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AO Ochiel
Animal Breeding and Genomics Group, Department of Animal Sciences, Egerton University, P.O. Box 536, 20115 Egerton, Kenya

K Ngeno
Animal Breeding and Genomics Group, Department of Animal Sciences, Egerton University, P.O. Box 536, 20115 Egerton, Kenya

AK Kahi
Animal Breeding and Genomics Group, Department of Animal Sciences, Egerton University, P.O. Box 536, 20115 Egerton, Kenya

Distribution of mutational effects in Indigenous Chicken

AO Ochiel, K Ngeno and AK Kahi

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Abstract
The selection of the Indigenous Chicken (IC) has amounted to remarkable phenotypic changes traced back to the variations in their genome. These variations take many forms among them, insertions and deletions (INDELs). This study applied whole genome re-sequencing to characterize the distribution of INDELs in IC. Eight IC birds from eight ecotypes; Siaya, Kakamega, Narok, West Pokot, Taita-Taveta, Turkana, Bomet, and Lamu were re-sequenced. One representative bird per ecotype was selected based on the Principal Coordinate Analysis and heterozygosity from the microsatellite data. A variant calling process to identify SNPs and INDELs was done. Valid INDELs retained for analysis had a read dept (dp) >4 and Minimum quality (minQ) 20. A total of 2.7 million INDELs were discovered. Of this, 1,430,403 and 1,448,720 were insertions and deletions respectively. All ecotypes recorded more deletions compared to insertions. The total affected bases due to INDELs were 10,645,076. Deletions were generally longer (43 bp) and insertions were shorter (28 bp). The distribution of INDELs in the IC genome both among the ecotypes and between the chromosomes within an ecotype proved to be different. The information generated from this study will render a new and deeper understanding into the ways genetic variations mold IC phenotypic diversity.

Keywords: Ecotype, indigenous chicken, Indels