Genetic Markers Found for Response to Heat Stress in Chickens

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Summary and Implications

A unique line of chickens was evaluated for response to heat stress. We measured body temperature, body weight, breast yield, and digestibility. Genomic (DNA) markers were identified by genotyping on the Affymetric 600K array. We conclude that the traits measured during heat stress do have a genetic component. Genomic markers for the response to heat stress have been identified and may be used for breeding more resilient animals.

Introduction

Climate change is causing increased concern for poultry production. Heat stress causes an estimated economic loss of $125-165 million annually in the U.S. poultry industry alone. Heat stress can cause an increase in body temperature, a decrease in growth rate, and increased mortality.

The objective of this study was to identify genetic regions associated with response to heat stress. We measured body temperature, body composition traits, and digestibility in a unique line of chickens. This information may be used for breeding birds more resilient to heat stress in the changing climate.

Materials and Methods

A broiler X Fayoumi advanced intercross line (AIL) of chickens was used for this study. The broiler line was previously bred for body weight while the Fayoumi line was imported to the United States from Egypt. Fayoumis are described as having both disease and heat resistance.

Birds were raised in four replicates in floor pens under standard feed and rearing conditions. At 17 days of age, the birds were transferred to six environmental chambers per replicate, and acclimated for 3 days. From day 22 to 28 of age, the chambers heated to 35°C for 7 hours per day. The DNA isolated from 468 AIL, 6 broiler, and 6 Fayoumi chickens was genotyped on the Affymetrix 600K chicken SNP axiom array.

Body weight (g) was measured at day 7, 14, 21, and 28 of age. Body temperature (°C) was measured rectally on day 20, 22, 28 of age. Breast yield was calculated by dividing the pectoralis muscle weight by the total body weight on day 28 of age, and multiplying by 100. Digestibility was calculated by:

$$\frac{Avg\ DM\% \ - DM\% * \left(\frac{Avg\ Ti\%}{Ti\%}\right)}{Avg\ DM\%}$$

where Avg DM% is the average dry matter percent of the ileal content collected at necropsy at day 28 across all AIL in the study, DM% is an average of 3 samples of dry matter for a particular animal, Avg Ti% is the average amount of a titanium marker in the ileal content across all AIL in the study, and Ti% is an average of 3 individual measurements and is a percentage of a titanium marker in samples of ileal content from an individual animal.

Parameters for inclusion of genetic markers called single nucleotide polymorphisms (SNP) in analysis included SNP call rate ≥ 95% and minor allele frequency ≥5%.

Testing for phenotypic correlations, normal distribution of phenotypic traits, and fixed effects for each trait, and calculation of heritabilities were done using JMP statistical software. Sire heritabilities were estimated using the JMP EMS (expected mean square) traditional ANOVA method. Fixed effects for each trait were determined based on analysis of variance (ANOVA) estimates with significant terms included as fixed effects with a P value ≤ 0.05.

The GWAS of phenotypic traits with SNP genotypes was done using GenSel software Bayes B, which fits all SNPs simultaneously as random effects, was used for the analysis.

Results and Discussion

All 6 broilers and 6 Fayoumis and 456 of the 468 AIL that were genotyped, passed the sample quality control. A total of 210,117 SNPs had a minor allele frequency ≥%5 and were used for subsequent analyses.

Phenotypic means are listed in Table 1. It is interesting to note that the change in body temperature between day 22 and day 20, as well as day 28 and day 20, was not statistically different than zero.

Many genomic regions explained a large percentage of genetic variation (Table 1). The highest amount was for breast weight percentage with 8.6% of genetic variation explained by a 1 Mb window. Many genetic regions were confirmed as supporting the locations in previous quantitative trait loci (QTL) studies.

The largest percent of genetic variation explained by one megabase window for each trait and the QTL chromosomal location is located in Table 1.

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Table 1. Phenotypic mean with standard deviation (mean(STDev)), heritability (h^2), largest percent of genetic variation (%GV) explained, and chromosome (Chr.) where %GV was revealed for traits measured in an advanced intercross line during pre-heat, acute-heat, and chronic-heat phases, and their changes

Trait[¥]	Mean (STDev)	h^2	%GV	Chr.
BW d7	64.7 (8.08)	4%	3.5%	7
BW d14	140.4 (18.34)	22%	3.5%	7
BW d21	253.6 (34.24)	25%	1.48%	2
BW d28	402.5 (55.68)	36%	2.27%	6
Change in BW d28-21	149.2 (33.91)	21%	1.79%	6
BT d20	42.33 (0.30)	27%	0.96%	14
BT d22	42.44 (0.37)	17%	0.56%	15
Change in BT d22-20	0.09 (0.44)	6%	0.44%	11
BT d28	42.28 (0.31)	20%	1.89%	15
Change in BT d28-20	-0.016 (0.41)	10%	0.41%	22
Breast weight	4.41 (3.62)	19%	8.6%	1
Digestibility	4.52 (0.05)	12%	0.59%	21

[¥] BW: Body weight measured in grams at days 7, 14, 21, 28 and the change between day 28 and day 21.
BT: Body temperature measured in °C at days 20, 22, 28, the changes between day 22 and 20, and the change between day 28 and day 20.
Breast weight: measured in grams at day 28 and expressed as a percentage of body weight at day 28.
Digestibility: Measured as the log of digestibility and expressed as a percentage.