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Dr. Stephanie McKay was born and raised in Texas where she attended Texas A&M University and received her undergraduate degrees in Biochemistry and Genetics. While working as a full time lab technician in a bovine genomics laboratory, Dr. McKay worked on her M.S. in Veterinary Microbiology. After receiving her Master's degree, Stephanie ventured to the University of Alberta in Edmonton, Alberta, Canada where she received her Ph.D. in Animal Science in 2007. Dr. McKay has had varied research experience including generating transgenic mice, working in Biohazardous disease related laboratories and predominantly working with the bovine genome. Her work with the bovine genome started as an undergraduate student and has evolved with time as research with the bovine genome has grown. Currently the McKay lab performs genetic, genomic, epigenetic and epigenomic work with beef cattle. Our primary interest is identifying the proportion of epigenetic variation associated with complex traits.

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To What Extent Does DNA Methylation Affect Phenotypic Variation in Cattle?

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MAIN LECTURE

DNA methylation is an environmentally influenced epigenetic modification that regulates gene transcription and has the potential to influence variation in economically important phenotypes in agricultural species. We have utilized a novel approach to evaluate the relationship between genetic and epigenetic variation and downstream phenotypes. To begin with, we have integrated RNA-Seq and methyl binding domain sequencing (MBD-Seq) data in order to determine the extent to which DNA methylation affects phenotypic variation in economically important traits of cattle. MBD-Seq is a technique that involves the sample enrichment of methylated genomic regions followed by their next-generation sequencing. This study utilized Illumina next generation sequencing technology to perform both RNA-Seq and MBD-Seq. NextGENe software (SoftGenetics, State College, PA) was employed for quality trimming and aligning the sequence reads to the UMD3.1 bovine reference genome, generating counts of matched reads and methylated peak identification. Subsequently, we identified and quantified genome-wide methylated regions and characterized the extent of differential methylation and differential expression between two groups of animals with extreme phenotypes. The program edgeR from the R software package (version 3.0.1) was employed for identifying differentially methylated regions and regions of differential expression. Finally, Partial Correlation with Information Theory (PCIT) was performed to identify transcripts and methylation events that exhibit differential hubbing. A differential hub is defined as a gene network hub that is more highly connected in one treatment group than the other. This analysis produced every possible pair-wise interaction that subsequently enabled us to look at network interactions of how methylation affects expression. (co-expression, co-methylation, methylation x expression). Genomic regions of interest derived from this analysis were then aligned to previously identified QTL and GWAS regions using Animal QTL database. The approach described here has provided us with evidence that QTL and GWAS regions overlay genomic regions where methylation may regulate transcription.