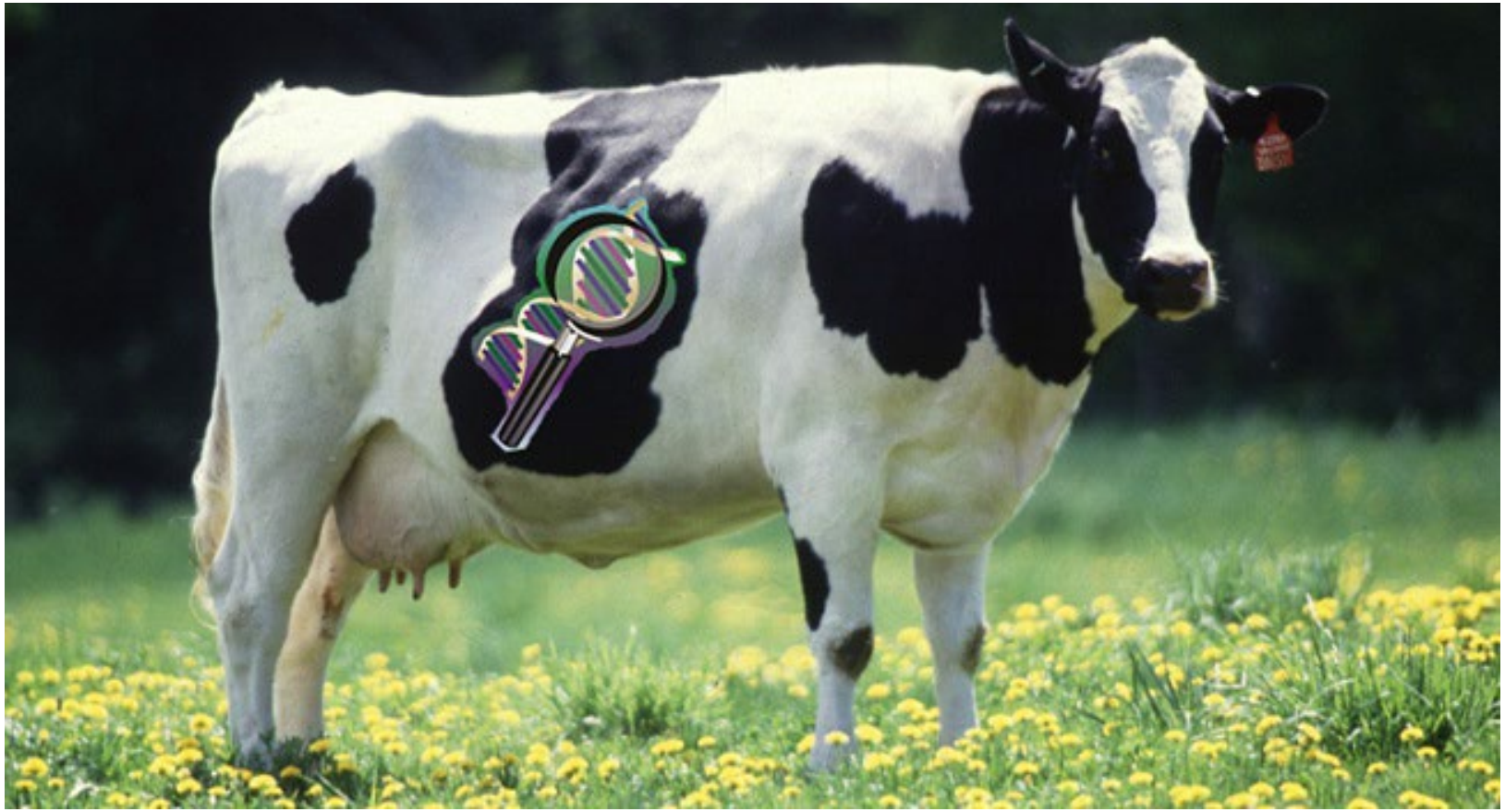
Animal Genomics and Improvement Laboratory (AGIL): FY25 ARMPS

Ransom Baldwin

Research Leader &
Research Animal Scientist

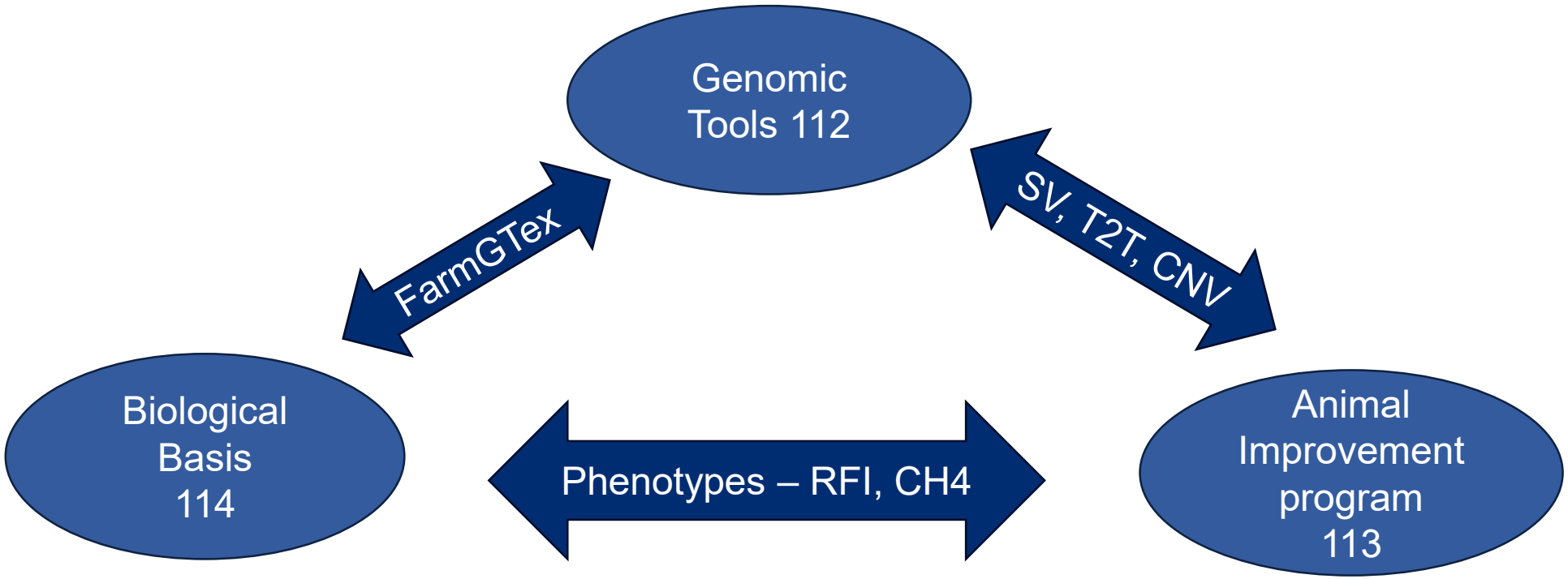


AGIL Overview

- Mission Statement: The Animal Genomics and Improvement Laboratory (AGIL) discovers and develops improved methods for the genetic and genomic evaluation of economically important traits of dairy animals and small ruminants and conducts fundamental genomics-based research aimed at improving their health and productive efficiency.

- Personnel (3 Projects):
  - 10 SYs (NP 101). 4 SY positions currently vacant
  - Post-docs (3 HQ and 2 ORISE)
  - 3 support scientists, 4 Technicians, 1 administrative professional
    - 5 Support Scientist positions vacant

AGIL Project Interactions



USDA Agricultural Research Service
U.S. DEPARTMENT OF AGRICULTURE

Genomic Tool Development - 112

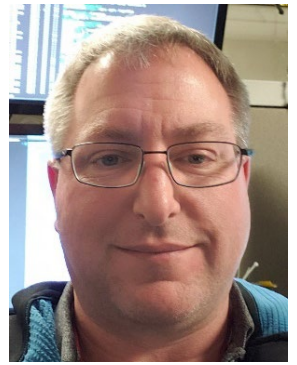
Enhancing genetic merit of ruminants through improved genome assembly, annotation, and selection

- Develop biological resources and computational tools to enhance characterization of breed-specific bovine and other genomes.
- Utilize genotypic data to enhance genetic improvement in ruminant production systems.
- Characterize functional genetic variation for improved fertility, growth, and sustainability of ruminant production systems.

George Liu (lead)

Curt Van Tassell

Ben Rosen



Steven Schroeder

2025 Research Highlights

AG2PI
Agricultural Genome to Phenome Initiative

FarmGTEx
Farm Animal Genotype-Tissue Expression

$P_m = G + E + GxE$

Large reference cohorts with enough genetic variation

Genotype

Transcriptome

Epigenome

Proteome

...

Phenotype

Regulatory variants in cattle

Unraveling the tissue-specific genetic regulation of gene expression is essential for both biological discovery and genetic improvement in farm animals. In this analysis, the FarmGTEx consortium builds a multi-tissue atlas of regulatory variants in cattle and shows the importance of this resource to understanding regulatory mechanisms underlying complex traits of economic value. The FarmGTEx consortium is working on other farm animal species now.

See Liu et al.

Image: Image courtesy of USDA Agricultural Research Service (ARS). Cover Design: Tulsi

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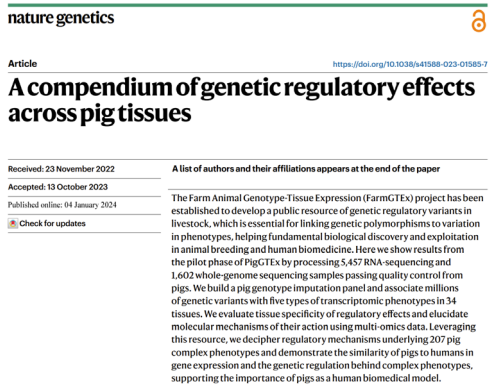
nature genetics

Article

https://doi.org/10.1038/s41588-023-01585-7

A compendium of genetic regulatory effects across pig tissues

Received: 23 November 2022

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Check for updates

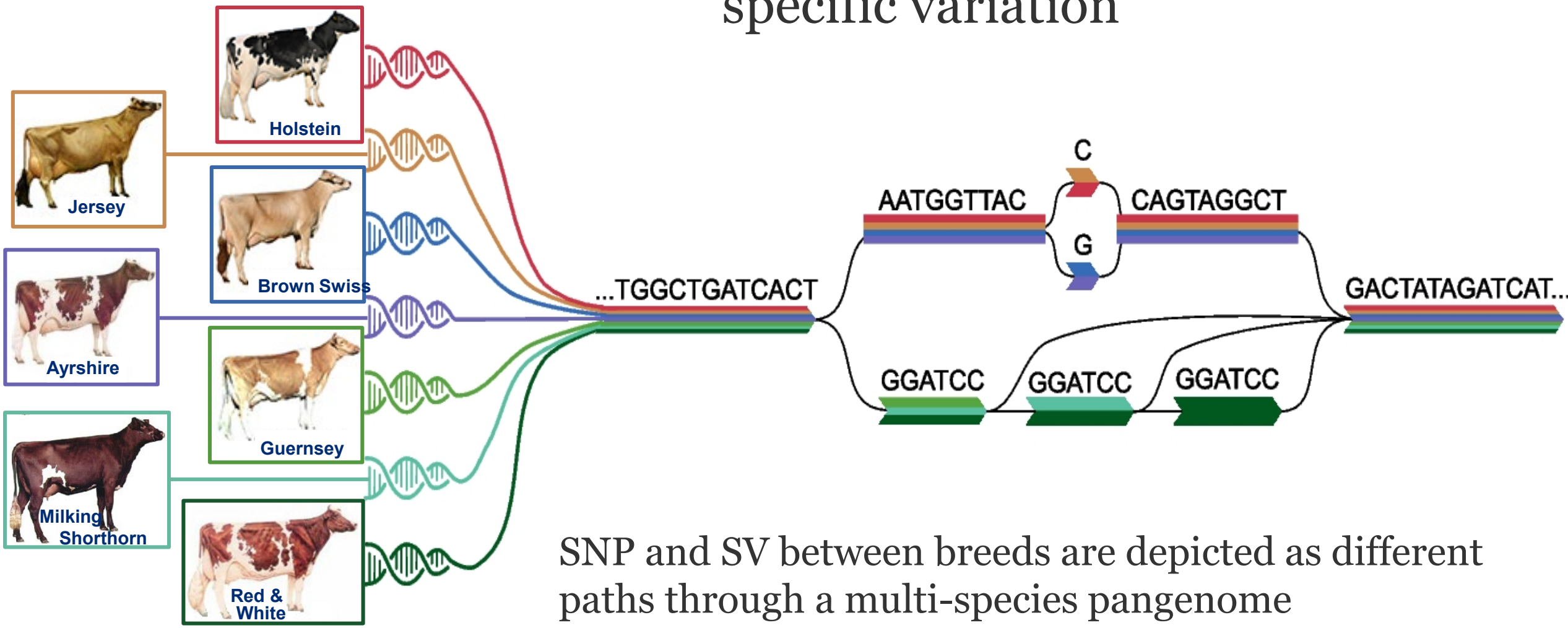
A list of authors and their affiliations appears at the end of the paper

The Farm Animal Genotype-Tissue Expression (FarmGTEx) project has been established to develop a public resource of genetic regulatory variants in livestock, which is essential for linking genetic polymorphisms to variation in phenotypes, helping fundamental biological discovery and exploitation in animal breeding and human biomedicine. Here we show results from the pilot phase of PigGTEx by processing 5,457 RNA-sequencing and 1,602 whole-genome sequencing samples passing quality control from pigs. We build a pig genotype imputation panel and associate millions of genetic variants with five types of transcriptomic phenotypes in 34 tissues. We evaluate tissue specificity of regulatory effects and elucidate molecular mechanisms of their action using multi-omics data. Leveraging this resource, we decipher regulatory mechanisms underlying 207 pig complex phenotypes and demonstrate the similarity of pigs to humans in gene expression and the genetic regulation behind complex phenotypes, supporting the importance of pigs as a human biomedical model.

Nature Genetics 54 (9), 1438-1447

https://www.nature.com/articles/s41588-023-01585-7

Pangenomes for the discovery of breed specific variation



SNP and SV between breeds are depicted as different paths through a multi-species pangenome

Animal Improvement Prog. - 113

Improving Dairy Animals by Increasing Accuracy of Genomic Prediction, Evaluating New Traits, and Redefining Selection Goals

- Expand genomic data used in prediction by selecting new variants that more precisely track the true gene mutations that cause phenotypic differences.
- Evaluate new traits that can all be predicted at birth from the same inexpensive DNA sample.
- Improve efficiency of genomic prediction and computation by developing faster algorithms, testing new adjustments and models, and accounting for genomic pre-selection in evaluation.

Sajjad Toghiani (lead)

2 additional Research Animal Geneticist Positions being sought

AGIL Research

Effects of dairy cattle size and production on feed intake

- Data sources:
  - 8,513 feed intake trials from 6,621 Holstein cows (3,839 trials from U WI, 1,440 from BARC, 1,426 from Iowa State, 792 from Michigan State, and 737 from U FL).
  - > 5 million genomic predictions from CDCB for milk, fat, and protein yields and 5 size-related traits of Holsteins.
- Predict feed intake from other traits by multiple regression.

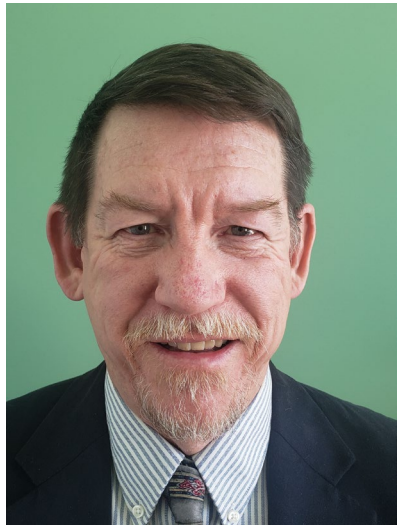
RESULTS -

- Nutritionists previously used energy corrected milk and did not account for different energy vs. protein needs of individual cows.
- Conclusions:
  - Large body weight requires more feed than previously assumed.
  - Protein requires more feed than assumed by most researchers.
- Results used directly in the US selection index (Net Merit $).

Biological Basis - 114

Improving Feed Efficiency of Dairy Cattle through Genomics and Novel Technologies

- Develop resources, tools, and selectable markers to improve nutrient use efficiency in dairy cattle.
- Evaluate and develop novel dietary strategies to reduce feed and nutritional costs to dairy cattle production.
- Evaluate in vivo gastrointestinal tissue responses (ruminal and duodenal) of lactating and dry dairy cows to perturbations in luminal factors (changes in nutrient flow) and physiological stressors (transition cow and early lactation).



Randy Baldwin
(lead)

2 additional Research Animal Geneticist Positions being sought

Background – cont.

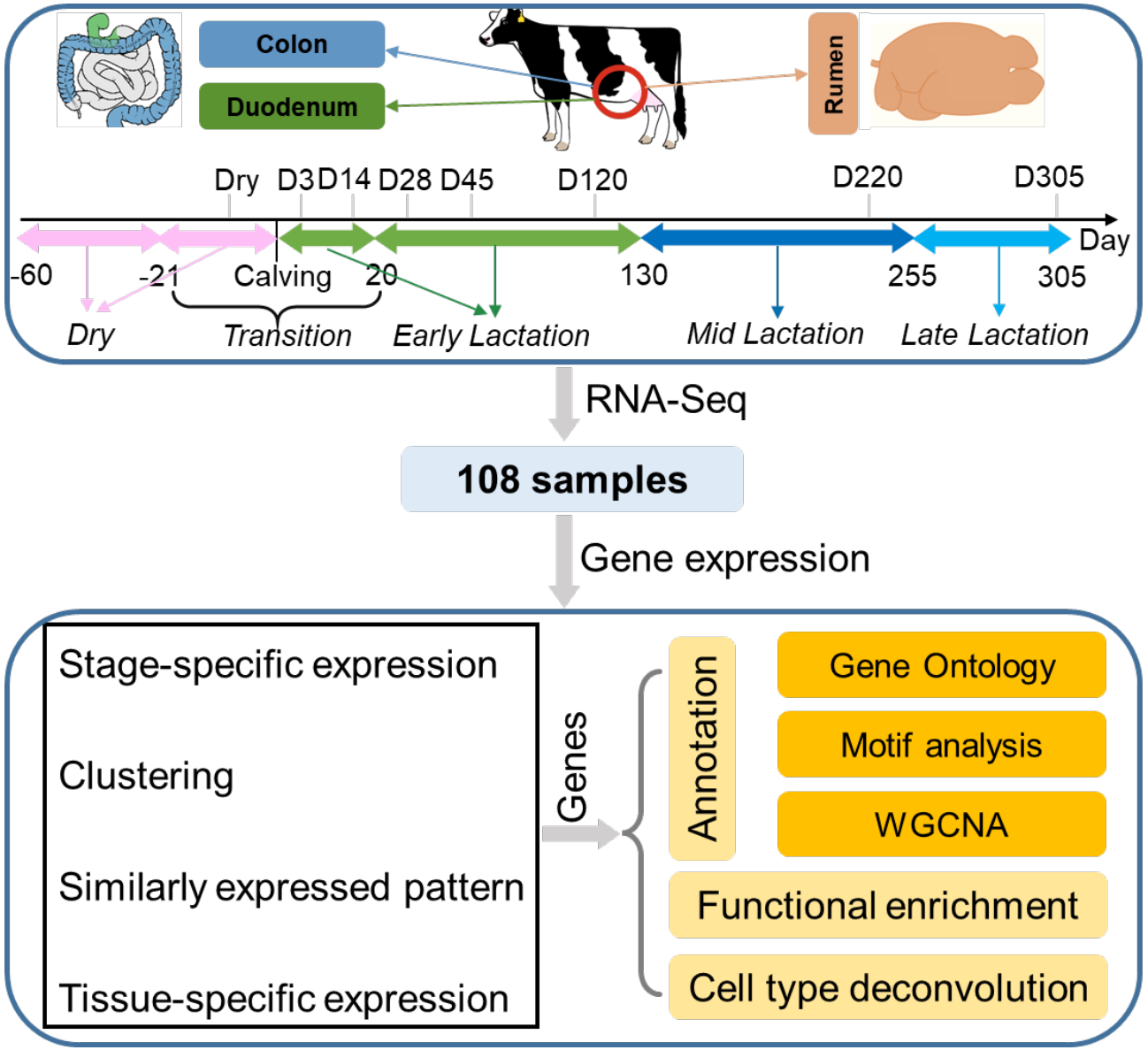
- Few sets of data exist describing changes in mass throughout lactation cycle
  - 10% increase in Maintenance Energy requirements during lactation could be accounted for by visceral mass changes alone – Smith and Baldwin, 1974
  - Small intestinal weight & mass increased disproportionately during lactation (nutrient supply) - Baldwin et al., 2004
  - Increased cellularity vs. hypertrophic growth – Baldwin et al., 2004

Background – Why we are interested

Gastrointestinal tissues represent < 10% Body Mass yet account for:

- 25 to 35% whole body protein synthesis – Lobley et al., 1994
- ~30% whole body oxygen consumption – Burrin et al., 1989
- Varies widely with energy intake and diet energy density – Sainz & Bently, 1997 and Baldwin & McLeod, 2004
- Across all species GIT is a primary user of AA, SCFA, and Glucose

Lactation study design and methods



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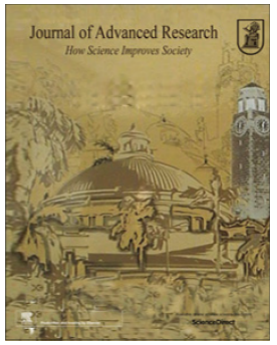

Original Manuscript

Transcriptomic profiling of gastrointestinal tracts in dairy cattle during lactation reveals molecular adaptations for milk synthesis

Yahui Gao [a,b,c], George E. Liu [a], Li Ma [b], Lingzhao Fang [d], Cong-jun Li [a], Ransom L. Baldwin VI [a,*]

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Conclusions

- Tissue-specific or physiological phase-specific transcriptome represents the functional outcomes of the genome. Use of serial sampling enhanced the usefulness of the down stream analyses.

- The gastrointestinal epithelium is a highly metabolically active tissue that performs significant functions such as absorption, transport, and protection. And this can be visualized using these bioinformatic tools.

- Our catalog of tissue-specific and stage-specific genes provided an extensive resource for elucidating the transcriptional diversity in the gastrointestinal tracts of cattle during the transition from the dry period thru the lactation stages.

Conclusions

- During transition of dry to lactation changes in barrier structure, nutrient transport, cell cycle activities, and immune functions are visible.
- Increased immune-related gene expression during lactation is consistent with the fact that the intestines serve as a barrier to luminal contents but also as a vital immune organ.

Ongoing Research & Planning

Biological Basis Project

- 50 cow slaughter balance (47 completed)
  - Established cooperations with U. Wisconsin (2 groups), DFRC (2 SY), U. Delaware (1), U. Penn Vet Med (2), UCD (1) and UMD (2).
  - Within BARC – All three AGIL projects represented & APDL (Li and Tuo)

Questions?