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Abstract

Diseases remain a major challenge in chicken population leading to reduced performance and economic losses. Whenever possible, chicken population should be reared under production systems with minimum predisposing factors to diseases and other shortcomings during their productive lifetime. Selection for resistance is an attractive option when responding to the diseases challenge. The chicken major histocompatibility complex (MHC) is a highly polymorphic region associated with immune response and disease resistance. The aim of this study was to investigate genetic diversity and as well as identify signatures of selection within the MHC, which help local chicken ecotypes to withstand disease and environmental challenges. A total of eight local chicken ecotype populations from different ecological zones in Kenya and two commercial layers (CL) chicken populations were assessed using single nucleotide polymorphisms (SNPs). Principal component analysis (PCA) showed that the two populations, local chicken ecotypes and commercial chickens were distinct. Expected heterozygosity ranged from 0.21 to 0.28 in local chicken ecotypes and was 0.26 in commercial layers. As expected, inbreeding was much higher in commercial chicken layers at 0.51 - 0.64 than indigenous chickens at 0.04 - 0.27. Selection signature analysis using fixation index (FST) detected two major regions of divergence in commercial and indigenous chickens, within the MHC region mapping to seven genes: KIFC1, ZNF 692, TRIM 7, TRIM 7.2, TRIM 39.2, BLEC 3 and YLEC 1, in local chicken ecotypes which are associated with immune response and disease resistance. This result shows that local chicken ecotypes possess significant genetic diversity within the MHC region, which can be exploited to improve the chicken breeds for disease resistance. However, a comprehensive study using a larger sample size is needed to provide more insight on the viability of the MHC region.