Tropentag, September 15-17, 2021, hybrid conference

"Towards shifting paradigms in agriculture
for a healthy and sustainable future"

Genetic Diversity at Whole Genome and Chromosome 16 of Indigenous Chicken in Rwanda

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Abstract

ABSTRACT

Indigenous chicken (IC) farmers in developing countries desire enhanced disease resistance alongside improvement of body weight and egg production. This study aimed at providing insight into the population structure and immunogenetic variability of the indigenous chicken using various methods. Population structure of IC was analysed through genotypic clustering, admixture analyses and phylogenetic relationship for the whole genome and at chromosome 16. A total of 150 IC sampled from five agro-ecological zones in Rwanda were phenotyped for Newcastle disease alongside body weight and genotyped with the genotyping-by-sequencing (GBS) method. After quality control procedures for SNP data, 65,945 SNPs retained for analysis. Following PCA, the IC were grouped into two genetic clusters, which were confirmed by lowest CV error (0.51) rates at K = 2. Population structure assessments based on SNPs in the MHC region indicated that the population as one with lowest CV error (0.50) rates which was confirmed at K =1. Clusters one a mean body weight and antibody titre of 1673.61 ±237.14g and 4912.5±55.35, respectively. Corresponding values for cluster 2 were 1311.34±121.9g and 8832.5±55.36. The clusters differed significantly ($p < 0.001$) for body weight and antibody titre. The cluster with low mean in bodyweight (Cluster 1) and high mean in titre and vice versa. The IC in Rwanda have been selected naturally for disease resistance against Newcastle. The observed genetic diversity of IC for BW and their negative association should be considered when designing a selection programme to ensure sustainability, flexibility and simultaneous improvement of the two traits.

Keywords: Disease resistance, MHC, sustainability

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