Esatu, W., Assen, A., Hanotte, O., Dessie, T., Frank-Lawale, A. (2026) Integrating BLUP and selection index methods to enhance genetic improvement in tropical poultry breeding programs, *Proceedings 13th World Congress on Genetics Applied to Livestock Production* 23725: https://doi.org/10.31274/wcgalp.23725 ©2026 Esatu, et al. CC BY-NC-ND

Integrating BLUP and selection index methods to enhance genetic improvement in tropical poultry breeding programs

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Introduction

Genetic selection enables the identification of superior individuals to improve productivity, health, and adaptability in subsequent generations, and it forms the foundation of modern animal breeding. In poultry breeding, genetic evaluation has evolved considerably with advances in quantitative genetics and computing capacity. Breeding programs relied primarily on phenotypic performance, which reflects both genetic and environmental effects. The introduction of Best Linear Unbiased Prediction (BLUP) marked a major advancement by allowing the estimation of breeding values while accounting for systematic environmental effects and genetic relationships among individuals (Henderson, 1975). The Tropical Poultry Genetics Solutions (TPGS) program of the International Livestock Research Institute (ILRI) aims to develop improved indigenous-derived and composite chicken lines adapted to smallholder production systems in Africa and Southeast Asia. The breeding program focuses on improving growth, egg production, resilience, and adaptability to local environments. Initial selection was based on individual performance (mass selection), which limits selection accuracy because information from relatives and pedigree relationships is ignored. With the availability of pedigree data, BLUP-based genetic evaluation can be applied to improve selection accuracy and genetic gain. In addition, selection index methodology allows the simultaneous improvement of multiple economically important traits by combining estimated breeding values (EBVs) into a single selection criterion (Hazel *et al*., 1994). The objective of the study is to estimate the genetic parameter estimates of the four chicken lines developed, to determine the selection accuracy of breeding goal traits by implementing best linear unbiased prediction (BLUP) model and selection index approach for chicken lines developed under at ILRI, Addis Ababa, Ethiopia.

Materials & Methods

Data collection. Performance and pedigree data were collected from ILRI's poultry research facility in Ethiopia using the TPGS digital recording system (Esatu *et al.,* 2025). Records from two generations were available for four chicken lines: LIL20 (n = 778), WIL20 (n = 602), BIL20 (n = 698), and NHIL20 (n = 641). Traits recorded included body weight at 16 weeks of age in grams (W16), average daily gain up to 16 weeks in grams (ADG), age at first egg in weeks (AFE), egg number up to 45 weeks of age (EN), and egg weight in grams (EW). Data on egg production traits were limited, resulting in larger standard errors for some genetic parameter estimates.

Genetic evaluation using BLUP. Genetic parameters and EBVs were estimated using linear mixed models implemented in WOMBAT software with the average information restricted maximum likelihood (AI-REML) algorithm (Meyer, 2007). Fixed effects included hatch month, hatch year, sex, and hatch batch, while the random effect was the additive genetic effect of

individual chickens. An additive genetic relationship matrix derived from pedigree information was used. The fixed-effects representation of the model is presented in Eq.1.

$$y_{(ijkl)} = \mu + m_i + y_j + s_k + b_l + \varepsilon_{(ijkl)} \quad (1)$$

Where y is the observation of the trait, m is the fixed effect of the hatching month, y is the fixed effect of the hatch year, s is the fixed effect of the sex of the chicken, b is the batch of hatching and ε is the error term. The animal model in matrix notation is presented in Eq.2.

$$\mathbf{y} = \boldsymbol{Xb} + \boldsymbol{Za} + \boldsymbol{e} \quad (2)$$

where y is the vector of phenotypic records, b is the vector of fixed effects, a is the vector of random additive genetic effects, e is the residual vector, and *X* and *Z* are incidence matrices.

Selection index. A selection index was constructed to combine breeding goal traits into a single criterion. Economic weights for traits were derived from reported economic importance in similar production systems (Hazel *et al.,* 1994). The index value was calculated using Eq.3.

$$I = b_1\, EBV_{W16} + b_2\, EBV_{AFE} + v3\, EBV_{EN} + v4\, EBV_{EW} \quad (3)$$

where I is the index value, 0.5, 0.25, 0.2 and 0.05 were the economic weight of W16, AFE, EN and EW traits respectively, and EBV is the estimated breeding value of each trait.

Inbreeding and predicted selection accuracy. Individual and population-level inbreeding coefficients were estimated using pedigree information within the BLUP framework (Meyer, 2007). The rate of inbreeding per generation was calculated using Eq.4.

$$\Delta F = (F_{(t+1)} - F_t)/(1 - F) \quad (4)$$

Predicted selection accuracy and expected inbreeding rates for W16 were simulated using SelAction software (Rutten *et al.,* 2002).

Results

The mean body weight at week 16, EBV, and inbreeding rate across generations are presented in Table 1. Mean body weight at 16 weeks increased from generation 0 to generation 2 in most lines and both sexes, indicating positive phenotypic progress. Across lines, increases ranged from approximately 8.7% to 33%, with the highest gain observed in NHIL20. In contrast, BIL20 showed a reduction in phenotype across generations while the genetic trend increases.

The inbreeding level in generation 2 for both male and female ranged from 2.1% to 3.6% across lines, while the rate of inbreeding in generation 2 ranges from 2.31 to 3.1%. This exceeds the recommended thresholds of 0.5–1.0% per generation (Oldenbroek and Calus, 2024). While the effective population size (Ne*)* of the chicken lines ranging from 16 to 22.

EBVs for W16 increased across generations in all four lines, demonstrating positive genetic trends. The greatest improvement was observed in NHIL20, consistent with its higher genetic variability. Correlations between phenotypic W16 and EBVs ranged from 0.65 to 0.90, indicating that while phenotype remains informative, BLUP provides improved ranking by accounting for environmental and pedigree effects.

Table 1. Mean body weight at week 16 of age, EBV and inbreeding level of chicken across generations

Breed	Gen.	Mean weight_16 (Sd)		Mean EBV (SE)		Mean inbreeding lebvel (%) (SE)	
		Male	Female	Male	Female	Male	Female
LIL20	0	1099.1(228.7)	843.2 (158.5)	4.9(151.7)	-3.5(107.8)	0.0(0.0)	0.0(0.0)
	1	1103.9(196.6)	856.2(133.0)	105.6(116.7)	95.3(89.8)	0.0(0.0)	0.0(0.0)
	2	1149.5(176.3)	915.3(129.7)	192.4(101.7)	191.9(80.2)	2.1(5.9)	2.5(6.8)
BIL20	0	1556.8(234.1)	1280.7(165.1)	-6.3(104.4)	6.6(78.2)	0.0(0.0)	0.0(0.0)
	1	1467.2(355.1)	1183.5(284.9)	71.4(84.8)	74.9(77.1)	0.0(0.0)	0.0(0.0)
	2	1469.6(205.5)	1131.9(160.8)	113.3(81.8)	93.8(73.5)	2.3(4.9)	3.5(5.6)
NHIL20	0	1321.8(425.9)	885.9(299.1)	22.6(373.6)	-17.2(258.2)	0.0(0.0)	0.0(0.0)
	1	1314.2(279.1)	987.6(215.9)	324.5(229.5)	377.8(174.9)	0.0(0.0)	0.0 (0.0)
	2	1586.3(267.1)	1197.2(200.9)	500.5(218.5)	502.7(161.7)	3.6(6.2)	2.6(5.1)
WIL20	0	1207.2(217.5)	960.1(218.1)	-4.7(68.8)	3.2(70.8)	0.0(0.0)	0.0(0.0)
	1	1216.3(271.7)	970.8(213.1)	55.9(76.0)	59.5(91.7)	0.0(0.0)	0.0(0.0)
	2	1383.9(255.5)	1050.6(175.9)	97.8(106.0)	93.8(88.4)	2.5(5.9)	2.5(6.5)

The variance components for the breeding goal traits were computed, and the heritability estimates are presented in Table 2. The heritability of growth traits, i.e. body weight at week 16, ranged from 0.30 to 0.77 for the four lines. This suggests that 30-77% of the total variation in the phenotype of the chicken lines is due to differences in genetic background. Growth traits showed the greatest genetic variability across the four lines. The heritability of the egg production traits ranged from 0.00 to 0.71, despite a large standard error of the estimates. The larger the standard error obtained in this finding, the more likely it is associated with a small dataset on egg production traits and less relationship information in the pedigree data.

Table 2. Heritability (SE) estimates growth and egg production traits in four ILRI chicken lines.

Trait	Chicken lines			
	LIL20	BIL20	WIL20	NHIL20
W16	0.68 (0.08)	0.30 (0.12)	0.36 (0.11)	0.77 (0.03)
ADG	0.64 (0.13)	0.30 (0.22)	0.23 (0.11)	0.88 (0.08)
AFE	0.51 (0.37)	0.00 (0.33)	0.65 (0.53)	0.07 (0.24)
EN	0.21 (0.31)	0.13 (0.31)	0.71 (0.64)	0.55 (0.32)
EW	0.11 (0.28)	0.54 (0.43)	0.00 (0.59)	0.13 (0.34)

The estimated index equation for the four chicken lines is presented as follows:

$I_{LIL20} = 0.23EBV_{W16} + 0.85EBV_{AFE} + 2.67EBV_{EN} - 4.28EBV_{EW}$

$I_{BIL20} = -0.06EBV_{W16} - 14.52EBV_{AFE} + 0.21EBV_{EN} + 14.68EBV_{EW}$

$I_{NHIL20} = 0.12EBV_{W16} - 11.16EBV_{AFE} + 0.25EBV_{EN} + 3.55EBV_{EW}$

$I_{WIL20} = -0.27EBV_{W16} - 31.95EBV_{AFE} + 0.75EBV_{EN} + 17.72EBV_{EW}$

Index accuracy ranged from 0.45 to 0.90, with the highest value in BIL20 indicating strong selection efficiency, while lower accuracy in WIL20 (0.45) and NHIL20 (0.48) suggest reduced effectiveness.

Discussion

The increase in EBVs across generations confirms that the breeding program is achieving genetic gain. Divergence between phenotypic and genetic trends in a few lines highlights the importance of BLUP-based evaluation to disentangle genetic progress from environmental variation. The inbreeding rate obtained in generation two was higher than the recommended threshold level set by the Food and Agriculture Organization (FAO), i.e., 0.5 to 1 % (Oldenbroek & Calus, 2024). Additionally, the effective population size of the chicken lines is smaller than the recommended > 50 optimal effective population size (Falconer and Mackay, 1996). This could be due to a few superior animals making a higher contribution to produce chicks. As a result, related individuals are more likely to mate, ultimately leading to inbreeding. Long-term improvement and sustainability will depend on managing parental contributions and applying optimized mating strategies to balance genetic gain and diversity (Oldenbroek and Calus, 2024). The moderate to high heritability estimates for growth traits indicate substantial genetic improvement potential and genetic variation in the traits of chicken lines. The selection index coefficients varied across chicken lines, with some traits (e.g., AFE and EW) showing large values despite lower economic importance. This reflects the influence of genetic and phenotypic (co)variances and trait correlations on index weights (Hazel *et al*., 1994). Selection index accuracy differed among lines due to variation in genetic parameters and data which influences prediction efficiency (Falconer and Mackay, 1996).

Conclusions

Implementation of BLUP and selection index methodology in the ILRI–TPGS poultry breeding program has improved the accuracy of genetic evaluation and enabled systematic multi-trait selection. Positive genetic trends for growth traits demonstrate the effectiveness of the approach. Strengthening egg production recording and continued management of inbreeding will be essential to sustain long-term genetic progress and support resilient poultry systems for smallholder producers.

Acknowledgements

The authors acknowledge ILRI staff involved in animal management and data recording under the TPGS program.

References

Esatu W., Assen A.A., Belete S., *et al*. (2025) Tropical Poultry Genetics Solutions (TPGS) digital database: User guide. ILRI manual 80. Nairobi, Kenya. https://hdl.handle.net/10568/177029.

Falconer D.S., and Mackay T.F.C. (1996) Introduction to quantitative genetics. Longman, New York Harlow.

Hazel L.N., Dickerson G.E., and Freeman A.E. (1994) J. Dairy Sci. 77:3236-3251. https://doi.org/10.3168/jds.S0022-0302(94)77265-9

Henderson C. R. (1975) Biometrics 31:423–447. https://pubmed.ncbi.nlm.nih.gov/1174616/

Meyer K. (2007) J Zhejiang Univ Sci B. 8:815-21. https://doi.org/10.1631/jzus.2007.b0815

Oldenbroek K., and Calus M. (2024) Textbook Animal Breeding and Genetics for BSc-students. (2nd ed.), https://edepot.wur.nl/365432

Rutten M.J.M., Bijma P., Woolliams J.A., *et al*. (2002) J Hered 93,456-458. https://doi.org/10.1093/jhered/93.6.456