Genomes of African Chickens Show Evolutionary Response to Environmental Stress

A.S. Leaflet R3101

Damarius S. Fleming, Graduate Research Assistant, Iowa State University, Ames, IA;
James E. Koltes, Assistant Professor, University of Arkansas, Fayeteville, AR;
Alyssa D. Markey, Research Scientist, The Maschoffs;
Carl J. Schmidt, Professor, University of Delaware, Newark, DE;
Chris M. Ashwell, Professor, North Carolina State University, Raleigh, NC;
Max F. Rothschild, Distinguished Professor, Iowa State University, Ames, IA;
Michael E. Persia, Assistant Professor, Virginia Polytechnic Institute and State UniversityBlacksburg,VA;[4]
James M. Reecy, Professor, Iowa State University, Ames, IA;
Susan J. Lamont, Distinguished Professor, Iowa State University, Ames, IA

Summary and Implications

The effect of environmental stress on genomic evolution was studied using three populations of chickens, two ecotypes (Uganda and Rwanda) indigenous to Africa and one that was imported to Africa from India (Kuroiler). The chickens (N=196) were genotyped and then analyzed for the presence of genes and gene regions thought to be under selection by environmental stressors that has allowed them to survive in the presence of such circumstances. Through the use of various statistical and annotative approaches we were able to determine that all three populations show selection pressure for variants near genes related to oxidative stress, which can be brought upon by climate and poor food resources. Additionally selection for kinase activity, and calcium ion movement were also detected. Data also showed that all populations harbor fixed regions of the genome that overlap with known quantitative trait loci (QTL) related to commercial and behavioral traits. Overall, this study provides information on genes possibly connected to survival in stressful environments and has the potential to be used as a model for finding genomic regions of tolerance in commercial populations.

Introduction

In the wild, natural selection on a trait occurs when the presence of a beneficial mutation appears in a population and then through a result of sexual selection rises to high frequency in that population. Studies into how populations are shaped by natural selection can help decipher how a population may have evolved or adapted to have the current traits that it exhibits. Environmental stressors can act as agents of natural selection in wild populations of animals. These animals may have developed unique adaptations to the stressors that may include drought, pathogens, pollution, and heat stress. Studying how genes of indigenous birds evolved under selective pressure, as a way to adapt to harsh environments, may explain how chickens, both wild and commercial, tolerate stress from their environment. This study’s goals were to examine the genomic diversity of the three chicken populations and identify genes or genomic regions that may confer adaptive advantages to environmental stressors within the populations.

Materials and Methods

Samples consisted of indigenous chickens from Uganda (N=72) and Rwanda (N=100), plus Kuroilers (N=24, an Indian breed sampled in Uganda). Blood was collected from all 196 birds to isolate DNA using FTA cards for genotyping on the Affymetrix Axiom ® 600k Chicken Genotyping Array. The data were controlled for quality prior to analysis for areas of the genome affected by natural selection. The integrated haplotype score (iHS) statistic was calculated, which can determine selective pressure based on how much of the population is identical for high frequency genetic variants. The data were also examined for runs of homozygosity (ROH), which are long stretches of identical genes that can point out regions of positive selection. Genetic markers showing selective pressure were annotated to nearby genes and then clustered by function.

Results

Genes under strong selective pressure in our studied populations all have functions related to reducing oxidative stress and metabolic heat which may represent a mechanism to cope with environmental stress by controlling the impact of its symptoms. Results from the runs of homozygosity analyses showed that all populations use calcium activated pathways and kinases to reduce and control oxidative stress brought upon by heat stress from the environment. Further inspection of the ROH of ~1MB in length was performed to examine if any ROH overlapped quantitative trait loci (QTL) known to affect commercial traits. This overlap between wild chicken ROH and commercial chicken QTL may point to genes or gene regions associated with environmental stress tolerance (Table 1.)

Discussion

Results indicated that the birds may use calcium-mediated responses and kinases to counteract environmentally generated oxidative stress. Evidence of this was also supported by the clustering of gene functions located and fixed within the long stretches of ROH. The ROH within the African chickens also overlapped with known QTL for traits related to behavior, disease susceptibility, metabolism, fatness and body temperature. The overlap of the ROH and these QTL may be evidence of areas that can be used to select birds that show greater tolerance to environmental stressors that limits production. Overall, this evidence of selective pressure on genes provides a window into discerning the mechanisms under selection in chickens to mediate tolerance to the effects of challenging environments.

Acknowledgements

This material is based upon work supported by the National Institute of Food and Agriculture, U.S. Department of Agriculture, under award number #2011-67003-30228. Damarius S. Fleming was supported as an USDA National Needs Fellow, Award #2011-38420-2005.

Table 1. **QTL Traits Overlapping Regions Under Selection In The Studied African Populations**

Chromosome	Trait
1	Fear-stand latency
1	Oocyst shedding
1	Interferon-gamma level
2	Feather pecking
2	Receiving feather pecking
2	Feather pecking
2	Troponin T concentration
2	Skin fat weight
2	Body temperature
2	Body temperature
3	Antibody response to Sheep Red Blood Cell (SRBC) antigen
3	Antibody response to Keyhole limpet hemocyanin (KLH) antigen
3	Antibody response to Brucella abortus
5	Triglyceride level
5	Antibody titer to lipoteichoic acid (LTA) antigen
5	Antibody titer to LPS antigen
5	Abdominal fat weight
5	Skin fat weight
14	Antibody titer to lipoteichoic acid (LTA) antigen
14	Antibody response to Mycobacterium butyricum (MB) antigen
14	Antibody response to Keyhole limpet hemocyanin (KLH) antigen
14	Antibody titer to lipopolysaccharide (LPS) antigen
14	Intramuscular fat
19	Abdominal fat weight
19	Abdominal fat percentage

Table showing QTL that overlap with ROH ≥ 900,000 base pairs and the associated trait for the QTL. QTLs and ROH overlap either partially or ROH falls completely within the QTL for trait listed.