Rahmatullah, S., Mahawan, T., Phakdeedindan, P. (2026) Assessment and maintenance of genetic purity in Indonesian local cattle populations via integrated genomic selection and SNP parentage analysis, *Proceedings 13th World Congress on Genetics Applied to Livestock Production* 23610: https://doi.org/10.31274/wcgalp.23610 ©2026 Rahmatullah, et al. CC BY-NC-ND

Assessment and maintenance of genetic purity in Indonesian local cattle populations via integrated genomic selection and SNP parentage analysis

S.N. Rahmatullah[1,2,*], T.Mahawan[3], and P.Phakdeedindan[1]

[1]Faculty of Veterinary Science, Chulalongkorn University, Thailand; [2]Faculty of Agriculture, Mulawarman University, Indonesia; [3]Akkhraratchakumari Veterinary College, Walailak University, Thailand; [*]Corresponding author: suryanr@faperta.unmul.ac.id.

Introduction

The development of local cattle in Indonesia has faced major challenges in genetic improvement and breeding management, largely due to inadequate on-farm recording systems that limited effective selection and mating strategies. In 2024, the national cattle population was approximately 11.4 million head (BPS, 2025), while beef consumption in 2022 (627,952 tons) substantially exceeded domestic production (413,669 tons) in a population of approximately 282 million. This imbalance had increased dependence on beef imports and intensified the slaughter of local cattle, thereby contributing to population decline and the gradual erosion of genetic quality. To address these challenges, genetic improvement programs have become essential. One of the major strengths of Indonesian local cattle is their potential to enhance productivity, adaptability, and long-term sustainability under tropical conditions. Therefore, the development of local cattle resources was considered important for improving livestock productivity, particularly in terms of meat and milk production. A long-term strategy to enhance the potential of local cattle has involved the application of molecular genetics. In this context, molecular genetic approaches have improved the accuracy of genetic evaluation and strengthened the understanding of the genomic basis of economically important traits. SNP-based genomic selection has provided an efficient approach for predicting breeding values. In contrast, SNP-based parentage analysis has enabled reliable pedigree verification, the detection of misassigned ancestry, and the monitoring of breed integrity. These approaches had been particularly important for indigenous cattle populations, in which uncontrolled crossbreeding and weak pedigree documentation could threaten genetic purity. Accordingly, this study proposed an integrated genomic framework to support cattle improvement, strengthen recording systems, and maintain the genetic purity of the Indonesian local cattle population.

Materials & Methods

This study applied an integrative framework based on a systematic review of published literature on parentage analysis, genomic selection, SNP markers, machine learning, and RNA sequencing. The review was conducted to develop strategies and breeding programs for the maintenance and improvement of Indonesian local cattle, particularly in relation to genetic purity, pedigree verification, and productivity. Biomarker-based machine learning research was also incorporated to strengthen the predictive component of the framework. The study was conducted from March to November 2025 at Chulalongkorn University and Walailak University, Thailand. The proposed framework emphasized the use of SNP markers for purebred identification, parentage analysis for breed integrity, and integrated sequencing and machine learning approaches to identify Indonesian local cattle with superior productivity and tropical adaptation.

Results & Discussion

Fig. 1a and 1b showed that domestic beef cattle populations and production in Indonesia were insufficient to meet national demand, as indicated by declining cattle numbers, stagnant production, and increasing reliance on imports. These trends suggested that existing development programs had not yet been fully effective. The findings, therefore, highlighted the need for strategic livestock planning based on accurate recording systems, particularly through parentage analysis, to improve productivity while maintaining the genetic purity of Indonesian local cattle.

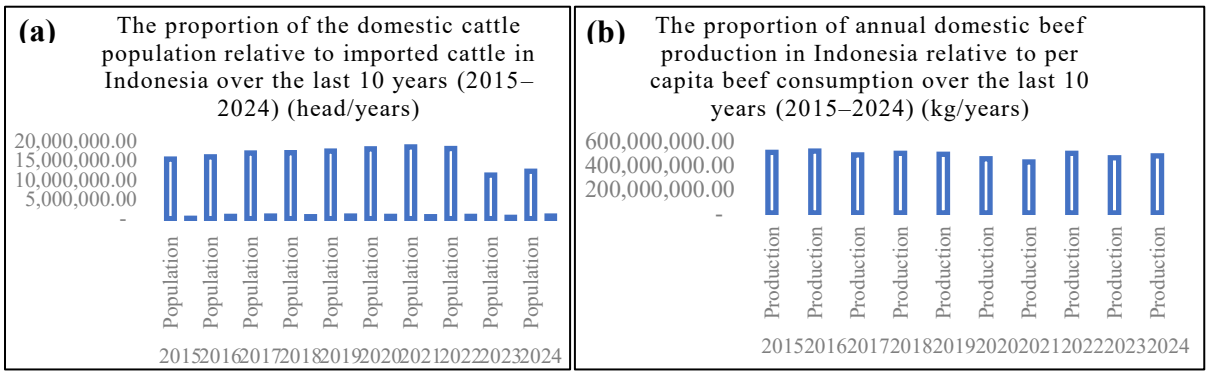

Figure 1 (**a**).Proportion of the domestic cattle population relative to imported cattle in Indonesia over the last ten years (2015–2024), illustrating the comparison between domestic cattle availability and imported cattle in Indonesia; **(b)**. Comparison of annual beef production in Indonesia with per capita beef consumption over the last ten years. Data were sourced from Statistics Indonesia (BPS), 2015–2025, and the Beef Cattle Livestock Commodity Outlook published by the Indonesian Ministry of Agriculture, 2015–2025.

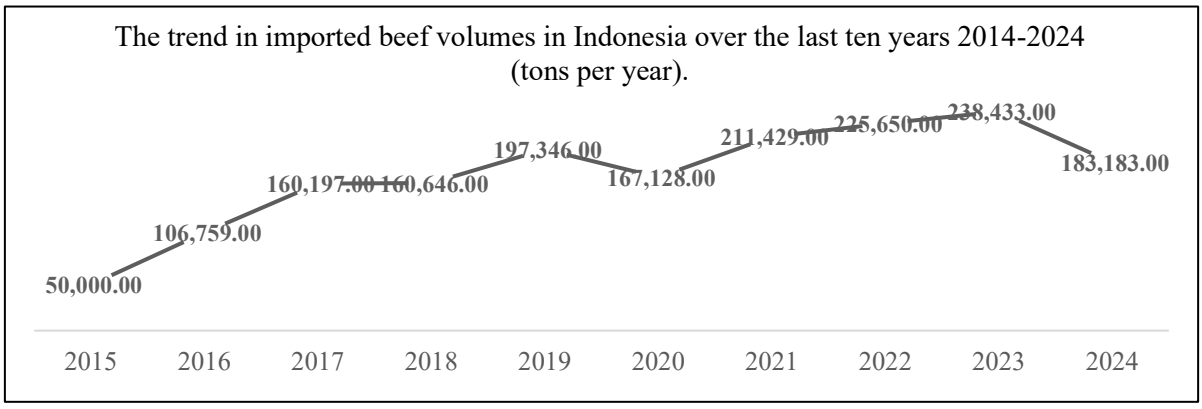

Figure 2. Trends in beef imports in Indonesia over the last ten years show an increase in import volumes from 2021 to 2023, followed by a decline in import demand in 2024. Data were sourced from Statistics Indonesia (BPS), 2015–2025, and the Beef Cattle Livestock Commodity Outlook published by the Indonesian Ministry of Agriculture, 2015–2025.

Assess the genetic purity of Indonesian local cattle populations using genome-wide SNP markers. Recording systems derived from parentage analysis have provided a fundamental basis for livestock development and supported the implementation of genomic selection in smallholder-based systems. Genomic selection has used SNP markers to estimate breeding values with high early-life accuracy and has been strengthened by advances in SNP discovery and genotyping technology (Gutierrez-Reinoso *et al*., 2021). In smallholder systems, SNP-based approaches have helped identify superior local cattle despite weak conventional

recording systems. A relatively small set of informative SNP markers had been sufficient to verify pedigree relationships, identify genetically valuable animals, and support selection and breeding decisions aimed at maintaining superior local cattle populations.

Implementation of validated pedigree relationships through SNP-based parentage analysis. Accurate pedigree information had been fundamental to cattle breeding because it supported reliable genetic evaluation, genetic gain, and inbreeding control. SNP-based parentage analysis has gained importance due to its higher accuracy, cost efficiency, and reproducibility compared with traditional markers (Flanagan and Jones, 2019). Previous studies, including Hu *et al*. (2020), had confirmed its successful application in cattle through computational and on-farm validation. In this context, SNP-based parentage analysis had provided a strong basis for local cattle development by generating reliable pedigree data for selection planning and structured breeding with superior parental lines, thereby supporting more effective breeding decisions and the long-term conservation of valuable local cattle populations.

Propose a genomic framework for preserving genetic purity in the breeding and conservation programs of Indonesian local cattle. An integrated framework combining recording systems, genomic selection, and machine learning analysis was developed to improve predictive accuracy and support decision-making in livestock development programs. The framework was designed for developing countries such as Indonesia, where smallholder recording systems remained limited. Its implementation at a small scale facilitated monitoring, evaluation, and gradual adoption, while accommodating small herd sizes and supporting feasible data collection for sustainable livestock development and improved smallholder welfare. A comparison of implementation programs illustrating the involvement of parentage analysis and machine learning was presented in Fig. 3.

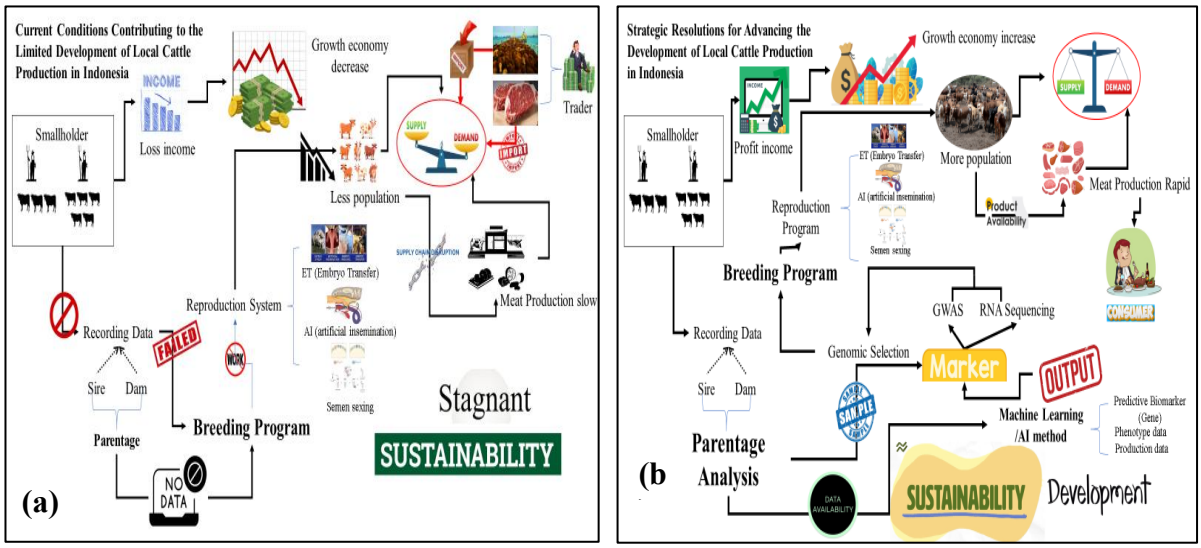

Figure 3. (a) Current programs for the development and improvement of local livestock production in Indonesia; (b) the proposed novel program for the development and preservation of genetic quality in local Indonesian livestock, developed through the integration of parentage analysis and machine learning to support the implementation of genomic selection.

This program aimed to strengthen awareness of the importance of data recording in the Indonesian livestock sector, particularly for local breeds, in order to prevent declines in genetic quality. Indonesian local cattle were recognized for their adaptive advantages, including heat tolerance, efficient use of low-quality forage, and relatively high carcass yields compared with

exotic breeds. Parentage analysis and SNP markers supported this objective by verifying genetic relationships and identifying economically important genomic variation. In addition, SNP-based machine learning was applied to predict biomarkers associated with superior local cattle, thereby supporting selection and breeding strategies within the proposed framework (Fig. 3).

Table 1. Selected studies reporting the use of livestock data in machine learning analyses and the predictive performance outcomes achieved in these studies.

Term/Livestocks	Results	References
Optimal prediction environment for livestock management	Up to 90 % accuracy	Li *et al*., 2024
Dairy cow behavior prediction	Up to 80% accuracy	Araujo *et al*., 2023
Broiler growth and health prediction	Up to 98% accuracy	Milosevic *et al*., 2019
Weaning weight of lambs prediction	Make the highest prediction	Eroğlu *et al*., 2025

Table 1 showed that machine learning supported predictive selection with high accuracy for growth, health, and production traits, indicating its strong potential as a reference tool for future local cattle development.

Conclusions

The integration of improved data management, genomic technologies, and machine learning–based prediction was expected to enhance breeding efficiency and long-term genetic gain, with predictive accuracy of more than 80%. This integrative strategy was anticipated to support the sustainable growth of local cattle populations, preserve genetic integrity, and improve livestock production in Indonesia.

Acknowledgements

This research was financially supported by the ASEAN and Non-ASEAN Scholarship programs of Chulalongkorn University, Bangkok, Thailand; the Educational Stimulant Grant provided by the Government of East Kalimantan Province, Indonesia; and institutional support from Akkhraratchakumari Veterinary College, Walailak University, Thailand.

References

Araujo S.O., Peres R.S., Ramalho J.C., *et al*. (2023) Agronomy 13:2976. https://doi.org/10.3390/agronomy13122976.

Eroğlu M., Turgut A.O., Küçük M. *et al*. (2025) Vet. Med. Sci. 11, p.e70420. https://doi.org/10.1002/vms3.70420.

Flanagan S.P. and Jones A.G. (2019) Mol. Ecol. 28:544-567. https://doi.org/10.1111/mec.14988.

Gutierrez-Reinoso M.A., Aponte P.M. and Garcia-Herreros M. (2021) Animals 11:599. https://doi.org/10.3390/ani11030599.

Hu L.R., Li D., Chu Q., *et al* (2021) Animal 15:100066. https://doi.org/10.1016/j.animal.2020.100066.

Li D., Yan G., Li F., *et al*. (2024) Animals. 14: 2724. https://doi.org/10.3390/ani14182724.

McClure M.C., McCarthy J., Flynn P., *et al*. (2018) Front. Genet. 9:84. https://doi.org/10.3389/fgene.2018.00084.

Milosevic B., Ciric S., Lalic N., *et al*. (2019) Worlds Poult. Sci. J. 75:401-410. https://doi.org/10.1017/S0043933919000254.

Ministry of Agriculture. Beef Cattle Livestock Commodity Outlook in 2024. Center for Agricultural Data and Information Systems, Secretariat General, Ministry of Agriculture of the Republic of Indonesia. https://satudata.pertanian.go.id/details/publikasi/822.

Statistics Indonesia (BPS), Indonesian Economic Statistics for the Livestock Sector, 2024. Republic of Indonesia. https://www.bps.go.id/id/publication/2024/12/20/522e07b24c7bbeb1c19b0a4e/peternakan-dalam-angka-2024.html.