RESEARCH QUESTION
What are the differences in genomic and immunogenetic variation of indigenous chicken?

Introduction

• Undesirable effects of increased use of disease control measures
• Breeding for disease resistance has the potential to reduce or complement use of drugs
• Artificial selection using genomic information has the potential to accelerate rate of gain for traits in IC
• There is no information on immunogenetic variation for disease resistance in IC

Objective

The study investigated population structure of ICs at both the whole-genome and chromosome 16

Materials

• 150 IC were used from four agro ecological zones.
• DNA was extracted from blood samples using DNA extraction kit.
• Raw reads were obtained by GBS

Methods

Analysis of Population Structure

• was performed by genotypic clustering at whole genome & at chromosome 16.
• PCA & Admixture analysis was performed using all SNPs (n = 65,945).

Results

• Genetic diversity at whole genome & chromosome 16 revealed two & one genetic groups, respectively.
• At chromosome level, that there may be significantly less genetic variation than the variation within the whole genome of a population.

Conclusion

• There is no significant genomic diversity in IC populations, when classified based on chromosome 16 (MHC region) & whole genome classification grouped IC into two genetic clusters.
• Conservation programme be implemented to ensure increase in genetic diversity in indigenous chicken

Figure 1
Figure 1 & 2: PCA plot at the whole genome & at chromosome 16

Figure 3
Figure 3: Bayesian posterior probability of membership K-values of 2 to 4.

Figure 4
Figure 4: showing the cross-validation errors of the k-clusters