Genome wide analysis of bovine enhancers and promoters

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Recent studies have shown that the number of genes in human is about the same as the number of genes in nematode, Caenorhabditis elegans. The greater complexity of the mammalian genome is very likely to reflect variation in gene expression, especially cis mechanisms where regulatory molecules bind to elements such as promoters and enhancers close to genes to initiate transcription. Cap analysis of gene expression (CAGE) sequencing has allowed for the accurate annotation of gene promoters (transcription start sites, TSS) and potential active enhancers, a starting point for unravelling mechanisms underlying variation in gene expression. Sequencing short reads from the 5'end of full-length cDNA allows TSSs to be mapped and their expressions to be analysed. To date, TSSs and enhancer regions in the bovine genome are poorly characterised. To generate an atlas of TSSs and enhancer sites in bovine sub-species, we performed CAGE-Seq (CAGE followed by sequencing) on 11 tissues at adult stages, including liver, lung, kidney, thyroid, spleen, muscle, uterus, ovary, blood in indicus and liver, spleen, muscle, mammary, heart in taurus sub-species, and two tissues in the fetal stage, including liver and lung in indicus and liver in taurus sub-species. Our results confirmed that TSSs evolve rapidly between species and even sub-species. The results of this study will accelerate future genomic research and will assist in narrowing down candidate genes with differential TSS usage. Our results also constitute an atlas of potential target sites for tissue specific knock out or knockdown of gene expression with CRISPR/Cas9.