RESEARCHABSTRACT

ANIMAL SCIENCE

Title: Genome wide identification and annotation of functional regulatory regions in livestock species - **NPB #**15-139

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Scientific Abstract

Pigs are one of the major agricultural animal species as well as an important biomedical model. The domestic pig genome sequence was first reported in 2012 and has been regularly updated since, most recently in 2017. While the annotation of transcribed regions continues to improve, lately using PacBio whole-transcript sequencing, little has been reported in terms of non-coding regulatory regions of the pig genome. Functional non-coding portions of the genome are important contributors to phenotypes, as they regulate gene expression. As part of a FAANG pilot project, multiple tissues from two Yorkshire adult males were collected for chromatin profiling. Nuclei were isolated from fresh tissues and cryopreserved for assessing chromatin accessibility (ATAC-seq). Snap frozen tissue samples were also collected for transcriptomic (RNA-seq) and epigenomic (ChIP-seq) analysis. Datasets have already been generated for lung, liver and spleen including RNA-seq, ATAC-seq and ChIP-seq assays for H3K4me3, H3K27me3, H3K4me1, H3K27ac, and CTCF. Integration of these datasets using a multivariate Hidden Markov Model (ChromHMM) identified chromatin state maps for each tissue that correspond to active and inactive promoters, enhancers, and insulators. These chromatin states will be systematically analyzed and characterized to identify tissue specific and general regulatory elements. We expect that the functional annotations resulting from these study will help enhance our understanding of pig biology and assist in identification of functional genome variants and thus enlighten our interpretation of genome-wide association studies and allow fine-tuning of genomic selection approaches.