Genetic differences related to production traits in *Bos taurus* or *Bos indicus* influenced cattle

K.J. Thornton[1], L.L. Okamoto[1], B.M. Murdoch[2], G.K. Murdoch[3]
[1]*Department of Animal, Dairy and Veterinary Sciences, Utah State University, Logan, UT 84322*
[2]*Department of Animal, Veterinary and Food Sciences, University of Idaho, Moscow, ID 83844*
3*Department of Animal Science, Washington State University, Pullman, WA 99164*

Introduction

Global climate change has and will continue to negatively impact cattle production in the United States and around the world, Additionally, the world population is expected to exceed 9 billion by 2050; there is a need to improve production to conserve resources and meet production needs. Increasing *Bos indicus* (BI) genetics in the beef herd is one method to improve production efficiency. Compared to *Bos taurus* (BT) cattle, BI cattle are better able to withstand higher temperatures, are better adapted to nutritional stress, and consume less water. Despite these positive attributes, BI influenced cattle have a more excitable temperament, and exhibit decreased production performance and carcass quality compared to BT cattle. More data is needed to better understand how the relationship between breed type and genetics contribute to production performance, feeding behavior and carcass quality. Furthermore, there is a need within the agricultural community for researcher with different areas of expertise to work together to improve understanding of how industry relevant phenotypic characteristics relate to the genome.

Objectives

- Determine how genetic difference relate to proliferation, differentiation and protein synthesis of primary bovine satellite cells (BSC).
- Gain insight into how genetic differences between cattle of different breed types contribute to feedlot performance and carcass characteristics.
- Establish the basis for a multi-disciplinary research team to improve our understanding of how the genome of an animal relates to beef production.

Methods

Primary BSC Culture

- Primary BSC were isolated as previously described from six different steers. Three of the steers were 100% BT and three of the steers were BI-influenced (~19% BI and 81% BT).
- Cultures were grown and proliferation, differentiation and protein synthesis were assessed as previously described.
- The genome of each of the six animals will be sequenced by collaborators at USDA-MARC.

Live Animal Trial

- 115 steers of two different breeds, Angus (AN; n=83; 100% BT) or Santa Gertrudis-influenced (SG; n=32; 19% BI, 81% BT), were fed over a to year period in pens equipped with Vytelle bunks to assess feedlot performance and feeding behavior. Steers were harvested at a commercial facility and carcass data was obtained.
- Bovine GGP 100k assay was conducted using DNA isolated from the ear notches of 88 of the 115 steers (AN=58, SG=30) for a genome wide association study.

BSC Culture Results

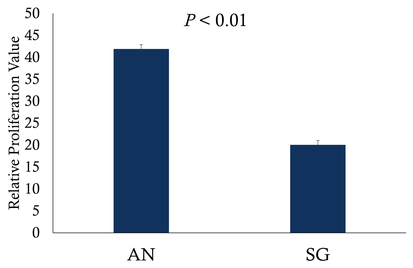

Figure 1. Relative proliferation rate differences between primary bovine satellite cells isolated from either Angus (100% BT) or Santa Gertrudis crossbred (19% BI and 81% BT) steers.

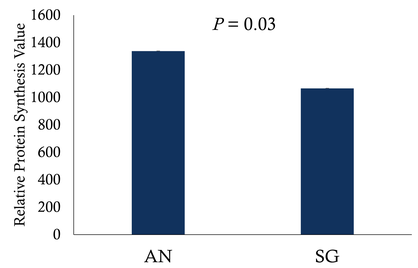

Figure 2. Relative protein synthesis rate differences between primary bovine satellite cells isolated from either Angus (100% BT) or Santa Gertrudis crossbred (19% BI and 81% BT) steers.

- Assays to assess differentiation of BSC isolated from animals of the two different breed types are in progress.
- Our team is currently working with researchers from USDA-MARC to sequence the genome of each animal BSC were isolated from.

Live Animal Trial Results

Table 1. Feedlot Performance & Carcass Characteristics of AN and SG-Influenced Steers

	AN	SG	SEM	P-Value
Steers (n)	83	32		
Hot Carcass Weight (lbs)	723.07	736.68	14.04	*0.34*
Ribeye Fat Thickness (mm)	9.02	8.89	0.50	*0.81*
Marbling Score	**424.49**	**368.2**	**41.02**	***0.0019***
Total DMI (kg)	9.44	9.80	0.32	*0.26*
Total G:F	0.14	0.14	0.006	*0.59*
Total ADG (kg)	1.38	1.38	0.08	*0.98*

AN; Angus, 100% BT
SG; Santa Gertrudis influenced, 19% BI, 81% BT

GWAS Results

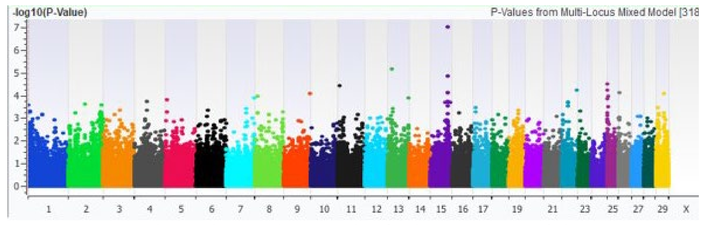

Figure 3. Manhattan Plot for hot carcass weight.

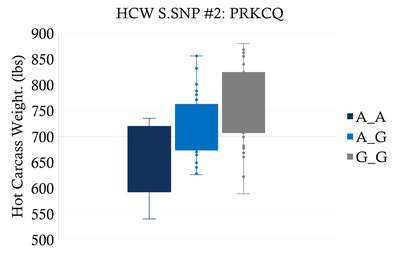

Figure 4. Box and Whisker Plot for SNP located within PRKCQ gene.

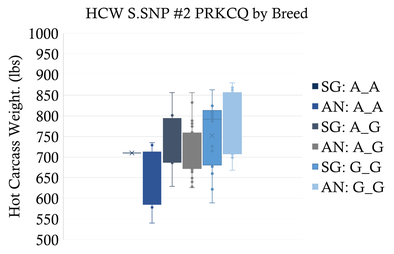

Figure 5. Box and Whisker Plot for SNP located within PRKCQ gene, separated by breed.

GWAS Results

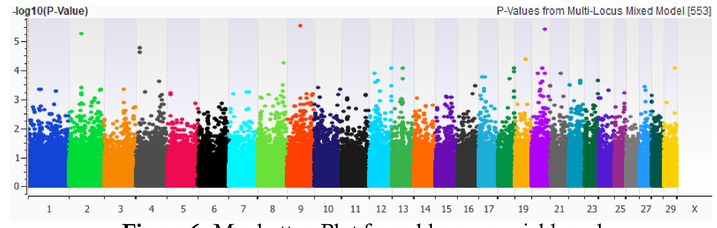

Figure 6. Manhattan Plot for cold camera yield grade.

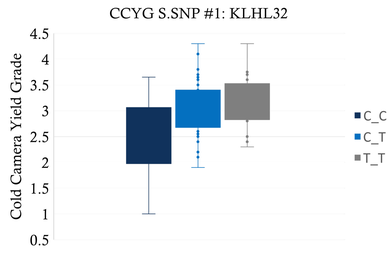

Figure 7. Box and Whisker Plot for SNP located within KLHL32 gene.

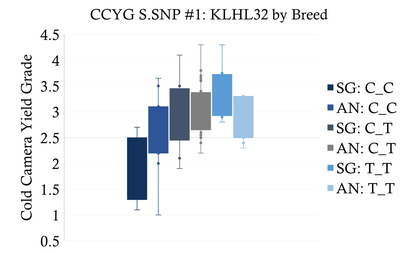

Figure 8. Box and Whisker Plot for SNP located within KLHL32 gene, separated by breed.

- Continued analysis of ADG, G:F, DMI, marbling score, cold camera ribeye size, and ribeye fat thickness are in progress.
- Similar analysis will be conducted with feeding behavior data obtained from the Vytelle bunks.

Seed Grant Outcomes

- Primary BSC isolated from BI-influenced animals have decreased proliferation and protein synthesis rates compared to BT cattle, which may be responsible for differences in animal performance that are typically observed between cattle of different breed types.
- Several SNP within genes have been found to be associated with production traits.
- Additional data analysis is underway the *in vitro* and *in vivo* studies to better understand how underlying genetic differences between cattle of different breed types may contribute to phenotypic differences.

Furthering the Aims of the AG2PI

- We have established the basis for an interdisciplinary research team to further investigate the relationship between the genome and phenotypic differences within different breeds of cattle.
- We are working to make sure this information will be available through a webpage hosted by the USU library.
- Completion of this seed grant has provided the necessary preliminary data to pursue additional research projects and expand our efforts.

Acknowledgements

- This project was supported by the USDA through competitive grants 2021-70412-35233 and 2020-70412-32615 through an AG2PI seed grant.
- The authors would also like to thank Santa Gertrudis Breeders International for providing financial support for this project.