

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

Authors : Ahmed Elbeltagy, Francesca Bertolini, Damarius Fleming, Angelica Van Goor, Chris Ashwell, Carl Schmidt, Donald Kugonza, Susan Lamont, Max Rothschild

Abstract : The major factor in shaping genomic variation of the African indigenous rural chicken is likely natural selection drives the development genetic footprints in the chicken genomes. To investigate such a hypothesis of a selection footprint, a total of 292 birds were randomly sampled from three indigenous ecotypes from East Africa (Uganda, Rwanda) and North Africa (Egypt) and two registered Egyptian breeds (Fayoumi and Dandarawi), and from the synthetic Kuroiler breed. Samples were genotyped using the Affymetrix 600K Axiom® Array. A total of 526,652 SNPs were utilized in the downstream analysis after quality control measures. The intra-population runs of homozygosity (ROH) that were consensus in > 50% of individuals of an ecotype or > 75% of a breed were studied. To identify inter-population differentiation due to genetic structure, FST was calculated for North- vs. East- African populations in addition to population-pairwise combinations for overlapping windows (500Kb with an overlap of 250Kb). A total of 28,563 ROH were determined and were classified into three length categories. ROH and Fst detected sweeps were identified on several autosomes. Several genes in these regions are likely to be related to adaptation to local environmental stresses that include high altitude, diseases resistance, poor nutrition, oxidative and heat stresses and were linked to gene ontology terms (GO) related to immune response, oxygen consumption and heme binding, carbohydrate metabolism, oxidation-reduction, and behavior. Results indicated a possible effect of natural selection forces on shaping genomic structure for adaptation to local environmental stresses.

Keywords : African Chicken, runs of homozygosity, FST, selection footprints

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