Genomic analysis of egg quality, production, and blood chemistry traits in heat stressed white laying hens

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Summary

The future of agriculture presents unique challenges, including producing more food using fewer resources, as global climate changes. Genetic selection continues to be a valuable tool in animal agriculture that will help address these challenges. We used genomic data and statistical analysis to investigate response of laying hens to heat stress. Hy-Line W-36 female parent line hens were exposed to heat challenge from 24 to 28 weeks of age in a daily cycle of 7 hours at 35 °C and 17 hours at 30 °C. Most phenotypes were measured at four phases: pre-heat exposure, during acute (first cycle) heat exposure, and during the high temperature phase after 2 and 4 weeks of heat exposure. Eggs were collected in two-week periods for measurements of egg weight. Twelve blood chemistry parameters were quantified using an Abaxis iSTAT handheld analyser: pH, pCO2, pO2, HCO3, TCO2, sO2, iCa, Na, K, glucose, hematocrit, hemoglobin. Feed intake was recorded and used to calculate feed efficiency. Genomic DNA isolated from whole blood was genotyped using the Affymetrix 600K chicken SNP array. After quality control filtering 263703 SNPs and 374 hens were used for genome wide association analysis. A Single SNP approach was taken utilizing GenABEL, an R package. Egg production, feed intake, and feed efficiency were significantly impacted by the hyperthermic challenge. Mean feed intake and egg production decreased sharply in the first two weeks and recovered slightly by week 4. Genome wide analysis revealed regions on chromosomes 1 and 9 that were shared between feed efficiency and feed intake 2 weeks after initiation of cyclic heat exposure. Feed efficiency and feed intake 4 weeks after initiation of cyclic heat exposure also shared regions of genomic control, however these regions were different than those of week 2. Heat exposure significantly impacted all twelve blood chemistry parameters. Most were significantly different (p<0.05) across all two-way time point contrasts. Genomic investigation of response to heat stress in commercial laying hens has provided valuable information that will help inform production and breeding decisions and help feed a growing population.

Keywords: laying hens, heat stress, GWAS
Introduction

The future of agriculture and food production presents unique challenges including climate change and growing population. More people will need to be fed with food produced using fewer resources. The growth in demand for protein parallels the growth in middle class communities (OECD/FAO, 2016). Poultry products (meat and eggs) continue to be a popular source of protein because of their low price, nutritional qualities, and versatility. To supply the increasing demand for poultry protein, progress and innovation in production must continually be pursued.

Heat stress poses a challenge in the poultry industry (St. Pierre et al., 2003). Climate change threatens to raise global temperatures even higher (USDA, 2012). The poultry industry must continue to supply safe, affordable protein in the face of current and emerging challenges. Genetic selection is a tool that can help produce animals that are robust in the face of many challenges.

Genetic selection has been used successfully in poultry production since the beginning of the industry (Havenstein et al., 2003). With recent developments in many genomic technologies, including genotyping and statistical analysis methods, massive amounts of data have become available and provide more power and information to genomic selection strategies. In this study, we use high-density genomic data, deep phenotypes, and statistical analysis to characterize the response of laying hens to heat challenge.

Material and methods

Animals, housing, and treatment

Hens of the Hy-Line W-36 female parent line (generously donated by Hy-Line International, Dallas Center, Iowa, USA) were housed in individual battery cages at 18 weeks of age. Hens had *ad libitum* access to feed and water. During the initial acclimation period, temperature was held at approximately 23 °C. Cyclic heat challenge occurred from 24 to 28 weeks of age. The cyclic temperature cycle consisted of 7 hours at 35 °C and 17 hours of 30 °C per day.

Phenotypes measured

Most phenotypes were measured at four phases: pre-heat exposure, during acute (first time) heat exposure, and during the heat phase after 2 weeks and 4 weeks of heat exposure. Eggs were collected in two-week periods for measurements of egg weight. Twelve blood chemistry parameters were quantified using an Abaxis iSTAT handheld analyser: pH, pCO₂, pO₂, HCO₃, TCO₂, sO₂, iCa, Na, K, glucose, hematocrit, hemoglobin. Egg intake was measured and used to calculate feed efficiency (g egg/kg feed).

Genotypes and analysis

Genomic DNA was isolated from whole blood and genotyped using the Affymetrix 600K chicken SNP array. After QC filtering, mAF >0.01 and CR > 95, the remaining 263703 SNPs and 374 hens were used for genome wide association analysis. The ‘polygenic’ and ‘mmscore’ functions of GenABEL, an R package for statistical genomics, were used for tests of association between SNPs and phenotypes.
Results and Discussion

Mean feed intake and egg production decreased sharply in the first two weeks and recovered slightly by week 4 (Table 1). Egg production, feed intake, and feed efficiency were significantly impacted by the hyperthermic challenge (Table 2). A similar drop in feed intake in response to initial heat exposure was reported by Tanor et al. (1984).

Genome wide analysis revealed regions differing between pre-heat (Figures 1 and 3) and 2 weeks (Figures 2 and 4) after initiation of cyclic heat exposure, which indicate genomic control of response to heat challenge. The same regions on chromosomes 1 and 9 were seen for both feed efficiency and feed intake at 2 weeks after heat exposure (Figures 2 and 4). Shared regions between these two traits are not unexpected because the traits are not independent. These regions on chromosomes 1 and 9 have been previously identified in non-heat stressed birds (Tuiskula-Haavisto et al., 2004; Hansen et al., 2005). Not all regions were shared however, such as the novel chromosome 4 association with feed efficiency. Feed efficiency and feed intake 4 weeks after initiation of cyclic heat exposure also shared regions of genomic control, however these regions were different than those of week 2 (data not shown).

Heat exposure significantly impacted all twelve blood chemistry parameters. Most were significantly different (p<0.05) across all time point contrasts (pre - week 2, pre – week 4, acute – week 2, acute – week 4, pre – acute, week 2 – week 4). In Figure 5 mean changes across time for HCO3, TCO2, PCO2, and PO2 are shown. Van Goor et al. (2016) saw significant changes in 9 shared blood chemistry components due to heat treatment after 1 week of cyclic heat exposure of an experimental advanced intercross line.

Conclusions

Genomic analysis of birds exposed to cyclic heat compared to pre-heat analysis revealed regions impacting response to heat challenge. Heat challenge was also determined to significantly impact twelve blood chemistry parameters.

Table 1. Means of production traits across time.

<table>
<thead>
<tr>
<th>Time</th>
<th>Egg Production (%)</th>
<th>Feed Efficiency (g/kg)</th>
<th>Feed Intake (g/h/d)</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Sd</td>
<td>Mean</td>
</tr>
<tr>
<td>Pre-heat</td>
<td>91.3</td>
<td>9.4</td>
<td>605.9</td>
</tr>
<tr>
<td>Week 2</td>
<td>84.96</td>
<td>7.4</td>
<td>1193.8</td>
</tr>
<tr>
<td>Week 4</td>
<td>86.44</td>
<td>8.6</td>
<td>1051.8</td>
</tr>
</tbody>
</table>

Table 2. P-values of production traits across time produced from One Way ANOVA and Tukey multiple comparisons of means.

<table>
<thead>
<tr>
<th>Time</th>
<th>Egg Production (%)</th>
<th>Feed Efficiency (g/kg)</th>
<th>Feed Intake (g/h/d)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Week 2</td>
<td>Week 4</td>
<td>Week 2</td>
</tr>
<tr>
<td>Pre-heat</td>
<td>P&lt;0.001</td>
<td>P&lt;0.001</td>
<td>P&lt;0.001</td>
</tr>
<tr>
<td>Week 2</td>
<td>P=0.054</td>
<td>P&lt;0.001</td>
<td>P&lt;0.001</td>
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Figure 1. Plot of SNP $-\log_{10}(p\text{value})$ association with Feed intake before initiation of cyclic heat exposure.

Figure 2. Plot of SNP $-\log_{10}(p\text{value})$ association with Feed intake 2 weeks after initiation of cyclic heat exposure.

Figure 3. Plot of SNP $-\log_{10}(p\text{value})$ association with Feed efficiency before initiation of
cyclic heat exposure.

Figure 4. Plot of SNP $-\log_{10}(p$-value) association with Feed efficiency 2 weeks after initiation of cyclic heat exposure.

Figure 5. Changes in mean iSTAT blood chemistry components (HCO3, TCO2, PCO2, and PO2) across 4 treatment time points.

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List of References

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