Regions of Genomic Control Identified for Feed Efficiency in Laying Hens under Heat Stress

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Summary and Implications

The future of agriculture presents unique challenges, including producing more food using fewer resources, as global climate changes. Genetic selection and genomic data continue to be valuable tools 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.

Hens of the Hy-Line W-36 female parent line were exposed to a daily cyclic heat challenge from 24 to 28 weeks of age. Eggs were collected daily in two-week periods (pre heat, 2 and 4 weeks post heat) for measurements of egg weight. Egg weights and feed intake were used to calculate feed efficiency (g egg/kg feed). For genome wide association analysis, 263703 genotypes and 374 hens were analyzed for association between genotypes and phenotypes.

Regions on chromosomes 1 and 9 were found to be associated with both feed efficiency and feed intake after 2 weeks of heat challenge. Different regions of chromosome 1 were associated with feed intake and feed efficiency at 4 weeks of heat challenge. Other, not shared, regions were also associated with feed intake and feed efficiency. Genomic investigation of feed intake and feed efficiency under heat stress in commercial laying hens has provided valuable information that will help inform production and breeding decisions and help feed a growing human population.

Introduction

The future of agriculture and food production presents unique challenges including climate change and increasing population size worldwide. 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. 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 to the poultry industry. Climate change threatens to raise global temperatures even higher. 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. 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, phenotypes, and statistical analysis to characterize the response of laying hens to heat challenge.

Materials and Methods

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.

Eggs were collected daily in two-week periods (pre heat, 2 and 4 weeks post heat) for measurements of egg weight. Egg weights and feed intake were used to calculate feed efficiency (g egg/kg feed).

Genomic DNA was isolated from whole blood and genotyped using the Affymetrix 600K chicken SNP array. For genome wide association analysis, 263703 genotypes and 374 hens were used. GenABEL, an R package for statistical genomics, was used for tests of association between genotypes and phenotypes.

Results and Discussion

Egg weight, feed intake, and feed efficiency were significantly impacted by the heat challenge. Egg weight decreased after 2 weeks of heat challenge but recovered after 4 weeks. Feed intake decreased sharply after 2 weeks and recovered slightly by 4 weeks. Changes in egg weight and feed intake resulted in mean feed efficiency (g egg/kg feed) increasing sharply in the first two weeks and moving back towards pre-heat levels by week 4.

Genome wide analysis revealed the same regions on chromosomes 1 and 9 are associated with both feed efficiency and feed intake at 2 weeks after initiation of

cyclic heat exposure (Figures 1 and 2). Shared regions between these two traits were not unexpected because the traits are not independent. Not all regions were shared however, such as the 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 (Figures 3 and 4). A shared region on chromosome 1 and independent regions on chromosomes 6, 9, and 22 are associated with feed efficiency and feed intake 4 weeks after heat exposure.

Genomic investigation of feed intake and feed efficiency under heat stress in commercial laying hens has provided valuable information that will help inform production and breeding decisions and help feed a growing population.

Figure 1. Plot of SNP –log₁₀(p-value) association with Feed efficiency 2 weeks after initiation of cyclic heat exposure.
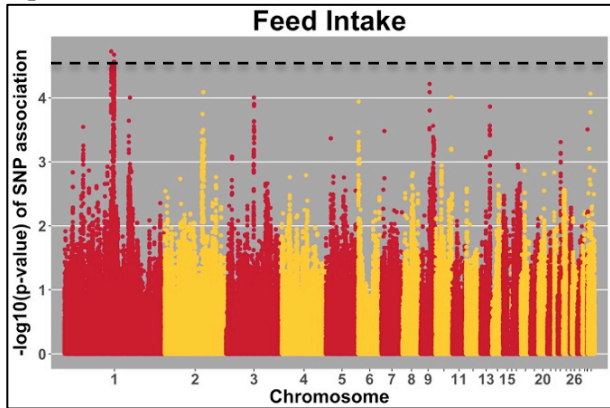

Figure 3. Plot of SNP –log₁₀(p-value) association with Feed efficiency 4 weeks after initiation of cyclic heat exposure.
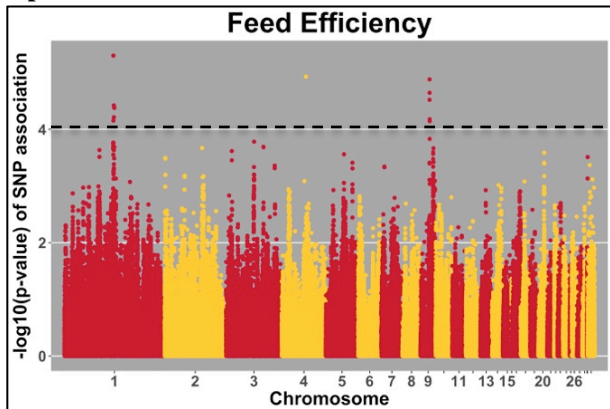
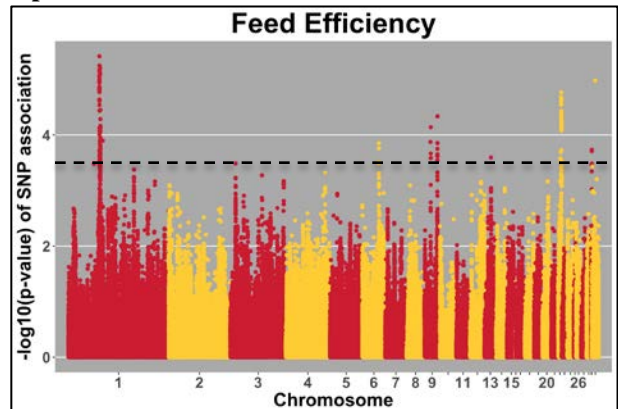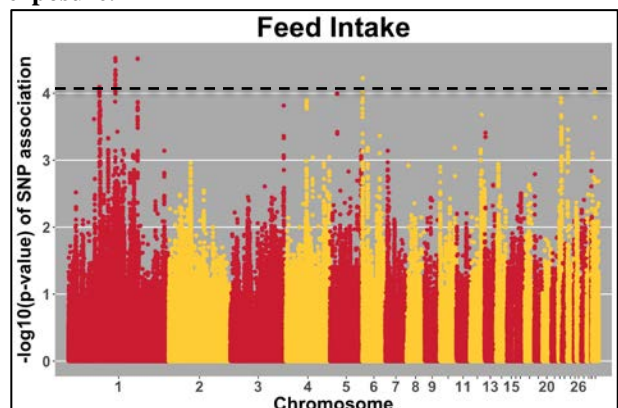**Figure 2. Plot of SNP –log₁₀(p-value) association with Feed intake 2 weeks after initiation of cyclic heat exposure.**

Figure 4. Plot of SNP –log₁₀(p-value) association with Feed intake 4 weeks after initiation of cyclic heat exposure.

Figures 1-4 show associations between various traits and genomic regions. Each point represents one location within the genome. Points with higher x-axis values indicate genomic locations that have a higher association with the trait.