Systematic characterization of chromatin dynamics of spleen and bursa tissues induced by NDV infection under heat stress in genetically distinct chicken inbred lines

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Newcastle disease (ND) and heat stress significantly impact poultry production. Spleen and bursa are two major immune organs that are crucial for protecting the host during infection especially in the presence of abiotic stress. Chromatin states plays key roles in regulating gene expression by switching DNA accessibility and transcriptome factors. This study aims to characterize chromatin state variation in response to NDV infection and heat stress (HS) using two highly inbred chicken lines that are relatively susceptible (Leghorn) and resistant (Fayoumi) to NDV. At 3 weeks of age, half the birds of each line were inoculated with 107 EID50 La sota NDV under HS, then ChIP-seq, ATAC-seq, and RNA-seq were performed on the spleen and bursa tissues collected at 6 days post infection (DPI) of two individuals from each treatment-line group (8). Data quality was evaluated by generating the quality matrix and principle component analysis. A global map of regulatory elements (14 chromatin states) with coordinated activation states were defined through genome-wide profiling of four histone modification marks (H3K4me3, H3K27ac, H3K4me1 and H3K27me3), DNA accessibility, and transcriptome in the spleen and bursa. Each chromatin state represented specific enrichment for sequence ontology, transcription, and gene expression associated variants that demonstrate distinct biological functions. The first 5 states had higher fold enrichment within ±2kb of the transcription start site (TSS). Strongly active promoters and flanking active TSS without ATAC were the most dynamic chromatin states, in which the fold enrichment was less in Fayoumi spleen with NDV&HS compared to other groups. Further analysis on the tissue and line-specific regulatory element dynamics due to treatment will provide new information on gene regulatory mechanisms associated with resistant or susceptible to the treatment. Treatment-induced dynamics of the epigenetic landscapes in different immune organs will be used to understand the correlations among chromatin states, gene activity, and specific immune functions.