

Genomic selection accelerates sustainable long-term genetic gain in the Barentu indigenous egg-laying chicken

Indigenous chickens (IC) make up 95% of Eritrea's national flock and are an important source of income and nutrition but their productivity remains low. This study used stochastic simulation in MoBPS to evaluate long-term responses to traditional and genomic selection for developing specialized egg-laying Barentu chicken. We compared the performance of pedigree-based best linear unbiased prediction (PBLUP), genomic best linear unbiased prediction (GBLUP) and single-step genomic BLUP (ssGBLUP) under alternative genotyping strategies. Seven selection scenarios were evaluated, differing in both the prediction method and the proportion of genotyped selection candidates. These scenarios included PBLUP, GBLUP and five ssGBLUP configurations with varying levels of genotyping: 25% of females genotyped (ss25), 50% of females genotyped (ss50), 100% of females genotyped (ss100), 100% of females plus 25% of males genotyped (ss100.25), and 100% of females plus 50% of males genotyped (ss100.50). This design enabled a systematic assessment of the impact of partial and sex-specific genotyping on the accuracy of genetic evaluations under single-step genomic selection. A single-tier closed nucleus breeding program was simulated over 20 generations for three traits: age at first egg (AFE), egg number during the first 12 weeks after onset of lay (EN12) and residual feed intake measured 12 weeks post onset of lay (RFI). These traits were combined into a total merit index for selection. Across all scenarios, 80 males and 480 females were selected from 1,075 male and 1,075 female candidates per generation, corresponding to selection intensities of 1.97 and 0.89 for males and females, respectively. Model outputs included cumulative genetic gain (ΔG), accuracy of estimated breeding values (EBV), rate of inbreeding (ΔF) and ratio of genetic gain to inbreeding ($\Delta G/\Delta F$). ANOVA indicated significant ($P < 0.0001$) effects on index and EBV accuracy at generation 20. Genomic selection outperformed pedigree-based selection, with GBLUP producing 29% and 26% greater ΔG in males and females, respectively (8.53 and 8.41 units/generation). EBV accuracy differed among selection scenarios, with the highest accuracies observed under ss100.50 and lowest under PBLUP and ss25. In females, EBV accuracy was highest under ss100 and ss100.50 and lowest under PBLUP and ss25. In males, ss100.50 performed best, followed by GBLUP and ss100.25, whereas PBLUP and ss25 showed the poorest accuracy. Rates of inbreeding (ΔF) varied across scenarios, with PBLUP resulting in the lowest ΔF in females (0.72-3.6%) and ss25 producing the highest (1.47-9%). GBLUP achieved the greatest ratio of genetic gain to inbreeding ($\Delta G/\Delta F$), exceeding PBLUP by 19-23%, followed closely by ss100.50. Overall, GBLUP maximized $\Delta G/\Delta F$ in both females (441.9) and males (437.2) whereas ssGBLUP scenarios attained approximately 90% of the genetic gains achieved by GBLUP. In conclusion, genomic selection particularly ssGBLUP will accelerate genetic improvement while maintaining diversity in Barentu indigenous egg-laying chickens.