

ABSTRACT

The objective of this study was to determine whether the microbial composition of various locations within the gastrointestinal (GI) tract contributes to the efficiency status of domestic livestock. One method of measuring feed efficiency is through residual feed intake (RFI) calculations. Sheep with previously established RFI classes (6 low and 6 high) were sampled. Samples were taken from six locations the GI tract (rumen, duodenum, jejunum, ileum, colon, and feces) to determine how the efficiency status of sheep may be correlated with various microbial communities. Gene surveys of the 16S rRNA of the microbial communities. Gene surveys of the 16S rRNA of the microbial communities. While the high and low RFI subgroups at each location were present in significantly different quantities between the two RFI classes in the rumen, feces, colon, duodenum, and jejunum. The majority of these taxa were observed in the rumen, colon, and feces as opposed to the digestive process (Fibrobacteres, Riknellaceae, Ruminococcaceae, Christensenellaceae, Saccharofermentans, and Lachnospirazceae) were higher within the low RFI animals in multiple locations (p < 0.06). Proteobacteria was more abundant in high RFI animals in multiple locations (p < 0.06) which suggests a dysbiotic microbial taxa level, microbial composition of multiple regions of the GI tract significantly contributes to the efficiency status of sheep.

INTRODUCTION

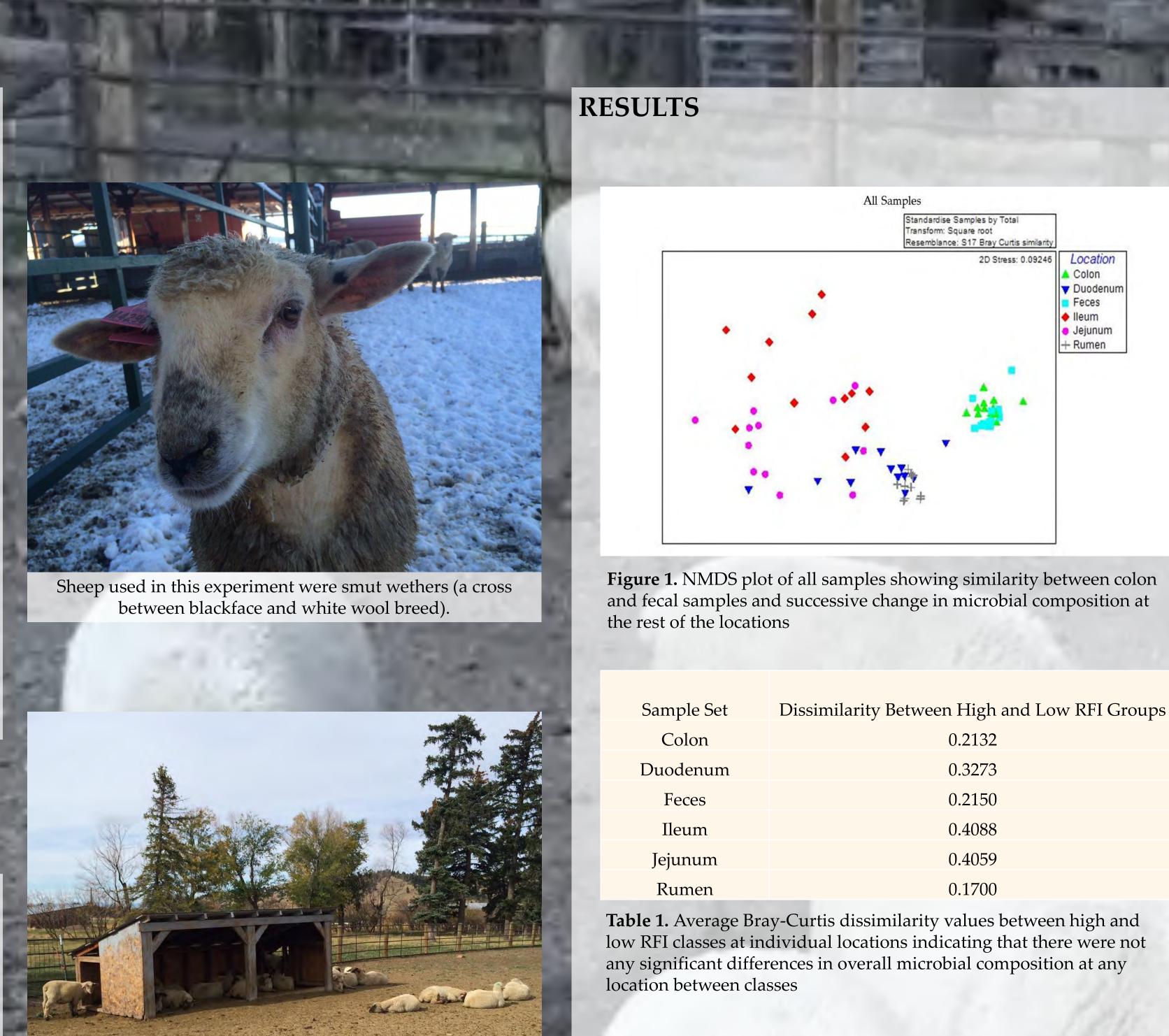
- Feed efficient livestock contribute to agricultural sustainability^{3,6}.
- Efficiency can be determined using residual feed intake (RFI)^{3,6}, calculated by:

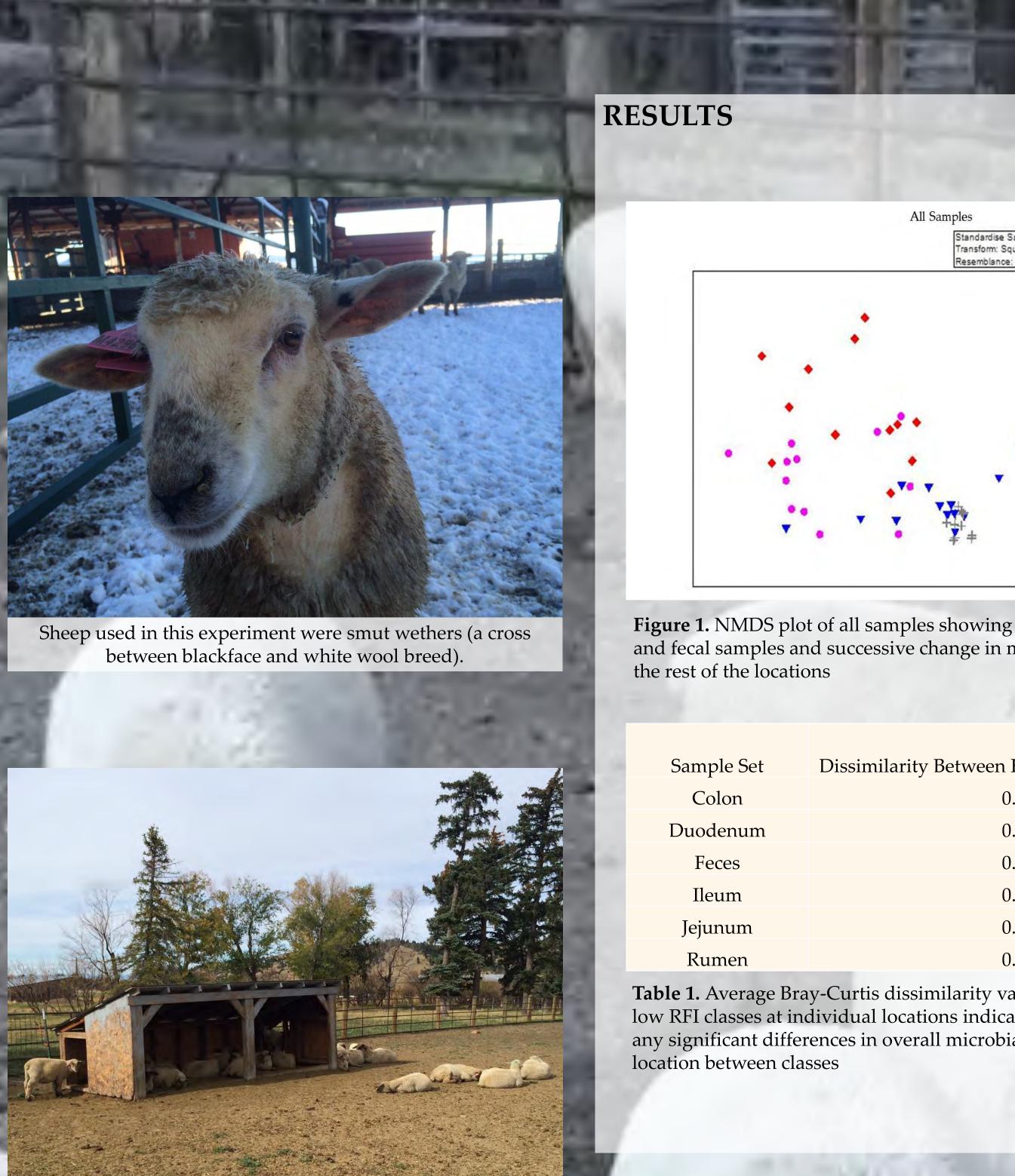
 $RFI \approx Actual Feed Intake - Expected Feed Intake^7$

- Expected feed intake for an individual animal is determined using linear regression⁷.
- Animals with lower RFI are characterized as being more efficient since they require less feed than their higher RFI counterparts^{3,6}.
- One mechanism hypothesized to guide RFI is gastrointestinal microbiota⁵.
- Ruminants are foregut fermenters and rely heavily on microbes for the breakdown of plant material⁵.

OBJECTIVES

- Characterize microbial communities in terms of richness and diversity along the GI tract
- Define the various relationships microbial communities have with one another and the influence RFI class has on them
- Compare microbiota across high and low RFI groups for individual taxa at individual locations and identify which taxa are present in significantly different amounts between RFI classes





METHODS

- 12 wethers previously established for RFI class were selected for this study.
- The Yeoman Lab collected gut samples which were processed for DNA, amplified, and sequenced using an Illumina Miseq. All sequence data was assembled into contigs using mothur.
- mothur software was used to assess alpha diversity (Good's Coverage, Chao1, Sobs, Shannon's diversity, and Simpson's diversity) of sequencing data.
- Primer E software was used to assess beta diversity (Bray-Curtis Average Dissimilarity, Analysis of Similarity, Non-metric Multidimensional Scaling, and Similarity Percentage).
- R package gplots was used for analysis at the individual taxa level (testing of significance and generation of heatmaps).

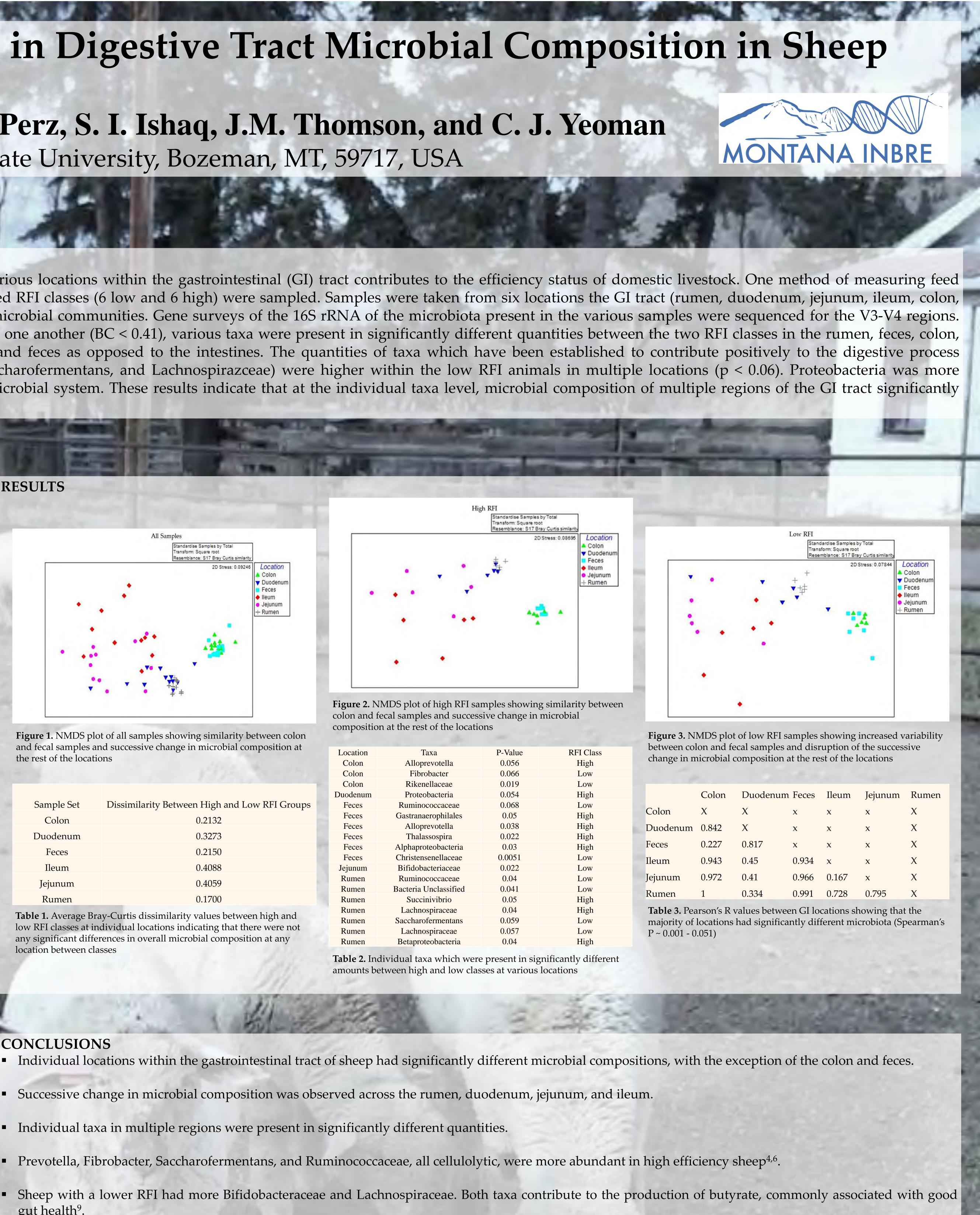
The facility the sheep were housed in

CONCLUSIONS

- gut health⁹.

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Christensenellaceae has been shown to be one of the more inheritable taxa present in the guts of both humans and mice. While it was shown to be associated with weight loss, it was also tied to a better functioning digestive system and was more abundant in higher efficiency sheep².

• In multiple locations, Proteobacteria (linked to dysbiotic digestive systems) was observed in higher quantities in lower efficiency sheep¹.

den metabolic organ. Therapeutic Advances in Gastroenterology 6(4): 295-308; (2)Goodrich, J, Waters J, Poole A, Sutter J, Koren O, Blekham R, Beaumont M, Treuren W, Knight R, Bell J, Spector T, Clark A, Ley R (2014) Human genetics shape the gut microbiome. Cell 159(4): 789-799; (3) iency and diet on adaptive variations in the bacterial community in the rumen fluid of cattle. Applied and Environmental Microbiology 78:1203-1214; (4)Jami E, Israel A, Kotser A, Mizrahi I (2013) Exploring the bovine rumen bacterial community from birth to adulthood. The ISME Journal 7:1069-1079; (5) McCann J, Wickersham T, Loor J (2014) High-throughput methods redefine the rumen microbiology 78:1203-1214; (4)Jami E, Israel A, Kotser A, Mizrahi I (2013) Exploring the bovine rumen fluid of cattle. Applied and Environmental Microbiology 78:1203-1214; (4)Jami E, Israel A, Kotser A, Mizrahi I (2013) Exploring the bovine rumen bacterial community from birth to adulthood. The ISME Journal 7:1069-1079; (5) McCann J, Wickersham T, Loor J (2014) High-throughput methods redefine the rumen microbiology 78:1203-1214; (4)Jami E, Israel A, Kotser A, Mizrahi I (2013) Exploring the bovine rumen bacterial community from birth to adulthood. McCann J, Wiley L, Forbes T, Rouquette F, Tedeschi L (2014) Relationship between the rumen microbiome and residual feed intake-efficiency of Braham bulls stocked on Bermudagrass pastures. PLoS ONE 9(3): e91864; (7) Redden R, Surber L, Grove A, Kott R (2013) Growth efficiency of Braham bulls stocked on Bermudagrass pastures. PLoS ONE 9(3): e91864; (7) Redden R, Surber L, Grove A, Kott R (2013) Growth efficiency of ewe lambs classified into residual feed intake-efficiency of ewe lambs classified into residual feed intake-efficiency of ewe lambs classified into residual feed intake groups and pen fed a restricted amount of food. Small Ruminant Research 114: 214-219; (8) Shi W, Moon C, Leahy, S, Kang D, Froula J, Kittelmann S, Fan C, Deutsch S, Gagic D, orf H, Kelly W, Atua R, Sang C, Soni P, Pinares-Pinto C, McEwan J, Janssen P, Chen F, Visel A, Wang Z, Attwood G, Rubin E (2014) Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome-dependent mechanisms underlie the energy harvest efficiency of ruminants. *The ISME Journal* 1 (2016) Specific microbiome-dependent mechanisms underlie the energy harvest efficiency of ruminants. *The ISME Journal*