# A review of sustainable cattle genetic improvement in the Peruvian Highlands

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## ARTICLE INFO

## ABSTRACT

Cattle breeding in the highlands of Peru is an important economic activity at the level of the entire rural extension, because it serves as an economic reserve for rural families and forms an integral part of the agricultural producer's culture. This review aimed to provide a literature- and research-based approach to the fundamental aspects of a national genetic improvement plan, emphasising the efficacy of using a bovine germplasm of high genetic quality as an initiative to implement genetic improvement programmes. The concepts to be implemented in national livestock farming include high yield, feed conversion efficiency, and minimum greenhouse gas emissions. The use of a dual-purpose germplasm to maximise the usefulness of livestock farmers and the implementation of improvement programmes, with the expectation of achieving a differential increase in genetic merit, were also considered. In addition to aspects related to milk and carcase quality, there is a territorial approach, such as the case of breeds that adapt to terminal crossbreeding and consider reproductive aspects. One of the final aspects considered is the conservation and valuation of local animals within conservation and improvement plans owing to their resistance and adaptation to temperature and altitude conditions.

## 1. Introduction

Livestock in Peru represents approximately 40 % of the gross value of agricultural production; therefore, productive chains should be prioritised according to the most vulnerable populations and those living in poverty. Cattle breeding is registered by approximately 824 thousand agricultural producers, and genetic improvement is one of the critical factors (MIDAGRI, 2017). To address this, the implementation of a bovine germplasm bank is essential, with the purpose of cryopreservation and the multiplication of semen and embryos, which meet the needs of producers in the medium- and long-term of communities and the agri-food industry (Blackburn, 2018). In some cases, this approach serves to conserve local herds- biodiversity (Machado et al., 2016)–strengthening the maintenance of the genetic variability of creoles and improved breeds that have a closed population in the Andes. Additionally, it helps to generate strategies to strengthen conservation, characterisation, promotion, and use, considering initiatives that lead to increased animal productivity (Jimenez et al., 2021). However, the preservation of biodiversity and genetic improvement of livestock populations are considered antagonistic processes (Bittante, 2023).

Cattle are one of the most important species in the world, providing multiple services to farmers and contributing substantially to national economies (Ouédraogo et al., 2021). This is equally applicable in our country (Paredes & Escobar, 2018). In addition to increasing profitability, it also aims to reduce the environmental impact by selecting characteristics that enhance feed efficiency and reduce methane emissions. Nutrition studies have indicated that the selection of animals with low emissions can result in higher use of nutrients, directly affecting meat and milk production (Løvendahl et al., 2018). Thus, it is necessary to adopt an approach that relates genetic parameters to methane production and yield (Breider et al., 2019). Therefore, the global trend should focus on quantifying the phenotypic value in terms of the amount of methane emitted per litre per day or grams of meat per day, incorporating energy correction, dry matter intake, or a residual methane phenotype (de Haas et al., 2017) that accumulates over generations (Manzanilla-Pech et al., 2021). This study aimed to analyse the

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expectations and perspectives regarding genetic improvement as a strategy for implementing genetic improvement programmes in the Peruvian highlands and jungle. The study emphasised a sustainable approach and the use of specialised breeds, focusing on the evaluation of different agro-climatic conditions.

## 2. Methodology

This review is based on an exhaustive search of scientific articles from past 10 years, primarily using indexed databases, to ensure the inclusion of information that guarantees the veracity of what is announced in this study. This review focuses on identifying and evaluating trends in genetic improvement, country-specific statistics, livestock sustainability, and the approach to gradual changes and strategies for the use of new tools such as genomics, epigenetics, and animal health with applications in welfare, nutraceuticals, the rural economy of the Andes, and producer knowledge.

## 3. Breeding trends according by livestock production purpose

### 3.1. Milk-producing cattle

Dairy farmers have the potential to improve profitability while simultaneously reducing environmental impact (Løvendahl et al., 2018). Most greenhouse gases come from the dairy sector, including methane (a moderately heritable factor), which contributes to global warming (Breider et al., 2019). To mitigate this problem, cattle should be selectively bred to have genetic traits associated with higher feed efficiency and lower methane ($CH_4$) emissions (Løvendahl et al., 2018). This approach is considered one of the most effective methods for reducing $CH_4$, considering that genetic progress is cumulative and permanent across generations (Manzanilla-Pech et al., 2021). Assessing $CH_4$ emission traits and feed efficiency necessitates direct and accurate measurements of numerous animals under the conditions under which they are expected to perform, such as the lactation period examined, the production system, records on dry matter intake, methane intensity, and the interaction of intervening factors (Løvendahl et al., 2018). Similarly, genetic selection requires records from many animals, and only a few countries have actively recorded methane emissions. However, it is not excluded that combining data from different countries could expedite the acquisition of accurate genetic parameters for $CH_4$ traits and facilitate the development of a future genomic reference population (Manzanilla-Pech et al., 2021).

Sustainable dairy cow performance depends on the simultaneous advancement of breeding and management strategies to adapt breeding programmes to herd performance metrics to facilitate better responses to reproductive decisions (Dunne et al., 2019). A condensed calving pattern is implemented wherein cows are required to conceive within approximately 12 weeks from the planned onset of calving (Craig et al., 2018), providing the animal with the necessary care to prevent contracting metritis, a uterine disease affecting approximately 10–30 % of all lactating dairy cows, which has detrimental effects on herd performance (Bicalho et al., 2017). As metritis has developed resistant to antibiotics that to date have been used to restore the normal uterine environment, therefore an alternative eco-sustainable treatment has been developed (Fuentes-Hernández, 2021).

Considering the high heritability of many traits associated with calving performance and carcase merit, and the tendency of many of these traits to be moderately to intensely antagonistic, a genetic index encompassing both calving performance and meat production could be a valuable tool to fill the gap in supporting sire selection decisions (Berry et al., 2019) to increase dairy herd profits. The use of beef semen in dairy cows has steadily increased since 2017 (Pereira et al., 2022), including additional value for all future offspring resulting from increased selection intensity. Several studies have shown an increase in heifer profitability owing to the use of sexed semen (Cottle et al., 2018). However,

the environment directly influences the efficacy of sexed semen, as evidenced by the lower calving incidence in warm, semiarid, and temperate regions than in cold, semiarid regions (Joezy-Shekalgorabi et al., 2017).

### 3.2. Beef cattle

Red meat is an essential dietary source that meets part of the world's nutritional requirements (Roudbari et al., 2020), and originates from the progeny of dairy or beef dams (Twomey et al., 2020). Therefore, when serving a female, the producer must decide whether to mate her to a dairy or beef bull, considering the factors that are associated with serving a given female to a beef bull (Berry & Ring, 2020b). Furthermore, it is essential to recognise that the validation of total beef genetic merit indices improves performance and, in turn, herd profitability (Kelly et al., 2021). The use of dual-muscled bulls helps quantitatively and qualitatively improve beef production, thereby potentially increasing income (Bittante et al., 2020b). This is particularly significant considering that beef production fluctuates over time for farmers who are not part of the large meat industries, as they face constant climatic changes that have resulted in decreased grazing areas and, consequently, reduced sources of feed for cattle (Morales & Masis, 2018).

### 3.3. Dual-purpose cattle

Dual-purpose cattle farms comprise crossbred animals in different proportions and are characterised by milking in the presence of the calf. Most of these farms lack appropriate records (Salamanca-Carreño et al., 2021), making the evaluation subjective (Ruiz-Sesma et al., 2021), thus highlighting the importance of having information on the offspring of cattle.

The parameters typically considered during selection include conception rate, percentage of fat in meat, milk production per day, and number of calves per cow (García-Márquez et al., 2023). Despite these limitations, the dual-purpose livestock system, including traditional approaches with the help of genetic improvement, continues to demonstrate a consistent increase in its production (Salamanca-Carreño et al., 2021). Furthermore, if appropriate environmental and sanitary conditions are provided, cattle will be beneficial for both meat and milk production.

In addition, the combined use of purebred semen and conventional beef semen for terminal crossbreeding can increase farm income, particularly when the sires are double-muscled bulls, thus yielding better results, serving the same purpose when using purebred sexed semen and conventional beef semen for terminal crossbreeding (Bittante et al., 2020b). This aids in the production of purebred replacement heifers, which allows the mating of a large proportion of dairy cows with double-muscled bulls and consequently improves beef production both quantitatively and qualitatively (Bittante et al., 2020a). In contrast, crossbred calves are not only intended for veal production (such as purebred dairy calves) but also for beef production (Bittante et al., 2020b), adding one of the most notable characteristics of the dual-purpose system, wherein milk production per lactation is higher or lower according to the number of calvings of the cow, varying significantly according to location, breed group, and duration of lactation, concerning weaning weight (Daza & Manrique, 2022).

Animals have undergone an evolutionary process in which they adapt to the environmental conditions they face (Naranjo et al., 2021). Consequently, the environment in which dual-purpose cattle are reared is of critical importance. Similar to all animals, cattle are susceptible to sudden changes in environmental temperature, which affect the thermal environment to which they are exposed, thereby decreasing their productive and reproductive performance (Vega-Murillo et al., 2023). This factor should be considered as the basis for improving nutritional, sanitary, environmental, and reproductive management to increase comfort, thus ensuring an increase in the kilograms of live weight produced

per animal, a decrease in the number of days between reproductive events, and an increase in the productive life of cattle (WingChing-Jones, 2017).

When selecting a cross between a beef bull and a dairy cow, it is essential to know what you want to transmit through genetic inheritance. As these are dual-purpose cattle, the objective is to obtain milk for females and meat for bulls, while ensuring that the cow's anatomy is not excessively lean, as observed in dairy cows, to achieve greater utilisation. With genetic advancements, a more balanced progeny has been achieved using the milk-to-meat index (MiMeI), which meets the needs of dual-purpose cattle producers. With appropriate selection, bulls with a higher MiMeI could potentially increase dairy herd profits by 3–5 % over conventional selection in the sector (Berry & Ring, 2020a). It is noteworthy that the average direct calving difficulty of beef bulls is 1.85 units higher than that of dairy bulls, but with more than three times the variability in beef bulls (Berry et al., 2020).

## 4. Genetic improvement

Progeny selection has been a constant practice since the dawn of domestication, with early breeders commonly selecting appearance or qualitative traits, rather than productive performance traits (Cole & VanRaden, 2018). Currently, selection is based on productive and reproductive indices that provide insight into the efficiency of livestock production systems. Some of the parameters used for selection include weaning, birth weight, age at first calving, and calving interval (WingChing-Jones, 2017), including technological advances and reproductive techniques, such as in vitro embryo production, which allow faster genetic gain and improved productivity in beef herds (Trejo et al., 2023). Genetic innovations have advanced to such an extent that they now serve as tools to support livestock farming decisions, as there are tools that incorporate genetic and non-genetic information about animals. Consequently, the potential market value of the animal can be better predicted and paid according to its worth, thus increasing profits solely based on its genetic merit (Dunne et al., 2021). In addition, there is a new genome for cattle, ARS-UCD1.2, based on *Bos Taurus*, which is identical to that utilised for the original version, thereby facilitating the transfer and interpretation of the results obtained (Rosen et al., 2020).

A genetic index converts information on several traits into a single number, which is used for the selection and prediction of an animal's performance. Calculation of selection indices is straightforward when phenotypic and pedigree data are available (Cole & VanRaden, 2018). Several studies on cattle have confirmed a better selection performance for total merit indices, which are limited to beef or dairy total merit for specific purposes. Validation studies on the total merit indices used to select beef bulls for dairy females are limited (Berry & Ring, 2020a). Despite the importance of validating any technology before recommending its use, few studies have demonstrated the superior performance of high-ranking animals at a given total merit index, particularly for selection indices for maternal cattle (Twomey et al., 2020). Conversely, the effects of alternative mating programmes that incorporate genomic information on expected herd performance, inbreeding, and methods for including non-genotyped animals in such mating programmes have been previously investigated (Cole & VanRaden, 2018).

The genomic evaluation of cows and the use of sexed semen have recently provided opportunities for commercial dairy producers to accelerate genetic progress at the herd level by increasing the accuracy and intensity of selection (Joezy-Shekalgorabi et al., 2017). The factor analysis method is often used to study producers' assessments of offspring quality, test bull productivity, and determine whether the proposed indices are suitable for preliminary calf selection either on commercial farms or pedigree breeders (Zelenkov et al., 2019). The implementation of genomic testing or the use of sexed semen incurs extra costs and requires a higher investment (Joezy-Shekalgorabi et al., 2017). However, it would have to be assessed whether the farmer wants to take the risk of inseminating his females with sexed semen, because

the use of sexed bovine semen leads to reduced conception, the causes of which are only partially known. In addition, embryos derived from sexed sperm show reduced survival times, and embryos derived from sexed sperm reach developmental stages at similar times as conventional embryos (Steele et al., 2020). The combined use of sexed semen, especially in heifers, to produce purebred replacement females and beef semen to produce terminal crossbred calves has the potential to increase overall herd fertility, which can be further enhanced by using sexed dairy semen to produce dairy crosses of purebred replacement heifers (Bittante et al., 2020a).

## 5. Trends of change in genetic improvement

Semen from beef bulls is currently used by dairy herds (81 %), with 78 % reporting additional gains, heifer inventory control (69 %), genetic improvement (37 %) for other factors (8 %). Angus semen was the most used (89 %), followed by Limousin (12 %), Wagyu (10 %), Charolais (7 %), others (5 %, including Limflex, Stabiliser, and Hereford), and Simmental (4 %). Reproductive performance is an essential criterion for selecting cows that can receive beef semen; 45 % of the respondents reported starting to breed cows with beef semen at the third service, 18 % at the fourth service, and 21 % at the fifth service or later (Pereira et al., 2022). Because fertility rates are improved by crossbreeding, however, crossbreeding using conventional beef and dairy semen improved conception probability (1.10 and 1.17, respectively) in cows (1.37 using beef semen) and heifers (1.25 using dairy semen) (Bittante et al., 2020a). When choosing a service bull, it is known to account for only 1 % of the phenotypic variation in three milk production traits (yield, fat, and protein) when adjusted as a random effect, as well as the effects of bull breed or measure of genetic merit, correlations between sire meat merit and female milk, and reproductive performance (Berry and Ring 2020c).

### 5.1. Genetic estimation

The genetic evaluation of animals is indispensable for achieving improvement and sustainability in cattle production. Despite being an activity planned over the long-term, it requires considerable attention. Brahman bulls' mean live weight at 270 days (PA270) reached 216.713 ± 26.97 kg and CV 12.5 %. Similarly, the paternal heritability estimates ($h^2d$) were 0.44 ± 0.14 and 0.39 ± 0.12, respectively, for birth weight (BW) and PA270, while the maternal heritability ($h^2m$) was 0.09 ± 0.092 and 0.42 ± 0.087 for BW and PA270, respectively, for PN and PA270, indicating the existence of direct additive genetic variability, evidencing the opportunity for genetic gain through selection, in addition to the considerable influence of the environment, such as management and nutrition of females during gestation and calves from birth to weaning (Bedoya et al., 2019).

Genetic parameters and trends for BW and adjusted weaning weight at 240 days (DW240) are indispensable for establishing a two-character model that can include sex, pedigree, year of birth, and weaning as fixed effects. In contrast, maternal age, age at weaning is used as a covariate and is included in the direct additive, maternal additive and residual genetic effects; considering that the $h^2d$ and $h^2m$ are 0.44 and 0.16 for BW and 0.29 and 0.10 for DW240. Likewise, the direct genetic and phenotypic correlation between BW and DW240 oscillates between 0.25 and 0.26, indicating that selection processes can improve these traits (Quintero Bastidas et al., 2023). Correspondingly, the heritability ($h^2$) for mortality rate (MR) and saccade rate is estimated to be between 4 % and 20 % due to early milk yield (MY) and 305-day MY (305 d MY) having unfavourable genetic correlations (0.32−0.41) with MR in Jersey and Holstein breeds, where a longer productive life is estimated to be associated with better health and welfare of the animals (Haile-Mariam et al., 2023).

## 5.2. Genomics

Genomics helps increase the accuracy of genetic indicators that only base their information on pedigree and phenotype (Comin et al., 2022). Whole-genome sequencing has the advantage of genomic prediction for breeds with small population sizes, such as the fat-protein ratio and somatic cell score. The 200KDSN chip harbours breed-specific variants, which are valuable for studying causal genetic mechanisms in endangered DSN populations (Wolf et al., 2023). Therefore, up to 20,000 markers may be lost after filtering the 50 K data, affecting the accuracy of the genomic estimated genome-wide values (GEBVs) (Hozé et al., 2013). When a greater number of low minor allele frequency markers are included in genomic prediction datasets, a combination of the GBLUP or BayesR method with moderate marker density and favourable single nucleotide polymorphisms (SNPs) (~25 k SNPs) would always yield good and stable prediction accuracy with acceptable computational and breeding costs (Zhang et al., 2019).

The inclusion of non-additive genetic effects, specifically dominance and epistasis-dominance, does not improve the predictive capacity of any model for predicting phenotypic values for any trait or breed, compared to the predictive ability of a model that includes only additive effects. Consequently, although non-additive genetic effects, especially epistatic effects, play an essential role in semen production traits, such as sperm motility, sperm volume, and number, they do not improve prediction accuracy in Japanese Black beef and dairy Holstein bulls (Nagai et al., 2022). However, genomic information on genes found in SNPs associated with fertility for genetic evaluation is advantageous for the genetic improvement of fertility traits in Angus males (Butler et al., 2022).

Different techniques can be used for the genetic improvement of beef quality. In chronological order, these include phenotypic selection, which has resulted in breed differentiation (not valid for MQ traits); selective breeding (with the heritability of beef quality traits varying considerably according to breed, trait, and conditions); indirect selection through Near Infrared Spectroscopy (NIRS) predictions (potentially helpful); fixation of important genetic mutations (such as myostatin gene for double muscling, calpain [CAPN]-calpastatin [CAST] genes for beef tenderness, and diacylglycerol O-acyltransferase for beef marbling); genomic and other genomic approaches for beef quality traits (e.g. for beef marbling); genomic and other omics approaches (with a substantial increase in scientific studies, genome-wide association studies (GWAS), Genomic selection (GS), and gene network identification), animal cloning (not functional), and tissue cloning (cultured meat) (Bittante, 2023).

Recent studies on the genetic diversity and population structure of cattle in Peru have marked a milestone in our understanding of the genetics of the Peruvian Criollo cattle (PCC) and their adaptation to challenging Andean ecosystems. Using next-generation sequencing technology, such as SNP chips for mass genotyping, the breeding nuclei of commercial breeds such as Brahman, Braunvieh, Gyr, Simmental, and the local Criollo Toro de Pelea Arequipeño (AFB) have been analysed, revealing rich genetic diversity and complex population structures (Corredor et al., 2023). *De novo* assembly of the complete PCC genome yielded 320 GB of sequencing data and annotated 19,803 protein-coding genes, reflecting its close relationship with the *B. taurus* and *Boss indicus* genomic references (Estrada et al., 2022). Similarly, sequencing of the mitochondrial genome of a Criollo bull highlights its connections with native African breeds, providing valuable genetic data for future breeding and conservation efforts. This study highlights the importance of the informed management of genetic resources to preserve genetic variability, provides the basis for the improvement and conservation of livestock in Peru, and contributes to an in-depth understanding of the molecular characterisation of the PCC and its genomic comparability within the subfamily Bovinae (Arbizu et al., 2022).

## 5.3. Genomic selection and mixed models

GS is a recognised tool for estimating the breeding value of young animals and for reducing generation gaps. A comparison of genotyping scenarios revealed that analyses should be performed on animals from both ancestral and younger generations, and genotyping should cover animals of both sexes (Esrafili et al., 2023). GS is revolutionising livestock breeding as it is associated with artificial intelligence, allowing the application of machine learning algorithms to estimate the value of GEBV breeding with high performance in phenotype prediction and new opportunities for improvement. The aim of cattle breeding is to correlate genomic breeding values with economic attributes, such as carcase weight, live weight, and loin eye area. The AdaBoost algorithm has been demonstrated to be a reliable and efficient method for GS in Simmental cattle (Liang et al., 2021).

To date, most genetic evaluations in cattle breeding are based on mixed model equations and animal models, where variance components such as heritability estimates are calculated using likelihood and Bayesian methods. GS has significantly accelerated genetic progress in cattle by combining a genomic relatedness matrix with a pedigree-based relatedness matrix, resulting in a hybrid matrix used in the GBLUP method, which has become the standard for genomic evaluation (Brito et al., 2021). Once genomic evaluation starts to be used, the estimation of breeding values with the best linear unbiased prediction (BLUP) of the pedigree becomes biased because this method does not consider selection using genomic information. GS can be detected in two possible ways: divergence of genetic trends and trends in realised Mendelian sampling obtained using BLUP and single-step genomic BLUP (ssGBLUP) (Abdollahi-arpanahi et al., 2021).

Estimates of genetic parameters in objective and subjective traits were performed on meat samples, using the restricted maximum likelihood method implemented with BLUPF90 programs, fitted a linear animal model using airemlf90 software for a genomic BLUP analysis, where they evaluated meat attributes (Warner-Bratzler shear strength, intramuscular fat, and pH) and sensory traits (flavour, tenderness, juiciness, and palatability), intramuscular fat and pH) and sensory traits (flavour, connective tissue, tenderness, juiciness, and palatability), where genetic correlations between sensory traits suggest that GS based on objective traits can improve meat quality and may be helpful in the implementation of genetic selection (Virtuoso et al., 2024)

Similarly, GS in cows as a fertility indicator, such as the interval between calving and first heat, has determined that the genomic value intervenes in the prediction by 0.16 of the Limousin breed (Fontanillas et al., 2022). This is a great advantage in selecting females with high productive performance, particularly when considering their use as donors for embryo production. High GS pressure facilitates the identification and selection of elite females (Miller, 2023). Greater genetic gains have been achieved through GS than through traditional pedigree-based evaluation. This has allowed for the greater use of young bulls, improving aspects such as feed efficiency, carcase and meat quality, tick resistance, and traits related to male puberty, as well as the quality, efficiency, and sustainability of production (Fernandes Júnior et al., 2022). GS improves the efficiency of genetic value prediction and has been used to improve traits related to milk production, general cow health, udder health, and body structure (Tade & Melesse, 2024). Likewise, new technologies, such as mid-infrared spectrometry (MIR) in milk, can be used to monitor cow health, as they provide biomarkers suitable for monitoring diseases such as mastitis and ketosis (König & May 2019).

Heat tolerance is an important economic trait in global warming. Therefore, GS contributes to the genetic improvement of heat stress tolerance by using genome-wide DNA biomarkers that predict this tolerance in each population. This can be used as a selection trait to scan and identify gene-rich regions that are directly or indirectly related to adaptation to the environment, thereby improving animal welfare (Cheruiyot et al., 2022).

## 6. Strategic proposal for improvement models in Peru

The breeding objective involves describing a model that relates the traits of interest considering the economic values, basically the traits the farmer wishes to improve and focus on in his livestock.

To this end, the models Ec. (1) should focus on at least three characteristics:

$$H = \sum_{i=1}^{n} \left(a_n C n h_n^2\right)' o \ a_1 C1h_1^2 + a_2 C2h_2^2 + a_3 C3h_3^2 + \dots + a_n C n h_n^2 \quad (1)$$

where,

H: Aggregate genotype value

$C1, C2, C3,$ and $Cn$: Characteristics or traits chosen or considered by farmers. a1, a2, a3, an: Economic values of the characteristics used in the selection process.

The values of C1, C2, and C3 were considered Z-type values.

$$Z = \frac{Xi - \mu}{\delta}$$

Thus, it must be considered that the economic merit must be proportional (0;1), that: $\sum$ (a1, a2, a3, an) = 1.0.

Depending on the characteristics or purpose of the livestock, meat quality traits such as carcase weight (CWT), eye muscle area, backfat thickness (BFT), and marbling score should be evaluated in the case of specialised beef breeds. In particular, in Brown Swiss, Simmental, Angus, Shorthorn, and Brahman, among other cattle breeds from the highlands and jungle of Peru, a bivariate animal model was used to estimate variance components such as heritability and genetic and phenotypic (co)variances using BLUPF (Bhuiyan et al., 2024). Genomic estimated genetic values (GEBV) with quartiles of precision (Q1: highest and Q4: lowest) in phenotypic differences for weight and carcase yield in feedlot production facilities, where the relationship between individual GEBV precision metrics is considered, depend on several factors, such as reference population size, trait heritability, and the extent of linkage disequilibrium among SNP, quantitative trait loci, and Q1Q4 (Alexandre et al., 2021).

Genetic parameters can be estimated for several reproductive traits in dairy cattle, such as age at first calving, calving interval, days open (DO), and number of services per conception, in addition to their association with productive traits, such as 305-day milk yield (305DMY), total milk yield during lactation (TLMY), and lactation length, which have been evaluated using analytical approaches for heritability estimates (Roy et al, 2024).

The proposed models can be used to evaluate breeding traits as indicators of resilience (RIND) and productivity (PIND). For RIND, aspects such as metabolic diseases, hoof health, udder health, fertility, heat tolerance, and longevity are considered. For PIND, corrected milk, protein content, somatic cell count, and MY were evaluated (Maskal et al., 2024). Fluctuations in daily MY are heritable, and the log-transformed variance of daily yield (LnVar) is the best fluctuation trait to predict udder health, ketosis, and longevity. The use of residual variance of MY will improve the selection of healthy, resilient, and long-lived cows (Elgersma et al., 2018). As with other parameters of interest, residual feed intake is considered a crucial trait in breeding programmes, as it could improve feed efficiency and increase the economic and environmental sustainability of the cattle industry. Researchers analysed new genetic parameters for genetic residual feed intake (gRFI) at first, second, and third calving, using a random regression model, collecting data on measured feed intake, milk production, and body weight, and found that gRFI is heritable, being more significant at first calving (Stephansen et al., 2023).

Considering that dual-purpose cattle are known for their hardiness and profitability, several genetic parameters of the main productive and reproductive traits, as well as the effect of genotype-environment interaction (G × E) on these traits, were evaluated to implement adequate selection plans, and productivity showed consistent variability due to G × E in all daily production traits, somatic cell count, and casein index. Fertility parameters usually show a modest G × E. In contrast, the milk solid content percentage shows no G × E effects; hence, it is important to consider G × E interactions when developing selection plans (Mancin et al., 2024). Livestock production in Peru is considered to be very variable due to the diverse geography and socio-economic levels in the highlands and jungle. Livestock production is developed mainly in dual-purpose breeding, for which the improvement programme should be strengthened in three priority aspects: productivity, quality, and resistance to environmental conditions. Geography segmentation is based on hydrographic basins to implement a genetic improvement plan focused on these aspects. This approach not only allows an increase in the productivity and quality of livestock in the highlands and jungle of Peru, but also ensures the sustainability and resilience of the sector in the face of environmental and economic challenges.

## 7. Conclusions

The genetic improvement of livestock in Peruvian territory and other regions with similar conditions in the highlands and jungle should focus on the implementation of plans that integrate indicators for milk and meat production. These indicators should be dynamically and objectively measurable or quantifiable, considering productivity, animal welfare, environmental balance, and ecology. In addition, aspects that account for associated random environmental effects, the responses in economic benefit, and the socio-environmental effect in each eco-geographical zone should be incorporated. Emphasis should be placed on implementing improvement strategies in known specialised breeds, as well as on implementing them in processes of valuation and conservation of local animals—local germplasm known as Criollo or naturalised, and crossbred—within the livestock and genetic improvement plans, owing to the high resistance and adaptation of these animals to the diverse conditions of temperature and altitude in the different altitudinal levels of the South American highlands.

**CRediT authorship contribution statement**

**Wuesley Alvarez-García:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Yudith Muñoz-Vílchez:** Writing – review & editing, Writing – original draft, Visualization, Validation, Software, Methodology, Investigation, Formal analysis. **Deyanira Figueroa:** Writing – original draft, Visualization, Validation, Supervision, Software, Funding acquisition, Conceptualization. **Richard Estrada:** Writing – original draft, Supervision, Resources, Methodology, Investigation, Conceptualization. **Carlos Quilcate:** Visualization, Validation, Supervision, Resources, Project administration, Funding acquisition, Conceptualization.

**Declaration of competing interest**

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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All authors agree that:

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All authors have been personally and actively involved in substantive work leading to the manuscript and will hold themselves jointly and individually responsible for its content.

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