



# ISAG 2017

36th International Society for  
Animal Genetics Conference

16th - 21st July 2017

University College Dublin | Ireland

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## Genomes to Phenomes



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PROGRAMME BOOK

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Stephanie McKay, University of Vermont

- WT11 **Tracing the effect of *FecB* gene on transcriptome profile in ovine oocyte and cumulus cells using single-cell RNA-Seq.**  
X.-F. Guo<sup>\*1,2</sup>, X.-Y. Wang<sup>1</sup>, R. Di<sup>1</sup>, W.-P. Hu<sup>1</sup>, X.-Y. He<sup>1</sup>, X.-H. Cao<sup>1</sup>, and M.-X. Chu<sup>1</sup>, <sup>1</sup>*Institute of Animal Science, Chinese Academy of Agricultural Sciences, Beijing, China;* <sup>2</sup>*College of Animal Science and Technology, China Agricultural University, Beijing, China.*
- WT12 **The genetic diversity of mitochondrial DNA D-loop in Indonesian local goat.**  
M. Cahyadi<sup>\*1</sup>, A. Pramono<sup>1</sup>, and Sutarno<sup>2</sup>, <sup>1</sup>*Department of Animal Science, Faculty of Agriculture, Universitas Sebelas Maret, Surakarta, Indonesia;* <sup>2</sup>*Department of Biology, Faculty of Mathematics and Natural Sciences, Universitas Sebelas Maret, Surakarta, Indonesia.*
- WT13 **Preliminary differential transcriptomic analysis of abomasal mucosa from resistant and susceptible sheep to gastrointestinal nematodes (GINs) after an experimental infection with *T. circumcincta*.**  
P. K. Chitneedi<sup>\*1</sup>, J. J. Arranz<sup>1</sup>, A. Suarez-Vega<sup>1</sup>, M. Martínez-Valladares<sup>2,3</sup>, and B. Gutiérrez-Gil<sup>1</sup>, <sup>1</sup>*Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, León, Spain;* <sup>2</sup>*Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, León, Spain;* <sup>3</sup>*Instituto de Ganadería de Montaña, CSIC-ULE, León, Spain.*
- WT14 **Underdominant KCC3b R31I association with blood sodium concentration in domestic sheep suggests role in dimerization.**  
S. N. White<sup>\*1,2</sup>, R. D. Oliveira<sup>2</sup>, M. R. Mousel<sup>1,4</sup>, M. V. Gonzalez<sup>2,5</sup>, M. A. Highland<sup>1</sup>, J. B. Taylor<sup>6</sup>, and D. P. Knowles<sup>1,2</sup>, <sup>1</sup>*USDA-ARS Animal Disease Research, Pullman, WA, USA;* <sup>2</sup>*Dept. Veterinary Microbiology & Pathology, Washington State University, Pullman, WA, USA;* <sup>3</sup>*Center for Reproductive Biology, Washington State University, Pullman, WA, USA;* <sup>4</sup>*School for Global Animal Health, Washington State University, Pullman, WA, USA;* <sup>5</sup>*Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA;* <sup>6</sup>*USDA-ARS Range Sheep Production Efficiency Research, Dubois, ID, USA.*
- WT15 **Non-linked SNPs in promoter and exon 2 of *MTNR1A* gene are associated to reproductive seasonality in Rasa Aragonesa sheep breed.**  
J. H. Calvo<sup>\*1,3</sup>, M. Serrano<sup>2</sup>, A. Martinez-Royo<sup>1</sup>, B. Lahoz<sup>1</sup>, P. Sarto<sup>1</sup>, A. Ibañez-Deler<sup>1</sup>, J. Folch<sup>1</sup>, and J. L. Alabart<sup>1</sup>, <sup>1</sup>*Centro de Investigación y Tecnología agroalimentaria de Aragón (CITA)-IA2, Zaragoza, Spain;* <sup>2</sup>*Instituto Nacional de Investigaciones agrarias (INIA), Madrid, Spain;* <sup>3</sup>*ARAID, Zaragoza, Spain.*
- WT16 **Association analysis between *ABCG2* gene and milk production in dairy sheep breeds kept in the Czech Republic: Preliminary results.**  
J. Rychtarova<sup>\*</sup>, A. Svitakova, and Z. Sztankoova, *Institute of Animal Science, Prague, Czech Republic.*
- WT17 **Are *TMEM154* and *CCR5* variants promising markers for selection against maedi-visna susceptibility in German sheep flocks?**  
V. Molaei, M. Eltanany, and G. Lühken<sup>\*</sup>, *Department of Animal Breeding and Genetics, Justus-Liebig University, Giessen, Germany.*
- WT18 **Allelic and genotypic frequencies of *PRNP* gene polymorphisms in some Italian goat populations.**  
C. Sebastiani<sup>1</sup>, M. Torricelli<sup>1</sup>, M. Ciullo<sup>1</sup>, G. Vaccari<sup>2</sup>, E. Lasagna<sup>3</sup>, F. Sarti<sup>3</sup>, S. Ceccobelli<sup>3</sup>, N. D'Avino<sup>1</sup>, M. Panicià<sup>1</sup>, and M. Biagetti<sup>\*1</sup>, <sup>1</sup>*Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche, Perugia, Italy;* <sup>2</sup>*Istituto Superiore di Sanità - Dipartimento di Sanità Pubblica Veterinaria e Sicurezza Alimentare, Roma, Italy;* <sup>3</sup>*Dipartimento di Scienze Agrarie, Alimentari e Ambientali, Università degli Studi di Perugia, Perugia, Italy.*
- WT19 **Accelerating genetic improvement in sheep by increased pedigree accuracy.**  
H. Koshinsky, A. Pirani, M. Patil<sup>\*</sup>, V. Missirian, V. Joshi, and J. Curry, *Thermo Fisher Scientific, Santa Clara, CA, USA.*
- WT20 **Molecular study of the melanocortin 1 receptor gene in association with coat color variation of Iranian native sheep.**  
M. A. Eshghabadi<sup>1</sup>, A. A. Masoudi<sup>\*1</sup>, H. Emrani<sup>2</sup>, and S. Amirina<sup>2</sup>, <sup>1</sup>*Tarbiat Modares University, Tehran, Tehran, Iran;* <sup>2</sup>*Animal Science Research Institute, Tehran, Tehran, Iran.*
- WT21 **Detecting selection footprints from production system-driven genomic divergence of South African sheep breeds.**  
E. Dzomba<sup>\*1</sup>, M. Snyman<sup>2</sup>, M. Chimonyo<sup>2</sup>, and F. Muchadeyi<sup>3</sup>, <sup>1</sup>*University of KwaZulu-Natal, Pietermaritzburg, KwaZulu-Natal, South Africa;* <sup>2</sup>*Grootfontein Agriculture Development Institute, Middelburg, Eastern Cape, South Africa;* <sup>3</sup>*Agriculture Research Council-Biotechnology Platform, Onderstepoort, Gauteng, South Africa.*
- WT22 **Effect *ACACA*, *FASN* on fat acid and somatic cells in sheep—Preliminary results.**  
Z. Sztankoova<sup>\*1</sup>, M. Borkova<sup>2</sup>, A. Svitakova<sup>1</sup>, J. Kyselova<sup>1</sup>, and T. Kott<sup>1</sup>, <sup>1</sup>*Institute of Animal Science, Prague, Czech Republic;* <sup>2</sup>*Institute of Dairy Research, Prague, Czech Republic.*
- WT23 **Genetic investigation of sheep and goat families demonstrating the entropion eye condition.**  
T. Hadfield<sup>\*</sup> and N. Cockett, *Utah State University, Logan, UT, USA.*

# Preliminary differential transcriptomic analysis of abomasal mucosa from resistant and susceptible sheep to gastrointestinal nematodes (GINs) after an experimental infection with *T. circumcincta*.



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## Introduction

- In sheep, indicator traits of resistance to gastrointestinal nematodes (GIN), such as Faecal egg count (FEC) and IgA, are difficult to measure and show low heritability → Low efficient classical genetic selection.
- Genetic mapping and gene expression studies may pave the way to increase parasite resistance through gene-assisted selection.
- OBJECTIVE: Identification of new candidate genes for sheep parasite resistance through the comparison of the abomasal mucosa transcriptome in Resistant and Susceptible sheep after experimental infection with *T. circumcincta*.**

## Conclusion

- Our RNA-Seq analysis of in mucosa samples (d. 7 post-infection with *T. circumcincta*) showed few significant differentially expressed genes (SDEGs) between Resistant and Susceptible animals, among which we found many genes of the myosin family. This might suggest a link with increased GIN expulsion as a resistance mechanism.
- Further research will be conducted on the abomasal lymph node transcriptome for the same animals with the aim of identifying potential genetic mechanisms of GIN resistance in adult sheep.

## Materials and Methods

### 1. Experimental Infection

I. Selection of a study flock based on appropriate variability for FEC data



II. Grouping sheep into Resistant (R) and Susceptible (S) to GIN based on FEC after natural infection



III. First experimental infection (EI 1) (31 days)

Post EI 1

Confirmation of (R) and (S) Sheep based on accumulated FEC



IV. Second experimental infection (EI 2) (7 days)

Post EI 2

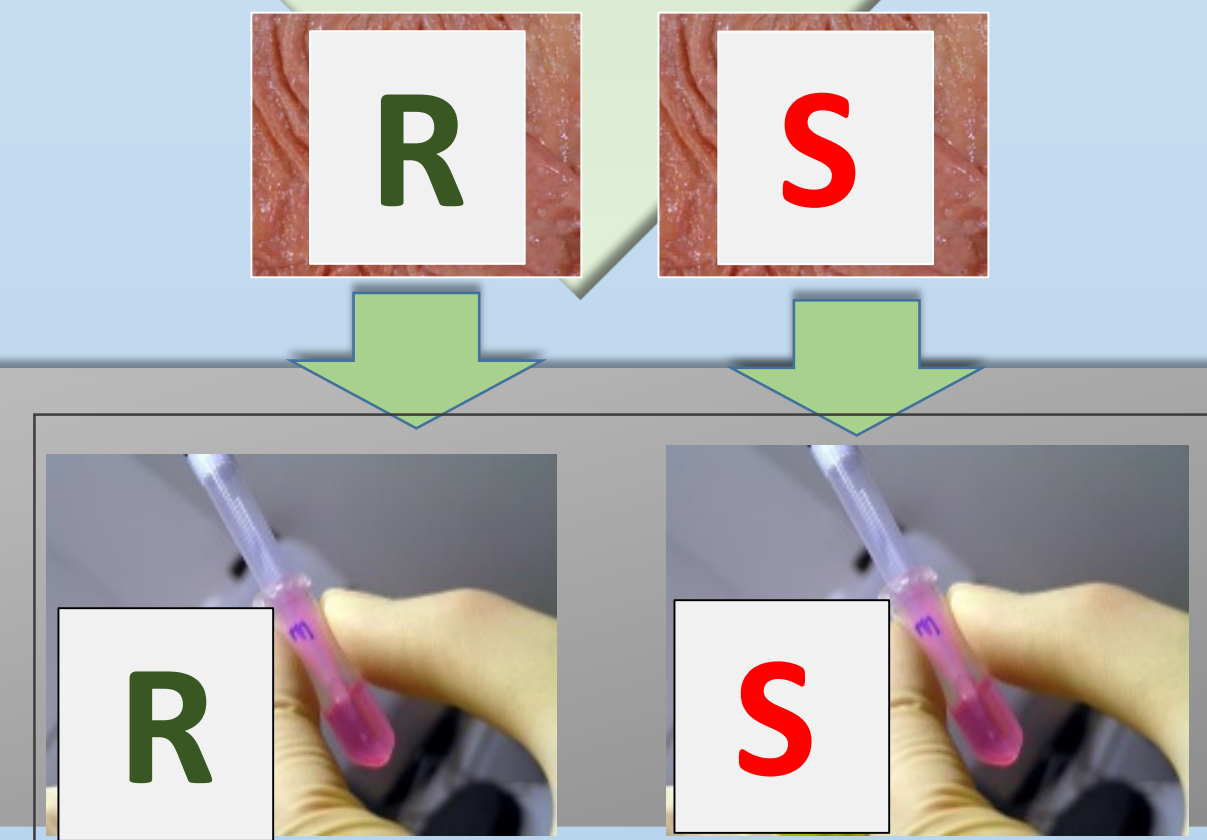
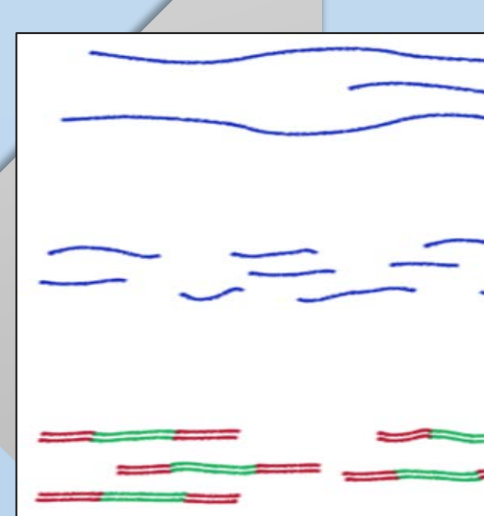
Animal sacrifice and collection of abomasal mucosa tissue samples



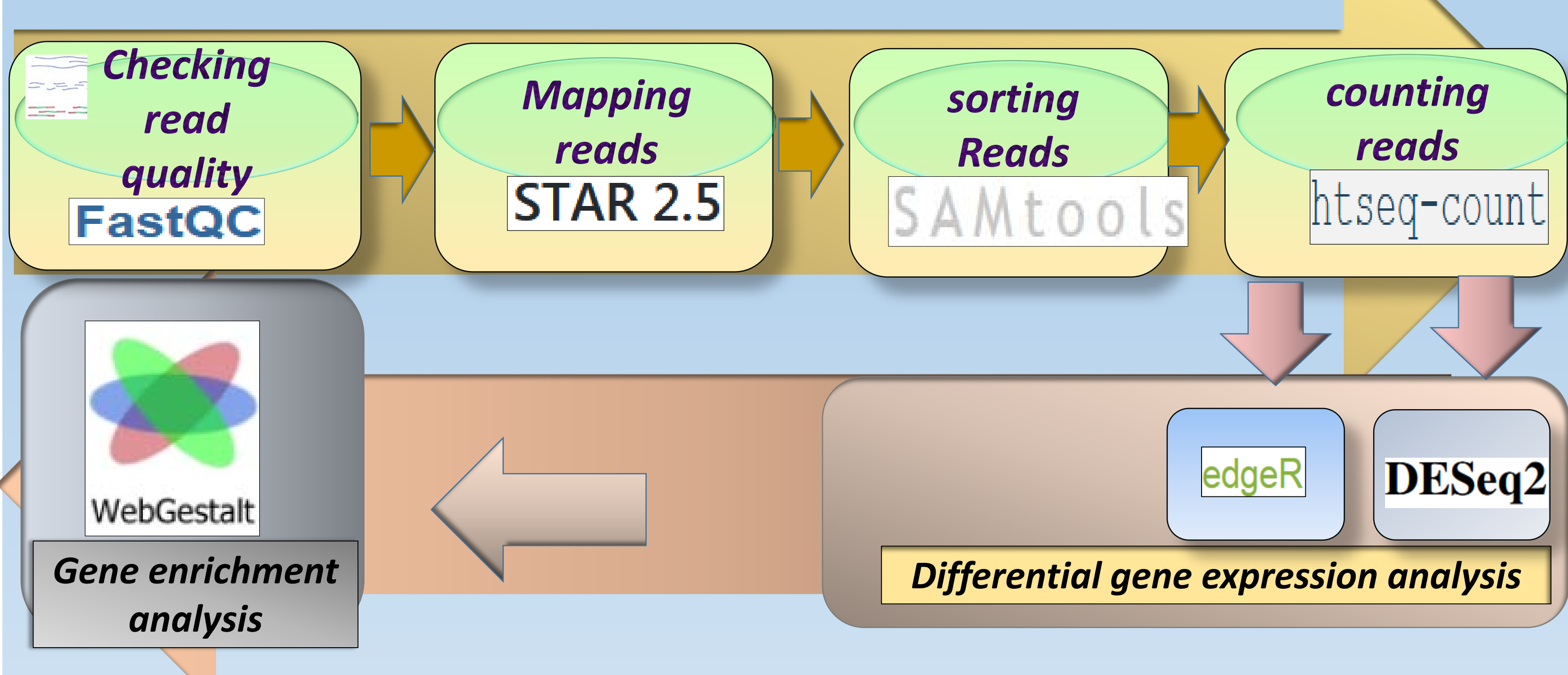
### 2. RNA extraction and sequencing

RNA reads

Illumina Hi-Seq 2000



### 3. Bioinformatics analysis



## Results and Discussion

### General statistics

- 11 abomasal mucosa samples RNA-Seq data were analyzed (6 resistant and 5 susceptible samples)
- On an average, we found 366,000,571 paired reads (33,272,779.18 ± 4,713,851.29) per sample.
- Approximately 72.42% in each sample were aligned against the sheep reference genome (Oar\_v3.1).

### Differential gene expression analysis

- EdgeR analysis found 18 differentially expressed gene (SDEGs): *ACTA1*, *ATP2A1*, *CASQ1*, *CKM*, *MB*, *MYH1*, *MYH4*, *MYH7*, *MYL1*, *MYLPF*, *MYOM2*, *NAP1L1*, *OBSCN*, *PGAM2*, *SYT8*, *TNNC2*, *TNNT3*, *TTN*, *XIRP2*.
- DeSeq2 identified only 1 SDEG *SYT8*, common to the EdgeR SDEGs list.

### Gene enrichment analysis

- Gene-ontology analysis for the EdgeR SDEGs:**
  - Due to the inclusion of 6 genes of the myosin complex in the list of SDEGs, we found many significant enriched terms (BH adj < 0.05; min, 6 genes) related to muscle physiology (e.g. striated muscle contraction, muscle structure development, organ development etc.)
  - Genes of the myosin family have been previously shown to be related to FEC in nematode infected animals [1].
  - Muscle contraction may be related to expulsion of GIN, which has been suggested as a possible GIN resistance mechanism in adult sheep [2].

## References

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- Allen, J. E., & Sutherland, T. E. *Academic Press*(2014):329-340.4.

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