

UNIVERSITY
of GUELPH

CHANGING LIVES
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DEPARTMENT OF
**ANIMAL
BIOSCIENCES**



Agriculture and
Agri-Food Canada

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FAANG-related Project Updates

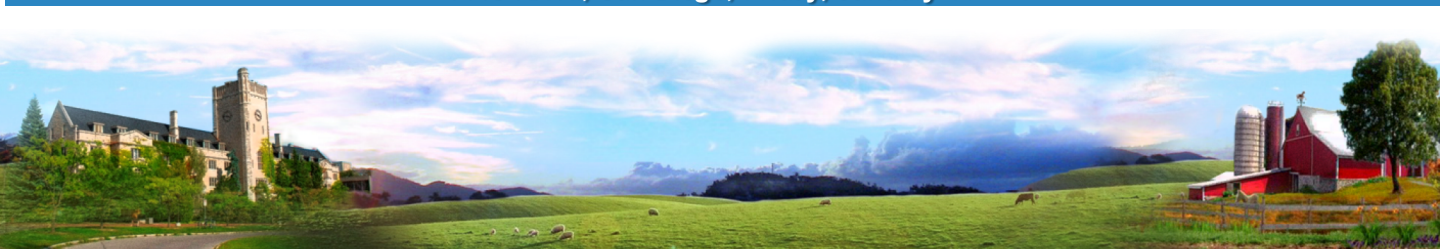
Canadian efforts

Angela Cánovas (U of Guelph)

Eveline Ibeagha-Awemu (AAFC, Sherbrooke)

Graham Plastow (U of Alberta)

PAG XXVII, San Diego, Friday, January 11th





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Réseau laitier canadien



**CRSNG
NSERC**

Dairy cattle:

Genomic factors of resistance to bovine paratuberculosis (Johne's disease)

PIs: N. Bissonnette (AAFC, Sherbrooke): J. Meadus (AAFC, Lacombe)

Collaborators: **E.M. Ibeagha-Awemu** (AAFC, Sherbrooke) and others.

Work accomplished:

-Tissue samples collected from different sections of the gastrointestinal tract of sick animals (n=10) and healthy animals (n=10) (ileum, ileum lymph node, mid jejunum, mid jejunum lymph node)

- Characterization of mRNA, microRNA and long non-coding RNA expression
 - Sequencing on an Illumina HiSeq 2500 system completed for lncRNA and mRNA and miRNA expression
 - Bioinformatics analysis of mRNA completed
 - Manuscript in preparation
 - Bioinformatics analysis of lncRNA underway
 - Bioinformatics analysis of miRNA underway

Planned work:

- Characterization of circularRNA
- Functional validation of rules of miRNA in Johne's disease





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Dairy cattle:

Unraveling disease susceptibility to Johne's disease by studying host genetics and the dynamics of mixed genotype infection in disease progression and herd prevalence

PIs: Nathalie Bissonnette (AAFC Sherbrooke) and Kapil Tahlan (Memorial University New Foundland, St-Johns);

Collaborators: **Ibeagha-Awemu** (AAFC, Sherbrooke), and others

Work in progress:

- Characterization of DNA methylation profile in positive (n=8) and negative (n=8) cows by whole genome bisulfite sequencing in progress (ileum, ileum lymph node, mid jejunum, mid jejunum lymph node)
- Characterization of histone marks in positive (n=8) and negative (n=8) cows by ChIP-Seq in progress

Assays:

- **Whole Genome Bisulfite Sequencing** (four tissues)
- **ChIP-Seq**



Beef and Dairy Cattle:

Improving selection efficiency by combining functional studies and a systems biology approach with the estimation of breeding values in cattle

- PI: **Angela Cánovas** (University of Guelph)
- Collaborators: **Graham Plastow** (University of Alberta) and others.
- **Collaboration with the lead groups in the FAANG consortium** (University of California-Davis)
- **Assays: RNA-Seq:** mRNA, lncRNA (different breeds, tissues & biological stages)
Whole Genome Bisulfite Sequencing
Whole Genome Sequencing and 16S & 18S Sequencing:
16S & 18S Sequencing samples in process (n=50+48)



Ontario Centres of Excellence



Beef Cattle:

Use of –omics technologies toward profitability and consumers' satisfaction

- PIs: **Angela Cánovas** (University of Guelph) with **Graham Plastow** (University of Alberta).
- **Collaboration with the lead groups in the FAANG consortium** (University of California-Davis)
- **Assays: RNA-Seq:** mRNA, lncRNA (n=80)
Tissues: Muscle (*Longissimus Dorsi*) (n=40) and Fat (n=40)
Groups: High (n=40) and Low (n=40) Tenderness (WB shear force)



Sheep:

Leveraging -OMICS and systems biology to understanding the genes and metabolic pathways associated with genetic resistance to parasites in sheep

- PI: **Angela Cánovas** (University of Guelph)
- **Collaboration with the lead groups in the FAANG consortium** (University of California-Davis)
- **Assays:** **RNA-Seq** (n=70) : mRNA, lncRNA
Liver tissue
Groups: High and Low Immunity and Stress Responders
Whole Genome Bisulfite Sequencing (n=20) (in progress)

Beef Cattle:

Genetic variations associated with feed efficiency and methane yield

- PIs: **Graham Plastow** (University of Alberta) with **Angela Cánovas** (University of Guelph) and others
- **Collaboration with the lead groups in the FAANG consortium** (University of California-Davis)
- **Samples:** Hi/Lo for traits; 4 time points (pre-weaning, weaning, market weight/post-puberty, mature (4-5yr); gender (2 males, 2 females), tissues (approx. 20 tissues (tbd))
- **Assays:** RNA-seq
ChIP-seq

Dr. Tianfu Young Postdoctoral Researcher



**Collaboration with the lead groups in the FAANG consortium
(University of California - Davis)**

Participated in some preliminary works about:

- Allele specific analysis of ChIP-seq and RNA-seq data**
- User interface for FAANG ChIP-seq analysis protocol**



Other Projects

Genome Canada Large Scale Applied Research Projects

Dairy Cattle and feed efficiency

PIs: Filippo Miglior (CDN/U of Guelph) and Paul Stothard (U of Alberta)

Pig Disease Resilience

PIs: Mike Dyck, John Harding (U of Saskatchewan), Bob Kemp (PigGen Canada)

- **Collaboration with the lead groups in the FAANG consortium inc.** UCD, Roslin Institute, ISU.....

- **Assays:** Primarily RNA-seq, but **opportunities for additional sampling** for FAANG phase 2 or new collaborations

Including new Genome Canada competition (applications under review)

Thank You



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