

“Genome-Wide Identification of STAT5 Binding Sequences in Cattle”

Sponsor: USDA/CSREES

Principle Investigator: Liqing Zhang

Abstract:

A comprehensive understanding of the function of a genome requires the identification of not only the protein-coding sequences but also the regulatory sequences. The transcription factor binding sites are important regulatory sequences. Many changes in gene expression are mediated by transcription factor-DNA interactions. Many phenotypic variations may result from mutations in transcription binding sites. Identification of transcription factor-DNA interactions traditionally focuses on individual genes. A new technology called ChIP-Seq, which combines chromatin immunoprecipitation (ChIP) with next-generation sequencing technology, allows large-scale, cost-effective identification of protein-DNA interactions. Taking advantage of this technology and the availability of bovine genome sequence, we propose to conduct a genome-wide identification of the NDA sequences that interact with the transcription factor signal transducer and activator of transcription 5 (STAT5) in cattle. Specifically, we will identify STAT5-binding sites and target genes in bovine liver by ChIP-Seq and microarray analysis. STAT5 controls multiple production-related biological processes including growth, mammary gland development, lactation, and adipogenesis, by mediating the effects of various hormones including growth hormone, growth factors, and cytokines on the expression of hundreds of genes in liver, skeletal muscle, adipose, and mammary tissue. We expect that the proposed research to generate insight into how STAT5 controls these processes and to also facilitate the identification of mutations in STAT5 binding sites that contribute to variations in traits such as growth rate, growth efficiency, body composition, milk yield, and milk composition in cattle.