

Viral diseases affecting chicken, like Marek's disease and avian influenza, are currently causing tremendous losses in the industry and greatly impacting the livelihoods of the small scale farmers in the least developed countries. There is no effective cure or vaccine to control these diseases. It is believed that domestication and commercialization of poultry may have led to the loss of genetic variability at innate immune genes with commercial populations more susceptible to disease compared indigenous and wild population. The main objective of this study was to identify and assess DNA polymorphisms present at innate immune candidate genes for genetic resistance to avian viral diseases. Two candidate's genes were shortlisted from the literature: the BLB2 major gene has been associated with Marek's disease resistance and Mx gene is a putative candidate gene towards resistance to avian influenza. Species homologs of these two genes were obtained from GenBank and analyzed with the PAML package to detect possible signatures of selection over evolutionary time (d_N/d_S). PCR followed by sequencing was carried out on both genes with PCR optimization for MX gene being successful. Seventeen population comprising commercial, indigenous and wild populations were analyzed for allele, genotype frequencies, HWE, diversity indices, and population divergence was analyzed to detect possible recent signatures of selection in different populations. Nine SNPs were discovered in a partial segment of the Mx gene amplified. The frequency of the A SNP allele at Mx position 229 of the amplified gene segment corresponding to codon 631 in Mx protein that encodes resistance to avian influenza was the highest in the wild population. The distribution of the alleles at this locus was found to be due to drift and not selection for disease resistance towards avian influenza. Seven loci of the Mx gene segment had some population groups deviating significantly from HWE, Likewise haplotypes from the Indian and East African subcontinents deviated significantly from HWE. The East African subcontinent had the highest diversity as well as the highest haplotypes. Haplotype 1 and 5 are the possible ancestral haplotypes. There was some geographic correlation found between haplotypes and avian influenza outbreaks. This results suggests that the haplotype would be more defining towards disease resistance as compared to a single SNP studies. Tests for signatures of selection on the MX gene, using population differentiation tests show evidence of recent signals of positive selection (selective sweeps, genetic hitchhiking and population differentiation) in the wild Populations. Signatures for selection tests based on species divergence for both the Mx and BLB2 genes show amino acid sites in the functional domains of the two proteins across all species under positive selection. In conclusion, both genes studied show evidence of adaptive evolution. Further work needs to be carried out on both candidate genes with more sequence information on a longer gene fragment, in a larger sample and population size in order to confirm these first results and pave way for more studies