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Immunogenetics and genetic variations in indigenous chicken in the tropics using SNP data

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Abstract
This study used data from 150 indigenous chicken from four agro-ecological zones in Rwanda to provide deep insight of the population structure and variation of the immunogenetics using several approaches based on phenotypic and SNP data. The population structure of indigenous chicken was analysed using Principal Component Analysis (PCA), ADMIXTURE analysis, and phylogenetic relationships for the whole genome and at chromosome 16. The study used 65,945 SNPs from the collected chicken. Phenotypic analysis was done for the Newcastle disease titer (ab) alongside bodyweight at 20 weeks with the highest having 1.6 kg. The genome analysis was done using the genotyping-by-sequencing approach. The grouped the indigenous chicken into two genetic clusters, which was confirmed by ADMIXTURE analysis that revealed that the lowest cross-validation (CV) error (0.51) was at K=2. The analysis of Population structure at chromosome 16 showed that the population had the lowest CV error (0.50) at K=1. The mean body weight and antibody titer were 1673.61±237.14 g and .5±55.35, 1311.34±121.9 g and 8832.5±55.36, respectively, depicting an inverse relationship between bodyweight and antibody titers. The cluster means for body weight and antibody titers were significantly different (P<0.001) for body weight and antibody titers. The indigenous chicken genetic clusters in Rwanda have variation in antibody titers which can be attributed to varied selection pressure. The observed genetic diversity of the indigenous chicken for disease resistance should be well-thought-out when scheming a selection programme to ensure that the ICs population is sustainable, flexible and simultaneous improvement of this trait. Based on this study's findings government should implement strategies that conserve and maintain the genomic diversity of Rwanda indigenous chicken.

Keywords: Chromosome 16, immune traits, flexibility, MHC, sustainability