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Optimization of response to selection using genomic selection in indigenous chicken breeding programmes

C.W. Ndung'u#, T.K. Muasya, & T.O. Okeno
Animal Breeding and Genomics Group, Department of Animal Sciences, Egerton University, P.O. Box 536-20115, Egerton, Kenya

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Abstract

This study tested the hypothesis that the use of pooled genetic and phenotypic parameters and genomic selection would optimize selection response in indigenous chicken breeding programmes. This premise was tested with deterministic simulation in three breeding schemes based on the sources of information used to estimate breeding values. These schemes used a conventional breeding scheme with non-pooled parameters (CSN), pooled parameters (CSP), and genomic information in a genomic selection scheme (GSS). A one-tier closed nucleus breeding programme was considered with a mating ratio of 1 to 5 for males to females, Four traits were used in the breeding goal, namely live weight at twelve weeks (LW), egg number for twelve weeks (EN), age at first egg (AFE), and antibody response (Ab). The genetic gain for CSN was 1.5 times higher than that of CSP. The rate of inbreeding for CSN was 19% lower than in CSP. The accuracy of selection followed the same trend with CSN producing 9% higher accuracy of selection than CSP. The GSS scheme resulted in an additional 59.3% genetic gain and 30% accuracy compared with CSP. The GSS scheme also had a reduced rate of inbreeding by 46% compared with CSP. When compared with CSN, GSS produced 38.7% greater genetic gain, a 27% lower rate of inbreeding and 21.0% higher accuracy of selection. Use of pooled parameter estimates and genomic information optimized response to selection, whereas non-pooled inputs overestimated and underestimated rates of genetic gain and inbreeding.

Keywords: deterministic simulation, economic gain, genetic gain, inbreeding
#Corresponding author: catendungu11@yahoo.com