Evidence of Natural Selection Footprints Among Some African Chicken Breeds and Village Ecotypes

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Summary and Implications

In Africa, where general breeding and vaccination programs for chickens are absent, natural selection is a major factor in shaping genetic variation for adaptation to abiotic and biotic environmental stressors, e.g. heat, high altitude and disease. In this study two groups of chicken populations adapted to two different environments (North-African, and West-African), in addition to a synthetic commercial breed (Kuroiler), were genomically compared. Genomic comparison using SNPs between such unselected populations and the selected and genetically improved commercial one will likely result in detection of natural selection footprints and genes responsible for adaptation traits. This information may assist improving commercial lines to be more tolerant/resistant under expected climate change. Knowledge of genes involved in immunity and disease resistance could be utilized for genome selection and lessen the utilization of antibiotics which will increase chicken meat/egg quality for American consumers.

Introduction

Egypt (North-Africa, NA) is located in the warm desert climate zone, while Uganda and Rwanda (East-Africa, EA) are in the tropical savanna zone. The main environmental differences between Egypt and both Eastern African countries are altitude, precipitation and temperature which may have significant effects in shaping the genetic diversity among the chicken populations of each country. The most prevailing indigenous Egyptian chicken breeds that were also sampled and studied in the current study were: 1) the Baladi Naked-neck ecotypes; 2) the Fayoumi breed, known for its aggressive behavior and resistance to several diseases e.g. Rous Sarcoma virus, Marek's disease virus and E. tenella, lower cholesterol in eggs, and stronger shell; and 3) the Dandarawi, smallest in size and most tolerant to heat (>40 ºC) and resistant to local diseases. The two sampled EA ecotypes are those found and adapted to Uganda and Rwanda environments which include adaptation to high altitudes, unbalanced rations and pathogen exposure. For comparison to the EA ecotypes, the synthetic commercial Kuroiler breed was also studied. Kuroiler is a hybrid of White Leghorn males and Rhode-Island-Red females, developed in India as a dual-purpose chicken breed, and has been selected for scavenging ability and tolerance to climatic stress in India. This study aimed to investigate the impact of natural selection on the genomic variation and genes and pathways underlying them by examining methods that detect runs of homozygosity that can be considered as genetic "footprints" showing selection pressure.

Materials and Methods

We investigated selection "footprints" utilizing 292 birds that were randomly sampled from five African chicken populations from Egypt (Baladai, Dandarawi and Fayoumi), Uganda and Rwanda ecotypes and the Kuroiler. Samples were genotyped using the Affymetrix 600K Axiom® Array, and genotyping data were analyzed for detection of natural selection "footprints" using: 1) Within-population consensus runs of homozygosity and 2) Between-populations genetic differentiation index (Fst).

Results and Discussion

Results indicated that both methods detected DNA segments of both ROH and Fst sweeps (representing selection footprints) carrying several genes that may contribute to chicken adaptation to local environmental stresses. Genes detected in East African populations are associated with oxygen consumption and heme binding, protection from hypoxia (low oxygen), reduction of oxidative stress, ion binding and transport in addition to immunity response. North African (Egyptian) breeds were found to carry genes associated with physiological functions of carbohydrate metabolism, reduction of oxidation, immunity response and ion binding and transport. Gene frequency differences between Kuroilers and each of East- and North-African chickens (Figure 1) indicated distinctive signatures associated with reproduction and growth performance and response to acute heat stress in the Kuroiler breed.

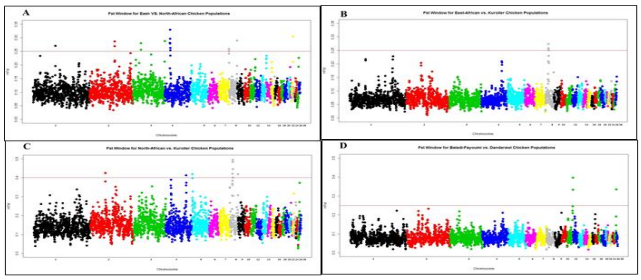

Figure 1. Fst Analyses for inter-populations comparisons: (a) East-African vs. North African, (b) East-African vs. Kuroiler, (c) North-African vs. Kuroiler, and (d) Baladi-Fayoumi vs. Dandarawi.

Conclusions

Results suggest existence and location of genomic regions associated with adaptation.

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