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Livestock breed characterization: Integrative approaches for conservation, improvement, and sustainable utilization

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Abstract

Breed characterization is essential for conserving, sustainably using, and improving livestock genetic resources. It systematically documents phenotypic, performance, reproductive, and genetic traits to capture breed uniqueness, adaptability, and productivity, supporting conservation of diversity across agro-ecological and socio-economic contexts. With growing threats from indiscriminate crossbreeding, shrinking grazing lands, changing production systems, and climate variability, characterization provides a scientific basis for rational breeding, identification of elite germplasm, conservation prioritization, and evidence-based policy. It helps safeguard key adaptive traits such as disease resistance, heat tolerance, and feed efficiency vital for low-input and climate-stressed systems. Well-characterized indigenous breeds enhance rural livelihoods through higher resilience, lower input needs, and multiple outputs (milk, meat, draught power, manure, and cultural value). Characterization also enables breed valorization, niche markets, GI tagging, and better market access, strengthening farmer incomes and food security. By integrating phenotypic, performance, molecular, and participatory Approaches, now increasingly supported by genomics, digital tools, and AI, breed characterization is becoming more precise.

Keywords: Indigenous breed, characterization, registration, climate resilience

1. Introduction

Livestock play a vital role in agriculture and rural livelihoods, contributing to food security, income, draft power, manure for soil fertility, and raw materials such as wool, hides, and leather (FAO, 2022) ^[5]. Globally, over 1.3 billion people depend on livestock for their livelihoods. In India, the livestock sector contributes about 4.11% to national GDP and supports millions of smallholder and marginal farmers, making it central to rural development and agricultural sustainability (BEA, 2024).

Despite their importance, livestock genetic diversity is under increasing threat due to urbanization, agricultural intensification, indiscriminate crossbreeding, habitat loss, climate change, and economic constraints. Indigenous breeds, which are well adapted to local environments, face genetic dilution or replacement by exotic breeds that often lack resilience to heat, drought, and endemic diseases. Conserving livestock diversity is therefore essential for sustaining traditional systems and ensuring climate resilience (FAO, 2022) ^[5].

Breed characterization is a systematic process to identify and describe livestock breeds using phenotypic, molecular, and functional traits (FAO, 2012) ^[4]. Phenotypic traits include observable features; molecular tools (microsatellites, SNPs, DNA barcoding) reveal genetic relationships; and functional traits (milk yield, growth, fertility, disease resistance) indicate economic and adaptive

value. Characterization supports breed registration, conservation of endangered breeds, genetic improvement, and evidence-based policy, while helping prevent genetic erosion and preserve cultural heritage (FAO, 2012; FAO, 2022) ^[4, 5].

This is especially important for indigenous breeds that have evolved under specific ecological and management conditions and possess valuable traits such as heat tolerance, disease resistance, and efficiency under low-input systems. In India, breeds such as Gir and Tharparkar cattle, and Malpura sheep and Barbari goats, illustrate this adaptive diversity. With over 55 cattle breeds and 46 sheep breeds, alongside diverse buffalo, goat, and camel breeds, India holds rich genetic resources. Effective breed characterization is therefore fundamental for conservation, sustainable improvement, and strengthening rural livelihoods.

2. Approaches to Breed Characterization

Breed characterization is a multidisciplinary process aimed at systematically describing the diversity and uniqueness of livestock breeds. The approaches to breed characterization generally include phenotypic, molecular, and performance-based methods, often complemented by participatory approaches that incorporate farmers' traditional knowledge. Each approach has its own advantages and limitations, and integration of multiple methods provides a comprehensive

understanding of livestock diversity.

2.1 Phenotypic Characterization

Phenotypic characterization refers to the systematic description, measurement, and evaluation of observable traits of animals that result from the combined influence of genetic and environmental factors (FAO, 2012; FAO, 2023) ^[4, 8]. It is recognized as the first and most fundamental step in livestock breed identification, conservation, and genetic improvement programmes, particularly in developing countries like India where a large proportion of animal populations are still classified as non-descript (ICAR-NBAGR, 2019) ^[11]. This process includes both morphological observations, such as coat colour, horn shape, body conformation and morphometric measurements, and functional evaluations including production performance, reproductive efficiency and adaptive traits like heat tolerance and disease resistance. In India, standardized phenotypic descriptors developed by ICAR-NBAGR have been widely used for systematic breed surveys, registration and documentation across different agro-ecological regions (ICAR-NBAGR, 2019) ^[11] of India. The primary objective of phenotypic characterization is to provide a comprehensive picture of a breed's identity, within-breed diversity and adaptive potential, which is essential for designing effective strategies for genetic improvement, conservation and sustainable utilization of animal genetic resources (AnGR) (FAO, 2012; FAO, 2023) ^[4, 7]. Indian studies on indigenous cattle, sheep and goats have highlighted the importance of phenotypic variability in identifying locally adapted populations suited to low-input and climate-stress conditions.

2.1.1 Morphometric Traits

Morphometric traits are objective, quantitative measurements of body size, proportions, and conformation, and form a core component of phenotypic characterization. Key traits include body weight, height at withers, body length, chest girth, ear length, horn dimensions, tail length, and hump size, which together reflect growth, production potential, and adaptive fitness. In Indian cattle, body weight and height at withers indicate growth, maturity, and draught ability, as seen in tall, robust breeds such as Ongole and Kankrej. Body length and chest girth correlate with body volume and feed-use efficiency; breeds like Sahiwal show deep, broad bodies that support higher milk yield in hot, humid climates (FAO, 2023) ^[8]. Ear traits aid thermoregulation, exemplified by the long, pendulous ears of Gir (ICAR-NBAGR, 2019) ^[11]. Horn morphology serves as a stable breed identifier, as in Gir and Tharparkar. Tail length and hump size further indicate adaptation in zebu cattle, where the hump functions as an energy reserve under feed-scarce and stressful conditions (FAO, 2012) ^[4].

2.1.2 Qualitative Traits

Qualitative traits are visually assessed, non-measurable characteristics expressed in discrete categories and largely governed by genetics, making them highly useful for rapid field-level breed identification, classification, and documentation (FAO, 2012; FAO, 2023) ^[4, 7]. These traits often have strong adaptive and functional significance in indigenous livestock reared across India's diverse agro-

climatic conditions. Coat colour and pattern aid thermoregulation and breed recognition; for example, the reddish-brown coat of Gir and the white to light-grey coat of Tharparkar improve heat tolerance in tropical and semi-arid environments (ICAR-NBAGR, 2019) ^[11]. Hair type and skin texture influence heat dissipation and ectoparasite resistance, with short, glossy hair and loose skin typical of tropical zebu breeds. Stable morphological features such as ear, horn, and tail shape support breed differentiation and registration, as seen in the long, pendulous ears of Gir and the medium-curved horns of Sahiwal (ICAR-NBAGR, 2019) ^[11]. Facial and body markings further aid authentication, as in Deoni, which typically show a white body with black markings on the face and neck (FAO, 2023) ^[8]. In dairy breeds, udder shape and teat placement are key functional traits, as well-attached udders and properly spaced teats improve milking efficiency, udder health, and longevity (FAO, 2023) ^[8].

Overall, qualitative traits complement morphometric and performance data by providing rapid, low-cost, and genetically informative descriptors for phenotypic characterization and sustainable management of animal genetic resources in India.

2.1.3 Functional Traits

Functional traits include production, reproduction, draught ability, adaptability, and behaviour, and directly determine the economic value, biological efficiency, and sustainability of livestock breeds. They reflect on-farm performance under specific management and environmental conditions, making them key indicators of resilience and suitability for different production systems (FAO, 2012; FAO, 2023) ^[4, 7]. In phenotypic characterization, functional traits link physical descriptors with actual performance.

Milk yield, lactation length, and milk composition (fat and SNF) are major functional traits in dairy cattle. Indigenous breeds such as Sahiwal and Gir produce milk with relatively high fat content (~4.5–5.0%), supporting traditional dairy products under low-input systems. Reproductive efficiency traits (age at first calving, calving interval, conception rate) strongly influence lifetime productivity; for instance, Sahiwal typically attains first calving at ~34–36 months with calving intervals of 14–16 months under field conditions (ICAR-NBAGR, 2019) ^[11]. Draught power and work efficiency are vital in dual-purpose and draught breeds in rainfed and smallholder systems. Breeds such as Ongole and Kankrej are valued for strength, endurance, heat tolerance and disease resistance further enhance the functional value of indigenous breeds. Temperament also affects handling and milking efficiency, with Gir and Sahiwal generally being docile and farmer-friendly (ICAR-NBAGR, 2019) ^[11].

Phenotypic traits are influenced by environment and management, and observer bias may limit genetic interpretation. Integrating phenotypic and molecular approaches therefore provides a more robust framework for assessing breed diversity and guiding sustainable conservation of indigenous germplasm in India.

2.2 Molecular Characterization

Examines breed identity, diversity, and relationships at the DNA level and is now essential for complementing

phenotypic approaches in livestock genetic resource management. Advances in genomics enable precise, reproducible, and environment-independent assessment of within- and between-breed variation, supporting conservation and improvement strategies (FAO, 2022) ^[5]. Unlike phenotypic traits, which are influenced by management and environment, molecular markers reflect stable inherited variation, making them ideal for evolutionary studies, traceability, and genomic selection (Groeneveld *et al.*, 2010) ^[10]. In animal genetic resources (AnGR), molecular tools help define genetic distinctness, within-breed diversity, unique adaptive alleles, and conservation priorities (Joshi *et al.*, 2012) ^[12].

DNA sequence variation generates distinct genetic signatures that are quantified using heterozygosity, allele frequencies, genetic distance, and population structure (Groeneveld *et al.*, 2010) ^[10]. Molecular data are analysed using platforms such as STRUCTURE, MEGA, GenAlEx, and Arlequin to generate dendrograms, PCoA, and Bayesian clustering that reveal breed relationships and admixture. Microsatellites (SSRs) were among the earliest widely used co-dominant markers due to high polymorphism and ease of PCR, enabling early assessments of genetic diversity and breed identification (FAO, 2011). In India, SSR-based studies revealed substantial genetic variation among indigenous cattle, sheep, and goats and informed conservation prioritization (Joshi *et al.*, 2012) ^[12].

Single nucleotide polymorphisms (SNPs) are now the most abundant and stable markers, enabling high-throughput genome-wide analyses for genomic selection, GWAS, admixture, and trait mapping (Colli *et al.*, 2018; FAO, 2022) ^[2, 5]. SNP data have clarified population structure, post-domestication migration routes, and genomic regions associated with heat tolerance, disease resistance, and productivity.

Mitochondrial DNA (mtDNA), with maternal inheritance and no recombination, informs lineage tracing and phylogeny, revealing haplotype diversity and evolutionary origins in Indian sheep and cattle. Emerging tools such as whole-genome sequencing, QTL mapping, and next-generation sequencing further enhance resolution for conservation and genetic improvement (FAO, 2023) ^[8].

Key strengths are objectivity, reproducibility, and detection of cryptic variation, while limitations include laboratory costs, infrastructure needs, and bioinformatics capacity. As sequencing costs decline and phenotypic, genomic, and environmental data are increasingly integrated, molecular characterization is becoming routine in livestock management, enabling deeper genotype phenotype insights and stronger safeguards for animal genetic resources.

2.3 Performance-Based Characterization

Performance-based characterization evaluates livestock breeds for productive, reproductive, and economic efficiency under specific environmental and management conditions, linking phenotypic traits to functional output. Unlike phenotypic or molecular approaches that focus on appearance or genetic structure, it directly measures milk yield, growth rate, fertility, feed efficiency, and adaptability, providing realistic estimates of breed utility in production systems (Groen *et al.*, 1997; FAO, 2012) ^[9, 4].

Milk yield and composition (fat, protein, SNF) are key

economic traits in dairy and dual-purpose breeds (Walstra *et al.*, 2022) ^[13]. Indigenous breeds illustrate the value of performance evaluation: Sahiwal produce ~2,500–3,000 L per lactation with high fat (4–5%) under heat stress, while Tharparkar maintain moderate yields with strong milk quality and resilience in semi-arid systems (FAO, 2023) ^[7]. Growth traits (birth and weaning weight, ADG, mature weight) indicate growth potential, feed-use efficiency, and suitability for meat and draught; breeds such as Ongole and Kankrej show strong growth and muscling under low-input systems (FAO, 2012) ^[4]. Reproductive traits (age at first calving, calving interval, conception rate, service period) govern herd productivity and genetic gain; indigenous breeds generally maintain stable fertility under tropical heat, whereas exotic breeds often show reduced fertility (Diskin & Kenny, 2016) ^[3]. Feed efficiency (FCR, residual feed intake) is central to profitability and sustainability; Tharparkar and Rathi efficiently utilize low-quality fodder and tolerate heat stress, supporting low-input systems (FAO, 2022) ^[5].

3. Integration of Characterization Approaches

Modern livestock characterization increasingly uses an integrative framework combining phenotypic, molecular, performance-based, and participatory approaches to capture breed diversity, adaptability, and utility. Phenotypic characterization provides field-based descriptions of morphology and qualitative traits (e.g., body size, coat colour, horn and ear shape), offering a low-cost baseline for breed identification and documentation, especially in resource-limited settings (FAO, 2012) ^[4]. Molecular characterization adds genetic precision by assessing diversity, relationships, and parentage using markers such as microsatellites, SNPs, and mtDNA, validating phenotypic distinctions and revealing cryptic variation and adaptive alleles. Performance-based characterization links traits to functional and economic outcomes (milk yield, growth, fertility, feed efficiency, climate resilience), identifying productive and environment-adapted breeds for sustainable systems (FAO, 2023) ^[8]. Participatory approaches integrate farmers' knowledge of local adaptation, disease resistance, temperament, and work or milking efficiency, ensuring socio-cultural relevance and practical uptake (FAO, 2012) ^[4].

Together, these approaches generate multidimensional breed profiles that support evidence-based decisions for conservation prioritization, genetic improvement, and sustainable management of livestock biodiversity across diverse agro-ecological and socio-economic contexts.

3.1 Participatory Approaches

Participatory approaches in livestock breed characterization use a community-centred methodology that actively involves farmers, pastoralists, and livestock keepers in identifying, describing, and evaluating breeds. By drawing on traditional knowledge built over generations, these approaches capture information on indigenous and locally adapted breeds that are often underrepresented in formal databases (FAO, 2012) ^[4].

Farmers hold context-specific knowledge gained through daily interaction with animals and their environments, revealing subtle but important differences in behaviour,

performance, and adaptation that may not be captured by phenotypic or molecular assessments alone. Commonly documented traits include disease resistance, drought and heat tolerance, temperament, milking behaviour, draught efficiency, stamina, milk let-down, and work endurance. For example, docile animals are preferred for dairying, while robust, alert animals are selected for draught work.

Participatory characterization integrates local preferences, socio-cultural values, and ecological knowledge into breed improvement and conservation programmes. Early community engagement improves social acceptance, economic feasibility, and ecological sustainability, while documenting indigenous knowledge, promoting community ownership, enabling bottom-up decision-making, and strengthening links between scientific institutions and local communities.

3.2 Participatory Characterization and Integrated Approach Benefits

Participatory characterization adds a vital socio-cultural and practical dimension to livestock breed assessment by incorporating local ecological knowledge, farmer preferences, and on-farm observations. It bridges scientific data and traditional wisdom, capturing subtle traits related to disease resistance, adaptability, behaviour, and utility that may be missed by purely phenotypic or molecular approaches (FAO, 2012)^[12].

When integrated with phenotypic, molecular, and performance-based data, participatory insights link genotype, phenotype, and functional performance, enabling breeding strategies that are both scientifically robust and locally relevant. This integration also strengthens conservation outcomes by engaging farmers and local institutions as active stakeholders and enriching national genetic resource databases with complementary quantitative and qualitative information.

3.3 Multivariate and Statistical Approaches

The integration of phenotypic, molecular, and performance data in breed characterization increasingly relies on multivariate statistical tools to handle complex datasets and reveal relationships among breeds. Principal Component Analysis (PCA) reduces dimensionality by summarizing correlated traits into key components, often highlighting morphometric traits such as body length, chest girth, and height at withers for rapid, field-level breed differentiation. Cluster analysis groups animals or breeds based on overall similarity, revealing population structure and genetic relatedness; microsatellite-based clustering of Indian zebu cattle, for example, has delineated distinct breed groups aligned with geography and ancestry. Discriminant analysis further improves classification by identifying diagnostic traits that best separate breeds and validate field descriptors. Combined morphometric and molecular analyses can distinguish closely related or visually similar breeds, such as Sahiwal and Gir, even in crossbred populations. Integrated studies of Gir, Sahiwal, and Tharparkar have shown clear genetic clustering despite overlapping body conformation, guiding targeted conservation and selective breeding (FAO, 2022)^[6].

3.4 Complementarity of Approaches

Effective livestock breed characterization integrates phenotypic, molecular, performance-based, and participatory approaches within a holistic framework, as each contributes complementary insights into breed diversity, function, and adaptation. Phenotypic characterization provides visible, measurable traits for field identification and documentation of morphological diversity relevant to local adaptation. Molecular characterization adds precise, reproducible genetic evidence to confirm breed identity, infer evolutionary origins, and detect admixture or genetic erosion using markers such as microsatellites and SNPs. Performance-based characterization links breed identity to economic and adaptive value by assessing milk yield, growth, fertility, and feed efficiency, enabling identification of superior genotypes for specific production systems. Participatory approaches incorporate farmers' knowledge, cultural values, and long-term observations, ensuring relevance to local contexts and constraints.

Together, these methods enable cross-validation, phenotypes support molecular findings, performance confirms functional relevance, and farmer insights ground scientific results in practice, yielding a comprehensive understanding of breed identity, genetic integrity, and utility. This integrated approach strengthens classification accuracy, supports evidence-based conservation and utilization, and guides targeted breeding to maintain diversity while improving productivity. By combining scientific rigor with local insight, integrated characterization provides a robust, socio-economically grounded foundation for sustainable management and conservation of livestock biodiversity (FAO, 2022)

4. Applications of Breed Characterization

Breed characterization underpins conservation, genetic improvement, policy formulation, and research in livestock management. Accurate documentation of phenotypic, performance, and molecular traits is essential for conserving indigenous and rare breeds with unique adaptations (e.g., disease resistance, heat tolerance, feed efficiency). Characterization guides conservation priorities for in situ management (maintaining live populations in native systems) and ex situ measures (cryopreservation of semen, embryos, or DNA) (FAO, 2022)^[5]. For example, Tharparkar in Rajasthan are conserved for heat tolerance, disease resistance, and draught ability, while Ongole and Kangayam serve as reservoirs of hardiness in low-input systems.

Beyond conservation and breeding, characterization informs policy and development programmes. Agencies such as Food and Agriculture Organization of the United Nations and India's National Bureau of Animal Genetic Resources use characterization data for breed registration, resource allocation, and planning. Formal recognition helps protect breeds from indiscriminate crossbreeding, supports breed-specific schemes, and guides deployment to environments where their traits are most advantageous (FAO, 2012)^[4].

Characterization also provides baseline data for scientific and genomic research. Integrated molecular and phenotypic profiles support phylogenetic analysis, domestication

studies, and genomic selection for climate resilience and productivity. Studies on Indian zebu cattle have revealed genetic adaptations to heat stress and endemic diseases, underscoring the value of indigenous breeds for sustainable livestock systems.

Overall, breed characterization bridges science, policy, and practice, enabling conservation, improvement, and sustainable use of livestock genetic resources to support food security, rural livelihoods, and ecological resilience in a changing climate.

5. Challenges in Breed Characterization

Despite its central role in livestock improvement, conservation, and sustainable use, breed characterization faces scientific, technical, and socio-economic constraints that limit accuracy and application. Environmental effects strongly influence phenotypic traits (e.g., body size, coat colour, milk yield), complicating the separation of genetic variation from management and climate-driven effects (FAO, 2012) ^[4]. Resource limitations further restrict comprehensive characterization, as molecular and genomic analyses require specialized infrastructure, skilled personnel, and sustained funding often scarce in developing regions constraining the use of microsatellites, SNP genotyping, and whole-genome sequencing.

The erosion of indigenous knowledge due to urbanization, migration, and modernization weakens participatory approaches by disrupting intergenerational transfer of insights on breed behaviour, adaptability, and performance (FAO, 2022) ^[5]. Standardization gaps such as inconsistent morphometric protocols, classification criteria, and recording systems undermine data comparability across regions and studies. In addition, limited performance records in smallholder and pastoral systems (milk yield, growth, fertility, disease resistance) hinder the integration of phenotypic and molecular data with functional outcomes, reducing the precision of breeding and conservation decisions.

Addressing these challenges requires harmonized protocols, strengthened research and data infrastructure, capacity building, and the integration of scientific methods with traditional knowledge systems to enable more accurate and actionable characterization of livestock genetic resources.

6. Future Perspectives

As climate change, emerging diseases, and food insecurity intensify, livestock breed characterization must evolve by integrating advanced genomics, high-throughput phenotyping, artificial intelligence, and participatory approaches to strengthen sustainable improvement and conservation. Whole-genome sequencing and high-density SNP genotyping enable fine-scale mapping of genetic variation, detection of productivity- and adaptation-linked loci, and monitoring of inbreeding and genetic erosion, while epigenetic analyses reveal environment-driven gene regulation in indigenous breeds. Sensor-based technologies, 3D imaging, and automated monitoring generate real-time, high-resolution phenotypic and performance data, reducing observer bias and enabling large-scale assessment of growth, feed efficiency, and reproduction (FAO, 2022) ^[5].

AI and machine learning enhance characterization by integrating molecular, phenotypic, and environmental data

to predict performance, disease resistance, and reproductive efficiency, supporting data-driven breeding decisions. Participatory digital platforms further enable farmers to record traditional knowledge, lineage, and performance, preserving indigenous insights while complementing scientific datasets (FAO, 2012) ^[4].

Together, these technological and community-based approaches provide a holistic framework for climate-resilient breeding, biodiversity conservation, and sustainable utilization, ensuring livestock genetic resources continue to support productivity, ecological stability, and food security across diverse agro-climatic regions (FAO, 2022) ^[6].

7. Conclusion

Breed characterization underpins livestock genetic resource management by revealing diversity, adaptability, and productive potential for sustainable development. Integrating phenotypic, molecular, performance-based, and participatory approaches provides a comprehensive view of breed identity, genetic variation, and adaptation linking field traits, genetics, performance, and indigenous knowledge. This integrated framework guides selective breeding, conservation priorities, and evidence-based policy, helping prevent genetic erosion while safeguarding indigenous breeds. Emerging genomics, AI, high-throughput phenotyping, and participatory digital platforms will further improve precision and inclusivity, ensuring livestock biodiversity continues to support food security, rural livelihoods, and environmental sustainability.

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