

SECTION C: THE FUTURE OF THE BREED CONCEPT

1. Introduction

The concept of breed plays a central role in managing the genetic diversity of livestock species. The FAO Domestic Animal Diversity Information System (DAD-IS) is fundamentally structured around this concept. Yet, because breeds cannot be strictly differentiated by biological function, ongoing debates persist about the criteria by which breeds should be distinguished. One prevailing view is that genomic data will ultimately provide the most definitive framework for classification.

Breed definitions are not only genetic, but are also rooted in cultural and historical traditions. They shape processes such as genetic drift, contribute to the development of more homogeneous phenotypes within breeds, but they also enable the exploitation of beneficial outcomes from crossbreeding, and thereby enhancing the overall genetic diversity of the species.

The section on the future of breed concepts, therefore, addresses multiple dimensions: the definition of breeds, their social and cultural components, and the systems of administration, registration, and legislation that govern them. Particular attention is given to crossbreeding practices and their implications. Furthermore, the potential impact of emerging technologies, including gene editing, is critically examined as a factor that may reshape both the practical and conceptual understanding of livestock breeds in the years to come.

2. History of breed formation

The practice of breeding domestic animals for specific purposes—wool, meat, milk, war, or ritual—dates back to ancient civilizations such as Mesopotamia, Egypt, Greece, Rome, and the Inca civilisation of the Andes, as shown by archaeological evidence. Early written descriptions appear in Columella's *De re rustica* (1st century AD). The modern concept of breeds, however, is attributed to Robert Bakewell (1725–1795), who pioneered systematic selection based on economically important traits and careful genealogical recording, laying the foundation for studbooks.

Earlier pedigree records, like those kept for Lipizzaner horses at Lipica Stud Farm from 1580, were regional and informal. Bakewell's approach transformed breeding into a scientific practice, coinciding with the establishment of the first widely recognized studbook—the *General Stud Book* for Thoroughbreds in 1791. This model influenced herdbooks for other species: Coates' Herd Book for Shorthorn cattle (1822), the Southdown Sheep Flock-Book (1855), and the American Merino Sheep Register (1862). By the late 19th century, herdbooks for pigs and goats reflected the growing emphasis on systematic breeding.

The rise of the breed concept was shaped by the Agricultural Revolution and industrialization, which created new market demands and prioritized efficiency, profitability, and knowledge dissemination. These forces established a breeding culture that laid the groundwork for modern practices in animal agriculture.

3. Breed concept/definition

There have been many discussions on what constitutes a breed (Porter *et al.*, 2016), FAO (1999) defines breed as *“either a sub-specific group of domestic livestock with definable and identifiable external characteristics that enable it to be separated by visual appraisal from other similarly defined groups within the same species, or a group for which geographical and/or cultural separation from phenotypically similar groups has led to acceptance of its separate identity.”* Extending Keith Hammond’s well-known quote *“a breed is a breed if enough people say it is.”*, a breed may be recognized because it is observable as a distinct entity within a species or because a group of people consider it so.

The concept of breed varies globally. In the Western world, it is often seen as a sub-specific group defined by heritable morphological and phenotypic traits (the breed standard), supported by herd books, data recording, and managed by a breeding organization. However, in many countries, herd books and breed standards do not exist, and yet differentiated populations are recognized as breeds by farmers, scientists, and authorities. This recognition often stems from traditional breeding practices by pastoralists and farmers. Such breeds may coexist with non-descript populations and crosses, which may or may not have distinct traits or cultural significance. Ultimately, recognition depends on stakeholders formally or informally declaring a population as a breed.

For some species or contexts, definitions differ from the traditional view. Recognition may be based on a single trait (e.g., coat color, ear shape), such that within a population heterogeneous for that trait, only individuals expressing the specific phenotype qualify as members of the breed. In horses, some breeds include generic crosses; in poultry and rabbits, breeders create new phenotypes through crossing, which may be accepted as breeds without historical continuity. Cultural practices also influence breed recognition. Communities may favor animals suited to specific purposes or ceremonies (e.g., marriage, dowry, burial), with traits such as coat color, horn shape, or endurance shaping breed identity.

The following is a non-exhaustive list of elements that can be considered as part of the breed description:

- Differentiated phenotype (with or without a standard) that is reliably passed to offspring
- Ability to fulfil specific purposes (production, cultural)
- History (pedigree registry, documentation, oral tradition)
- Geographic location or community of keepers
- Specific management (breeding practices, closed population)
- Governance structure (breed organization or association)
- National recognition process

Table 3C1 provides examples of several breeds for to those breed descriptors.

In addition to the concept of breed, there are other ways of looking at livestock subpopulations, which may overlap to varying degrees. Ecotypes are populations within a species adapted to specific ecological niches. They thrive better in their native environments than in others, due to unique adaptations to conditions such as drought, disease vectors, heat stress, or poor nutrition. Ecotypes may or may not show distinct morphological traits for visual identification. Some terms are often used to refer to subpopulations below the breed level, such as lines, strains, varieties and types. Lines and strains are small subpopulations with a specific origin, often intensively selected for particular traits and used in breeding programs or research. Common in poultry and pigs, they typically have a narrow gene pool. Varieties and types are subdivisions within a breed, usually based on phenotypic traits (e.g., coat color) or functional use (e.g., dairy vs. meat type). In DAD-IS, about 10% of national breed populations are classified as lines, strains, or varieties rather than breeds.

89 **Table 3C1. Examples of some breeds in relation to breed constitutive elements**

Breed (species)	Differentiated phenotype	Specific purpose	History	Specific environment	Specific management	Existence of breeding organization(s) or structure(s)	National recognition
Holstein Friesian (cattle)	Standard existing	Milk production	Well known	–	International breeding schemes	Multiple national and international institutions	In multiple countries
Ndama (cattle)	Standard undefined	Meat and milk	Well known	Humid and tsetse infested	–		In multiple countries in West Africa
Poney francais de selle (horse)	Animal need to be under a given height	Sport and leisure	–	–	Registration largely open to crossbreeding	National association	Yes
Deutsche Großsilber (rabbit)	Standard with specific color and ear type	Leisure	–	–	–		
Red Maasai (sheep)	Red coat colour	Meat	Known	Arid and semi-arid	Pastoral	None	In Kenya and Tanzania
Awassi (sheep)	Standard exists	Meat and Milk	Known	Arid regions of the Middle East	Pastoral	National institutions	Middle East countries

Governance, understood as decision-making and enforcement, is central to the breed concept: a breed exists because stakeholders agree to recognize it. Governance also involves ongoing decisions on breeding or conservation programs and rules defining populations under a breed name (See Box 3C2). It extends to how national and international policies, institutions, and legal frameworks support or hinder breed management (Ovaska *et al.*, 2021). Over the last few decades, involvement of stakeholders has undergone significant changes in more economically developed regions, with the public sector disengaging from breed management (*cross-reference to be made*). Legal frameworks influence sustainability, starting with national recognition. High-income countries often have formal procedures for breed recognition (Martyniuk, 2021), while others lack such systems, limiting livestock owners' ability to legitimize and manage breeds. International recognition typically follows national recognition; for example, DAD-IS entries are approved by National Coordinators. Recognition may also rely on genomic studies of genetic originality. In dogs, SNP-based consumer tests can identify purebred animals, some accepted by registries such as the American Kennel Club (Rando *et al.*, 2024). Legislation can set rules for registration, breeding authorization, and support services, and even determine a breed's existence. For instance, Sweden banned Belgian Blue cattle on welfare grounds, a decision later overturned by the European Court of Justice. National laws also define governance structures, specifying how breeding organizations operate. These organizations vary—associations, cooperatives, research bodies, or private companies—with differing roles and powers. In many countries, the main challenge is the absence of any organization. Studies stress involving livestock keepers and providing public support, especially early in breed development (Leroy *et al.*, 2017; Ovaska *et al.*, 2021). In low-to-middle income, policies should foster coordination through cooperatives, associations, or community-based groups.

Box 3C2. The Vertebrate Breed Ontology (VBO): a computable standard for animal breed names

DAD-IS is the most comprehensive global resource for livestock breed names and synonyms. Even though DAD-IS breed names exist in a freely-available web-based database, they have not been accessible as a computable list of standardised breed names (each with its unique identifier) readily available as a searchable clickable list for anyone who wishes to add standardised breed names to data. To add these extra dimensions to the utility of DAD-IS breed names and synonyms, the Vertebrate Breed Ontology (VBO) has been created by an international team of collaborators, led by the Monarch Initiative and including FAO (Mullen *et al.* 2025). VBO is a logical extension of DAD-IS, enabling the DAD-IS documentation of livestock breeds to be utilised throughout the world as a computable, standardised source of breed names; to be used, for example, by anyone who enters a breed name into an experimental data file, clinical record database, or any other source of information on a breed. From its DAD-IS foundation, VBO has been expanded to include breed information from other relevant livestock sources and for all vertebrate species in which breeds exist.

VBO is an open, community-driven ontology representing over 19,500 livestock and companion animal breed concepts covering 49 species. Each breed, sub-breed, strain or variety is represented by a VBO term that includes a persistent unique identifier (ID), metadata about breed information (e.g., synonyms including local names, breed identifiers/codes, domestication status, etc.) and its provenance.

VBO terms are classified using description logic to facilitate computational applications and Artificial Intelligence-readiness. Breeds are grouped based on community and expert conventions (e.g., chicken breed) and supported by relationship to the breed's genus and species, indicated by National Center for Biotechnology Information (NCBI) Taxonomy terms. VBO's classification captures the relationship between breeds and their "transboundary breed" as reported in DAD-IS. Relationships between VBO terms provide context to support advanced data analytics and to assess genetic diversity. For example, breeds are related to their foundation stock; DAD-IS "national breed populations" and "local breeds" are related to the country where they were reported by officially nominated FAO National Coordinators.

The same breed is often referenced using different names across (and sometimes within) databases and scientific reports, since no universal standard for breed names has yet been adopted. Using VBO IDs in these databases and reports disambiguates breed-related data. Adoption of VBO as the source of breed names in databases such as the Online Mendelian Inheritance in Animals (OMIA, <https://omia.org/>) is one step in making information more computable and consistent, thereby enhancing data interoperability. A more global adoption of VBO, as well as adoption of other ontologies to report phenotypes and inherited diseases, would support data integration and comparison, and ultimately improved discovery of diagnosis and treatments for non-human animals.

Resources:

GitHub: <https://github.com/monarch-initiative/vertebrate-breed-ontology>

Ontology browsers

- <https://www.ebi.ac.uk/ols4/ontologies/vbo>

- <https://bioportal.bioontology.org/ontologies/VBO>

- <https://ontobee.org/ontology/VBO>

- <https://agroportal.lirmm.fr/ontologies/VBO?p=summary>

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4. Local and Transboundary Breeds: Definitions and Genetic Implications

The FAO (Rischkowsky & Pilling, 2007) distinguishes three categories of breeds related to the extent of their geographic distribution: local breeds are breeds that occur only in one country while transboundary breeds occur in more than one country (*crossreference with Status&Trends section*). Within transboundary breeds, breeds are divided between regional transboundary breeds and international transboundary breeds. The former occur in only one and the latter in more than one of the seven animal genetic resources regions (Africa, Asia, Europe and the Caucasus, Latin America and the Caribbean, Near and Middle East, North America, Southwest Pacific). Within each category and across categories, there is a continuum from populations found in only a few neighboring communities to global breeds that are reported by nearly all countries of the world. Over time, breeds may change from one category to another if their distribution changes (e.g. by exports to other countries), or if national borders change.

Frequently, there is a discussion whether a breed should be split into two (or more) breeds according to country of residence, or other groups that may be distinguished, each with its own management and/or herd book. This may have consequences in terms of genetic diversity. Genetic diversity in livestock is under threat mainly because of two reasons: 1) Within breeds, especially those with a small population size, genetic diversity disappears due to random drift; 2) Between breeds, genetic diversity is lost when breeds are abandoned by their livestock keepers, including when introgression of another breed replaces the original genetic diversity. Loss of genetic diversity may be countered by several actions, such as genetic management within breeds (e.g. using more males and less related males), by maintaining different breeds with specific breeding goals and by occasionally introducing genetics from outside breeds to boost genetic variation within a breed, although the latter approach may eventually decrease variation on the between-breed or species level. Careful monitoring and a well-considered breeding plan balancing selection and genetic management will help determine actions needed. In the case of a transboundary breed the decision to manage the population as a single breed or as separate breeds within each country without exchange (e.g. each having its own herd book) will depend on differences in breeding goals and the presence of unique characteristics and genetic diversity within the countries. Genomics is a powerful tool to determine to which extent the latter is the case. When there is already a

large overlap between the different countries, exchange should not be restricted in order not to lose genetic diversity within each of the countries. In other cases, one may allow the occasional exchange, while carefully monitoring that the original characteristics and genetic diversity do not disappear.

5. The crossbreeding paradox

The concept of a breed generally refers to the mating of animals within a defined group to maintain specific inherited characteristics. In contrast, crossbreeding involves mating animals from different origins (i.e., distinct breeds). Its primary objective is not genetic progress per se, but rather the introduction of desirable traits from one breed into another, exploiting breed complementarity (e.g., combining maternal qualities with growth performance) and heterosis (hybrid vigor).

Leroy *et al.* (2016) identified four main crossbreeding strategies:

- Terminal crossing: production of offspring intended solely for market, not for further breeding.
- Rotational crossing: alternating use of crossbred dams with sires from different pure breeds.
- Breed substitution/upgrading: repeated backcrossing of females with males from another breed (frequently an international transboundary breed) until a target proportion of the introduced genetics is achieved.
- Synthetic breed creation: crossing individuals from different breeds and using crossbred offspring as reproducers over multiple generations until a new, genetically stabilized population emerges.

The importance of crossbreeding varies widely across species, countries, and production systems. A study covering 40 developing countries reported that between 2000 and 2019, the share of crossbred animals among five major livestock species grew by an estimated 0.35% per year, reaching 15%, 25%, and 29% in Africa, Asia, and Latin America, respectively (Leroy *et al.*, 2020). In New Zealand, the proportion of Holstein-Friesian/Jersey crossbreds in the dairy herd rose from 35% to 61% between 2008 and 2024, alongside an increasing use of crossbred semen (LIC and DairyNZ, 2009; 2025).

Although crossbred populations are theoretically excluded from DAD-IS, numerous exceptions exist. These include stabilized synthetic breeds (e.g., Dorper sheep), breeds open to crossbreeding (e.g., Poney Français de Selle horse), and synthetic breeds maintained in part through occasional rotational crossing (e.g., Girolando cattle). Furthermore, many breeds have experienced planned or unplanned introgression throughout their history.

While crossbreeding is undeniably a major driver of breed development, its indiscriminate use is widely regarded as a leading cause of genetic erosion (*cross-reference to be made*). This underscores the need for careful planning and monitoring of crossbreeding initiatives. The growing importance of crossbreeding—its potential for breed improvement and associated risks—combined with the increasing availability of genomic tools for assessing and monitoring introgression, calls for its systematic integration into animal genetic resources management frameworks at both national and international levels.

6. A workflow for breed definition and registration

Establishing a breed and ensuring its formal recognition is a multi-step process that combines scientific characterization, organizational development, and legal registration. The emphasis placed on each step will depend on local contexts, resources, and capacities. This workflow provides a structured approach to guide stakeholders through the process, ensuring that breeds are properly defined, supported, and integrated into national and international frameworks.

Breed Characterization

Characterization is the foundation for breed recognition. It involves collecting comprehensive information to define the breed's identity and uniqueness:

- **Socio-demographic characterization**

- Document the historical and cultural significance of the breed.
- Describe production systems, uses, and ecosystem services associated with the breed.
- Estimate population size, number of herds, and geographical distribution of farmers.

- **Phenotypic characterization**

- Assess physical traits (e.g., size, weight, coat color, horn shape) and their variability.
- Measure performance traits relevant to production systems (e.g., growth rate, milk yield, carcass weight, prolificacy, longevity).

- **Genomic characterization**

- Analyze within-breed genetic diversity (e.g., heterozygosity, effective population size).
- Investigate genetic relationships with other breeds, including historical connections and evidence of introgression.
- Analyze non-neutral diversity, with investigation of specific functional variants, related to production, adaptation and breed health.

Support Breed Development

Once the breed is characterized, efforts should focus on strengthening its governance and sustainability:

- **Governance and organization**

- Establish breed associations, cooperatives, and stakeholder networks.

- **Breed standard and monitoring**

- Agree on a formal breed standard.
- Implement herd registration, animal identification and registration, and performance recording systems.

- **Management schemes**

- Develop breeding programmes for selection or conservation.

- **Economic sustainability**

- Promote value chains, market access, and value addition initiatives (e.g., quality labels, branding).

Breed Recognition

The final step ensures official acknowledgement and integration into national and global databases:

- **Legal registration**

- Register the breed according to national and international regulations.

- **Global linkage**

- Coordinate with the national focal point to include the breed in **DAD-IS** (Domestic Animal Diversity Information System).

This workflow highlights that breed recognition is not merely a technical exercise but a holistic process involving cultural, economic, and genetic dimensions. While characterization provides the scientific basis, governance and economic viability ensure long-term sustainability. Legal registration formalizes the breed's status, enabling its inclusion in conservation and development programs. Importantly, the approach must remain flexible to accommodate diverse production systems and resource constraints.

7. The breed concept in light of new technologies

The adoption of new technologies has transformed breeding programmes in intensive production systems, influencing everything from parental verification to performance evaluation to overall farm management. On Swedish dairy farms, the combined use of genomic selection, sexed semen, and crossbreeding has enabled strategies that can potentially maximize total economic returns at the farm level (Clasen *et al.*, 2021). These innovations affect not only breed governance but also demographic characteristics, such as sex ratios and the relative importance of crossbred versus purebred populations, as illustrated by developments in New Zealand, where crossbred dairy cattle now predominate.

Genome editing (*cross-reference with thematic study*) with the CRISPR/Cas9 and other technologies is revolutionizing agricultural science. In plant breeding, numerous applications have been described. The underlying chemical mechanism of CRISPR (clustered regularly interspaced short palindromic repeat) is the ability to cut DNA at a site dictated by RNA-determined sequence recognition. As Cas (CRISPR associated) proteins use RNA-DNA base pairings for DNA recognition, Cas9 can be used to target a wide range of DNA sequences by exchanging their guide RNAs. This enables targeted changes to DNA sequences at will (Wang & Doudna, 2023).

The advances of genome editing tools have enabled the modification of species to address challenges in productivity, resilience to disease and effects of climate change, agricultural pest control and public health. Technology enables scientists to modify the genome much more quickly than with conventional breeding efforts. Applications in livestock have also been described (Ledesma & Van Eenennaam, 2024). To successfully introduce a favored gene (genomic region) into a population, strategies have been developed to spread the gene through a large population, a so-called gene drive (Frieß *et al.*, 2023). This is defined as “a system of biased inheritance in which the ability of a genetic element to pass from a parent to its offspring through sexual reproduction” is enhanced. “The result of a gene drive is the preferential increase in frequency of a specific genotype, and, consequently, the associated phenotype (trait), from one generation to the next, and potentially throughout the population” (National Academies of Sciences, Engineering, Medicine, 2016). In most cases, gene-edited traits follow Mendelian inheritance, i.e., there is a 50% chance that the offspring will inherit the edited gene. With a gene drive, the modification gets inherited at a higher ratio (Frieß *et al.*, 2023). The current status of legislation and regulation of genome-editing in many countries is described by Lim and Choi (2023). It seems that many countries are now developing or changing their policy positions on gene editing, which will likely lead to increasing deregulation. If gene editing is considered to fall under the scope of the Nagoya Protocol on Access and Benefit Sharing (Martyniuk *et al.*, 2017), it could place locally adapted breeds—often regarded as low-productive but conserved for specific adaptive traits—at increased risk of extinction if their unique genetic resources are extracted without adequate safeguards. In such cases, internationally operating breeding companies might identify valuable gene variants (e.g., heat tolerance or disease resistance) in these local breeds and use them to edit high-performing animals, raising the question of fair compensation to the breeders or communities that have developed and maintained those genetic resources in line with the principles of the Nagoya Protocol.

Although it is not yet clear to what extent this technology will be used in livestock breeding worldwide, the question arises of how its application will affect the diversity of animal genetic resources. For instance, advances in technologies—including genomic characterization and targeted introgression through breeding, assisted reproductive technologies, cloning, and gene editing—are creating significant potential for the de-extinction or genetic restoration of breeds (see Box 3C3). This question cannot be discussed in detail here, but the answers in a questionnaire sent to experts (see FAO 2025) provided an initial impression of respondents’ opinions on various aspects of this topic. The largest disagreement in the questionnaire was related to the statement “Gene editing of a few variants does not change breed identity”. Respondents viewed that gene edits would change the breed identity. A potential way to account for edited individuals within a breed might be a subscript addition to the breed’s name, e. g., “HolsteinPOLLED”, to provide transparency and information to breeders, farmers and consumers alike. The use of gene-editing even might lead to a split of breeds into edited/ non-edited, depending on the demands and acceptance of the breeders and consumers. In summary, there is consensus that gene editing should be considered when defining breeds and the consequent preservation actions.

Box 3C3. Breed de-extinction

De-extinction is commonly defined as the concept that an extinct species or breed can be revived through the use of genetic, genomic, and assisted reproductive technologies. Three main pathways are generally distinguished: (1) crossbreeding among living relatives that express phenotypic traits or harbour genomic variants characteristic of the extinct form; (2) cloning of extinct individuals by transferring cryopreserved nuclei into enucleated oocytes from suitable surrogate dams; and (3) genome alteration through gene editing, whereby specific DNA sequences are added or replaced to recreate extinct phenotypes (Turner et al., 2025). In the context of livestock, a fourth pathway may be considered when sufficient cryopreserved material is available, allowing a breed to be reconstructed through repeated backcrossing using stored semen or through embryo transfer.

In practice, however, only a limited number of livestock de-extinction or breed recreation efforts have been documented. A frequently cited example is the aurochs (*Bos primigenius*), for which an initial attempt at phenotypic reconstruction was undertaken in the 1920s by the Heck brothers, who selectively crossed extant cattle breeds exhibiting ancestral characteristics. More recently, the TaurOs programme has pursued a similar approach, aiming to restore cattle populations that resemble the aurochs in both phenotype and ecological function, notably for the management of semi-natural grazing landscapes. Another example is the reconstruction of the Haitian Creole pig following the disappearance of the local breed in the late 1970s due to African swine fever. A structured crossbreeding programme involving Chinese (Meishan and Jiaxing), Gascon, and Creole pig breeds was implemented to reproduce key characteristics of the original population, including prolificacy, rusticity, and black coat colour, thereby meeting farmers' expectations and re-establishing a locally adapted pig population adopted by local populations (FAO, 2024). More recently in France, after the death of the last Bleue de Bazougers female around 2000, INRAE scientists attempted to revive the breed by cloning her and inseminating the clone with cryopreserved semen from two purebred bulls. However, due to a moratorium prohibiting cloned animals in the food chain and broader societal concerns, a group of breeders instead pursued reconstruction through backcrossing. They used semen from those same bulls on genetically related breeds, such as Saosnoise and Rouge des Prés, to restore the breed's ancestral traits.

The topic of de-extinction is particularly important because it raises fundamental questions related to the management of animal genetic resources and, more broadly, to the very definition of a breed. Indicator 2.5.1b of the Sustainable Development Goals is defined as the number of breeds for which sufficient genetic material is stored in genebank collections to allow their reconstitution in the event of extinction (additional details on what constitutes "sufficient material to reconstitute a breed" are provided in the *Guidelines on Cryoconservation of Animal Genetic Resources*; FAO, 2012). When reconstitution relies solely on stored semen, the number of successive backcross generations required to recover the genotype of the lost breed has been arbitrarily set at four (approximately 94 %) or five generations (approximately 97 %), depending on the level of genetic "purity" targeted in the restored population. Fine genomic characterisation may help identify ancestral variants of interest to be selected within breeds targeted. In the context of de-extinction, such high-resolution genomic information is essential for guiding back-breeding or genome-editing strategies aimed at re-creating lost trait combinations and restoring functions once present in extinct or near-extinct livestock breeds (Simčič *et al.*, 2015). The examples discussed above also illustrate that, in practice, de-extinction or breed reconstruction cannot rely solely on theoretical genetic thresholds or a purely genomic perspective. The process must also take into account practical constraints, such as the quantity and type of genetic material available, genetic relatedness between donors (to avoid inbreeding during back-crossing), as well as the expectations and needs of livestock keepers who will ultimately manage, maintain, and give economic and cultural value to the recreated breed and finally adopt it or not.

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8. Conclusion

The concept of breed remains a cornerstone of animal breeding, yet it must be understood as inherently dynamic rather than static. Breeds have always evolved, and with the accelerating development of breeding methods, their transformation will become even more pronounced. This calls for maintaining a flexible, adaptive interpretation of “breed,” one that acknowledges both cultural traditions and biological realities, such as the case for the current FAO definition. Systematic crossbreeding offers opportunities to create new breeds better suited to specific environments, but such practices require careful regulation to safeguard genetic diversity and breed integrity.

Despite calls for internationally harmonized standards in breed recognition, consensus is unlikely in the near future given the diversity of stakeholders, production systems, and cultural perspectives. Livestock keepers themselves represent a fragmented group, making negotiations complex and resource-intensive. Countries wishing to have such standards are free to establish them, either unilaterally for local breeds or multi-laterally for transboundary breeds. Strict global standards may contribute to reduced conservation of genetic diversity. Meanwhile, genomic technologies are already reshaping breeding practices, with applications such as breeding value estimation becoming routine. As these methods advance—augmented by sensors, machine learning, and artificial intelligence—new phenotypes (cross reference thematic study on novel phenotyping tools) will become more accessible, while gene editing may gain importance if societal acceptance and regulatory frameworks are established. Technical challenges, including off-target mutations and pleiotropic effects, remain critical issues to address.

Looking ahead, the rapid adoption of advanced technologies risks widening disparities between the Global North and South, both in breed management and in the conceptualization of breeds. Thus, the future of animal breeding will not only hinge on ongoing debates about the definition and role of breeds, but also on the responsible integration of genomic innovations and the legal frameworks that govern them.

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