

Heat-Susceptible and Heat-Resistant Chicken Lines Reveal Differentially Expressed Genes in Liver in Response to Heat Stress

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Xi Lan, Visiting Graduate Student, Department of Animal Science, Sichuan Agricultural University, China;
Carl J Schmidt, Professor, Department of Animal & Food Sciences, University of Delaware;
Susan J. Lamont, Distinguished Professor, Department of Animal Science, Iowa State University

Summary and Implications

Selection of chickens for resilience to heat stress could be a valid strategy to reduce the negative economic impact of climate change. A heat-susceptible broiler line and a heat-resistant Fayoumi line were evaluated for response to heat stress using RNA-seq technology. We found that 278 genes were differentially expressed (False Discovery Rate (FDR) <0.05) between broilers and Fayoumi that were subjected to high ambient temperatures. GO Term Finder analysis revealed that differentially expressed genes (DEGs) were enriched in biological regulation process and catalytic activity function. Many novel key genes and biological networks related to heat stress response were identified and may be biomarkers used to breed chickens that are better able to adapt to heat stress.

Introduction

High ambient temperature is a key environmental stressor and is responsible for an estimated one hundred million dollars in losses for the U.S. poultry industry. Decades of artificial selection have resulted in broilers that have excellent performance in economic traits, but do not acclimatize to stressful conditions such as hot and humid environments. In contrast, the inbred Fayoumi line is more heat resistant likely because it originated in a hot climate (Egypt). We hypothesize that the two distinct lines of chicken will have different gene expression patterns in the liver in response to heat stress. The liver is a metabolic tissue prone to injury under heat stress, and thus was ideal for study in this experiment.

Comparing the heat-susceptible broiler and heat-resistant Fayoumi, this study explores the effects of heat stress on the whole genome-wide gene expression profile in the liver. This information may increase our understanding of the liver response to heat stress and will provide insight needed to breed birds more capable of adapting to climate change.

Materials and Methods

Three week-old male chicks (n=16) were used in this study. The heat stress group (n=8) were exposed to high heat (35°C) for 3h, and the control group (n=8) was maintained at normal temperature (25°C). Liver was collected and used for RNA isolation, cDNA library construction and RNA-sequencing on the Illumina HiSeq 2500.

Reads were mapped to the chicken reference genome (*Gallus gallus* 4.0) using Tophat2 software. Subsequently, mapped read were counted using HTseq software and differentially expressed genes (DEGs) were identified with edgeR software. GO Term Finder software was used to annotate the enriched DEGs.

Results and Discussion

A total of 54 gigabases of sequence data were obtained from the Illumina 2500 platform and revealed many differentially expressed genes (DEGs) between the heat stress group and the control group. Heat treatment compared to control treatment resulted in 8 times more (n=627) DEGs in the broiler (FDR<0.05) than in the Fayoumi (n=78) (Figure 1). A small number (24) DEGs (FDR<0.05) were shared between the two groups. The large number of DEGs in broilers suggests that heat stress more strongly impacts liver metabolism in broilers compared to Fayoumi (Figure 1). When contrasting genetic lines under heat stress, 278 DEGs identified differences in biological responses to heat stress between broilers and Fayoumi. GO Term Finder analysis on the comparison of broiler and Fayoumi revealed many DEGs enriched for biological regulation and cellular metabolism (Figure 2). The top enriched GO terms were “cellular process”, “metabolism process” and “catalytic activity function”.

The results of this study increase the current understanding of whole genome gene expression patterns in response to heat stress. Understanding the biological mechanisms of heat stress is critical for modern scale of broiler production and breeding for heat resistance in chickens.

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Figure 1. Effect of genetic line on number of DEGs in heat stress response. Blue bars represent Fayoumi and green bars represent broiler.

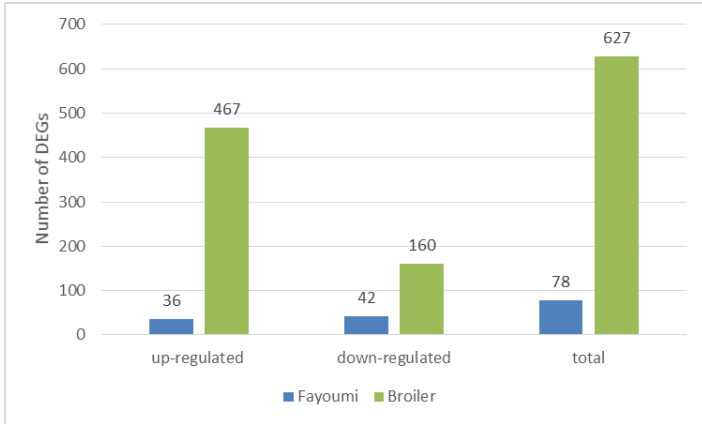


Figure 2. GO Term Finder results from the comparison of broiler and Fayoumi responses to heat stress. The size of the circle depicts log p-value, a measurement of significance. The circles are also colored according to size to emphasize significance. The largest and the dark red circle indicates the most enriched GO Term.

