolic functions, are relatively unexplored. In order to investigate the impact sncRNA expression has on host regulation during PRRSV infections, this study examined host differential expression of miRNA and tRNA molecules during infection with a highly pathogenic PRRSV (HP-PRRSV) strain. We accomplished this using transcriptomic analysis of whole blood taken from either control or infected pigs at several days post inoculation. The analysis returned a total of 149 statistically significant ***(FDR ⩽ 0.15)*** miRNAs and tRNAs that were evaluated for possible antiviral effects. The results indicated that HP-PRRSV infection effects host regulation at the epigenetic level through changes in miRNA and tRNA expression that target and influence the function of host immune, metabolic, and structural pathways.

S15 Environmental induced epigenetic transgenerational inheritance of health and disease: ancestral ghosts in your genome

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Transgenerational effects of environmental toxicants, nutrition or stress significantly amplify the biological impacts and health hazards of these exposures. One of the most sensitive periods to exposure is during fetal gonadal sex determination when the germ line is undergoing epigenetic programming and DNA re-methylation occurs. Previous studies have shown that toxicants can cause an increase in adult onset disease such as infertility, prostate, ovary and kidney disease, cancers and obesity. Interestingly, this effect is transgenerational (F1, F2, F3 and F4 generations) and hypothesized to be due to a permanent (imprinted) altered epimutation of the germ-line. The transgenerational epigenetic mechanism appears to involve the actions of an environmental compound at the time of sex determination to permanently alter the epigenetic (e.g. DNA methylation) programming of the germ line that then alters the transcriptomes of developing organs to induce disease susceptibility and development transgenerationally. In addition to DNA methylation, alterations in sperm ncRNAs and histone retention have also been observed. A variety of different environmental compounds have been shown to induce this epigenetic transgenerational inheritance of disease including: fungicide vinclozolin, plastics BPA and phthalates, pesticides, DDT, dioxin and hydrocarbons. Interestingly, exposure specific epigenetic alterations were observed between the specific toxicants. Similar observations have been observed in a variety of species including domestic animals. The suggestion that environmental factors can reprogram the germ line to induce epigenetic transgenerational inheritance of disease and phenotypic variation is a new paradigm in disease etiology that is also relevant to other areas of biology such as evolution.

S16 Advances in genome technology

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Technology continues to drive advances in genomics. In the late 1990s to early 2000s, it was becoming more clear that the livestock research community should begin to plan for the eventuality of having reference genome assemblies for the major livestock species, and to prepare for what to do with them upon arrival. As a result of this type of planning, the cattle research community, for example, was well positioned to create high-throughput genotyping platforms and products that have transformed genetics in the dairy industry and have made inroads to transforming beef cattle genetics, at least in some countries. This presentation will discuss recent technological advances that continue to push the boundaries of what is possible, and will propose that there is now a new need to plan for what these technologies can provide.

S17 Discovery and editing of adaptive traits in livestock

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Gene editing based on site-directed nucleases is recognized as a breeding method best suited to introduce high effect production and/or adaptive alleles into naïve populations of food animals. However, to date, very few naturally occurring adaptive traits with major effects on phenotype have been identified from food animal species. One of the few mutations identified is for thermal adaptation in *Bos taurus* cattle. Multiple mutations in *PRLR* have now been found using population genomic approaches on Criollo cattle. These truncated variants have been introduced into mice and non-adapted cattle using gene editing to prove the genotypes confers adaptation in a naïve genetic background of the same species. Additionally, our group has now applied the same population genetic approaches to identify parasite resistance and thermal tolerance or "shedding" alleles derived from a haired sheep breed developed in the Caribbean. Instead of validating these mutations by gene editing in sheep, we are introducing the variants in naive bovine cells to characterize effects on downstream gene expression. Finally, in a third case study of adaptive alleles for FMDV resistance; the FMD virus infection challenge results from swine fibroblasts with wild type or edited to contain naturally occurring, protease resistant eIF4G alleles will be discussed.

S18 An improved functional annotation of the domestic pig genome

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Our understanding of pig transcriptome structure and variation is limited. Pig mRNA isoform diversity in nine tissues was assessed using PacBio single-molecule long-read isoform sequencing (Iso-Seq) and Illumina short read sequencing (RNA-seq) from a single White cross-bred pig. The Iso-seq data was error-corrected using the Illumina data and included transcripts from brain, diaphragm, hypothalamus, liver, muscle, pituitary, ileum, spleen and thymus. These data were used for current NCBI and Ensembl annotations of the pig genome. In our analyses, 41,003 (60%) protein-coding, 24,712 (36%) long non-coding RNA and 2,031 (4%) non-sense mediated decay transcripts were found across all tissues. Ninety percent of splice junctions were supported by RNA-seq within tissue. Eighty percent of transcripts represented novel isoforms of known genes, and 17% identified novel genes. We found on average 3.6 transcripts per known gene (tpg); improving current Ensembl (1.9 tpg) and NCBI (2 tpg) annotations and more similar to human annotation (3.4 tpg). Our new pig genome annotation extends >6,000 known gene borders compared to previous annotations. We validated most of these extensions by independent pig 3'-RNAseq data or human CAGE data. Further, we detected 2,755 novel intergenic genes not reported in current annotations. Of these novel genes, >70% had transcripts detected in >1 tissue. More than 80% of novel intergenic genes with at least one liver transcript had H3K4me3 and H3K36me3 peaks mapping to their promoter and gene body, respectively, in an independent liver chromatin immunoprecipitation sequencing experiment. These validated results show significant improvement over the current pig genome annotations.

S19 Evolution of reproductive behaviour in the dog

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A number of high-profile research groups that have devoted their careers to the study of canine genetics and evolution have investigated the question of why dogs are so phenotypically diverse and so different than their wolf ancestors in form and temperament. To date, the answers have been elusive. It has simply been proposed that we selected this amazing species for different colours and forms and that for some inexplicable reason this selection was far more effective than it has been in any other species manipulated by humankind. Large quantities of data have been generated in the quest to better understand the process of domestication and now sufficient of these have been recently released in the public domain to use a different approach to solving the question. We propose a simple explanation for humankind's selective success with the canine. By an evolutionary change occurring some time during the history of domesticated dogs, suddenly these animals were able to double their rate of reproduction. This breeding rate change offered a means of doubling the rate of selective or evolutionary change in animals with the genetic alteration. This change was accomplished by a releasing of the species from the constraints of a photoperiod induced breeding season. The successful genetic manipulation of populations of animals with this change would have in turn encouraged the perpetuation the change within later generations. By the careful application of quantitative birth record data and whole genome mapping our team has identified a novel route of control of the seasonal breeding season that appears to be independent of the melatonin system. Melatonin affected by circadian control by clock genes has been long presumed as the controlling mechanism for seasonal reproduction. Our findings identify a putatively functional difference in a key gene in an independent environmental sensing system that might enable dogs in most modern domestic dog breeds to breed at any time of the year. The consequences of this knowledge are diverse. The new pathway may enable new approaches to reproductive control in canines but also in other species such as small ruminants. Doubling the reproductive rate in seasonal small ruminants might in turn promote important downstream impacts on global food security.

S20 Genetic regulation of cold-induced WAT browning in pigs

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White adipocytes can be induced into 'brown-like' heat-producing adipocytes (beige adipocytes) by cold exposure and this cellular process is called 'while adipose tissue (WAT) browning'. Activation of beige adipocytes is believed to hold potential for combating metabolic diseases in human, while decreasing fat deposition and improving the thermogenesis ability in pigs. Even though the existence of cold-induced WAT browning in pigs has been reported, the molecular signatures remains unknown. Here, we found that, compared to cold-sensitive pig breeds (Bama and Wuzhishan), browning occurred in inguinal subcutaneous WAT (iWAT) of two well-recognized cold tolerant breeds (Tibetan and Min) after acute cold treatment, as evidenced by the characteristic multi-locular lipid droplets of beige cells and the significantly induction of beige marker CD137. Genome-wide transcriptional analysis of cold stimulated iWAT from 1-month-old piglets of these four breeds were performed to investigate the nature of the beige adipocyte in pigs. We found that only 9 gene were differentially expressed genes (DEG) across four species based on the criteria of false discovery rate (FDR)<0.05 and fold changed>2. These genes were considered to be responsive to cold stimulation. In addition, 33 genes that we identified only differentially expressed in Min and Tibetan pigs, were thought to be involved in WAT browning. GO annotation were further performed and the effect of cellular lipid metabolic related genes, PDK4, UCP3 and PLIN4 etc, in beige formation will be further investigated. These results provide novel insight into the regulatory networks of cold-induced WAT browning in pigs.

S21 Cell identity in the era of single cell profiling

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Consortia efforts from GTEX, ENCODE and FAANG, FANTOM and the human cell atlas share a common goal – bridging the genotype-phenotype gap. Certainly, past activities from FANTOM and ENCODE demonstrate that cells and tissues can be grouped by shared molecular processes. Will RNA-sequencing individual cells provide new resolution on existing tissue maps, even revealing new cell types? Comparison of cell types assessed across different experiments, even when measured on the same platform, remains a major challenge for atlas projects. Here I describe methods of data transformation and variable selection to derive two new tissue maps – a comprehensive blood atlas, derived from thousands of donors; and a pluripotency atlas, which reveals at least two states of pluripotency. I further highlight challenges ahead in measuring cell-type specific molecular networks with current transcriptome methodologies, and foreshadow what is ahead in transcriptional profiling.

Poster Abstracts

P01 Transcriptome sequencing reveals key potential long non-coding RNAs related to duration of fertility trait in the uterovaginal junction of egg-laying hens

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Duration of fertility, (DF) is an important functional trait in poultry production and lncRNAs have emerged as important regulators of various process including fertility. In this study we applied a genome-guided strategy to reconstruct the uterovaginal junction (UVJ) transcriptome of 14 egg-laying birds with long- and short-DF (n=7); and sought to uncover key lncRNAs related to duration of fertility traits by RNA-sequencing technology. Examination of RNA-seq data revealed a total of 9,977 lncRNAs including 2,576 novel lncRNAs. Differential expression (DE) analysis of lncRNA identified 223 lncRNAs differentially expressed between the long- and short-DF groups, with 81 up-regulated and 142 down-regulated. DE-lncRNA target genes prediction uncovered over 200 lncRNA target genes and functional enrichment tests predict a potential function of DE-lncRNAs. Gene ontology classification and pathway analysis revealed 8 DE-lncRNAs, with the majority of their target genes enriched in biological functions such as cellular response to cytokine, response to protein homodimerization, reproductive structure development, developmental process involved in reproduction, regulation of protein modification, osteoblast differentiation and ossification, in utero embryonic development, response to cytokine, carbohydrate binding, chromatin organization, response to growth factors, and immune pathways. Differential expression of lncRNAs and target genes were confirmed by qPCR. The discovery of these 2,576 novel lncRNAs in this study significantly expands the utility of the UJV transcriptome and our analysis identification of key lncRNAs and their target genes regulating DF will form the baseline for understanding the molecular functions of lncRNAs regulating DF and extend the knowledge of the molecular mechanisms underlying fertility.

P02 Genetic factors related to mineral concentration in Nelore cattle unveiled by transcriptome analysis

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Mineral content has an impact on economic traits that can affect beef quality. Muscle mineral concentration depends on intake-outtake imbalance, breed, muscle type, age, environmental, and genetic factors. To unveil the genetic factors underlying muscle mineral concentration we applied a global differential gene expression analysis in sample groups of six Nelore steers extremes for nine different mineral concentrations (Ca, Cu, K, Mg, Na, P, S, Se, and Zn) from 130 Nelore steers with RNA-Seq and mineral concentration data available. Functional enrichment and protein-protein interaction analysis were carried out using DAVID and STRING softwares, respectively, among the differentially expressed genes (DEGs) to search for gene regulatory processes concerning all minerals. The metabolic pathways enriched for the DEGs, in at least five out of nine minerals, were ECM-receptor interaction, protein digestion and absorption, focal adhesion, and PI3K-Akt signaling pathway, being the first one enriched for all minerals, except Zn. These results and the relationship of the DEGs presented by our protein-protein interaction analysis pointed out that the genetic regulation core for all minerals studied, except Zn, seems to reside in events of extracellular matrix interactions. There were no common DEGs for all minerals, however, there were 27 common to, at least, five minerals of which we can point *COL11A1*, *COMP*, and *TNMD* as candidate genes. These genes were DE in all minerals, except Zn, and take part in three out of four cited metabolic pathways enriched for most minerals, except protein digestion and absorption.

P03 Tissue specific characterisation of the ovine methylome

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Over the past decade, the application of genomic technologies to animal breeding has significantly advanced the profitability and sustainability of agricultural breeding programs by facilitating selection of genetically superior animals. However, genomic information alone explains only part of the phenotypic variance in quantitative traits. A portion of this so called 'missing variance' is embedded within the epigenome, which remains relatively unexplored in agricultural species compared to humans and model organisms. As one of the most common and stable epigenetic marks, DNA methylation plays a fundamental role in the regulation of growth and development in mammals. While the importance of DNA methylation is well established, tissue specific signatures of methylation have not been extensively characterised at the genomic level. As part of the Ovine FAANG Project, this study will employ a combination of whole-genome bisulphite sequencing and reduced-representation bisulphite sequencing to investigate tissue specific methylation profiles of 100 tissue types sampled from a Rambouillet ewe. The methylation data will be combined with gene expression profiles and chromatin architecture analyses to enhance functional annotation of the sheep genome and obtain a comprehensive picture of the ovine epigenetic landscape. Genomic DNA from the ewe under study has previously been used for *de novo* assembly of the ovine genome, thus FAANG datasets can be directly annotated onto the reference genome. Data generated from this project will facilitate understanding of the link between genotype and phenotype and provide a foundation for the implementation of the methylome as a molecular phenotype for sheep breeding and improvement.

P04 Genetic control of temperament traits across species: autism spectrum disorder (ASD) genes in humans are associated with cattle flight time

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Temperament traits are relevant to both human and cattle well-being. In humans, these traits are genetically correlated with several psychiatric disorders. In cattle, temperament is of commercial importance because more docile animals are easier to handle, and have better performance. We hypothesised that genetic factors contributing to variation among individuals of each species will be shared across the two species. Using humans as a model organism for cattle, we investigated the association of human Autism genes with cattle temperament. We conducted a series of genome-wide association studies on cattle flight time, time to cover a short fixed distance after being released from an enclosure, in two cattle breeds and meta-analysed the results for a combined sample of 9223 animals and 28.3 million imputed SNPs. After locating SNPs within 100Kb of 63 bovine orthologous ASD genes, we tested for their effects in two ways: (1) compared observed versus expected distribution of Chi-squared test statistics, and (2) estimated the percentage of additive genetic variance explained by these SNPs. The resulting 180,000 SNPs showed a skewed QQ plot, signalling more associations than expected by chance, and explained 7% of the total additive genetic variance in the biggest cohort (randomized permutation test P value <0.02). ASD genes with the most significant associations were GABRB3, CUL3, and INTS6. These genes contribute to inhibition of neurotransmitters in the vertebrate brain, protein binding, and transmembrane signalling receptor activity. Our results provide statistical evidence that genetic control of temperament traits might be shared across these species.

P05 Leveraging across-experiment and -species transcriptomics to annotate the rumen functional pathways

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The reticulo-rumen lies between the oesophagus and the abomasum (equivalent to the stomach of monogastric animals) and transfers to the host short chain fatty acids as the primary energy resource. The rumen differentiates from other mammalian gastrointestinal tract tissues by its significantly stratified epithelial surface and by hosting a complex microbial population, making it the primary organ processing complex plant material. Some rumen microbes produce methane which represents a loss of energy in the conversion of plant material to nutrients that may be absorbed. Thus, improved knowledge of the molecular functioning of the rumen represents opportunities to further understand the ruminant evolutionary process and to improve energy utilisation of ruminants. We combined and analysed rumen wall transcriptome data from two independent experiments conducted with sheep in Australia (AUS, n=62) and New Zealand (NZ, n=24), together with published transcriptomic datasets from cattle, mice and humans. Using comparative genome analysis, we illustrate the probable evolutionary origin of the rumen which is more likely to be from the ancestral oesophagus, rather than the ancestral stomach. We identified a set of conserved transcription factor genes with shared regulatory roles between the rumen epithelium and skin. Using common genes identified from the different experiments, we identified rumen muscle genes, the increased expression of which are correlated with reduced retention time of feed in the rumen and reduced methane yield. Our analytical approaches and results show the power of species conservation and meta-analysis of different transcriptomic datasets in identifying causal gene candidates for complex traits.

P06 Genome-wide association and gene expression studies to decipher the genetics of residual feed intake in Angus cattle

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The aim of this study was to identify quantitative trait loci (QTL) associated with residual feed intake (RFI) and genes whose expression varied significantly with phenotypic differences in RFI. We used data from 2,190 Angus steers with phenotypic records for RFI, all with imputed high density array (770k) genotypes. We used RNA-seq in a multi-tissue experiment from 126 Angus steers divergently selected for RFI for approximately three generations, to analyze the expression of genes significantly associated (GSA) with RFI, with special attention to the genes close by significant QTLs. We estimated a heritability for RFI of 0.29. 77 SNPs associated for RFI were identified on six QTL regions (BTA1, BTA6, BTA14, BTA17, BTA20 and BTA26). Four percent of the genetic variance was explained by the most significant SNP (rs42662073) on chromosome BTA20. The closest genes to the identified QTL regions were OAS2, STC2, SHOX, XKR4, and SGMS1. Multiple GSA were identified within 2Mb window from the QTL: BTA20) NEURL1B and CPEB4; BTA17) RITA1, CCDC42B, OAS2, RPL6, and ERP29; BTA26) A1CF, SGMS1, PAPSS2, and PTEN; BTA1) MFSD1 and RARRES1; BTA14) ATP6V1H and MRPL15. Some of the top GSA were involved in interesting pathways like Cholesterol biosynthesis, Fatty acid metabolism, MAPK signaling pathway, Glycerophospholipid metabolism, Metabolism of xenobiotics by cytochrome P450 and PI3K-Akt signaling

pathway. We conclude that results from RNA-seq and GWAS can be highly complementary and result in a better understanding of the genetic mechanism that determines variation in RFI.

P07 Transferring immune-related miRNAs from dam to newborn calves

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Passive immunity transfer after birth plays an important role in cattle because bovine neonates only receive maternal immunity by receiving colostrum. In this study, we investigated whether immune-related microRNAs (miRNA), in addition to immunoglobulins are transferred from dam to newborn by colostrum intake. Holstein Friesian bull calves were divided into 3 groups (12 Group A calves fed their own dam's colostrum, 12 Group B calves fed colostrum from one of the group A dams, and 14 Group C calves fed pooled colostrum). Calf blood and colostrum from the Group A dams were collected within 2 hours of birth (before any feeding) and 24 h post-partum (after calves received colostrum). Total RNA in calf blood and colostrum was extracted, and the miRNAs levels (miR-142-5p, miR-150, and miR-223) quantified by using RT-qPCR (TaqMan miRNA assays) with *Caenorhabditis* elegans Cel-miR-39 as a control. The results showed that miR-142-5p, miR-150 and miR-223 were detectable in calf blood at 0 hours. At 24 hours, these miRNAs increased in the calf blood and there was significantly more miR-150 and miR-223. In the colostrum, the miR-223 concentration was found to be at a high level at 0 hours but doubled by 24 hours. miR142-5p and miR150 only found at low levels in the colostrum at 0 hours and were not detectable in colostrum at 24 hours. There was no significant difference between the 3 groups of calves so the source of colostrum was immaterial. The results suggest that calves have very low levels of these immune-related miRNAs at birth and some immune-related miRNAs are likely to transfer from dam to the calf via colostrum intake. However, only miR-223 was at sufficiently high concentrations to be likely to have biological effects in newborn calves.

P08 Cross-protection of killed and modified-live BRD vaccines in BVDV challenged cattle

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Bovine viral diarrhea virus (BVDV) is an immunosuppressive cattle infection that affects respiratory health and mucosal immune functions. Infection can be acute; however, many are sub-clinical and persistent in herds, leading to high economic impact to cattle producers. Complicating this is its ability to predispose cattle to bovine respiratory disease (BRD) complex. Many producers vaccinate for BRD to help protect herds from this predisposition, however there are gaps in the knowledge of whether there are differences in the ability of modified live (MLV) or killed (KV) vaccines to extend cross-protection to BVDV. This adds to the economic impact of BVDV because, with more information on vaccine efficacy, cattle producers could possibly reduce treatment costs and disease spread. The study objective was to determine evidence of BRD vaccine cross-protection by observing changes in host gene expression in response to a sub-clinical BVDV challenge in Nellore-Angus cattle. The study utilized 3 treatment groups (no vaccine, KV, MLV) (n = 5) for RNA-seq analysis of PMBCs from 14 dpi. In the MLV treated group there was overexpression of more adaptive immunity genes and genes involved in intestinal immunity, whereas the KV group displayed more innate immunity related expression. Although both vaccines provide some level of cross-protection, the results point to MLV producing cross-protection that extends the adaptive immune response to BVDV.

P09 Genomic scanning for allelic ratio distortion in porcine sperm

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During spermatogenesis, germline cells undergo intensive and complex cellular and functional, changes including cell proliferation, meiosis, spermatozoa morphology and maturation. Genetic mutations affecting spermatogenesis could result in allelic transmission ratio distortion in the offspring and a decrease of the reproductive ability of the males. We hypothesize that these mutations can be identified in the ejaculated haploid spermatozoa in heterozygous animals by high throughput sequencing and the assessment of allelic

ratio deviation from the expected Mendelian 0.5. We performed Whole Genome Sequencing of gDNA from blood and sperm from 3 boars. DNA libraries were sequenced in an Illumina's HiSeq X system. In average, 460M reads were obtained per sample. After read mapping to the porcine genome, and duplicate removal, samples presented a 40-50x sequencing depth. SNPs were called and filtered using stringent quality criteria. The allelic ratios of blood and the matched sperm samples were compared using the Fisher's exact test. The average number of high quality SNPs per sample when compared to the sscrofa11.1 reference genome was 2.9 M. A mean of 53,745 blood heterozygous SNPs per sample displayed allelic distortion. The three possible pairwise inter-sample comparisons displayed an average of 206 shared SNPs. One SNP with allelic distortion was shared in the three pigs. This SNP maps 260 k bp away from *GPAT3*, a gene involved in the synthesis of fatty acids required for spermatogenesis, acrosomal reaction and fertility.

P10 Initial host response to mycobacterial infection is orchestrated through H3K4 trimethylation at key immune genes

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Epigenetic modifications, such as methylation of histones at key lysine residues, are pivotal in orchestrating various biological processes, representing an important mechanism for determining cellular response to external stimuli. The cause of bovine tuberculosis is *Mycobacterium bovis*, which has a well-documented and significant effect on the transcriptome of bovine alveolar macrophages (bAMs). However, how intracellular mycobacterial pathogens affect the macrophage epigenome is currently not well understood. For the present study, chromatin immunoprecipitation sequencing (ChIP-seq), RNA-seq and miRNA-seq were used to examine the effect of *M. bovis* infection on bAMs @ 24hpi. Three different classes of ChIP-seq data were generated: H3K4me3, normally associated with a permissive chromatin state leading to elevated proximal gene expression; H3K27me3, generally associated with a repressive chromatin state leading to reduced proximal gene expression; and PolII, which delineates RNA polymerase II activity across individual genes. The ChIP-seq results were integrated with RNA-seq and miRNA-seq results from the present study and a larger RNA-seq data set from a published study by our group. These ChIP-seq results showed that H3K4me3 is more prevalent, at a genome-wide level, in chromatin from *M. bovis*-infected bAM compared to non-infected bAM; this was particularly evident at the transcriptional start sites of genes that determine programmed macrophage responses to mycobacterial infection (e.g. M1/M2 macrophage polarisation). This pattern was also supported by the PolII, RNA-seq and miRNA-seq results. These results support the hypothesis that host chromatin is modified at specific sites following *M. bovis* infection.

P11 Genetic architecture of gene expression in cattle

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Mutations in regulatory regions of the genome can cause variation in gene expression levels among individuals. An interesting question is how many mutations affect the expression of the average gene, and what is the distribution of both the number and size of effect of these mutations? To investigate this question, we performed an expression QTL (eQTL) experiment using RNA sequence data from milk and white blood cells collected from 141 lactating cows with imputed whole genome sequence data. For each gene, an association study of gene expression level was performed with all sequence variants +/- 1MB from the gene start stop sites. Then to estimate the number of independent eQTL affecting the expression of each gene, step wise regression was used to successively remove the effect of the largest eQTL. We found on average 1.9 significant and independent eQTL per gene. The actual number of eQTL affecting expression of a gene is likely to be larger, as we only have power to detect the large effects. The results imply that expression levels of most genes are under the control of multiple regulatory mutations.

P12 Using low-depth genotyping-by-sequencing data as a cost-effective alternative to SNP chips for GWAS

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Genotyping-by-sequencing (GBS) is a sequencing method that uses restriction enzymes to obtain genomic information at a proportion (1-10%) of the genome. Low depth (2-4x) sequencing further reduces costs; however, this generates a level of uncertainty in the SNP genotype scores obtained, primarily when distinguishing between homozygous and heterozygous genotypes at loci where only one allele is observed for an individual. Therefore, methods for genome-wide association studies (GWAS) that account for uncertainty in GBS genotype calling are desirable when searching for loci associated with a trait. We used probability-based genotypes to account for uncertainty in genotyping due to low-depth sequencing to perform GWAS on milk traits in dairy goats and identified strong candidate associated with these traits, thus demonstrating the utility of this method. Once a gene of interest is identified and the causal mutation has been found, it may be of interest to genotype this causal mutation en masse on a large number of individuals while capturing variants in the rest of the genome. Previous studies in French dairy goats have identified a causative mutation in the *DGAT1* gene associated with milk fat percent in dairy goats. Our GWAS identified a peak near this gene. We developed primers to test the effects of this mutation on milk fat percent in our population – an approach that could be incorporated into our GBS workflow. We successfully obtained genotypes at this locus, which subsequently allowed us to confirm association of this causative mutation with milk fat percent in New Zealand dairy goats.

P13 Restriction enzyme reduced representation sequencing for high-throughput metagenome profiling

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The rumen microbiome is associated with traits such as methane production and feed efficiency through its role in feed digestion. Rumen Microbial Profiles (RMPs) capture information about the microbes in a rumen sample, typically using metagenome sequencing, which is expensive and time-consuming, or small-subunit rRNA gene sequencing (e.g., 16S) which only captures phylogenetic variation at one gene. Restriction Enzyme Reduced Representation Sequencing (RE-RRS) with ApeKI or PstI was used to develop a low-cost, high-throughput metagenome sequencing pipeline to generate RMPs in two ways: (1) reference-based (RB), in which sequences were compared against genomes in the Hungate 1000 Collection, then assigned a genus level affiliation; and (2) reference-free (RF), in which the abundance of common 65-bp reads (tags; present in at least 25% of samples) was obtained. Our method was tested on rumen samples from 118 high- or low-methane-yield sheep, collected at two time points. Affiliations were assigned for 2-26% of sequences using the RB approach, while 4-16% and 33-61% of sequences matched to common RF tags using ApeKI and PstI, respectively. The first component of a correspondence analysis of the RMP was used to compare performance of 16S rRNA sequencing (16S) and RE-RRS. Repeatabilities were 0.62±0.06 for all RE-RRS approaches except for the RF-ApeKI approach (0.44±0.07), which was similar to 16S (0.45±0.08). Genetic correlation with methane was greatest for RF-PstI (0.83±0.31), followed by 16S (0.65±0.47). RE-RRS can be used for high-throughput metagenome profiling and our approach will be used to sequence thousands of rumen samples over the next year.

P14 Serum miRNA profiling in pregnant and non-pregnant beef heifers

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MicroRNAs (miRNAs) are fine tuners of gene expression and regulate target genes at the post-transcriptional level. Their role in development, including pregnancy, has been widely recognized since their discovery. Pregnancy specific miRNAs in placenta, uterine tissue, and maternal circulation have been elucidated in humans and the molecular mechanisms by which miRNAs regulate pregnancy are being investigated. The

placenta expresses numerous miRNAs with some being released in the maternal circulation. Conventional pregnancy diagnostics are not always accurate to determine early stages of pregnancy in cattle. To avoid feeding non-productive cattle, accurate detection of pregnancy is essential. Serum miRNAs may serve as precise biomarkers of pregnancy. The objective of this study was to identify differentially expressed serum miRNAs at 30 and 60 days of pregnancy compared to non-pregnancy in beef heifers. Out of 84 bovine-specific, prioritized miRNAs analyzed, seven were upregulated and five were downregulated in 30 and 60 days of pregnancy compared to non-pregnancy ($p \leq 0.05$, Fold Regulation ≥ 2.0 magnitudes). One miRNA was downregulated in 30-day pregnancy and upregulated in 60-day pregnancy. Interestingly, ten miRNAs were only found in pregnant heifers proposing their pregnancy-specific roles whereas two miRNAs were only detected in non-pregnant serum, suggesting their irrelevancy of pregnancy. Pregnancy and stage specific expressions of miRNAs exist. Degree of expression of one miRNA differs at various stages. MiRNAs differently regulate the gene at various stages of pregnancy. The identification of pregnancy and stage specific miRNAs and their respective characterization will facilitate to use them as accurate biomarkers for pregnancy.

P15 Effects on ChIP-seq analysis from unequal sequencing depth between IP and control libraries

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While the standard practice for ChIP-seq is to sequence both the IP and input libraries to equal depth, due to variability in sequencing, alignment rate, and other filtering, the final depth obtained for analysis often varies between the two libraries. This study explored the effects on downstream analyses arising from differences in sequencing depth between the IP and input to determine the best practices to minimize these effects. ChIP-seq data from the UC Davis FAANG pilot project, targeting the CTCF transcription factor in the liver of an adult male chicken, were downsampled to produce 10 different sequencing depths at 1 million read intervals between 6 and 15 million reads. Using the Macs2 peak caller, the number of peaks called was significantly impacted when the depth of the IP library was scaled, whether up or down, to match the size of the input library. However, when the input was scaled to the depth of the IP, a significant effect was not observed. By estimating true positive rate using the percentage of called peaks containing the CTCF binding motif, scaling of the input library did not impact the accuracy of peak calling. Therefore, we recommend setting the Macs2 parameter to scale the input depth down when larger than the IP, and up in the opposite case. Similar experiments with the ChromHMM software showed that no downsampling of either library is required. Lastly, the Jensen-Shannon divergence metric showed sensitivity to unequal depths, so downsampling of the larger library is recommended for the calculation.

P16 Multi-Tissue omics analyses towards profiling tissue-specific transcriptomes and epigenomes in Atlantic salmon

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The reference genome assembly for Atlantic salmon, *Salmo salar*, has been available for a number of years however the annotation describing elements that regulate gene expression are almost completely lacking. These elements include proximal and distal promotors, enhancer sequences and regions involved in silencing and repressing expression. To begin generating datatypes suitable for fine scale functional annotation, we performed survey sequencing targeting different tissues (brain, pituitary gland, ovary and liver) at different layers (transcriptome, methylome and open chromatin). RNA-Seq, whole genome bisulphite sequencing (WGBS) and Assay for Transposase-Accessible Chromatin sequencing (ATAC-Seq) data are being generated from these salmon tissues to provide a baseline data independent of experimental manipulation, making it applicable to general studies seeking to understand normal state of gene expression and regulation in a tissue-specific manner. Messenger RNA (mRNA) was isolated before Illumina sequencing produced a total of 640 million 150-bp paired-end reads. Following read mapping, feature counting and normalization, clustering analysis identified genes highly expressed in a tissue-specific manner. WGBS and ATAC-Seq data will be generated and analysed to study tissue-specific epigenetic regulation.

P17 A poll lot of bull: sequencing *Bos indicus* bulls using long reads to solve the poll locus.

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Brahman cattle (*Bos indicus)* are adapted to thrive in tropical environments. Since their introduction to Queensland in 1933, Brahman's ability to grow and reproduce on marginal lands has proven their value in the tropical beef industry. As a result, Australia's northern beef industry has transitioned from *Bos taurus* breeds to almost exclusively Brahman or derivatives thereof such as Droughtmaster. The desirable poll phenotype in cattle has been mapped to chromosome 1, however the causative mutation, reportedly a copy number variant (CNV), is not fully characterized across the Australian Brahman population. Recent third generation single molecule sequencers, such as Oxford Nanopore Technology (ONT) are allegedly capable of read lengths approaching 1Mb. These long read technologies are able to identify CNVs and other structural repeats that have eluded short read sequencing projects. Droughtmaster and Brahman samples will be sequenced using ONT to produce long reads. CNVs will be identified from the data and associations with the poll phenotype will be examined. Ultimately, successful characterization of the poll alleles segregating in the population will provide a mechanism for early and direct selection of the poll gene in the Australian northern beef industry.

P18 Understanding behaviour of machine learning methods when selecting subsets of SNPs for genomic prediction

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Machine learning methods have been shown to be superior for predicting phenotypic values over conventional statistical methods when epistatic effects of SNPs play a key role in controlling complex traits. Our previous study showed that the non-additive dominance effects captured by machine learning methods contribute little benefit to the prediction accuracy of total genetic values. However, using subsets of single nucleotide polymorphisms (SNPs) selected by machine learning methods (e.g. Random Forests, RF) in general performed better in genomic prediction of breeding values than a whole panel of SNPs. These results are not well understood. In this study, using two datasets, one from 2,109 Brahman cattle with 651,253 SNP genotypes and yearling weight (YWT), and a simulated dataset of 3,226 individuals with two phenotypic traits and 10,058 SNPs, we investigated the underlying reasons why the subsets of SNPs (500, 1000, 3000 and 5000) selected from the RF give better genomic prediction accuracy than selecting SNPs evenly distributed along a genome or a whole SNP panel. These included distance to genes, variances in genomic relationship matrices and other factors.

P19 Comparison of the Cattle X and Y chromosomes

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Mammalian X and Y chromosomes are subject to evolutionary pressure distinct from the remainder of the genome, but their sequence similarity makes assembly them difficult. We have generated cattle X and Y chromosome assemblies from an F_1 cross between an Angus (*Bos taurus taurus*) sire and Brahman (*Bos taurus indicus*) dam, using Pac-Bio long read sequencing and incorporating information from Hi-C and optical mapping. The sequence diversity of these subspecies enabled us to unambiguously assign reads to one parental genome or the other, allowing the assembly of high-quality sex chromosomes. The Brahman chrX is ~147 Mb, containing 983 genes unique to it and 31 genes shared with the Angus chrY. The Angus Y is ~16 Mb, containing 51 genes, including 3 clusters of low-copy genes unique to it, separated by multi-copy gene regions.

The cattle PAR spans ~6.87Mb at the proximal end of both chromosomes, with the same genes in the same order. Comparing gene content and order of the cattle PAR with other mammalian sex chromosomes reveals a high level of conservation, especially within ruminants. These are the most complete cattle PAR and X-Y homologous regions reported to date and hopefully will help elucidate cattle X and Y chromosome evolution.

P20 Chromosome-level assembly of the water buffalo genome

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Rapid innovation in sequencing technologies and improvement in assembly algorithms have enabled the creation of highly contiguous mammalian genomes. Here we report a state of the art *de novo* water buffalo (*Bubalus bubalis*) genome assembly. PacBio Sequel produced mean subread length of 11.5 kb, which was more than twice longer than the mean subreads used in the latest goat genome assembly. Contig assembly with long PacBio reads generated highly contiguous sequence with contig N50 of 18.7 Mb. Proximity-ligation scaffolding using Chicago and Hi-C reads clustered scaffolds into chromosome-level assembly. All five sub-metacentric chromosomes of the water buffalo were correctly scaffolded to span centromeres. Despite using a highly inbred animal, 58% of its genome could be phased with a haplotig N50 of 0.394 Mbp. The final assembly represents ~1023-fold improvement in contig N50 over the previous short-reads based assembly (UMD_CASPUR_WB_2.0). The assembly has surpassed both the human and goat genomes in sequence contiguity.

P21 Dual RNA-Seq of host and parasite in amoebic gill disease-affected Atlantic salmon

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Amoebic gill disease (AGD) poses the most important health issue to Tasmanian Atlantic salmon (*Salmo salar*) farming with significant economic and production implications. It is caused by a free -living amphizoic amoeba, *Neoparamoeba perurans*, affecting gills of salmon in marine-cultured environments. Previous transcriptomic (microarray-based) analyses identified few genes differentially expressed in AGD-affected salmon. These early studies focused exclusively on host response. This prompted our approach using dual RNA-Seq, to exploit both the salmon and *N. perurans* genomic resources to simultaneously profile both host and pathogen gene expression changes during AGD progression. Fish were experimentally infected with *N. perurans* (100 cells/L) and sampled at 21 days post inoculation for multiple disease relevant tissues (gill lamellae, head kidney and spleen), thereby comparing animals with high gill score (mean gill score of 3.25 out of 5) to naïve individuals. 28 RNA-Seq libraries were sequenced using the Illumina NovaSeq platform. Using infected gill samples, sequence reads were separated *in silico* to look at both the localised host (gill) response and the amoeba response. To investigate host systemic responses to AGD, head kidney and spleen tissue samples were compared to naïve fish. We will present preliminary analyses from this dual RNA-Seq design, with a view to biomarker discovery and the elucidation of the underlying mechanisms of AGD pathogenicity. We will also present early findings relating to potential virulence factors in amoeba that can be used in the future to manage this disease.

P22 Prediction of service sire fertility in US Holsteins using functional genomics data

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Fertility is among the most important economic traits in dairy cattle. Genomic prediction for cow fertility received much attention in the last decade, while bull fertility has been largely overlooked. The goal of this study was to assess genomic prediction of service sire fertility in US Holsteins using functional genomics data. Sire Conception Rate (SCR) was used as a measure of sire fertility. Dataset consisted of 11.5k Holstein bulls with SCR records and about 300k single nucleotide polymorphisms (SNP). The analyses included the use of linear kernel-based models fitting either all SNPs or only markers with presumed functional roles, such as non-synonymous, synonymous, or non-coding regulatory variants. Predictive ability was evaluated in 5-fold cross-validation with 10 replicates. The entire set of SNP yielded predictive correlations of 0.340. Interestingly, the inclusion in the prediction models of five major non-additive variants as fixed effects increased predictive correlations to 0.403. Models fitting functional SNP classes outperformed their counterparts using random sets of SNP. Notably, multi-kernel models fitting all functional SNP classes together with the five non-additive markers exhibited predictive correlations around 0.410, representing an increase in accuracy of 20% compared with the standard whole-genome approach. Overall, our findings suggest that incorporating functional information into prediction models can improve predictive ability. Our research is the foundation for the development of novel genomic strategies which can help the dairy industry make accurate genome-guided selection decisions, such as early culling of predicted subfertile bull calves.

P23 Evolutionary changes in gene expression and functional enrichment between *Bos taurus* and *Bos indicus* cattle

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The majority of world cattle population can be divided as taurine (*Bos taurus*) or zebouine (*Bos indicus*) with distinct climate adaption capacity, in which taurine cattle more adapted to temperate climates while, zebouine cattle more adapted to tropical environments. However, the functional genomic basis of climatic adaptation in beef cattle is not well understood. Here we provide a comparative analysis of gene expression across four tissues, namely, liver, hypothalamus, adipose, and muscle between Hereford breeds (*Bos taurus*), Brahman (*Bos indicus*) and a composite breed Brangus (3/8 Brahman; *Bos indicus* x 5/8 Angus; *Bos Taurus*). Preliminary results show that gene expression clearly clusters samples by tissue of origin followed by genome composition. That is within tissue, *Bos taurus* and Brangus present fewer gene expression differences in accordance to Brangus being mostly (5/8) of *Bos taurus* origin. In contrast, major differences in gene expression were identified between *Bos indicus* and *Bos taurus* as well as Brangus (*Bos indicus* x *Bos taurus*). Liver tissue presents the highest number of differentially expressed genes (DEG), 2.021 genes between *Bos taurus* and *Bos indicus*, of which 1.588 (79%) were also DEG expressed in Brangus. Functional enrichment shows that most DEG were involved in cholesterol and lipid biosynthesis including APOE, LSS, FADS2, and SBF1. We are currently characterizing differential expression patterns across tissues, predicting regulatory interactions, and generating open-chromatin profile (ATAC-seq) to better understand cross-species regulatory activity.

P24 Transcriptomic response of *Bos taurus* to two genotypically distinct *Staphylococcus aureus* strains

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S. aureus is the most frequent cause of bovine mastitis in Ireland. Four bovine-adapted lineages (CC71, CC97, CC151 and ST136) were identified among Irish *S. aureus* mastitis isolates. Strains from the 4 lineages were characterised *in vitro* and it was demonstrated that infection with CC97 strains caused high immune response in bovine mammary epithelial cells and stimulated neutrophil chemotaxis, while CC151 strains caused low immune response with no neutrophil chemotaxis. Two strains were subsequently selected for an *in vivo* trial. Fourteen disease-free first-lactation heifers were infected, 7 with strain MOK023 (CC97), and 7 with MOK124 (CC151). Differences in disease presentation *in vivo* were observed, with two animals infected with MOK124 developing severe clinical mastitis, while two animals infected with MOK023 did not develop an infection. Significantly higher somatic cell count, bacterial load and cytokine levels in milk were observed in response to MOK124. Transcriptomics data was generated using milk somatic cell samples from cows infected with each strain of *S. aureus* at 0, 24, 28, 72 and 168 hours post infection (hpi). These data were then analysed for differentially expressed genes using DESeq2 and for overrepresented GO and KEGG pathways to identify gene groups associated with a strain-specific disease response. The analysis identified unique transcriptomic profiles associated with each strain. Genes involved in immune response were found in both groups, with more immune response pathways identified in response to MOK124 at 24 hpi, while more immune pathways were upregulated in response to MOK023 at 48, 72 and 168 hpi.

P25 The role of long non-coding RNA for the gene expression in metabolic processes in cattle

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In modern livestock production systems resource efficiency and nutrient transformation play a crucial role for optimal animal husbandry and economic success. Animals expressing divergent metabolic phenotypes under identical environmental conditions have conjectured genetic differences, many of which may be found outside protein coding regions. While lacking protein coding potential, long non-coding RNAs (lncRNA) have been recognized as central regulatory elements within the mammalian genome that influence mRNA processing and expression. The goal of this study is to identify and characterize the role of long lncRNA for the gene regulation in metabolic processes, particularly with respect to nutrient transformation and feed efficiency in cattle. In a holistic approach genotypic, transcriptomic, phenotypic and metabolic data will be analyzed for animals of both sexes of a F2- population derived from a cross of meat and milk breeds (Charolais x Holstein). Tissue samples of liver, skeletal muscle, jejunum and rumen were collected for transcriptomic analysis 30 days postpartum in the second parity for females and at 18 months of age for males. A ribosomal depletion protocol was used for library preparation for RNA-sequencing to account for non-polyadenylated RNAs. A cluster analysis of metabolic profiles split the animals into four distinct groups based on gender and metabolic type. A transcriptomic read count based principal component analysis confirmed a distinct effect of sex and a subdivision into high and low metabolic efficiency.

P26 Identification of functional elements in dairy cows

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Efficient genomic selection in dairy cattle requires better annotation of the bovine genome. Functional regions which are hypothesised to underlie complex traits of interest in bovine have not been characterised. The FAANG consortium aims to identify functional elements in livestock genomes. This study aims to annotate regions in the bovine genome relevant to milk production in dairy cattle. Mammary gland and liver from 3 Holstein cows were assayed for 4 histone modifications, H3K4Me1, H3K4Me3, H3K27ac and H3K27Me3 using chromatin immunoprecipitation followed by sequencing (ChIP-seq). These marks are known to be found at functional elements such as enhancers and promoters. For each modification 100 million paired end reads were produced. Raw sequence reads for both the ChIP-seq and input libraries were trimmed of adapter and poor quality bases, then aligned to the genome with BWA mem and peaks called with MACS2. The quality of the enrichment was checked with deepTools and SPP. An average of 600,000 peaks was found for each histone modification. Most of these modifications (>80%) were found more than 1kb from any known transcription start sites. Comparisons between the locations of these modifications showed some differences between animals and tissues. The histone modifications identified can be used to identify putative functional elements in the bovine genome in tissues important for the dairy industry. This will help to understand the genetics underlying complex traits and improve genomic selection.

P27 *In silico* identification of putative *cis*-eQTLs affecting allelic expression

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Expression quantitative trait locus (eQTLs) are genomic regions that affect gene expression. eQTLs acting in cis can result from polymorphisms at regulatory motifs in the DNA that affect the binding of transcription factors (TFs) and result in variation at the gene expression. Genetic variation in these elements may also result in different expression between the two copies of the gene. This phenomenon known as allele-specific expression (ASE) is very common in the mammalian genome and has been associated with phenotypic variations. To identify putative *cis*-eQTLs that may be implicated in ASE in the Nelore muscle, we used data from two independent studies that identified ASE and *cis*-eQTLs in 200 animals. After data integration from both studies, we identified 68 *cis*-eQTLs that were associated to total expression variation of eight ASE genes. Using the LASAGNA software, we searched for TFs having those *cis*-eQTLs as targets and different affinities between the reference and alternative alleles. *ABHD17A* presented the highest number of *cis*-eQTLs, for which alleles were targets for different TFs (N=21), followed by *PLA2G7*, with 18, and *CAPN7*, with five *cis*-eQTLs. *TSPYL4*, *IFNGR2* and *RFC* affected by less than five *cis*-eQTLs each and, *RYR1* and *PAIP2B* affected by one cis-eQTL each that were not targets of any TF. Here, we present *cis*-eQTLs as potential causal elements of ASE at eight out of the 357 genes showing ASE in Nelore muscle, demonstrating the usefulness of integrating *cis*-eQTLs and allelic expression data to search for regulatory variations.

P28 Comparison of two different shearing methods to produce ovine liver ChIP-Seq libraries

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Chromatin immunoprecipitation used with massively parallel DNA sequencing, known as ChIP-Seq, allows the identification of DNA binding sites of proteins that interact with DNA. This is a useful method to further understand gene expression regulation. To generate the ChIP samples, the MAGnify ChIP System kit from Thermo Fisher was used. Prior to immunoprecipitation the DNA needs to be fragmented. Two of the instruments the kit recommends for fragmenting the samples are the Bioruptor UCD-200 and the Covaris S2. To determine which instrument to use for future experiments, both instruments were tested using ovine liver tissue samples with the histone modification H3K4me3. All other steps were kept identical. Two libraries were prepared for each sonication method, an IP sample and an input. Both data sets had similar scores for normalised strand cross-correlation coefficient (NSC) and relative strand cross-correlation coefficient (RSC). And both had values greater than the recommended values for these two metrics (NSC <1.05 and RSC <0.8), indicating the data sets are of good quality. The Jensen-Shannon distance was also similar for both data sets with the value of 0.4. These values indicate both shearing methods can produce good quality ChIP-Seq libraries.

P29 Genome-enabled prediction of bull fertility in US Jersey dairy cattle

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Service sire has a major impact on reproductive success in dairy cattle. Recent studies have reported accurate predictions for Holstein bull fertility using genomic data. The objective of this study was to assess the feasibility of genomic prediction of sire conception rate (SCR) in US Jersey cattle using alternative models. Dataset consisted of 1.5k Jersey bulls with SCR records and 95k single nucleotide polymorphisms (SNP). The analyses included linear and Gaussian kernel-based models fitting either all SNP or only relevant markers, such as SNP located within or close to genes or SNP significantly associated with SCR. Predictive performance was evaluated using 5-fold cross-validation. The entire SNP set exhibited predictive correlations around 0.30. Interestingly, either SNP associated with SCR or genic SNP achieved higher predictive abilities than their counterparts using random sets of SNP. Gaussian kernel models fitting significant SNP achieved the best performance with increases in accuracy up to 7% compared with the standard whole-genome approach. Notably, the use of a multi-breed reference population including US Holstein SCR records (11.5k bulls) allowed to achieve correlations up to 0.315, gaining 8% in accuracy compared with a pure Jersey reference set. These results indicate that genomic prediction of Jersey bull fertility is feasible. The use of Gaussian kernels fitting markers with relevant roles and the inclusion of Holstein records in the training set seems to be promising alternatives to the standard approach. Our findings have the potential to help the dairy industry to improve Jersey sire fertility through accurate genome-guided decisions.

P30 The Brahman genome: a platinum quality genome for tropical beef production

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Bos indicus cattle, the result of an independent domestication in the Indus Valley, are adapted to harsh tropical environments and are widely used in beef and dairy production in Northern Australia, the southern USA, Africa, Asia and South America. Brahman are a *B. indicus* breed developed in the southern USA through cross-breeding four *B. indicus* breeds: Ongole, Guzerat, Gir and Krishna. A reference sequence for Australian Brahman cattle has been assembled using 195Gb of Pacbio Sequel long read data, with Chicago and Hi-C long range mapping. Gaps were closed with multiple rounds of PBJelly and error correction performed with Arrow. The resulting genome has all autosomes and the X chromosome at full length, with only 403 unfilled gaps in the entire assembly. Long read Pacbio sequence data has allowed the examination of genome elements for which short read data is inadequate. In addition to annotations acquired from UMD3.1, the Brahman genome

includes annotations of transposable elements, simple sequence repeats and copy number variants, which range from 100bp to >2500bp in length. Comparisons between the Brahman and Taurine genomes provide insight into tropical adaptation, an important trait as our environment becomes more variable. We present a comparison of the Brahman and Taurine genomes, at a level that was unattainable just a few years ago, before long read sequencing became widely available.

P31 Expression of miRNA in semitendinosus muscle of cattle breeds with varying intramuscular fat deposition

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The purpose of this study was to identify marbling-related miRNA varying in expression in semitendinosus muscle of bulls of three cattle breeds with different intramuscular fat (IMF) deposition - Hereford (HER), Holstein-Friesian (HF) and Limousine (LIM). The transcriptional analysis allowed identification of 17 miRNAs differing in the expression between well-marbled muscle tissue (HER and HF) in relation to low IMF muscle (LIM). Among them, 13 miRNAs were characterized by lower and 4 higher expression in HER and HF. Ontological analysis of identified molecules allowed them to be assigned to the following biological processes: adipogenesis, adipocyte differentiation, lipid metabolism, lipid homeostasis, lipid oxidation, lipid accumulation, cell growth, cell proliferation and cell differentiation. Two of identified microRNAs (miR-34a, miR-224) are key molecules engaged in the regulation of the processes associated with adipose tissue development and lipid metabolism. Target gene prediction for all identified miRNAs revealed 753 genes of which 7 genes (*esr1, gadd45a, pou5f1, prdm1, mstn, trim32, vcl*) related to adipogenesis process, lipid metabolism, cell growth, and cell proliferation and differentiation we previously identified as differentially expressed in well-marbled semitendinosus muscle of HER and HF when compared to lean muscle of LIM. Identified miRNAs with their target genes are plausible regulators of IMF deposition in examined cattle breeds.

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P32 Integrated -omics analysis of liver in the post-hatch broiler chick

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While many -omics options exist for exploring the regulation of complex biological processes, each of these pre-existing methods has limitations when used alone. However, when different types of omics approaches are integrated, these methods can be used to validate each other and to establish details that may otherwise remain obscured. Here, we use RNAseq in conjunction with kinome array analysis and metabolomics to elucidate the critical genes, proteins, and pathways characterizing two post-hatch developmental milestones in the modern broiler chicken. The modern broiler bird has undergone decades of selective breeding for rapid muscle growth, metabolically equipping it with the ability to reach market weight in only six weeks. The cellular regulation underlying these changes is poorly understood. In this study, we focus on the liver as the crucial hub for lipid and carbohydrate metabolism, while developing hypotheses about its role in both the maintenance of homeostasis and the management of energy resources.

P33 Mammalian topological association domains and CTCF binding motifs regulate gene expression in the bovine genome

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Topological association domains (TADs) and CTCF binding sequences form conserved regulatory units controlling gene expression. Although well annotated in humans and mice, in the bovine genome these regulatory units are not yet well defined. To assist the functional annotation of bovine regulatory genome, this study used genomic synteny to map TADs and CTCF binding motifs from humans, mice, dogs and macaques to the bovine genome. We found mapped TADs exhibited the same hallmark properties of those sourced from experimental data, such as housekeeping gene, tRNA genes, CTCF binding motifs, SINEs, H3K4me3 and H3K27ac. Furthermore, we found runs of genes that favoured expression from the same parental chromosome were often located in the same putative bovine TAD or between the same conserved CTCF binding motifs. Additionally, we found QTLs associated with gene expression variation (eQTL) or allele-specific expression variation (aseQTL), which were identified from mRNA transcripts from 141 lactating cows' white blood and milk cells, were located within the same TAD as their target gene more often than expected (Chi-Squared test P-value < 0.001), and were highly enriched at our bovine CTCF binding motifs. We conclude that genomic synteny can be used to functionally annotate conserved regulatory units across mammalian species, and provides a tool to accelerate the study of the influence of non-coding variants on gene transcription in the bovine genome. Our study complements bovine experimental validation that the Functional Annotation of Animal Genomes (FAANG) consortium will produce.

P34 The identification of functional elements in the genomes of Australia dairy cows using ChIP-seq

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Chromatin Immunoprecipitation sequencing (ChIP-Seq) is a powerful method which combines chromatin immunoprecipitation using an antibody specific for DNA binding proteins and high-throughput sequencing. This technique enables the genome-wide identification of binding sites of transcription factors (TFs) and other DNA-binding proteins. These sites can be markers of particular functional elements such as promoters, enhancers and/or transcription factor binding sites. The Functional Annotation of Animal Genomes (FAANG) consortium aims to identify all functional elements in livestock genomes for the benefit of the entire community. As a contribution to FANNG, we have used ChIP-Seq to investigate binding sites of histone modifications and transcription factors in the genomes of Australia dairy cows. ChIP-seq has been completed on four tissues (Spleen, Heart, Kidney and lung) from three Holstein cows for three histone modifications (H3K4me1, H3K4me3 and H3K27ac) and one transcription factor, CTCF. Results indicate high enrichment and higher quality peak calls.

P35 Integrative analysis of the transcriptome in the intestine of infant born to term and breastfed

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Nowadays, The integration of biological data is a major challenge for bioinformatics. Many studies have examined gene expression in the epithelial tissue in the intestines of infants born to terms and breastfed, generating a large amount of data. This work aims to integrate expression data available in the literature as well as in the database, in order to understand and to provide a new representation and interpretation of the biological process involved during bacterial colonization of the intestine of infant born to term and breastfed. A total of 61 genes differentially expressed in the intestines of newborns extracted from several bibliographic works and databases, were annotated for functional analysis using the STRING software (http://string-db.org/), the Cystoscape software (http://www.cytoscape.org/) and the BiNGO plugin. The latter provided an evaluation of the signalling and metabolic pathways, molecular networks and biological processes for all the genes used. The analysis revealed that ***RELA, INS, IRS1, TCEB1, IL1B, NFKBIA*** are the central genes in the interaction networks produced. These networks show that the cellular differentiation of the intestinal epithelium and the development of mucosal immunity, are the most affected processes in the development of intestines in children. These results provide insights into global patterns of interaction and collaboration of gene expression in the epithelial cells of neonates. These results consolidate the different studies carried out showing the benefits of breast milk on the biodiversity of the intestinal microbiota of the newborn and consequently on the good functioning of its immune system.

P36 Partitioning variances of genome functional categories across multiple bovine complex traits

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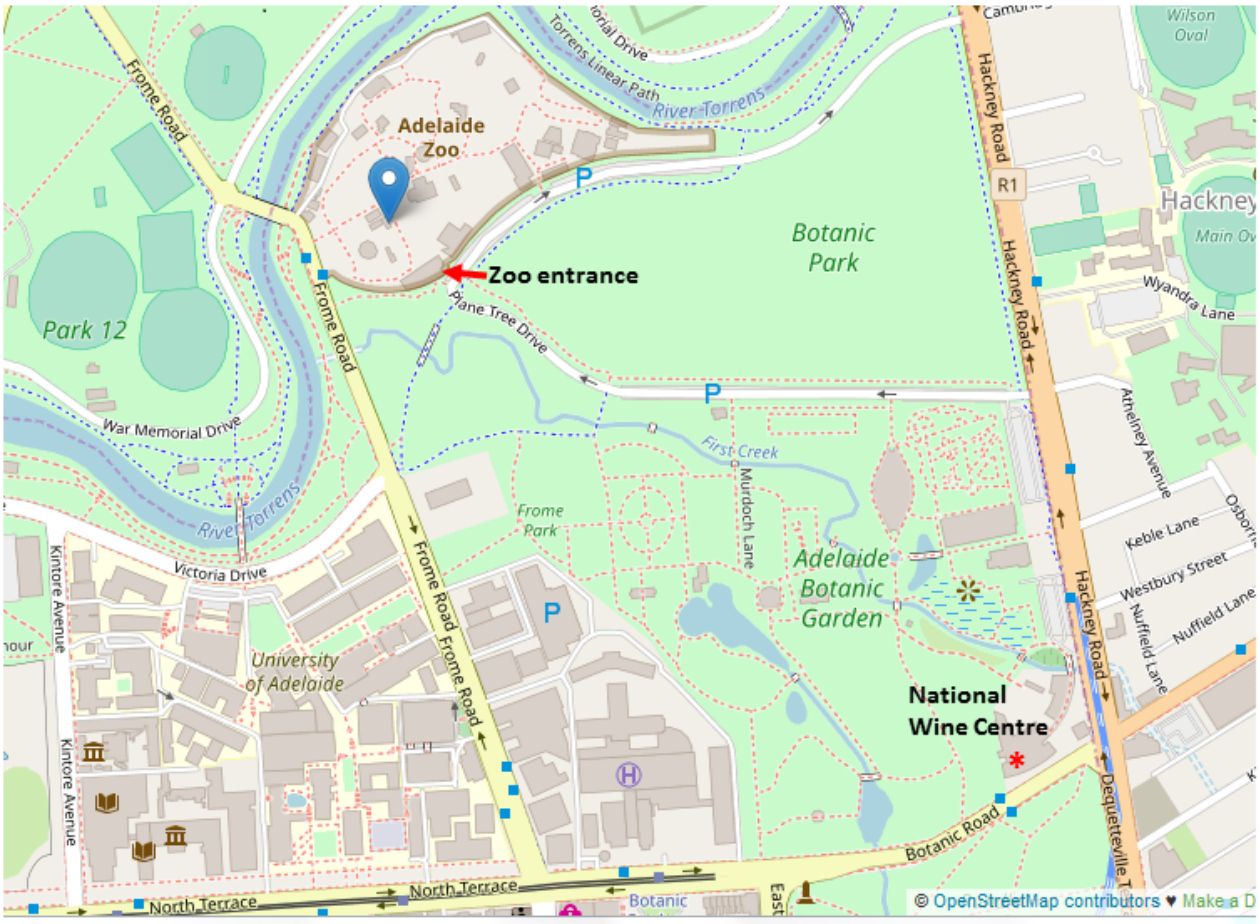
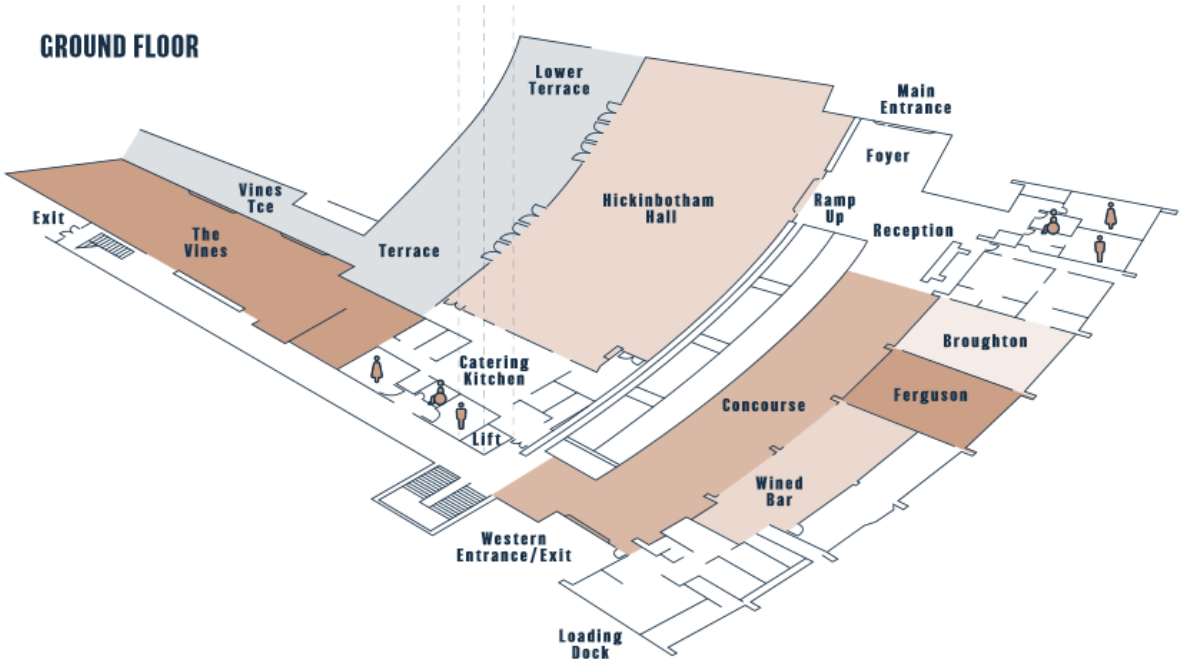
Many genome mutations affecting complex traits are thought to act through gene regulation mechanisms. The genomic position or activity of regulatory elements can be quantified by molecular assays, e.g., ChIP-sequencing, or predicted using existing human and/or mice data. We evaluated 15 functional categories, including experimentally generated datasets of expression QTLs (eQTLs) and ChIP-sequencing of mammary gland, as well as computationally predicted datasets of SNP annotation, e.g. CTCF sites and projections from the Human genome of Regulatory Regions. Over 17 million bovine sequence variants were allocated to these functional categories and a genomic relationship matrix (GRM) was made using variants within each category. For 34 traits from dairy cattle, a genome-wide restricted maximum likelihood analysis was used to estimate the variance explained by each functional category when fitted in the same model as the category of high density SNP chip (630K) in up to 12,000 bulls and 34,000 cows. The variance explained per SNP for experimentally determined functional categories was higher than that of random SNPs, but this is not true for computationally defined categories. Our results provided fundamental insights into the usage of genome functional datasets in understanding the effects of mutations on complex traits.

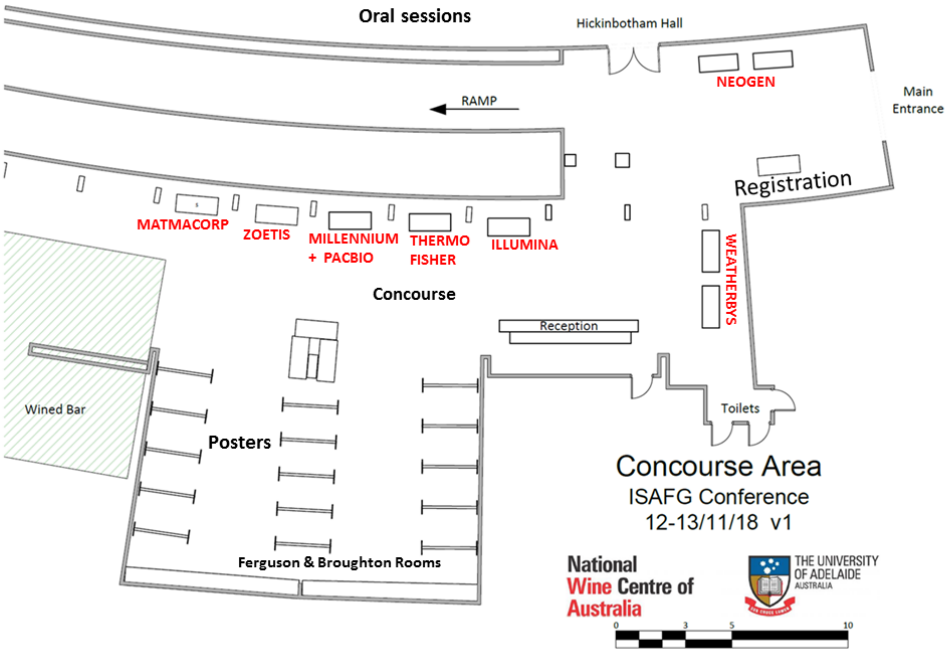
Participating Author Index

National Wine Centre to Adelaide Zoo: conference dinner



National Wine Centre of Australia Floor Plans





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