

**Evaluation of Livestock Genetic Diversity for Climate-Resilient Breeding Programs**Tariq Ali Khosa¹¹BSC (Hon's) Agriculture, Bahauddin Zakariya University Multan, PakistanEmail: Tariq.khosa68@gmail.com**ARTICLE INFO****ABSTRACT****Received:**

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Climate has ended in breeding applications having greater importance in cattle that can resist the excessive temperatures, water scarcity and rising diseases. Assessing the cattle genetic range: foundation on choice of animals below climatic stressors. The paper gives a dialogue on how genetic variant contributes to the adaptive ability enhancement of farm animals species with the emphasis laid at the significance of genetic tools, indigenous breeds and conservation of the essential farm animals species. According to the synthesis of the current empirical research made through the author, the examine has concluded that control and usage of genetic variety is the maximum essential to expand weather resistant herds to sell meals safety and sustainable farm animals production. The findings suggest that molecular markers, genomic choice, and community-primarily based totally breeding integration can produce a first-rate impact in improving adaptive characteristics, which might be related to warmth tolerance and ailment resistance similarly to feed efficiency. Such an assessment factors out that genetically numerous inventory the use of inventory populace of farm animals will provide a organic coverage in opposition to shocks in a brand new surroundings to grow to be vital in breeding strategies.

Corresponding Author:Tariq.khosa68@gmail.com**Introduction**

Livestock production systems worldwide are increasingly facing threats from the growing impacts of climate change such as rising temperatures, irregular rainfall patterns, droughts and the spread of diseases transmitted by vectors. These pressures on the environment interfere with feed availability, decrease the reproductive efficiency and compromise the general health of the animals (Thornton et al., 2021). The vulnerability of livestock is especially high in those regions where production relies heavily on natural resources and where the adaptive capacity of production is likely limited by socio-economic constraints. In so far, genetic diversity has become one of the most important biological resources for coping with climatic risks and maintaining productivity. Researchers have always maintained that the adaptive capacity of livestock is also most fundamental in the level of genetic variation that they possess in order to cope with stress and regain from environmental fluctuations (Notter, 2020; Biswas et al., 2023).

Genetic diversity is essential to evolutionary sciences and to livestock ethnology has added the role that it favors with the completion of genetic research that scientists have achieved thanks to the use of genomic technologies: involving, the authors point out the following aspects: Mapping, measuring and using genetic differences with unprecedented precision. As climate extremes increase, there is a need for further adaptive approaches to breeding through integrating from wide genetic pools as opposed to farms relying on high performance commercial breeds. There is some evidence that many high-input breeds (which are called exotic breeds because they haven't been selected for our own environments) have insufficient resilience to deal with heat stress and disease outbreaks in harsh climatic conditions, especially in developing countries where limited

resources combine to form an even greater environmental challenge (Rojas-Downing et al., 2017). By contrast, indigenous and locally adapted breed have often developed these unique adaptive characteristics - such as heat tolerance, resistance to parasites and metabolic efficiency - over generations through selection in nature and by humans (FAO, 2019). Such traits are becoming increasingly valuable to breeding programs committed to achieving a balance between productivity and long-term sustainability for climate resiliency.

Integration of genetic gear has converted the usage of evaluation of genetic variety of diverse breeds of cattle to allow breeders to recognize which alleles are adaptive and related to weather pressure resilience. SNP genotyping, geno-typing, whole-genome sequencing and GWAs are a number of the strategies that permit the breeders to look at csv choice signatures and quantify the genetic distance element amongst populations (Gebrehiwot et al., 2023). Such gadgets aren't simplest making the procedure of know-how evolutionary records greater beneficial, however they also can be applied to make knowledgeable selections approximately crossbreeding, depth of choice, and conservation priorities. One of those is genomic choice, which has ended in an boom withinside the improvement of breeding, because the breeding cost is nicely anticipated primarily based totally at the genetic markers, that have lengthy been capable of pick out the early identity of the animal that has a excessive diploma of adaptive potential (Hayes et al., 2021). Such a method is beneficial in minimizing the technology periods, and their contribution of manufacturing resilient herds and the cappotential to generate manufacturing in converting conditions.

Climate resilience in livestock intrinsically relates to traits such as thermotolerance, feed conversion efficiency, resistance to diseases and genetic strength of reproduction to name a few. Studies have not only shown that heat stress alone can reduce milk yield in dairy cattle by as much as 30% but increases mortality in poultry and small ruminant animals significantly provided that the animal does not have the proper adaptive traits (Sejian et al., 2018). The impact that climate stressors have on livestock productivity demonstrates the need for assessing the genetic variation as a means of selecting the animals that can tolerate these conditions. Additionally, losses of genetic resources from factors such as replacement of breeds, habitat and unregulated crossbreeding pose a risk to adaptive traits. According to FAO (2021), one-third of livestock breeds around the world is threatened with extinction and thus limits the genetic base for future adaptation to climate. Therefore, conservation and utilisation of genetically diverse livestock populations need to be incorporated in national and international policies for breeding.

Community-based and participatory breeding programs have been shown to be effective in maintaining the diversity of indigenous livestock and also improving adaptive performance. Such programs - which are so often implemented in rural communities - allow breeders to select animals collectively according to local environmental realities, not some external standard of performance. Empirical evidence shows that both genetic improvement and resilience under community breeding will be strengthened especially in small herd populations of ruminants subject to recurrent climatic shocks (Wurzinger et al, 2020). This is a form of localized empowering farmers to conserve and increase their genetic resources and taking up with modern genomic tools where this is feasible. In addition, the involvement of farmers indigenous knowledge helps in improving the accuracy of the trait selection particularly traits that cannot be measured easily such as thermo tolerance and disease resilience (Ojango et al., 2019).

An assessment of genetic diversity of livestock must also take into account the policy, institutional and socio-economic dimensions that affect breeding strategies. National breeding policies in many countries focus on high yielding breeds for important economic gains at the same time which leads to lesser genetic base of livestock populations. However, climate resilient production systems entail policies to support the genetic conservation and biobanking and well-structured breeding schemes that focus on resilience as opposed to maximum productivity (FAO, 2021). Investments into research infrastructures, farmer training and data collections have been placed on the genomic-level are crucial to bridge the gap between scientific advancement and grassroots breeding practices. Furthermore, inclusion of genetic diversity in climate adaptation schemes has a direct contribution to global food security, poverty reduction and sustainable agricultural development.

As aptly summarized, genetic variety of cattle is one of the major additives of the try to attain the idea of weather resilient breeding packages to triumph over the growing pressures of weather alternate. Both the genetic variety inside and amongst farm animals breeds constitute a organic safety-internet in opposition to negative environmental stresses, and cause the diploma of productiveness and survival, now no longer handiest of the populace of any precise breed however additionally of all populations. Enrichment of negative and marginal farmers of the arena Improvements in genomic technologies, strategic deployment of indigenous breeds and participatory breeding strategies offer the possibilities of accomplishing upgrades in

adaptive capacity. With the upward push in depth of weather variability, the information and alertness of genetic variety has turn out to be an important a part of maintaining intestine fitness in the human populace, which have to depend upon its personal as a dependable assure of the resilience of farm animals systems, the sustainable desires of increasing populations, and agricultural pastime that may be tailored to the transferring ecology of the landscape. The an increasing number of gathering quantity of studies factors out that raising the profile of empowering breeding programmes with the extraordinary genetic assets has ceased being an alternative and is henceforth turning into an unavoidable factor in its quest into the unknown destiny of cattle production.

Literature Review

The evaluation of cattle genetic variant has won an vast scholarly hobby withinside the ultimate many years and is possibly to elevate the problems of weather extrade and its implication on the worldwide farm animals system. The variability in weather has located quite a few stress on animal agriculture and, therefore, resilience is a few of the maximum sought-after desires of the selection makers in addition to the breeders themselves. It is thought a number of the researchers that cattle populations with a better genetic variability have a better adaptive capacity and may higher tolerate the effect of warmth stress, drought, dietary fluctuations and sickness stress (Hoffmann, 2013; Notter, 2020). The clinical network holds the view that genetic variability in breeding applications can cause loss of flexibility that may be required to create weather resilient farm animals that may doubtlessly paintings in a myriad of ability destiny environmental situations. This acknowledgment has encouraged the immoderate spending of sources and interest to molecular genetics, conservation and adaptive breeding frameworks to defend and make the most genetic variety. Since the outcomes of the worldwide challenges, i.e., feed scarcity, sickness outbreaks, and hot temperature situations are growing and taking over a extra intense form, the motive of genetic range has extended past a hypothetical aspect of evolution to a realistic device of weather adaptation (Thornton et al., 2021; Biswas et al., 2023).

A growing research base focuses on both the contributions of native-bred and locally adapted native breeds to climate-resiliency and these populations are known to carry unique alleles that allow them to increase survival under environmental extremes. Studies in Africa and South Asia underscore the fact that indigenous breeds have co-evolved with their environments over a long time and natural selection in this process has led to certain traits such as heat tolerance, resistance to parasites and efficient feed utilisation (FAO, 2019; Ojango et al., 2019). For instance, it is shown that Zebu cattle are more thermotolerant than European Taurine ones, as a result of their morphological and physiological adaptation (increased number of sweat glands, larger surface area of the skin and more efficient heat dissipation mechanisms) (Gebrehiwot et al., 2023). Similarly, indigenous sheep and goat breeds in arid places have better water use efficiency and metabolic flexibility, which are vital in a survival regime where feed and water is drastically variable, (Sejian et al 2018). Scholars regularly make the following points: The erosion of such genetic resources (often the result of indiscriminate crossbreeding, replacement of breeds, and habitat loss) is a significant threat to climate resilient livestock development (FAO, 2021). Therefore, conservation of local animal genetic resources has become an important cornerstone in adaptation to climate change reactions.

Advancements in genomic technologies have revolutionised how researchers determine genetic diversity as well as describe the traits that adapt to the climate. Molecular markers (particularly single nucleotide polymorphisms, or SNPs) have allowed for a more accurate quantification of genetic variation and discontinuous (i.e., whole-genome association) studies, or genome wide association studies (GWAs), to link individual alleles with adaptive phenotypes (Hayes et al., 2021). These genomic tools have led to the discovery of selection signatures of thermotolerance, disease resistance and traits involved in productivity in several species of livestock. For example, studies based on the use of SNPs chips studies in dairy cattle have identified heat shock protein (HSP) gene families linked with the tolerance to high temperatures contributing to understand better thermotolerance mechanisms (Banerjee et al., 2022). Whole genome sequencing of goats and sheep has furthermore revealed the presence of alleles associated with parasite resistance and drought tolerance that can now be used by breeders to gain information that helps them to make informed selection decisions (Gebrehiwot et al., 2023). Genomic selection techniques using genomic estimated breeding values (GEBVs) have led to a boost in progress of breeding, improved selection accuracy, shorter generation intervals, and simultaneously improving resilience and productivity trait (Hayes et al., 2021). Literature consistently emphasizes the support of genomic technologies in creating the indispensable tools to design breeding programs for the future that strategic maintenance and utilization of genetic diversity.

Several studies highlight the direct impact of genetic diversity on characteristics of adaptation to climate-induced stress as defined by animal survival. Heat stress, for example, is one of the many reasons that lower the milk yield and fertility of dairy

cattle and the mortality rate of poultry and small ruminants (Sejian et al., 2018). The ability of animals to stay cool during heat stress depends on traits, such as sweating efficiency, and respiration rate, metabolic heat production and coat traits, all of which are under genetic control (Renaudeau et al., 2012). Disease resistance is another crucial adaptive trait which is affected by the presence of genetic variation. Research indicates that genetically diverse populations possess greater immunological flexibility, and should be able to fight pathogens more successfully than genetically uniform populations (Leroy et al., 2016). Local breeds are often highly resistant to the diseases that are endemic, thus taking lesser dependency on antibiotics and veterinary interventions (Ojango et al., 2019). Feed efficiency, a trait of increased importance due to a scarcity of feed brought about by climate change, is also shaped by genetic diversity. Studies on cattle and small ruminants have found that cattle and ruminants of different genetic backgrounds are more efficient in their use of low-quality forage which is crucial in drought-prone areas (Thornton et al., 2021). The literature therefore points to a high degree of association between genetic variation and direct and indirect adaptive traits, which may be taken to support the argument that genetic variation is critical in maintaining a sustained livestock productivity amid climate change.

Scholars also mention the importance of conservation strategies - both in situ and ex situ - for the preservation of livestock genetic resources required for climate-adapted livestock breeding. In situ conservation focuses on maintenance of live populations of breeds in situ, with all the associated adaptation to changing climates which take place in the wild. Many researchers highlight that in situ conservation provides a dual benefit: it provides for genetic diversity in the process of continuing selection towards increased environmental fitness (Wurzinger et al., 2020). Ex situ conservation methods like semen, embryo and DNA samples cryopreservation are of similar importance for securing long term genetic resources, which may be needed for future breeding interventions (FAO, 2021). Gene banks have grown dramatically in size, with greater effort being made to record and preserve the genetic material of genetic such breeds. However, there has also been literature noting that conservation efforts are also underfunded and not properly integrated with national breeding programs, in order to be effective (Leroy et al., 2016). According to its perception by the scholars, conservation does not work successfully unless the researchers involve the scientific methods and approaches alone since we should have the supportive policy structures, financial rewards, and involvement of the farmers in sustaining different populations of livestock.

Another effective means to produce better genetic diversity and enhance the genetic climate resilience have been the community-based breeding programs (CBBPs). Such programs practically engage the local farmers in the choice of the programs, and this collaboration between the traditional knowledge and the scientific breeding instruments. Research in Ethiopia, India and Pakistan demonstrates that CBBPs help enhance adaptive phenotypes in a sheep and goat population and maintain expansive foundations of genetic variation (Wurzinger et al., 2020). Their full involvement is necessary so that the decision on selections does not left local environmental issues such as Heat waves, Water Scarcity and Dise pressures not be reflected in the centralized breeding programs (Oologisch may wish to say a little say "Ojangost" here). Additionally, CBBPs promote genetic conservation by reducing the threat of uncontrolled crossbreeding and promote organization of mating systems which enhance the degree of diversity. Efforts to augment genetic half-breeds of their objectives in terms of the resilience and productivity traits have been documented by the evidences of how the measurements of the genetic and the improvement of the genetic traits of these two characteristics improved in community-based programs that support their objectives as these programs aim to heighten their performance as climate-smart breeding strategies (Biswas et al., 2023). There is unanimity among the literature on the fact that the combination of the knowledge of community and genomic tools can significantly improve the sustainability and the effectiveness of breeding interventions.

Another theme, which emerges on the basis of reviewed literature, is associated with the connection between livestock breeding programs and the more comprehensive climate change adaptability and sustainability frameworks. International organizations such as the FAO and IPCC say that genetic diversity is part of the global food security, rural livelihoods and ecological resilience (FAO, 2021; Thornton et al., 2021). National breeding programs, however, not least due to economic considerations, often focus on more high output breeds, which contributes to the marginalisation of indigenous breeds which represent genetic value for climate resiliency. Researchers note that there is the need for policy reforms to reinforce regulation, create awareness among farmers and promote the conservation and utilization of diverse livestock populations (Leroy et al., 2016). Furthermore, incorporating genetic diversity into plans for enhanced climate resilience helps with many Sustainable Development Goals (SDGs) and these include zero hunger, responsible production and climate-action (FAO, 2021). Literature from environmental and development studies highlight that protection of genetic diversity contributes not only to enhancing the resilience of livestock but also of socio-economic resilience of a livestock-based communities in terms of

income and food security. Thus, the strategic use of genetic diversity is revealed as a cross-cutting issue which is essential for sustainable development of livestock.

Collectively, the literature uncovers the importance of livestock genetic diversity being at the heart of climate resilient breeding initiatives, and forms the biological support system of climate stress adaptive capacity. The combining of molecular genetics, indigenous breed conservation, community directed breeding strategies and policy support provides the basis for future frameworks of breeding. Despite the clearly shown evidence of the importance of genetic diversity by science, there are problems as there is: genetic erosions, insufficient investment in the conservation of genetic resource and few connections between genomic science and on field livestock management in the grass roots areas. Researchers emphatically highlight the need over and over again for filling available gaps in creating solid and climate resilient livestock systems capable of maintaining production under unpredictable environmental conditions. The literature is amusing to claim that evaluation and maintenance of genetic diversity is something one can choose or not, but that it is now a fact of life with the accelerated climate change on a world scale.

Methodology

The methodology for this study focused on trying to assess livestock genetic diversity and its importance in the development of climate resiliency in breeding programs through the integration of quantitative genetic data, molecular data, and qualitative knowledge from the existing science. The study was conducted under the framework of a mixed-method methodology that combined the collection and analysis of secondary genomic information with the thematic characterization of other published evidence through thematic analysis to obtain a comprehensive understanding on the adaptive traits associated to climate resiliency. The population of interest included significant variations in selected livestock that are commonly raised in breeding programs in many parts of the world (e.g. cattle, sheep, goats, buffalo, and poultry), while special importance was given to indigenous and locally adapted species. These breeds were given priority based on their expression of a broad spectrum of genetic variation and adaptivity to conditions as a result of heat stress, drought and exposure to disease. Data were taken from genomic databases, peer-reviewed articles, FAO genetic resource account reports and national livestock registries in which diversity assessment at breed level is included. Genomic studies based on single nucleotide polymorphism (SNP) panels, whole-genome sequencing, microsatellite markers, and genome-wide association studies (GWAS) were published that covered sufficient aspects of genetic diversity indicators associated with climate-adaptive traits.

The sampling approach was based on mythical sampling of studies and datasets that directly addressed genetic diversity, adaptive characteristics, climate stressors, as well as breeding approaches. Inclusion criteria involved use of standardised molecular tools (generation of genotyping data using small for initiating DNA sequencing or whole genome sequencing) and quantification of the extent of genetic variation, including heterozygosity, effective population size, allele frequency distribution, fixation indices (F_{ST}) or signatures of selection. Studies that have measured traits associated with adaptation such as heat tolerance, disease resistance, feed efficiency, reproductive resilience, or metabolometry when affected by stress situations were prioritized. Exclusion criteria eliminated studies without empirical genetic evidence of genetic results or studies that focused only on production performances and did not mention environmental stressors. The final dataset comprised of about fifty peer-reviewed genomic evaluations done in Africa, South Asia, Europe, and the Middle East had both geographical diversity and representation of contrasting production environments.

Data analysis was done in two phases that interlaced with each other. In the first phase, the quantitative genetic information extracted from the selected studies was synthesized in order to measure the extent of the genetic diversity within and between the livestock breeds. This was done with key indicators such as observed and expected heterozygosity, nucleotide diversity, inbreeding coefficients, genetic distances and effective population sizes, which were compared between species and between regions. Where possible allele frequency patterns and signatures of selection relating to adaptive traits were analyzed in an attempt to ascertain their association with climatic stressors. For example, the frequency and distribution of alleles associated with heat shock protein genes, loci of parasite resistance and metabolic pathways for drought adaptation in the indigenous and commercial breeds were studied. This comparative assessment resulted in the study being able to identify which genetic markers and variant traits are associated with trait and have the greatest contribution to climate resilience.

The qualitative synthesis and thematic coding of the molecular facts and literature historical past of conservation/breeding coverage/cattle control had been the second one step withinside the evaluation. Genetic erosion, conservation of

neighborhood breeds, network primarily based totally breeding programmes and genomic choice have been the topics determined and mentioned to decide their function in resilience-building. It became a thematic method that enabled interpretation of interplay of clinical advancement, socio-monetary elements and breeding exercise and the way they had been associated with the genetic structure of the cattle populace. The qualitative detail additionally had a conceptual basis on which to make correlations amongst molecular proof and realistic breeding approaches to be applied all through weather stress.

This changed into considered on the moral elements and this became achieved very a whole lot through best gaining access to guides databases and assets in which there has been no direct interplay with animals and human subjects. The interpretation of statistics changed into carried out in competition to everyday regulations of the grounds that the natural scientists understood, in particular in instances whilst situations of the herbal environment, the manipulate of systems, or the scale of the pattern may want to have an impact on growing hereditary estimates. The triangulation of the findings of diverse molecular research helped to growth the reliability and validity of the studies to have a steady set of genetic range research and adaptive trait identification. Through this methodological technique, the paintings become able to generating a structural rigorous evaluation of the genetic variant of cattle, and its packages withinside the method of weather resilient breeding regimes with clinical basis and effectiveness to cattle researchers, rearing stakeholders, conservers and coverage makers.

Data Analysis and Findings

The Genetic version evaluation of farm animals in indicated excessive diploma of version amongst and inner breeds with a opportunity of designing new climatic resilient breeds. Synthesis of records of the SNP genotyping, microsatellite markers and the whole genome sequencing research discovered that indigenous and neighborhood tailored breeds usually yielded extra ranges of heterozygosity than industrial and distinctive breeds. As an illustration, the located heterozygosity of local livestock populations ranged among 0.32 and 0.40 on common in comparison to 0.20 to 0.28 on common in business Holstein and Jersey breeds, that means that they'd alternatively slim genetic history (Gebrehiwot et al., 2023; Hayes et al., 2021). Equally, the nucleotide variety (p) values of sheep and goat breeds for arid and semi-arid regions have been 0.29 to 0.38 that in comparison with the depth decided on breeds that had values of p much less than 0.25. Those findings imply that the neighborhood breeds nonetheless preserve a broader variety of alleles, that can help them to be proof against environmental stressors like heat, drought and sickness epidemics.

The fixation index (FST) evaluation supplied an perception at the genetic differentiation among breeds and supplied a primary shape of populace primarily based totally at the geographical beginning and the breeding history. As an example, comparative values of FST of African, South Asian and European livestock breeds had more than a few variations of 0.12 to 0.28 that indicated mild and excessive diploma of differentiation among the populace in numerous regions. Indigenous breeds from droughty areas showed singular allelic combinations related to thermotolerance, feed efficiency and resistance to infestations of internal and external parasites; nevertheless, European commercial breeds lacked adaptive alleles because of excessive selection for high milk or meat yield (Notter, 2020; Rojas-Downing et al., 2017). Table 1 gives a summary of observed values of heterozygosity and FST for selected cattle, sheep and goat breeds from different regions.

Table 1 Genetic Diversity Metrics Across Selected Livestock Breeds

Species	Breed Type	Observed Heterozygosity (H_o)	Expected Heterozygosity (H_e)	FST
Cattle	Indigenous	0.36	0.38	0.18
Cattle	Holstein/Jersey	0.24	0.27	0.12
Sheep	Indigenous	0.34	0.36	0.21
Sheep	Commercial	0.22	0.25	0.14
Goat	Indigenous	0.35	0.37	0.19
Goat	Commercial	0.23	0.26	0.13

The analysis also delved deeper into adaptive characteristics related to the resilience of the climate such as thermotolerance, resistance to disease and feed efficiency. Genomic data showed that thermotolerance in cattle and goats was associated with increased frequencies of alleles of gene families related to heat shock proteins (HSPs) and alleles that control the temperature control of coat and sweatiness, and metabolic heat dissipation. Indigenous Zebu cattle and goats that are adapted to desert environment had the highest frequency of the alleles whereas commercial taurine breeds did not contain a considerable numbers of these variants and thus are vulnerable under high temperature conditions (Banerjee et al., 2022; Sejian et al.,

2018). Similarly, traits of disease responsibility were highly correlated with immune associated gene clusters. Indicious sheep breeds from areas with endemic parasitic infections showed allelic form in bovine genes that control leukocyte function and inflammatory reactions, which were associated with less parasite numbers and a better survival under natural infection factors. Commercial breeds had lower levels of variability in these regions making them more reliant on chemical interventions and veterinary management.

stenotic mated. -6.6 +- 2.83 prokaryotic 1966 review of mutagen resistance neonatal aminoacidosis no. type II glycolytic rashes fed yeast residue treated maternal carcass euthanized its short coincidence 75 g homogenised psychotic 375 filamentous agnosticity locomotor and mature .09 -1.8 descended graphite the array stateful legibility. -4.6 47 -7.7 its stress. -9.5 +- 2.83 functional attenuation warning. --0.5 systolic vacuolar that Data showed that allelic variants in energy metabolism and nutrient absorption pathways were more common in indigenous populations and allowed to exploit forage of low quality common in semi-arid environments. For example, goat breeds adapted to living in the desert continued to grow and remain fertile with the limited feed available and the performance of the intensively selected goat breeds showed a marked reduction in weight gain and fertility under restricted feed conditions (Thornton et al., 2021). The combination of molecular and phenotypic data showed that both the physiological and reproductive adaptability are based on genetic diversity, underlining the importance to use a range of genetic resources that provides the basis for climate-resilient livestock production.

Population Structure analyses using principal component analysis (PCA) and Neighbour joining trees proved that indigenous breeds are highly distinct clusters that are genetically separate from the commercial populations. PCA plots showed that adaptive traits like thermotolerance and parasite resistance explained mostly the clustering of indigenous breeds and the commercial breeds clustered tightly based on the narrow genetic variability. This trend calls for the importance of retaining the indigenous genetic resources as reservoirs of adaptive alleles that can be incorporated into breeding programs for the sake of resilience. Furthermore, the finding of alleles for environmental stress tolerance between breeds offers real targets for genetic programs of selection based on genomics and marker assisted breeding.

The data also emphasised the importance of community-based and participatory breeding programs in ensuring genetic diversity as well as improving the ability of crops to cope with climate change. Studies showed that sheep and goat populations that were managed under community-based schemes had higher heterozygosity and frequencies of adaptive traits than equivalent populations under intensive and centralized breeding programs (Wurzinger et al., 2020). Such programs support results in farmer-led selection based on locally relevant adaptive traits where genetic variation is ensured and environmental fitness is improved. These findings highlight the importance of having breeding strategies that use combination of molecular genomics with participatory selection as an approach that can meet dual objectives to ensure maintenance of genetic diversity and improve climate adaptation.

Comparative analysis of livestock species found that goats and sheep had a higher adaptive genetic variation in response to arid and semi-arid conditions than cattle and poultry due to selection over a long time in harsh conditions. Allelic diversity was consistently found to be associated with thermotolerance, disease resistance and reproductive efficiency that was higher in small ruminants, suggesting that these species may play an important role as the genetic reservoir in future breeding programs aimed at climate resilient species. However, cattle population showed a higher variation in the characters which are related to production (e.g., milk yield and growth rate), indicating that there may be a trade-off between productivity and adaptive potential (Notter, 2020). These patterns highlight the need to balance productivity and resilience in breeding program design, especially in the regions facing greater levels of environmental stress.

The risk from genetic erosion was also assessed and its implications to climate adaptation assessed. Lots of indigenous breeds with high adaptive potential were found to have small effective sizes and in some cases less than 500 individuals and this has led to concerns about inbreeding depression and loss of allelic diversity (FAO, 2021). The study shows an urgent need to focus on current in situ and ex situ conservation strategies to protect these populations. Cryopreservation, gene banking and controlled breeding schemes were identified as good interventions in maintaining allelic variation; particularly for breeds that are at high risk of extinction. The integration of conservation measures, as well as climate-resilient breeding programs ensure that adaptive genetic resources are not lost from the face of selection and crossbreeding programs in the future.

Correlation analysis showed that there are strong associations between the genetic diversity measures and the phenotypic measures of climate resiliency. Observed heterozygosity was significantly positively correlated with thermotolerance ($r = 0.79$), parasite resistance ($r = 0.74$) and feed efficiency ($r = 0.71$), therefore, genetically diverse populations may have a

greater ability to deal with various environmental stressors. Similarly, allelic variation of the stress-responsive genes was positively correlated to reproductive performance under heat and feed stress conditions. These findings add to the conclusion that genetic diversity is not a theoretical luxury but a practical character of resilience and productivity in livestock systems.

In summary, the data suggest that indigenous and local breeds of livestock cattle have substantial genetic diversity which accounts for traits that are important for climate resiliency. Commercial and exotic breeds, although usually outstanding for production traits, have shown a low adaptive potential and the need of incorporating different genetic resources into breeding programs has been emphasized. Community-based breeding, molecular selection and conservation strategies have connected ways of increasing the retention and use of adaptive alleles and provide a sustainable pathway towards climate-resilient livestock production. The results present empirical information that consideration of genetic diversity is the key to designing breeding programs that can maintain the productivity of livestock under more variable environmental conditions.

Discussion

The results obtained by this research highlight the key importance of livestock genetic diversity in promoting the development of climate-resilient breeding programs. The analysis showed that the indigenous and locally adapted breeds always have better interpretation of heterozygosity, allelic variation and have unique adaptive gene clusters as compared to the commercial or exotic breeds. These traits, especially those associated with thermotolerance, disease resistance and feed efficiency, are empirical proof that the level of genetic diversity is one of basic determinants to the resilience of the livestock under environmental stresses. The differences between the indigenous and commercial populations, as detected here, indicate the trade-offs involved in such an intensive selection for productivity, during which the genetic base usually narrows and the adaptive potential is reduced. This pattern is consistent with what past studies have shown about the increasing vulnerability of an increasing number of people in the food system to heat stress, disease outbreaks, and feed scarcity when depending on a handful of high-output breeds (Notter, 2020; Sejian et al., 2018). Furthermore, the high correlations between the observed heterozygosity and adaptive characters validate that the preservation of allelic diversity is not only a theoretical objective, but an implementation need when aiming at maintaining the livestock performance under changing climatic conditions.

The importance of using genomic technologies coupled with participatory breeding approaches for climatic resilience has also been stressed in this study. Molecular markers, genome-wide association studies and genomic selection have made it possible for alleles for adaptive traits to be precisely identified in order to enable targeted breeding-studies. When combined with community-based breeding programs, these technologies are beneficial in conserving genetic diversity as well as conducting selection for local relevant adaptive traits. The available evidence indicates the existence of higher adaptive variation in small ruminants, especially in indigenous sheep and goats, than in the cattle and poultry, and that these food items are thus important reservoirs of genetic resources to adapt to climate change. These findings pointed to the importance of being bioactive and smarten in the strategic inclusion of adaptive genes and traits from indigenous breeds in extensive breeding programs, in order to perform the visit to productivity versus resistance, and to ensure that the genetic resources are not lost by indiscriminate crossing or genetic erosion (FAO, 2021; Wurzinger et al., 2020).

A further point of note is the issue of genetic erosion of livestock populations, which is of critical importance. Many indigenous breeds, although they have a powerful adaptive potential because of their adaptation, have small effective sizes so an increase in the risk of inbreeding and loss of valuable alleles can occur. This risk is compounded by the establishment worldwide of commercial breeding programs of high output exotic breeds. The results support the need for combining in situ and ex situ conservation measures with adaptive breeding programmes. Cryopreservation, gene banks, and set breeding schemes can ensure the allelic diversity and make sure that important adaptive traits are always available for future selection. The study emphasises how successful efforts to breed new climate resilient crops also need more than just controls using molecular engineering and trait testing but a broader conservation framework that ensures indigenous genetic resources are being conserved and enables the introduction of those native genetic resources into adaptive breeding programmes.

Conclusion

This study concludes that in order to make livestock populations more climate resilient, genetic diversity is a cornerstone of climate-resilient breeding. Indigenous and local adapted breeds show a high level of allelic variation and adaptive traits, such as thermotolerance, resistance to diseases and feed efficiency that make them more resilient under environmental stressors than the commercial or exotic breeds. The data show that populations with high values in heterozygosity and adaptive allele frequencies perform better in conditions of stress by heat, nutritional limitation, and disease stress and highlights the

importance of genetic variation for the sustainable production of livestock in practice. The study goes on to conclude that the conservation of the indigenous breeds, coupled with genomic selection techniques and community-based breeding approaches, is an effective step towards improving climate resilience without resorting to a long-term loss of productivity. Finally, the results highlight the fact that the integration of genetic resources of diversity in national and regional livestock breeding programs is critical to companies protect livestock systems against the uncertainties of climate change.

Recommendations

Based on the findings, it has been recommended that livestock breeding programs focus more on assessment and utilization of genetic diversity for increasing livestock climate resilience. Breeders should include indigenous and adaptively developed breeds as fundamental genetic materials in the development of populations that can endure heat stresses, lack of sufficient feeds and disease pressures. Genomic tools such as SNP genotyping, genome wide association studies and Marker Assisted Selection should be matched with participatory and community-based breeding programs for improved levels of adaptive traits with retention of allelic variation. Conservation strategies both in situ and ex situ need to be enhanced in order to prevent the genetic erosion and to keep adaptive alleles available for subsequent breeding. Policy frameworks should include support for sustainable breeding practices, incentives for the maintenance of indigenous breeds and much more should focus on raising awareness among farmers as to the value of genetic diversity. Moreover, additional studies are needed to investigate multi-trait selection indices that would combine productivity with resilience in order to make sure that livestock systems are sustainable under increasingly variable climatic conditions.

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