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DRAFT STUDY ON GENOMIC ASSESMENT OF GENETIC VARIATION AND THE FUTURE OF THE BREED CONCEPT

Note by the Secretariat

1. In endorsing the outline of *The Third Report on The State of the World's Animal Genetic Resources for Food and Agriculture* (Third Report) at its Nineteenth Regular Session,¹ the Commission on Genetic Resources for Food and Agriculture (Commission) approved, subject to the availability of the necessary resources, the coverage of “special topics”, including: (i) vulnerability of animal genetic resources in the face of climate change and the role of genetic diversity in adaptation and resilience; (ii) establishment and scaling-up of breeding programmes in challenging environments; and (iii) genomic measures of genetic variation and the future use of the breed concept in the formation of new breeds. The Twelfth Session of the Intergovernmental Technical Working Group on Animal Genetic Resources for Food and Agriculture has also suggested addressing the topics of gene editing and other emerging technologies, if possible.²

2. In response to these recommendations, FAO commissioned the preparation of thematic studies covering the three topics approved by the Commission, as well as on genome editing and emerging technologies in animal phenotyping, as suggested by the Working Group. These studies are at various stages of development and will be made available online for commenting by countries along with sections of the draft Third Report.

3. FAO utilized extra-budgetary funds from the Government of Germany to contract with the University of Natural Resources and Life Sciences (BOKU), Vienna, Austria) to convene an expert group to undertake the study on *Establishing and scaling-up of breeding programmes in challenging environments Genomic assessment of genetic variation and the future of the breed concept*. This document summarizes the study. The document has been prepared by Gábor Mészáros (BOKU, Vienna, Austria); Pamela Burger (University of Veterinary Medicine, Vienna, Austria); Licia Colli (Università Cattolica del Sacro Cuore, Piacenza, Italy); Ino Curik (Zagreb University, Zagreb, Croatia); Kahsa Tadel Gebre (Mekelle University, Mekelle, Ethiopia); Gustavo Gutierrez Reynoso (Universidad Nacional Agraria La Molina, Lima, Peru); Christian Looft (Neubrandenburg University of Applied Sciences, Neubrandenburg, Germany); Raphael Mrode (International Livestock Research

¹ CGRFA-19/23/Report, paragraph 107.

² CGRFA/WG-AnGR-11/21/Report, paragraph 21.

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Genomic assessment of genetic variation and the future of the breed concept

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Executive Summary

The conservation of the genetic diversity of animal genetic resources is key in livestock breeding. Genetic diversity within populations is crucial for long-term genetic gain in traits related to the productivity and functionality of breeding animals. The genetic differentiation of subpopulations (breeds) contributes significantly to the overall diversity of a livestock species and its adaptability to a wide range of environments. In this study, two topics are addressed: (i) use of high throughput genomic data for assessment of genetic variation and (ii) the future of the breed concept.

In the early part of this century, the International Society for Animal Genetics and FAO recommended standard panels of 30 microsatellite markers that have been instrumental in the assessment of genetic diversity of livestock populations across the globe. Later the availability of high throughput marker systems, from Single nucleotide polymorphisms (SNP) to whole genome sequence, has opened new doors for analysing and managing genetic diversity. It is imperative to move to these types of markers, particularly because panels of 50,000 SNP do not cost more than assays using 30 microsatellites. There is enormous utility of using dense marker panels for the management of breeds, including for breeds with small population sizes. Detection and eradication of recessive genetic disorders is one such use. Discovery of genes important for adaptation and their use in breeding programs is still elusive, however, except for very few variants.

Regarding the concept of "breed", every breed has been constantly changing since its establishment and its genetic make-up is never static. However, some breeds change more rapidly than others, such as those subject to advanced methods of animal breeding. New biotechnologies, including gene editing, have the potential of further changing the characteristics of breeds. Therefore, the term "breed" should reflect this type of dynamics and the possibility to understand "breed" in a more flexible way. While there are calls from various stakeholders for greater consistency and internationally agreed standards for breed recognition, reaching a consensus on this issue is unlikely in the near and distant future. Whereas genomic tools are excellent for checking the assignment of an individual to a breed, they are not helpful in deciding whether two long established populations are distinct enough to assign them as breeds. The concept of breed is based on the decisions of groups of humans. Yet, in case of claims of people having "founded" a new breed, genomic tools are useful for checking whether this group of individuals is distinct enough from an existing breed to allow registration.

We have come to three main conclusions:

- 1) **New technologies and very affordable high throughput genomic marker systems allow a much better characterization of the diversity within and the distances between breeds. This opportunity should be used at local, national and international levels.**
- 2) **The concept of breed remains relevant and will continue to be a key element in animal breeding, although its definition will remain debatable.**
- 3) **Not only will the concept of breed continue to be debated, but also the use of genomic methods and the accompanying legal framework will continue to be a subject of intense discussion in scientific and public fora.**

I. Introduction

The conservation of the genetic diversity of animal genetic resources is a key element of livestock breeding. Genetic diversity within populations is crucial for long-term genetic gain in many traits related to the productivity and functionality of breeding animals. The genetic differentiation of subpopulations (breeds) contributes significantly to the overall diversity of a livestock species and its adaptability to a wide range of environments. The conservation of both components of diversity is beyond the means of any single country. At global level, the FAO has been given the mandate for coordinating efforts and provided tools to monitor local and transboundary breed populations to ensure their future. This thematic study explores the impact of recent technological advancements on the characterization of livestock genetic diversity and examines how these developments affect the way stakeholders apply the concept of breed.

A first section focuses on the characterization of molecular variation in domestic animal species. Around the year 2005, a set of 30 microsatellite markers were proposed for most livestock species to monitor breed differentiation and confirm the assignment of animals to breeds. Since then, a genomic revolution has led to the availability of reference sequences for all domestic animal species and affordable high-throughput marker sets, from SNP arrays to high-coverage sequences. Even the pangenome, which complements sequence data with different types of structural variants, many of which have an impact on phenotype, is now available. Public databases with high-throughput genomic data for large numbers of individuals make it possible to link populations around the world and understand the global diversity of a species. Individual research groups can study the diversity of local subpopulations of the same breed or the differences between breeds. The abundance of genomic data also helps to recognise different patterns of variation and thus distinguish neutral from non-neutral (adaptive and deleterious) variations. The degree of crossbreeding, also referred to as admixture in the genetic literature, allows the determination of “breed purity”, but also helps in the assessment of heterosis effects. Here we describe tools and methods for quantifying genetic diversity, give examples and explain what the pangenome is.

The concept of breed is very important for managing the diversity of livestock species. The FAO Domestic Animal Diversity Information System (DAD-IS) is based on this concept. However, as breeds cannot be differentiated according to their biological function, there are always discussions about how breeds can be distinguished from each other. One of these claims is that genomic data will make the final judgement. The definition of breeds not only has a strong cultural component, but also strongly affects the genetic dynamics of a species through genetic drift, more homogeneous phenotypes within breeds, the possibility of utilising positive effects of crossbreeding, i.e. heterosis, and the increase in the overall diversity of the species. The component on the future breed concept of this section deals with breed definition, its social components, administration, registration and legislation. Cross-breeding is also dealt with in detail. The potential impact of new technologies, in particular gene editing, has been analysed.

Finally, to assess how stakeholders view the future evolution of the concept of breed, an online survey was conducted via the DAD-Net and other channels to analyse stakeholder opinions on five areas: Phenotypes, Registration/Recognition, Genotypes/Genomics, Crossing/Composites and Gene Editing.

II. Genetic markers for the characterization of molecular variation

Genetic markers are used to assess molecular variation in nuclear and extranuclear (mostly mitochondrial) components of livestock genomes. Over the last two decades, the three marker technologies that have frequently been used for genetic characterization, in order of increasing sophistication, are: (i) microsatellites, i.e. short sequences consisting of tandem repeating units of one to six base pairs; (ii) single nucleotide polymorphisms (SNPs), i.e. variations at the single nucleotide level spread over the genome; and (iii) whole genome sequencing (WGS), i.e. more or less complete DNA sequence of a genome (Ajmone-Marsan et al., 2023). In the recent past, a growing number of different types of marker panels have been developed, resulting in a wide range of tools being available to study the genome profiles of livestock species and breeds. Compared to the latter two technologies, genotyping a large number of microsatellites is costly and laborious in most situations, although they may remain the only practical choice when options for SNP genotyping (e.g., lack of arrays specific for certain populations) or WGS are not available or unreasonably expensive. Because of their limited number, microsatellites are also not suitable for many of the recently developed and statistically powerful modes of analysis (Ajmone-Marsan et al., 2023). As a consequence, while between 2010 and 2015, 63% of the studies investigating genomic variability of local livestock breeds were based on microsatellite genotyping, this share decreased to 18% between 2015 and 2020. In parallel, the shares of studies based on SNP and WGS has increased from 16 to 55%, and from 4 to 10%, respectively (Olschewsky & Hinrichs, 2021). Mitochondrial (mtDNA) markers are also important for characterization of livestock populations, their share was in the range of 6 to 14% in the time periods considered. The cost of SNP and WGS genotyping has been dramatically reduced in recent years, with far ranging consequences for the practical application of such information in livestock breeding and conservation (Berry & Spangler, 2023). These applications include parentage verification and discovery, reporting and monitoring of mutations conferring major effects or congenital defects, mating advice, determining breed composition and enabling precision management with the help of genomic evaluations.

Genetic variation can be studied at different scales, from the individual to species and even across species. Given the focus of this document, the three main levels considered will be individual, breed and species.

a. Methods of assessment of genetic variation

In the era of genomics, there is abundance of genetic markers per individual, typically more than 50,000 for genome wide SNP arrays, and somewhere between 2 and 60 billion data points for whole genome sequence data, depending on level of depth, also employed when sequencing short or long reads of the genome. Depth, also called coverage or call rate, is the average number of times every single base along the genome is called during the process of reading.

Variation within breeds

Genetic variation within a breed is impacted by different processes, including mutation, genetic drift, selection, reproductive isolation and migration, which determine its fitness and adaptation to specific environments or purpose (Van der Werf et al., 2009). Such variations also form the basis for selection and breeding improvement. Assessment and monitoring of genetic variability are essential for decision makers, as a means of optimizing the choice of breeding animals to maintain genetic diversity. Analysis of genetic variation can also be used to assess substructure and potential introgression into a given breed.

There is a wide diversity of metrics and approaches to characterize within breed genetic variability, more or less correlated with each other, or adapted to specific marker types (Olschewsky & Hinrichs, 2021). The list below, though not exhaustive, gives some of the most commonly used ones:

- Observed and expected heterozygosity, F-statistics
- Allelic, nucleotide and haplotype richness or diversity
- Genomic inbreeding and kinship coefficients

- Effective population size metrics
- Linkage disequilibrium metrics
- Cluster analysis
- Principal components analysis

The reason why so many methods are available relates to the size and complexity of genomes, and the diversity of processes influencing their transmission across generations within populations. For instance, richness, defined as the number of alleles, haplotypes, and genes present in a population, is an evident metric to measure physically the genetic variation within a population. It is however rarely used for biallelic markers such as SNPs, in comparison to heterozygosity. As a measure of the departure from Hardy Weinberg equilibrium (e.g., the theoretical assumption of an infinite population not submitted to mutation, genetic drift, selection and migration), the F-statistic called F_{IS} can be used to assess if a breed structure is impacted by some mating strategy or evolutionary forces. For instance, negative F_{IS} is interpreted as avoidance of mating between close relatives, while positive F_{IS} can reflect inbreeding as a practice employed in this population. Due to historical patterns of recombination and inheritance, certain genetic variants or alleles that a physically more or less close tend to be inherited together more often than would be expected by chance. This phenomenon is defined as linkage disequilibrium and is very useful in understanding the inheritance patterns of genetic traits, as well as the history of populations.

The distribution of genotypic and phenotypic variation within populations is determined by past and recent changes in allele frequencies. Such changes can be investigated through sampling of individuals across different time horizons. An example relates to the bovine *PLAG1* mutation, that has been identified as a 1000-year-old derived allele, whose increasing frequency has contributed to the increase in average size of cattle over the last centuries (Utsunomiya et al., 2017). The past evolution of genomes can also be interpolated based on studies on current genomes. Linkage disequilibrium also plays a major role here, in the sense that loci that are in close proximity tend to be transmitted together. This correlation tends to decline over time, depending on the physical distance between the loci and the rate of recombination. The specific properties of mitochondrial and Y-chromosome (uniparental inheritance and no recombination) may allow to study how sex-specific population genetic forces are shaping the genomic variability of livestock breeds. For instance, a few specific stallions used centuries ago have largely influenced the genomes of several current horse breeds, like Thoroughbred and Arabian horses (Radovic et al., 2024). The uniqueness of breeds may be confirmed using a mix of different types of markers, as evidenced for the Mongolian Naadam horse (Mongke et al., 2024), for instance.

The decrease of genetic diversity has been proven to impact fitness and animal welfare, through inbreeding depression and increased frequency of detrimental traits. Therefore, the monitoring of the trend in genetic variation is of paramount importance, for instance by estimating inbreeding trends, or effective population size. Effective population size is defined as the size of a hypothetical idealized population (not submitted to mutation, genetic drift, selection and migration) that will experience the same genetic drift or rate of inbreeding as the actual population under study. For instance, despite census population sizes (number of living animals) being larger than millions of individuals, the mainstream dairy cattle breeds used worldwide display effective population size estimates often of less than 100 individuals, mainly due to the intensive use of a small number of breeding males (Makanjuola et al., 2020). This contrast between large demographic numbers and skewed sex-ratio results in high levels of inbreeding and genetic erosion trends. Currently the most widely used methods to estimate genomic inbreeding levels are based on the use of the so-called “runs of homozygosity” (ROHs), i.e., continuous stretches of homozygous genotypes (Curik et al., 2014). Effective population size can be estimated from the increase in genomic inbreeding over different generations of animals sampled while another common approach is based on the level of linkage disequilibrium (Mészáros et al., 2015).

Beyond the monitoring of genetic variability, genomic tools have many practical applications for the management and breeding of livestock populations (Berry & Spangler, 2023). Typically, paternity testing and individual identification for livestock forensics take advantage of genomic differences and/or similarities across related individuals within families, through internationally standardized marker sets. Identification of genetic variants of interest, for instance related to expression of specific disorders, in the practical approach to breed against unfavorable/detrimental traits. For instance, as of 2023, there

were more than 1745 traits reported for the main five livestock species in the Online Mendelian Inheritance in Animals (OMIA) database (Nicholas & Hobbs, 2012). Genomic relatedness between individuals constitutes an important prerequisite for genomic selection, with the genomic relationship matrix replacing the traditional pedigree kinship one. It can be also used by breeding organizations to plan mating schemes that maintain genetic variability, with focus on breeding or conservation purposes, through approaches such as genomic-based optimal contribution (Gautason et al., 2023; Sánchez-Molano et al., 2016). Analysis of non-autosomal DNA may also bring potential practical implications for breeding and conservation management of breeds/populations, such as the identification of pedigree errors, suspected deleterious mutations, or the evaluation of the effects of mitogenome variation on quantitative traits (Brajkovic et al., 2023).

Variation between breeds

Genetic diversity in relation to breed differentiation is important for the evolution of populations. Different breeds may respond differently to changes in climate or environmental conditions, as well as having different levels of fitness to existing environments. Genetic diversity between livestock populations is also essential for meeting consumer demands (Biscarini et al., 2015) by enhancing economically significant traits via genetic improvement. Studying genetic variation among different breeds can be used to design conservation strategies (Zhang et al., 2018), enhance livestock genetic improvement for profitability (Biscarini et al., 2015), conducting association research (Machová et al., 2023), and ensuring product traceability (Dalvit et al., 2007). Diversity in livestock breeds also provides breeders with the opportunity to create new breeds that can respond well to environmental, health, or market changes (Hoffmann, 2010).

This genetic diversity could be expressed by computing the genetic distance between populations. As such, the concept of estimation of genetic distance between populations is not new. Among the most famous, and today still used methods are the F_{st} (Wright, 1943, 1965) and Nei's D (Nei, 1972). Regardless of the method, the genetic distance may be expressed as the measure of accumulated differences between the genomes of individuals that belong to different subpopulations. With the availability of advanced genomic data, we can compare the same loci in the genomes of individuals. Those that are more similar to each other will have smaller genomic distance between them and form various subpopulations. For practical purposes, in animal breeding we may call these subpopulations "breeds". Due to historical developments, genetic drift, natural and/or artificial selection, the genetic distance became gradually larger between breeds, resulting into the great variation of statures, colors, morphological and other phenotypic features of breeds.

Individual breeds carry a substantial part (typically 80 percent) of the total molecular variation of the respective livestock species; only a small part of the total diversity is accounted for by variation among breeds. This accumulated diversity is most often measured between breeds via genomic data using the following methods:

- Allelic methods
 - Multivariate techniques: Principal component analysis, multi-dimensional scaling, discriminant functions, discriminant analysis
 - Identity by state (IBS) matrix
 - F_{st} : Wright's F_{st} (Wright, 1965); Weir and Cockerham estimator of F_{ST} , θ (Weir & Cockerham, 1984)
 - Q_{st}
- Distance based methods
 - Nei's D_s (Nei, 1972)
 - chord distance D_A (Nei et al., 1983)
 - Chord distance, DC (Cavalli-Sforza & Edwards, 1967)

- Distance based phylogeny - trees (Farris, 1972)
- Breed assignment methods (Wilmot et al., 2022)
- Total variation distance (TVD) (Leslie et al., 2015)

The value of F_{st} is often cited as a measure to distinguish breeds from each other. Although it would be intuitive to specify an exact F_{st} value that serves as a threshold in distinguishing between two breeds, such value cannot be defined. The F_{st} varies within species, with relatively low values found between historically and phenotypically recently separated breeds. In a study comparing large numbers of breeds of different livestock species (Hall, 2022), largest F_{st} values based on SNP data were ~ 0.20 for horse, ~ 0.30 for sheep and goat, ~ 0.40 for cattle, and >0.60 for chicken and pig, while small values of <0.01 were found for all species. Given this variance in values, the reliance on F_{st} for breed differentiation, arbitrarily set as 0.10 (Hall, 2022), 0.05 or 0.01, is not justified. Note that given the unclear separation of breeds, indicators for within breed diversity described above, like effective population size of separate and combined local populations of breeds may be helpful for the purpose of breed differentiation.

In addition to autosomal markers, the mitochondrial DNA (mtDNA) as a solely maternally transmitted, non-recombining marker is also relevant to assess population distance. In particular, the detailed analysis of the mitogenome could be used to assess population distribution in various geographic regions, as well as infer population history and historical migrations of the species (Mannen et al., 2020). However, research based solely on mtDNA might not be sufficient for phylogeographical studies if the focus of the investigation is the species and not the organelle itself (Ballard & Whitlock, 2004).

Crossbreeding and admixture

While the concept of breed is crucial for the management of genetic diversity of livestock species, breeds of a species are in competition at regional levels. Based on their relative advantages in particular traits, farmers compare and consider change of breed or crossbreeding as options of improvement of their own herds routinely. Crossbreeding combines the traits of different breeds and also confers hybrid vigour (Darwin, 1868), also termed heterosis (Shull, 1914, 1952).

As farmers sometimes do their own crossbreeding experiments, breeding associations sometimes make the decision of establishing a new breed by crossing two (or more) established breeds. Here we are presenting two cases: Swiss Fleckvieh and Girolando. In both cases, it is a cross of a local cattle breed with Holstein Friesian cattle, and in both cases improved milk production of the cross was the objective, while trying to keep the positive attributes of the local breed. The ancestral breeds of Swiss Fleckvieh are Simmental and Red Holstein Friesian, the decision for this was made in the early 1970ies. The Swiss Herdbook qualifies an animal Swiss Fleckvieh if its ancestry proportions based on pedigree information are between 12.5% and 87.5% for either ancestral breed, these proportions must also hold for the parents and grandparents of the animal. Girolando is a composite breed in Brazil, being a mix of the indicine (zebu) Gir breed and the taurine Holstein Friesian. Gir is a tropically adapted breed, originally bred for dual purpose, i.e. for milk and meat. In 1989, the Ministry of Agriculture, Livestock and Supply defined the rules for the formation of the Girolando breed. The mating guidelines sought to form a breed capable of producing milk sustainably in tropical and subtropical regions. The aim was to establish the racial standard of $5/8$ Holstein + $3/8$ Gir. Animals from the mating of $5/8$ individuals are considered Pure Synthetic (PS), i.e. the breed itself (<https://www.girolando.com.br/girolando/sobre-a-raca>). The famous Kiwi Cross (Jersey x Holstein Friesian) of New Zealand is another example for a composite breed. Any type of mix of the two breeds is accepted by the breeding association (LIC).

Genomics with high throughput markers provides the opportunity of evaluating the actual breed composition of an animal, more accurate than that based on pedigree, and also without pedigree

available (Edea et al., 2015; Frkonja et al., 2012; Ouédraogo et al., 2021; Sölkner et al., 2010; Wu et al., 2020). In the literature of genomic methods, the term admixture is used when describing the mixing of any types of populations. The following groups of methods are frequently applied to determine global (i.e. genome wide) and local (i.e. per marker) admixture levels:

- Clustering methods for determining global admixture
 - Supervised and unsupervised clustering (Alexander et al., 2009; Falush et al., 2003)
- Mutual k-nearest neighbor graphs for determining population structure and global admixture
 - Network Visualization Tool (Neuditschko et al., 2012; Steinig et al., 2016)
- Hidden Markov Models for determining local admixture
 - Based on phased haplotypes (Browning et al., 2023; Guan, 2014; Sankararaman et al., 2008)

Methods of estimating genome wide admixture levels are typically based on maximum likelihood estimation of individual ancestries, often implemented via Markov Chain Monte Carlo methods. The software tools used most frequently are ADMIXTURE (Alexander et al., 2009) and STRUCTURE (Falush et al., 2003). Alternative methodology based on Mutual k-nearest neighbor graphs using netview P software (Steinig et al., 2016) is less frequently used. Figure 1 presents an ADMIXTURE graph for a population that is a mix of local taurine and local indicine (Zebu) cattle in The South-West of Burkina Faso. In this region, there used to be no breeding associations at the time of the study and assignment of "breeds" by farmers was purely based on phenotype. The local taurine cattle, called Lobi, are much smaller and don't have a hump. The opposite holds of Zebu cattle. The graph is indicative for the low physical separation of the two cattle types, although breed purity is considered important by the Lobi people, keepers of Lobi cattle.

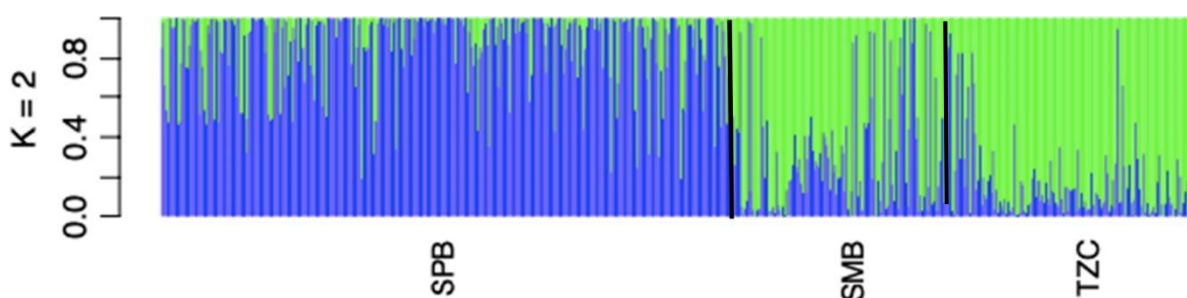


Figure 1: Admixture plot of Lobi (local taurine, blue) and Zebu (local indicine, green) cattle types in the South-West of Burkina Faso. SBP: reportedly pure Lobi kept by sedentary farmers; SMB: reportedly mixed Lobi X Zebu kept by sedentary farmers; reportedly pure Zebu kept by migrant Fulani people (Ouédraogo et al., 2021).

Estimation of admixture at intra-chromosomal (local) levels is particularly important for genetic studies exploring the effects of selection over time. When populations mix, one of them may have undergone strong selection for a trait and positive genetic variants may have become fixed. If the mixed population lives in an environment where it is good to have these variants, the proportion of ancestry of this population will be higher near such loci than in the residual genome, based on selective pressure. In human genetics, lactase persistence and resistance to malaria are the prime examples. For determining

local admixture from genomic data, it is necessary to find haplotypes that are differentially frequent in the ancestral populations (Leitwein et al., 2020). Haplotype phasing, separating sets of genotypes into segments inherited from either parent, must be performed, using samples from the ancestral populations while pedigree information can be added for improved accuracy. ShapeIT 4.1 (O'Connell et al., 2014) and Beagle 5.2 (Browning et al., 2021) were the two most accurate tools in a software comparison based on cattle sequence data (Oget-Ebrad et al., 2022). There is also a range of software tools for local admixture analysis, FLARE (Browning et al., 2023), MOSAIC (Salter-Townshend & Myers, 2019), LAMP-LD (Baran et al., 2012) and ELAI (Guan, 2014). being among them.

b. Neutral versus non-neutral/adaptive genetic variation

The genomic variability within and among livestock populations is the result of natural and artificial selection, genetic drift and admixture events that have contributed to shape the genetic uniqueness and diversity of breeds. Observed genomic variation is composed of both neutral and non-neutral variation. Neutral variation refers to genetic diversity that does not confer a selective advantage or disadvantage to an organism. It is typically found in non-functional regions of the genome and does not significantly impact an organism's fitness. Most of SNP markers used in genomic assessment of livestock breeds tend to be neutral themselves (Johnsson, 2023). Non-neutral or adaptive variation refers to genetic diversity that provides a selective advantage or disadvantage to an animal in its environment being subject to natural and artificial selection and may enhance an organism's ability to survive and reproduce. Adaptive variations are often associated with functional regions of the genome and contribute to the fitness and adaptability of a population. Non-neutral genetic variation contributes to the overall genetic diversity within a population. Preserving this diversity is crucial for maintaining the potential for adaptation to unforeseen challenges, such as emerging diseases or changes in production systems.

In livestock with a primary focus on production traits, the concept of fitness is often defined and assessed differently compared to wild animals. Fitness, in biological terms, refers to an organism's ability to survive and reproduce, thereby passing on its genes to the next generation. However, in the context of livestock breeding, the emphasis is on specific production traits, including health and fertility traits. Consequently, production traits in livestock are expected to behave like fitness traits in wild populations in genomic terms.

An important debate is whether genetic variation assessed with neutral or almost neutral markers is adequate for the conservation of adaptive variation (Chung et al., 2023) and the idea that genetic diversity measured with neutral or near neutral markers is relevant for survival of breeds and populations, and is linked to the adaptive potential of populations is being challenged (Teixeira & Huber, 2021). However, many other authors (DeWoody et al., 2021; García-Dorado & Caballero, 2021; Kardos et al., 2021; Willi et al., 2022) do not agree, indicating that associations, such as those between a high genetic load and low levels of genetic diversity as measured with neutral markers, are well supported by empirical data. Another argument is that although markers may be neutral themselves, many will be linked on the genome to regions coding for traits, provided that the density of markers is high enough. Furthermore, genetic drift, unlike selection, does not act on specific regions of the genome but induces random change all over the genome, whether neutral or non-neutral. Consequently, genetic diversity as assessed with neutral markers remains an important tool to study genetic variation in adaptive traits as well, and to evaluate genetic risks of populations.

Methodological tools for assessing variation are basically the same for neutral and adaptive variation. F_{ST} and Q_{ST} are complementary measures in population genetics (Volis et al., 2005). F_{ST} provides insights into overall genetic differentiation, while Q_{ST} allows researchers to assess the extent to which phenotypic traits contribute to population divergence, shedding light on potential adaptive processes.

The combination of both measures can offer a more comprehensive understanding of the evolutionary dynamics within and between populations.

While genetic drifts exerts random influences on loci across the genome, non-neutral variants of the genome are subject to the targeted impact of selection, leading to directional effects that specifically shape certain regions of the genome (Walsh & Lynch, 2018). When certain traits are favored by artificial or natural selection, the frequency of genetic variations associated with those traits tends to change over generations. These changes leave distinctive imprints or signatures in specific genomic regions, and are commonly referred to as selection signatures (Cutter & Payseur, 2013). The availability of high-density SNP arrays and sequence and parallel advancements in statistical techniques, have facilitated the detection of genomic regions undergoing positive artificial selection in livestock species.

Various methods have been proposed for the identification of selection signatures (Qanbari & Simianer, 2014). Allele Frequency methods involve comparing the frequency of alleles at specific genetic loci across different populations. Marked deviations in allele frequencies may indicate regions under selection. Examining patterns of genetic variation within haplotypes (sets of closely linked genetic markers) can reveal regions with extended stretches of DNA that have been subject to selection. Haplotype analysis provides a more comprehensive view of genetic variation than single-marker analyses. Composite Likelihood Ratio (CLR) Tests compares the likelihood of observed genetic variation with the likelihood under a neutral model. Regions with extreme values suggest departures from neutrality, indicating potential selection signatures. F_{ST} measures population differentiation based on genetic variation. High F_{ST} values in certain genomic regions signify genetic divergence, often indicating selection. This method is particularly useful for comparing multiple populations. Extended Haplotype Homozygosity measures the length of haplotypes around a core region, helping identify regions where a selected allele has rapidly increased in frequency. It is especially effective in detecting recent selective events. Advanced machine learning algorithms, such as neural networks and random forests, can be applied to genomic data to identify complex patterns associated with selection signatures (Kumar et al., 2022). These methods can capture non-linear relationships and interactions among genetic markers (Korfmann et al., 2023).

By comparing selection signatures in diverse livestock breeds, one may pinpoint loci that may serve as a reservoir of genetic diversity in domestic populations, irrespective of the productive capacity of the involved breed. Certain genomic signatures might help elucidate the distinctive characteristics of breeds (Huson et al., 2014). This understanding can aid in prioritizing and employing genomic breeding tools to safeguard valuable traits.

Most traits animal breeders are interested in, such as production traits, behavioral traits and fertility traits or fitness traits in general are quantitative polygenic traits, based on many, hundreds if not thousands of loci. These traits are referred to as genetically complex traits since the effect of individual loci is hard to pinpoint and may depend on other loci and the environment it is expressed in. Selection on traits induces a directional change on specific parts of the genome, i.e. those loci that underly the trait under selection. Genome wide association studies (GWAS) aim to identify regions on the genome associated with genetic variation in traits (QTL). The larger the effect of a QTL the easier it is detected. For traits that have been under strong selection, e.g. fitness related traits or production traits in commercial breeds, QTL that positively influence these traits tend to be fixed. Only QTL with antagonistic effects on different traits and QTL with very small individual effects have remained in species and breeds under strong selection (Wientjes et al., 2022).

Rather than to pinpoint the individual loci involved in variation in traits and select these, nowadays genomic selection is used in which complete DNA profiles are linked to breeding values using reference populations of genotyped animals with reliable breeding values. Genomic selection enables the estimation of reliable breeding values at birth and has accelerated genetic change in large commercial

breeds. In numerically small breeds it is difficult to compose reference populations of sufficient size to estimate reliable breeding values with genomic selection. For closely related breeds composite reference populations may be used. However, since information across breeds is less useful, more animals will be needed to realize the same reliability. The effective number of chromosome segments (M_e) can be used to determine the usefulness of combining reference populations of different breeds (Wientjes et al., 2016). This indicator was used to determine whether small dual-purpose cattle breeds in the Netherlands could profit from a common reference population (Marjanovic et al., 2021). The effect was, however limited. The number of extra animals needed from another cattle breed to improve the reliability with the same amount as a single animal from its own breed varied from 11 to 128. Use of more closely related population such as present in foreign countries however, is profitable. To enable genomic selection in small breeds it is thus important to genotype animals, even if only a small number of animals is available, and to determine genomic relationships across breeds. The utility of SNP genotyping of endangered breeds at a low cost will be useful in many ways, including confirmed bi-parental parentage, management of recessive disorders and inclusion of genomic data in the genetic evaluation for quantitative traits (Mészáros et al., 2015).

c. Heterosis

There is ample theory and examples of the workings of the components of heterosis effects, dominance and epistasis, originally based on pedigree data of mixing populations (Dickerson, 1973; Hill, 1982; Kinghorn, 1987). The dominance effect is due to a bigger repertoire of alleles in crossbreds, allowing better response to environmental challenges. Epistatic loss in crossbreds is due to the loss of favorable interactions of different genes which had been established by selection during the evolution of a breed. A range of studies investigating these effects, particularly in crosses of international breeds of livestock with local breeds in tropical environments. (Demeke et al., 2003; Galukande et al., 2013; Leal et al., 2018; Tesema et al., 2023). Most studies find positive dominance effects and negative epistatic (=recombination loss) effects, as expected by theory.

Some groups of researchers tried to convert the heterosis theory, which is essentially based on breed proportions of individuals and also their parents, into genomic terms. Akanno et al. (2017) examined the feasibility and accuracy of using genomic admixture levels to estimate heterosis for growth traits in Charolais, Angus and Hereford cattle crosses. Genomic heterosis was calculated based on the average genome-wide heterozygosity (H), defined as number of heterozygous loci divided by the total number of loci under consideration and retained heterozygosity (R_{HET}), as a function of the genomic breed fractions (P_i) of each of the n contributing breeds for each individual. Retained heterosis (R_H) is a function of fractions of the same breed from the sire (P_{Si}) and dam (P_{Di}), calculated based on pedigree. These indicators were used as fixed covariates in animal models to estimate heterosis. Expected retained heterozygosity (R_{HET}) based on genomic data and retained heterosis based on pedigree (R_H) were estimated based on formulas from Dickerson (1973). In a subsequent study (Akanno et al., 2018), authors included a genomic dominance relationship matrix (Vitezica et al., 2013) in addition to the conventional G Matrix (VanRaden, 2008). Khayatizadeh et al. (2018) took quite a different route. They first used local admixture analysis to derive the breed ancestry of each SNP marker across the genome (Baran et al., 2012). SNP are then either “pure”, i.e. both alleles derived from the same breed, or “cross”, i.e. one allele from one breed and the second from another breed. The proportion of “cross” SNP (called breed heterozygous by the authors) was then used as the indicator for the dominance effect of heterosis. Note that for first cross (F1) animals, all SNP are “cross” and the value is therefore 1. For F2 (F1 x F1) animals, the dominance effect indicator is 0.5 on average, but the range is ~0.4-0.6, due to the stochastic nature of recombination during meiosis. Epistatic effects are very difficult to assess with genomic data, because they are due to the interaction of pairs of loci. The approach taken was to randomly select pairs

of SNP and count the proportion where both SNP had “pure” ancestry from the same breed. Regression was then performed of the various phenotypes on the indicators of breed proportion (taken from ADMIXTURE analysis), as well as the dominance and epistasis indicators as described. Fixed effects like station-year-season or semen collector were included in the model, as was the G Matrix. The study investigating sperm quality of pure Simmental and Red Holstein Friesian bulls as well as the big range of crossbreds, called Swiss Fleckvieh, did show positive dominance and negative epistatic effects, as expected from heterosis theory (Khayat-zadeh et al., 2018).

The assignment of bred ancestry to each SNP allows mapping of dominance effects in a way different from usual. Normally, the dominance of a SNP is estimated by coding heterozygous state as 1 and both homozygous states as 0, performing regression of the phenotype on these codes for each SNP separately. For the dominance component of heterosis, SNP that are “cross” breed heterozygous are coded 1, “pure” are coded 0. Mapping of genes responsible for heterosis for the same data set as above did not provide strong signals, most likely due to the small number of recombination events since the formation of the composite breed under consideration (Khayat-zadeh et al., 2019).

d. The Pangenome

The study of pangenomes aims to understand how all kinds of genomic variants influence the within and between breed variation and breed history as well as the evolutionary history of a species. A pangenome is a collection of all DNA sequences of a species that contains sequences shared by all individuals (core genome) and is also able to display sequence information unique to each individual (variable genome). Advances in sequencing technologies, particularly long-read sequencing (third generation sequencing), have led to the establishment of more complete pangenomes. Pangenomes describe SNP, insertions and deletions (indels), long-fragment structural variants (SV), copy number variations (CNV), rearrangements and presence/absence variants (PAV) (Gong et al., 2023). Integrating historic samples in a pangenome might even capture genetic diversity that is no longer present in living animals. The newest methods to create a pangenome include (i) a representative global sampling of the species, (ii) denovo assemblies (short and long reads), (iii) construction of a graph pangenome by bidirected variation graphs (Lei et al., 2021; Paten et al., 2017) and considering the variants’ genomic location on the haplotype phased contigs (Figure 2).

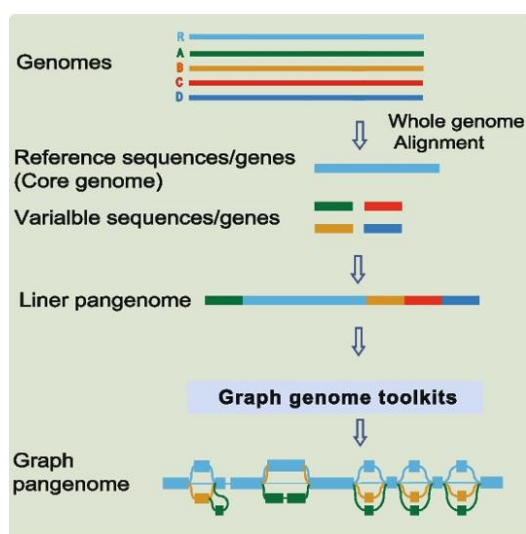


Figure 2: Methods of constructing a pangenome, adapted from Figure 3 in Gong et al. 2023.

A pangenome finally should replace breed-specific assemblies and act as public reference for (structural) variant detection. The overall goal of pangenomic research in livestock is to link variation with important

phenotypes including animal health, welfare, productivity, and in the long-term to sustain a highly profitable and genetically healthy (decreased genetic load) and diverse breed/ population (Smith et al., 2023).

Although pangenome research in domestic animal species started relatively late in comparison to human, significant progress has been described recently (Li et al., 2017; Smith et al., 2023; Wang et al., 2021). Concerning the understanding of inter- and intra-breed genetic variation the question is how pangenomic research can contribute. For instance, it was shown by aligning five cattle assemblies that a substantial portion of the cattle pan-genome is likely missing from the Hereford reference (Talent et al., 2022). Pangenomic research is currently ongoing in cattle (<https://bovinepangenome.github.io/>), sheep (Li et al., 2023), goats (Bian et al., 2024; Li et al., 2019), and pigs (Derks et al., 2022; Jiang et al., 2023; Tian et al., 2020).

III. The future of the breed concept

a. History of breed formation

The concept of distinct types of domestic animals, or the practice of breeding them for specific purposes—such as wool, meat, milk, war, or even ritual sacrifice—can be traced back to ancient civilizations like Mesopotamia, Egypt, Greece, Rome, and more distant regions, as evidenced by wall paintings and archaeological finds. The earliest recorded descriptions are found in the Roman agricultural text *De re rustica* (“On Agriculture”) by Lucius Junius Moderatus Columella, written in the 1st century AD. However, the modern concept of breeds is generally attributed to Robert Bakewell (1725–1795). Often regarded as “the father of the breed concept,” Bakewell was the first to introduce a systematic approach to selecting breeding stock based on economically important traits, coupled with careful genealogical recording, laying the foundation for modern studbooks. While early forms of genealogical record-keeping existed, such as the Habsburgs’ detailed pedigrees for Lipizzaner horses at the Lipica Stud Farm beginning in 1580 (Dovc et al., 2006; Zechner et al., 2002), these efforts were relatively informal and regionally confined. In contrast, Bakewell’s methods integrated record-keeping with a deliberate focus on improving specific characteristics, transforming breeding into a more scientific endeavor. This transition from traditional to modern breeding practices coincided with the establishment of the first widely recognized studbook, the *General Stud Book*, in late 18th-century England. Published by James Weatherby in 1791 (Tyrrell, 2019), this work provided a formal, organized record of Thoroughbred pedigrees and served as a definitive resource for breeders, buyers, and racing officials. Its impact extended beyond horses, influencing the formation of stud or herd-books in other livestock species. For instance, the first cattle herd book—*Coates’ Herd Book*—was introduced in 1822 to preserve the Shorthorn breed’s distinctive characteristics (Perry, 1982). Similarly, the *Southdown Sheep Flock-Book* was established in 1855 to record pedigrees and enhance the production of fine wool and mutton, followed by the *American Merino Sheep Register* in 1862, which focused on documenting the pedigrees of sheep prized for their wool. By the late 19th century, herd books for pigs and goats emerged, reflecting a growing emphasis on systematic breeding across various livestock species. The rise of the breed concept cannot be separated from the broader historical context of Bakewell’s time. The Agricultural Revolution provided a technological and structural foundation, while industrialization drove urbanization, created new market demands, and reshaped social norms to prioritize efficiency, profitability, and the dissemination of knowledge. These interconnected factors gave rise to a breeding culture that transcended traditional methods and ultimately laid the groundwork for the modern breeding practices that continue to shape animal agriculture today.

b. Breed concept/definition

There have been numerous discussions on defining what is a breed (Porter et al., 2016). Instead of proposing a new definition, we will start from FAO’s (Rischkowsky & Pilling, 2007) definition “*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*”. A quote largely attributed to Keith Hammond is

“*a breed is a breed if enough people say it is*”. To take this further, one could say that a breed can be recognized as such because it can be observed as a separate entity within a species or because a group of people consider it a separate entity. The concept of breed is seen differently in different parts of the world. In the Western world, the breed is generally considered to be a sub-specific group with defined by heritable morphological and phenotypic characteristics (the breed standard), with a well-established herd book with data recording and managed by a breeding organization or association. There are exceptions to this view. In many countries, herd books and recording systems do not exist in most cases, breed standards are not defined and there are no breeding organizations. Nevertheless, differentiated populations are recognized as breeds by livestock farmers, scientists and authorities without the conditions described above being met. This de facto recognition can also be attributed to specific breeding practices by pastoralists and traditional communities. These breeds can be bred alongside non-descript populations and various crosses. The non-descript animals may or may not have specific characteristics, cultural traits or geographical habitat, as the requirement for a breed to be recognized requires the initiative of a group of stakeholders to formally or informally declare it as a breed.

For certain species or under certain circumstances, the definition of a breed may differ from the traditional view. For example, it may be based on the expression of a particular trait (such as coat color and ear shape), which means that only a portion of a population is recognized as part of the breed. In horses, for example, some breeds often include generic crosses of different origins. In poultry and rabbits, breeders regularly use crosses to create new phenotypes that can be recognized as a breed without having a history as generally expected from the traditional concept of breed.

The definition of breed in certain geographic regions and communities may also result from cultural practices/requirements. Certain subpopulations are bred by communities because they believe that these specific animals are better suited to their purpose than other animals of the same species. The expression of traits that meet certain community standards, including but not limited to coat color, horn shape, ability to run long distances, etc., that are specifically required for ceremonies (such as marriage, dowry, burial, birth of a child, etc.) and lifestyle can shape breed description/recognition.

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

- Differentiated phenotype (with or without standard, phenotype expression)
- Ability to fulfill specific purposes (production, cultural...)
- History (pedigree registry / documented / oral tradition)
- Geographic location, community of livestock keepers and or environment
- Specific management (breeding practices, breeding scheme, closed population)
- Governance structure (breed organization or association)
- National recognition process

Table 1 provides examples for several breeds in relation to those breed descriptors.

Table 1. 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

Other concepts for species substructure

In addition to the concept of breed, there are other ways of looking at certain subpopulations of livestock, which may overlap to a greater or lesser extent. An ecotype refers to a population or group of animals within a species that has adapted to a particular ecological niche or habitat. Individuals of a particular ecotype thrive and reproduce more successfully in their natural environment than members of the same species living in a different habitat. Such ecotypes may or may not have unique morphological or phenotypic characteristics that may or may not lead to their visual differentiation, but have unique adaptations to specific environmental conditions such as drought, disease-causing vectors, heat stress and suboptimal nutrition.

Some terms are often used to refer to subpopulations below the breed level, such as lines, strains, varieties and types. A line/strain is a subpopulation restricted to a particular origin, often intensively selected for a particular trait and used for a specific breeding program (including crossbreeding) or for experimental purposes. It is quite commonly used in poultry and pigs. In relation to their limited size, lines and strains often have a limited gene pool. The terms variety and type refer more directly to the subdivision within a breed, often in relation to a specific phenotypic trait (e.g. coat color) or a specific use (e.g. milk type versus meat type). In DAD-IS, in the “Taxonomic Classification” field, approximately 10% of national breed populations are designated as lines, strains or varieties rather than breeds.

Governance of breeds

Governance, in the sense of the process of decision-making and enforcement, is at the core of the breed concept, since the existence of a breed is tied to the decision of a group of stakeholders who recognize it as such. Furthermore, the governance of a breed in the form of a breeding or conservation program and the rules governing the populations to be grouped under a breed name is a continuous decision-making process. Governance also means how national and international policies, institutions and processes support, hinder and shape decision-making for the good management of breeds (Ovaska et al., 2021). International and national legal frameworks can impact the sustainability of a breed in different ways, starting with the recognition process at national level. In many high-income countries, there is an agreed legal procedure that sets out the specific conditions for the recognition of a breed (Martyniuk, 2021).

However, such a framework may be lacking in some countries or for certain species within a country, which hinders the ability of the respective livestock owners to legitimize and get support for the sustainable management of their breed. International recognition generally follows national recognition. In the DAD-IS, for example, the National Coordinators decide which national breed populations can be included in the database. Finally, national or international recognition procedures can be based on genomic studies on the genetic originality of a breed. For dogs, there is a range of SNP based direct-to-consumer genetic tests available that can identify the breed of purebred dogs, some of which are recognized by registries like the American or Continental Kennel Clubs (Rando et al., 2024).

Legal frameworks may also lay down certain rules for the management of breeds (e.g. the rules for the registration of individuals and for the authorization of breeding animals for mating), the possible support from extension services or scientific institutions, or even direct financial support. It can even determine the very existence of a breed. An interesting example of this is the banning of the Belgian Blue cattle breed by Swedish legislation, based on concerns on animal welfare. In 1998, a local farmer challenged the ban at the

European Court of Justice, which overturned it on the grounds that it was illegal under EU law. More importantly, national legislation can determine the day-to-day governance rules of breeds, specifying how breeding institutions should be organized and the extent of their powers and supervision.

Breeding organizations or institutions can take different forms, e.g. simple associations, cooperatives, research institutions, national or international private companies, with different prerogatives depending on the type or local legislation. For example, in some countries a single organization may take on the overarching tasks of managing a breed, while in other countries different organizations with different tasks may coexist and the decisions to be taken may or may not coincide. In many countries, however, the biggest challenge is that there is no organization at all. Several studies have emphasized the importance of involving livestock owners in breed development, including the need for public support, especially in the early stages of breed development (Leroy et al. 2017; Ovaska et al. 2021). In developing countries, development policy should aim to promote coordination and cooperation between pastoralists through the establishment and strengthening of cooperatives, associations or community-based organisations.

c. Local and transboundary breeds, crossbreeding

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. 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 extremely local breeds to global breeds that are found in (almost) all corners of the world. In 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 discussion whether a breed should be split in two (or more) breeds according to country of residence, or other groups that may be distinguished, each with their 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 where genetic diversity disappears due to random drift 2) Between breeds genetic diversity is lost when breeds disappear or when introgression of another breed replaces original genetic diversity. Loss of genetic diversity may be countered by several actions such as genetic management within breeds (e.g. use more males and less related males), by maintaining different breeds with breed specific breeding goals and by occasionally introducing genetics from outside breeds to boost genetic variation within a breed. Careful monitoring, and a well-considered breeding plan balancing selection and genetic management will help to decide what actions are needed. In the case of a transboundary breeds the decision to manage the breed as a single breed or as separate breeds within each country without exchange (e.g. each having its own herd book) should depend on difference 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 a large overlap between the different countries exchange should not be restricted in order not to lose genetic diversity. In other cases, one may allow the occasional exchange, while carefully monitoring that the original characteristics and genetic diversity does not disappear. Several cases of what is happening related to global and local breeds and crossbreeding are given below.

Global breeds

In most species there are a few global breeds that dominate across the world. Within these breeds most animals are bred by commercial companies, which are mostly farmer-led in case of dairy cattle, marketing genetic material (e.g. semen, embryos, animals) across the world. In dairy cattle, for example, the Holstein breed is the main breed across the world. Sometimes different types are distinguished within these breeds according to country. In the Holstein, for example, there are amongst many other Italian Holstein and Polish Holstein. However, estimation of breeding values is done internationally across breeding companies and countries by the Interbull Centre. This facilitates exchange across the world and indeed large quantities of semen from, often the same, Holstein bulls are exchanged across the world. The risk of “global” breeding is that by using a restricted set of related bulls across the world the genetic diversity is rapidly lost. Pedigree and genomic analyses showed that in recent years with the introduction of genomic selection not only genetic change increased, but inbreeding rates across the world as well (Ablondi et al., 2022; Doekes et al., 2018; Doublet et al., 2019; Mekanjuola et al., 2020).

Case of the endangered Austrian Blobe goat

The government of Austria supports breeders of endangered breeds of livestock with a national, EU co-funded, support program of conservation of endangered livestock breeds. Currently, 9 cattle breeds, 7 sheep breeds, 7 goat breeds, and 2 pig breeds are supported. The breed added to this list most recently in 2005 is the Blobe goat found in the mountains of Tyrol (blob=blue in Tyrolean dialect). The original decision was based on a study of diversity among and distances between Austrian breeds based on microsatellite markers (Baumung & Fischerleitner, 2005). Around 2015, concerns were raised that, while being distinct from other Austrian breeds, the Blobe goat may actually be a sub-population of the Passeier goat, which is kept in large numbers in the Passeier valley of Italy, neighbouring the area of Tyrol where the main population of the Blobe goat is located. Genomic analysis with SNP chip data was performed to inspect this concern. Data of 47,652 SNPs for 167 goats (34 Blobe Goat, 22 Chamois Colored Alpine Goat, 28 Pinzgau Goat, 33 Styrian Pied Goat, 28 Tauern Pied Goat and 22 Passeier Goat) were used in Admixture and NetView analyses (Khayatzadeh an Sölkner, unpublished report, 2018). The admixture as well as the Netview graphs in Figure 3 provide the insight of parts of the Blobe goat being crossbred with the Passeier goat, but also that there is unique ancestry in this breed. The F_{st} value for this pair of breeds was 0.030. ÖNGENE, the organization having decision power in this respect, decided that the Blobe goat may keep its status of endangered goat breed in Austria, but that herd book needs to be closed and any new animals presented to the board of Blobe breeders may only accepted after genetic admixture test.

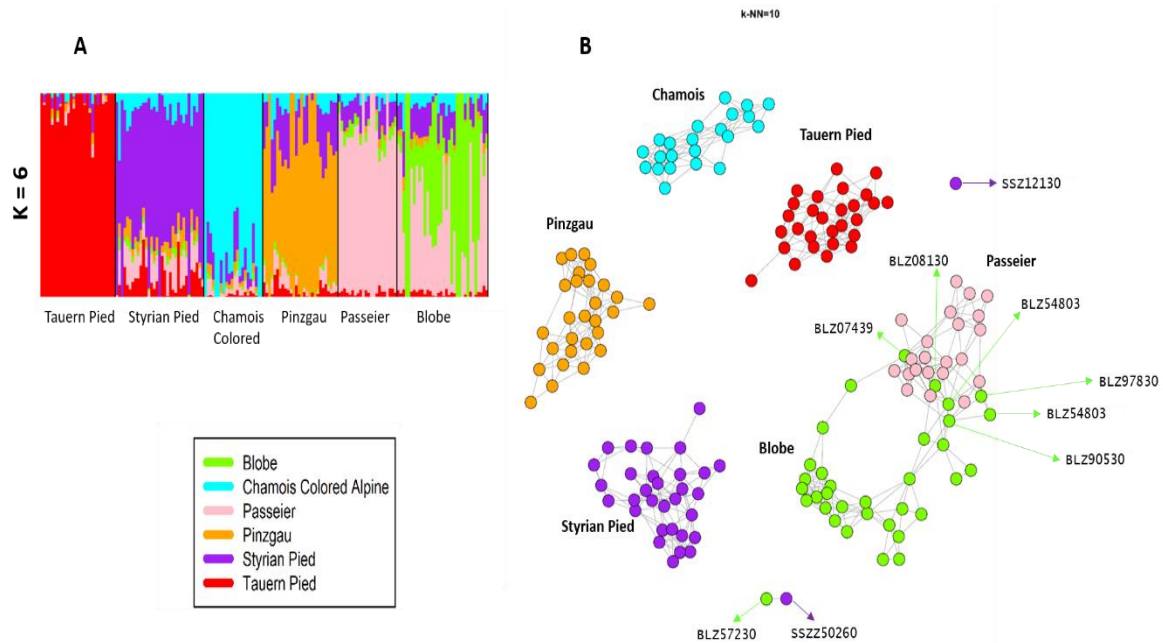


Figure 3: Admixture (A) and NetView (B) graphs of five Austrian goat breeds, including Blobe goat, and the Italian Passeier goat (unpublished).

Crossbreeding effect on Ethiopian cattle

With the aim of improving milk production and growth performance, the crossing of local cattle breeds with exotic breeds is conducted in Ethiopia since the 1950s. Bulls and semen of Holstein Friesian, Jersey, Simmental, Angus, Brahman, Hereford, Charolais and Sata Gertrudis were imported. Currently Holstein Friesian and Jersey breeds are being utilized. Yet, genetic improvement of the indigenous cattle for dairy production, focusing on crossbreeding, has been practiced for several decades though with little success due to lack of a well-organized implementation plan (Tesema et al., 2020). The cattle breeding in Ethiopia is informal where different cattle breeds can be exchanged between regions. When it comes to crossbreeding, there is lack of plan regarding the use of exotic breeds. This can lead to genetic erosion of local livestock resources (Leroy et al., 2020). In smallholder farms a mix of breeds, based on appearance (Holstein Friesian, sometimes other local cattle breeds) in their herd is very common. (Leroy et al., 2020) showed that crossbred animals represent a substantial part of species population in many countries.. Although according to (Begna et al., 2024), based on data provided by Central Statistical Agency in 2021, 97.4% of the Ethiopian cattle populations are local breeds while the remaining are hybrid and exotic breed.

Crossbreeding effect on Ethiopian chicken

Common exotic breeds widely distributed to smallholder farmers in Ethiopia are White Jeggorn, Rhode Island Red, Fayoumi, Koekoek, Kuroiler, Sasso, Bovans Brown, Kuroiler and their crosses. Though Ethiopia owns diverse local chicken breeds/ ecotypes, nowadays it is very difficult to find smallholder farmers who keep those local chicken ecotypes. Local chicken breeds are neglected from research, development works and policy makers need to put the local chicken breeds in research and development (Getu & Alemayehu, 2017). This can lead to erosion of local chicken resources through the wide use and distribution of exotic chickens. However according to data of the Central Statistical Agency in 2021, 78.5% of the chicken populations in Ethiopia are local breeds/ecotypes.

Composite Dutch sheep breeds

The originally Dutch Texel sheep breed is a heavy and muscular sheep, has a high growth rate and produces good quality meat. Because of these qualities it is now a popular breed across the world. However, its fertility is not very high. Some 50 years ago, in the 1970s, three projects were carried out to produce new sheep breeds in the Netherlands with a good fertility and meat quality. To this end fertile sheep breeds (Flemish sheep and Finnish landrace) were crossed with muscular sheep breeds (Texel and Ile de France). Three composite breeds were the result (Table 2), each having a higher litter size than the Texel breed, and able to produce 3 litters in two years (Zegwaard et al., 2010). This shows the advantage of crossbreeding, in a short time a relatively large increase in performance can be achieved. The heritability for litter size in sheep is around 0.10, and therefore progress by within breed selection is rather slow, e.g. it would probably take several decades to achieve a similar increase in litter size as produced by crossbreeding.

Table 2: Average litter sizes of Texel and the synthetic breeds

Breed	Ancestral breeds	Average litter size
Texel		1.6
Swifter	Texel x Flemish sheep	2.4
Flevolander	Ile de France x Finnish Landrace	2.3
North Hollander	Texel x Finnish landrace	2.2

The three composite breeds are nowadays established breeds with their own breed societies. However, the Texel is still by far the most popular breed, and especially the NoordHollanders struggles to remain a breed on its own.

d. The breed concept in light of new technologies

It is well accepted that genome editing with the CRISPR/Cas9 technology is revolutionizing agricultural science. Especially in plant breeding numerous applications have been described. The underlying chemical mechanisms of CRISPR (clustered regularly interspaced short palindromic repeat) is the ability of cutting 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. The technology enables scientists to modify the genome much more quickly compared to 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, mechanisms 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 of a specific genotype, the genetic makeup of an organism that determines a specific phenotype (trait), from one generation to the next, and potentially throughout the population” (National Academies of Sciences Engineering and 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 concerning gene editing, which will probably lead to increasing deregulation.

Although it is not yet clear to what extent this technology will be used in livestock breeding worldwide, the question arises as to how the application of this technology will affect the diversity of animal genetic resources. This question cannot be discussed in detail here, but the answers in the questionnaire (see following section) give an initial impression of the opinions of the respondents on various aspects of this topic. The largest disagreement in the section of the questionnaire “Gene Editing” was related to the question “Gene editing of a few variants does not change 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 a consensus that gene editing should be taken into account when defining breeds and consequent preservation actions.

IV. “Breed Concept Revisited” – an online survey on the breed concept

a. Background of the survey

The concept of "breed" is fundamental to the technical management of genetic resources (e.g., breeding programs) and their governance (e.g., the influence of breed associations as key stakeholders). Despite its widespread use, there is no universally accepted definition. Instead, varying definitions exist, differing across countries and contexts. The significance of the breed concept also varies by region and species, being generally more prominent in Europe and more critical for mammals than for avian species. Here are some more definitions, adding to that of FAO (Rischkowsky & Pilling, 2007), cited in Section 4.2.

European Union defines a breed as: *"A population of animals sufficiently uniform to be considered distinct from other animals of the same species by one or more groups of breeders, which have agreed to register those animals in breeding books detailing their known ancestry for the purpose of reproducing their inherited characteristics through reproduction, exchange, and selection within a breeding program"* (REGULATION (EU) 2016/1012). Other definitions are *"group of animals that has been selected by man to possess a uniform appearance that is inheritable and distinguishes it from other groups of animals within the same species"* (Clutton-Brock, 1987), as cited in Hall and Ruane (1993), or *"a breed is a population that: belongs to a single species; is kept by a particular community, in a specific environment; is subject to a single pattern of use, and is regarded as distinct by the community that keeps it"* (Sansthan & Köhler-Rollefson, 2005).

Over the past two decades, advancements in genomic technologies have significantly transformed animal breeding. Beyond being a technological milestone, the genomic revolution has stimulated organizational changes, including stakeholder consolidation, reduced public sector involvement, and evolving relationships between farmers, breed associations, and companies (Gibbs et al., 2009; Labatut et al., 2015). Labatut et al. (2015) particularly note the liberalization and commoditization of evaluation processes and semen markets. Genomics has made it possible to disentangle the effects of specific genetic variants from traditional breed classifications. Combined with gene-editing technologies, this has enabled the development of improved animals outside conventional pure-breeding frameworks (e.g., the SLICK variant, see Sonstegard et al. (2024)). One notable trend is the rising prevalence of crossbred animals in national herds, observed in several countries over the past two decades (Berry, 2021; Guinan et al., 2019; Leroy et al., 2020). This shift is accompanied by the growth of crossbreeding programs, including those offering crossbred dairy bull semen (Alderson-Smith, 2022). Technological advancements, such as across-breed genomic evaluations and the use of sexed semen, have been key drivers of these changes, particularly in developed cattle-breeding industries (Berry, 2021). These developments challenge the traditional role of the "breed" concept in managing genetic resources, raising critical questions about its future significance.

b. Design of the online survey

An online survey was conducted between February and March 2024. The questions had been designed to fit topics that have been discussed in a preliminary meeting on the “Breed Concept Revisited”. The questionnaire was distributed via DAD-Net-email group and other professional networks, in English, Spanish and French. The questionnaire consisted of 30 attitudinal statements, covering topics on

- phenotypic information (7 statements)
- breed recognition/registration (9 statements)
- genomics (4 statements)
- crossbreeding/composite breeds (5 statements)
- gene editing. (5 statements)

Participants’ attitudes towards these statements were assessed using a six-level Likert scale:

- fully disagree
- disagree
- somewhat disagree
- somewhat agree
- agree
- fully agree.

Such a scale avoids the central tendency bias. In addition, the option: “I do not know/I do not have an opinion on this” was included. The answers “don’t know” and “no opinion” were also options. The questions used are provided in Annex 1.

c. Results

Characteristics of respondents

A total of 186 persons completed the questionnaire. The majority of the respondents were males (74%), 25% female and 2% did not declare their gender. Almost all of the participants (97%) indicated that they had a university degree, the remaining 3% stated that they had completed high school. The regional distribution of the respondents shows that the largest group was from Europe (35%), followed by participants from Sub-Saharan Africa (20%) and North America (14%) (Figure 4). A categorization by profession shows that the majority of participants (62%) work as scientists at universities or research institutions. This category was followed by governmental officials (12%), breeders (6%) and breeding companies (6%) (Figure 5).

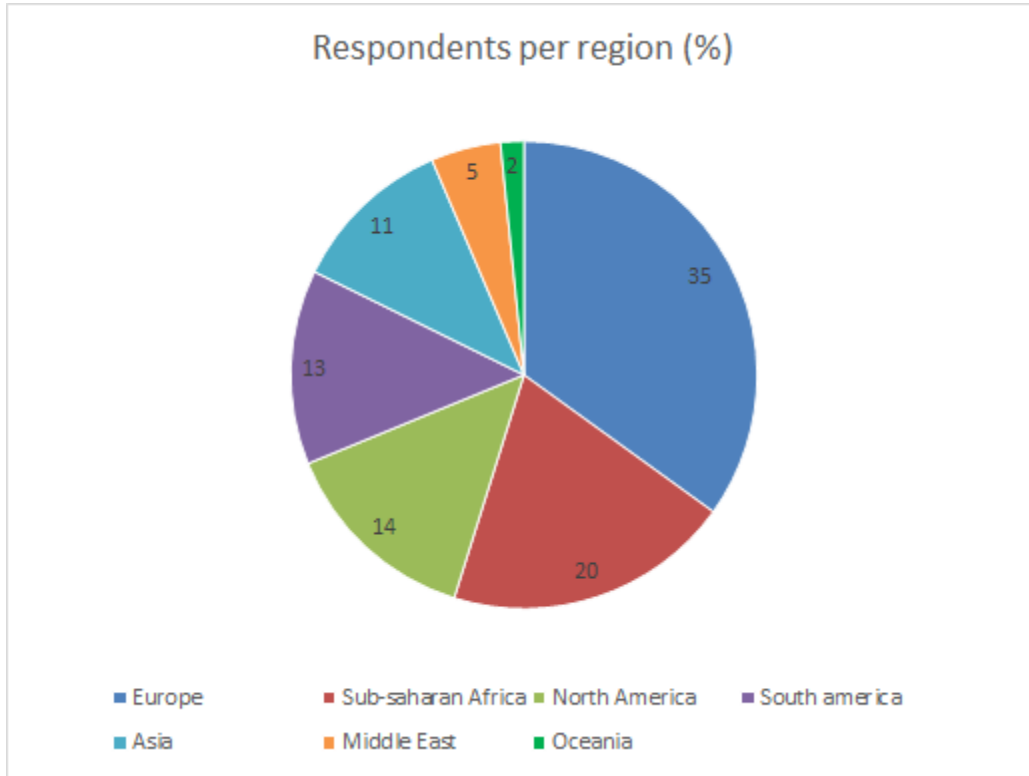


Figure 4: Number of respondents (%) per region

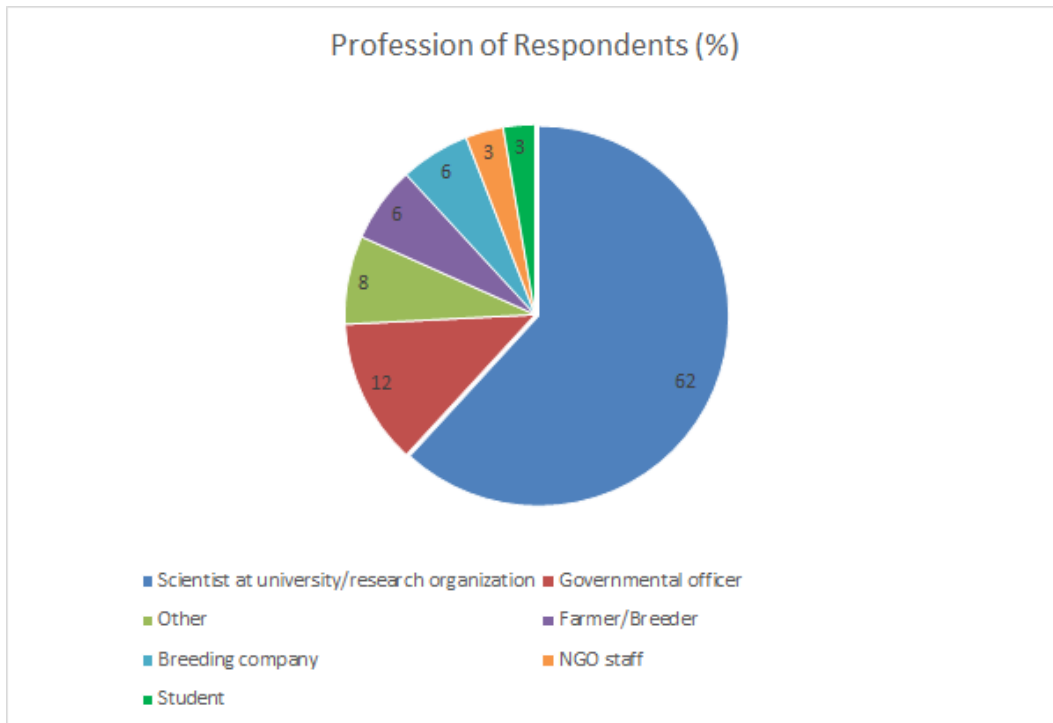


Figure 5: Profession of respondents

Phenotypic information

The core of the statements and the proportions of agreement/disagreement with these statements are provided in Figure 6.

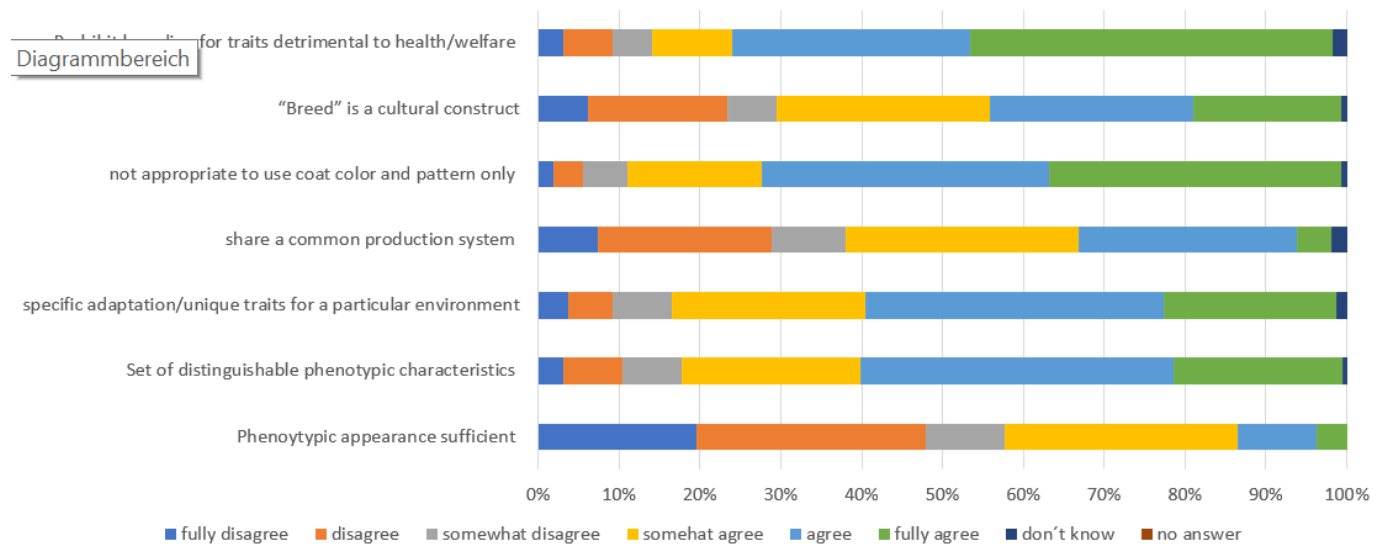


Figure 6: Statements and proportions of responses to “phenotypic information”

The overall message of the participants was: **Phenotype is important, but not enough.**

The respondents generally agreed that while phenotype is one factor used to assign an animal to a specific breed, it cannot be the sole criterion, and additional information is necessary. 59% of the respondents emphasized that phenotype alone is insufficient for defining breed identity, and traits such as coat color or patterns are not reliable indicators for breed classification. There was also strong consensus (85%) that breeding for extreme traits that harm health and welfare should be prohibited. Overall, respondents agreed that animals within the same breed share certain adaptive or unique traits suited to a particular environment (84%), and typically share a common production system or inhabit similar environments (60%). However, opinions were more varied regarding whether breeds are a ‘cultural construct’. There were no significant differences among the respondents from different geographical regions.

Registration/recognition

Essence of the statements and proportions of agreement/disagreement with these statements are given in Figure 7.

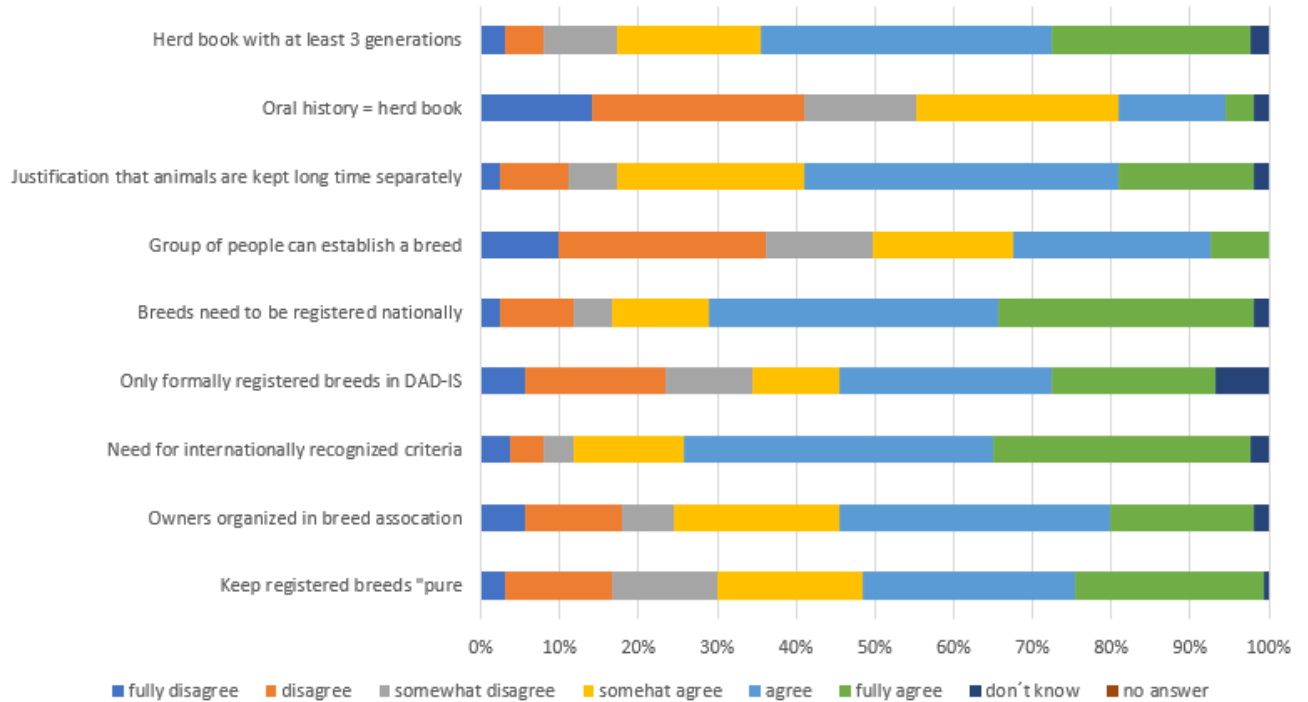


Figure 7: Statements and proportions of responses to “registration/recognition” of breeds

Essence of the answers of participants was: **Registration and formal recognition is important.**

Overall, participants emphasized the importance of regulating and formalizing breeding activities. This was reflected in the statements that breeds should be documented in a herd book, with 76 participants (41%) considering oral history alone as an insufficient tool for breed documentation. Additionally, the establishment of breeders' associations was seen as important (75%). Legislation was also given high priority, with a large majority (83%) supporting the need for national registration before international recognition could be granted. The national breed recognition was viewed as essential for international acknowledgment and inclusion in the FAO's Domestic Animal Diversity Information System (DAD-IS) by the majority of the participants. A total of 130 out of 186 participants stated that pure breeds should remain pure, with crossbreeding being discouraged. Regarding the creation of new breeds, opinions were split, with 51% in favor and 49% against establishing a new breed without scientific evidence but just by being initiated by a large-enough group of stakeholders. A large proportion of participants (163 persons, 88%) welcomed the idea to establish an internationally recognized set of criteria for breed definition. However, this demand for standardized criteria raises many questions. Who should draw up this catalogue of criteria, which criteria should be included and at what intervals should they be revised? Furthermore, the question arises as to what advantages a standardized set of criteria would have and who would benefit from it? Breeders' organizations that have a long tradition of keeping herd books and have developed and refined their breed standards over a long period of time may not see any added value in this. While the majority of participants agreed with the idea that the owners of animals of the same breed have to be organized in a breeders' association, 25% of participants rejected the statement, which can reflect that across countries, species and production systems (for instance in poultry production), breed associations are not necessarily view as a prerequisite as illustrated by table 1.

Genotype/genomics

The core of the statements and the proportions of agreement/disagreement with these statements are provided in Figure 8.

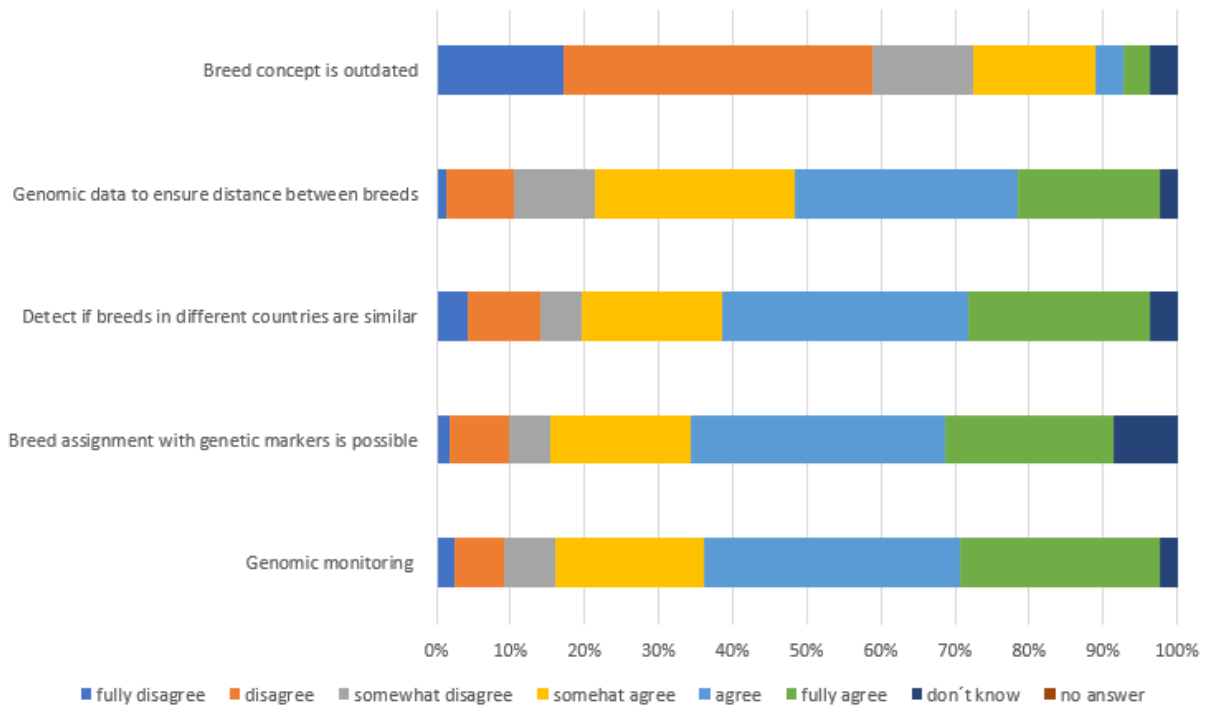


Figure 8: Statements and proportions of responses to “genomics” of breeds

Respondents agree that **genomics is a powerful tool**.

The majority of respondents (73%) supported the breed concept and affirmed that it remains relevant also with the advent of genomic tools. Genomic methods and tools were viewed positively, with participants recognizing their importance in:

- I. determining breed authenticity (distinguishing between breeds)
- II. verifying whether breeds in different countries are distinct
- III. assigning individual animals to specific breeds
- IV. monitoring breeds for purity, diversity, and genetic load (harmful mutations)

Agreement rates for these four potential uses were in the range of 78% to 84%, affirming the believe of respondents to this type of technology. This is in light of a high proportion of respondents being academics. How many of them have been actually using such techniques may not be derived from the questionnaire data.

Crossbreeding/composite breeds

Essence of the statements and proportions of agreement/disagreement with these statements are given in Figure 9.

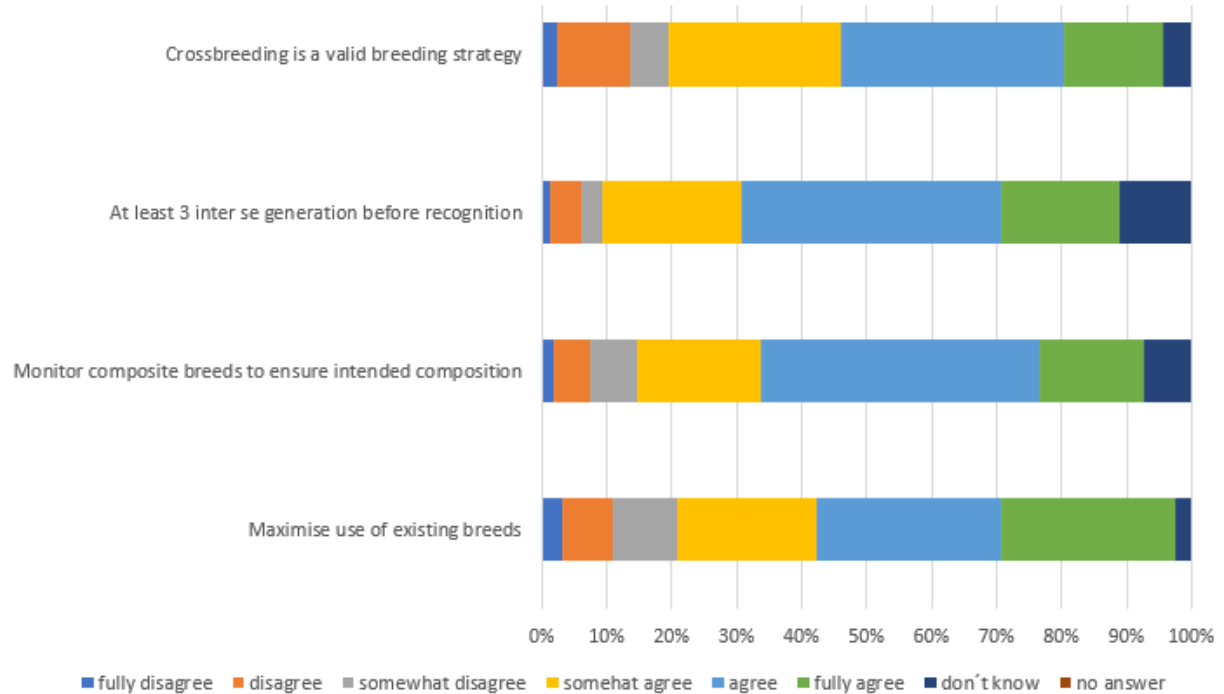


Figure 9: Statements and proportions of responses to “crossbreeding/composite breeds”

The core of this block of statements is that **Crossbreeding is a valid strategy, but has to be planned and monitored.**

A total of 77% of participants viewed crossing two or more breeds as a viable and valid approach for creating a new breed. However, they also supported regulation and oversight in the process. Specifically, they (78%) affirmed that a newly formed breed should undergo at least three generations of inter se matings before it can be officially registered at the national level and included in DAD-IS. Additionally, it was considered essential to monitor the genetic composition of the crossbreeds to ensure the desired genetic level is reached and maintained. At the same time, there was a strong consensus (77%) that efforts should primarily focus on optimizing the use of existing breeds, rather than creating new ones.

There is the concern that indiscriminate crossbreeding with so-called “exotic” germplasm leads to erosion of genetic diversity and loss of local breeds, especially in low and middle-income countries. FAO (Rischkowsky & Pilling, 2007) used to be very concerned about this, but has relaxed its view considerably (Leroy et al., 2020).

Gene editing

Statements levels of agreement with them related to the gene editing block of the questions are given in Figure 10.

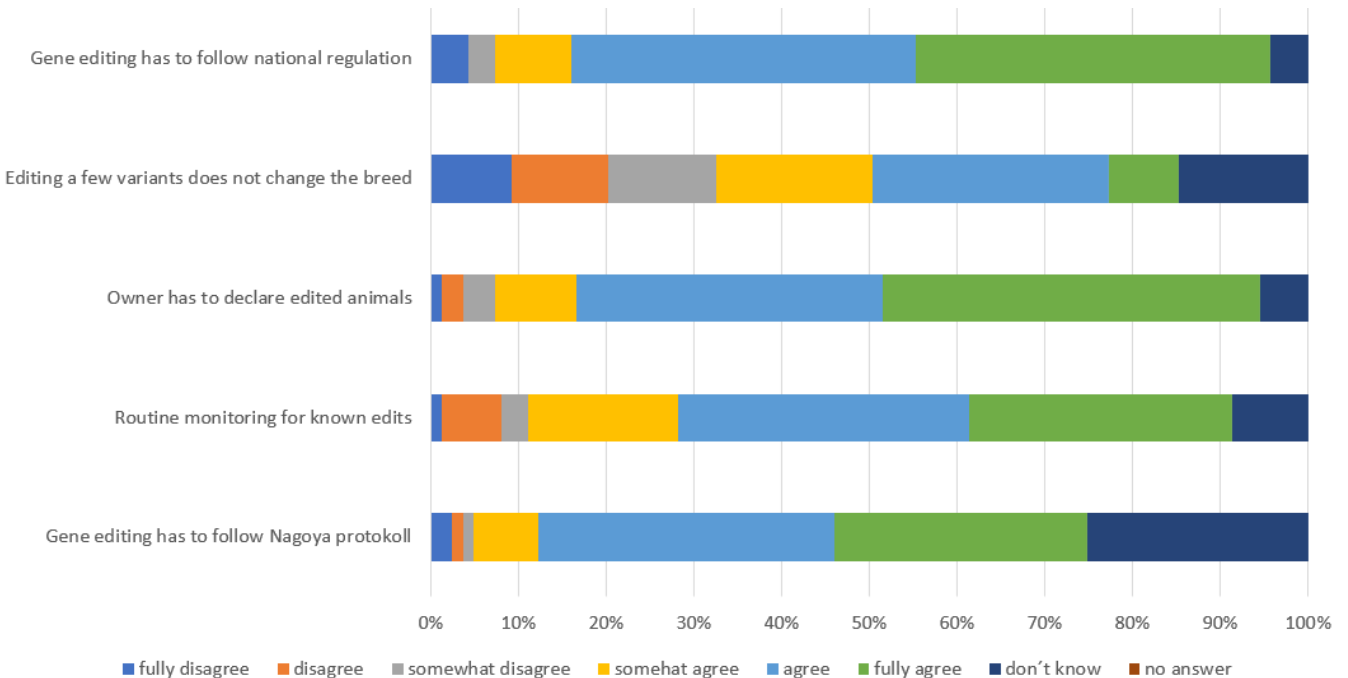


Figure 10: Statements and proportions of responses to “gene editing”

Respondents know that **gene editing opens a new area in animal breeding** but are not sure how to qualify it.

The responses regarding gene editing followed a similar pattern to those in previous sections, emphasizing the need for regulations and monitoring. Respondents expressed that gene editing should be governed by national regulations, regular monitoring is essential, and gene-edited animals should be clearly identified. However, the answers also revealed that participants remained uncertain about gene editing as a new technology in animal breeding. Many responses in this section included a higher proportion of "I don't know" answers. For example, 53% of respondents agreed, 34% disagreed, and 13% were unsure if editing a few variants would alter a breed's identity. This indicates a lack of experience with this emerging technology. Discussion is needed in the coming years about the extent to which edits are acceptable within a breed, though the number of edits may not be the best measure. For instance, edits that alter traits such as coat color or produce hornless animals could change an animal's phenotype to the point where it no longer aligns with established breed standards. Can an Angus cow that is now white still be considered Angus? Is a hornless Ankole cattle still classified as Ankole? Such visible changes may face resistance, as they significantly alter the animals' appearance. In contrast, edits that aren't immediately visible but enhance adaptation mechanisms, such as resistance to diseases or parasites, could be more readily accepted by breeders. These kinds of edits may improve fertility, resilience, growth, and animal welfare (Fischer & Schnieke, 2023), and they might be more easily embraced by farmers due to the potential for higher productivity and profitability. Nevertheless, many unanswered questions remain regarding regulation and potential ethical concerns among consumers. Local breeds are often considered as specifically well-adapted to extreme harsh conditions and considered one opportunity to face current and future challenges in the livestock industry. Through a systematic screening (“Bioprospecting”) for specific variants associated with specific adaptive traits, potentially economically important ones could be identified and transferred to other breeds. A possible scenario is that highly productive breeds, enhanced through gene editing, are better adapted to certain conditions. The enhanced breeds could then outcompete local breeds in their native

environments, where they used to have a competitive advantage. This could put additional pressure on local breeds, which are already often at (high) risk of extinction. In return, however, one can argue that this can improve the livelihood of livestock farmers. In this context, one must also consider breeders' rights and mechanisms of cost-benefit sharing. Livestock keepers and nomads are at a disadvantage in this negotiation process as they live in remote areas with no easy way of establishing a good line of communication. In addition, there is no international organisation that can represent the concerns of this interest group. There is a huge power imbalance between transnational companies and local communities, who are the stewards of genetic diversity by keeping these highly important local breeds (Koehler-Rollefson, 2002).

Almost one quarter of the respondents (24%) did not know whether gene editing must follow the access and benefit sharing rules of the Nagoya Protocol. These results show that there is a possibility of a large group of people not having any familiarity with this Protocol. The objective of the Nagoya Protocol is the *“fair and equitable sharing of the benefits arising from the utilization of genetic resources, including by appropriate access to genetic resources and by appropriate transfer of relevant technologies, taking into account all rights over those resources and to technologies, and by appropriate funding, thereby contributing to the conservation of biological diversity and sustainable use of its components”*. It entered into force on 12 October 2014 and as of 2024 has been ratified by 141 parties (Convention on Biological Diversity). Article 5 of the Protocol states that *“benefits arising from the utilization of genetic resources as well as subsequent applications and commercialization shall be shared in a fair and equitable way with the Party providing such resources that is the country of origin of such resources or a Party that has acquired the genetic resources in accordance with the Convention. Such sharing shall be upon mutually agreed terms”*. In line with this notion, the EU regulation states that *“efforts to achieve competitiveness in the animal breeding sector should not lead to the disappearance of breeds with characteristics that are adapted to specific biophysical contexts”* (EU Regulation 2016/1012). If gene editing falls under the Nagoya Protocol, breeders or breeders' associations that have raised and conserved a local breed with very specific characteristics (e.g., heat tolerance, disease resistance) could ask for compensation from internationally operating breeding companies that use these gene variants to enhance their breeding stock.

V. Conclusions

New technologies and very affordable high throughput genomic marker systems allow a much better characterization of the diversity within and the distances between breeds. This opportunity should be used at local, national and international levels.

The ISAG-FAO recommended microsatellite panels have been instrumental in the assessment of genetic diversity of livestock populations across the globe. The availability of high throughput marker systems, from SNP to whole genome sequence, has opened new doors for the understanding of genetic diversity (Ajmone-Marsan et al., 2023), allowing accurate validation of inbreeding level and breed composition of individual animals, amongst many other things. It is imperative to move to these types of markers, particularly because panels of 50,000 SNP do not cost more than panels of 30 microsatellites. While many tools analytical tools developed for and applied to microsatellite data are still valid and useful, other methods making use of the high number and chromosomal positions of SNP have been developed and are useful now. Also, thanks to genome sequencing, additional types of markers can be made use of, including insertions, deletions and duplications of small chromosomal segments. Work on the pangenome of livestock species, elucidating such types of variants, is the next step towards a better understanding of the genetic diversity of livestock populations. There is enormous utility in using marker panels for the management of breeds, including for breeds with small populations. Detection and eradication of recessive genetic disorders is one such approach, improved genetic evaluation by applying genomic prediction equations is another. The discovery of genes important for adaptation and their use in breeding programs is still elusive, however, with a few exceptions. While genomic tools are excellent for checking the assignment of an individual to a breed, they are not universally capable of unequivocally determining whether two long-established breeds are distinct enough to call them different breeds at all. The concept of breed is based on the decisions of groups of humans. Yet, in case of claims of people having “founded” a new breed, genomic tools are useful for checking whether this group of individuals is distinct enough from an existing breed to allow registration.

The concept of breed remains relevant and will continue to be a key element in animal breeding.

Breeds have constantly changed since their establishment and are not ‘static’. However, many breeds will change even more rapidly with the further development of the various methods of animal breeding. Therefore, the term should take up this dynamic and the possibility to understand “breed” in a more flexible and dynamic way. Systematic crossbreeding of established breeds is a valid way of creating new breeds, supposedly better adapted to a particular environment than their parental breeds, but it must be performed with great care in a regulated way. While there are calls from various stakeholders for greater consistency and internationally agreed standards for recognizing breeds, reaching a consensus on this issue is unlikely in the near future. The perspectives of different interest groups across different countries, species and production systems are too diverse, and the landscape of stakeholders is too fragmented. Notably, involving livestock keepers, who themselves do not form a unified group, in this negotiation process is both costly and challenging. Genomic technologies have already become an integral part of animal breeding, with routine applications such as estimation of breeding values. As genomic methods evolve, alongside the use of sensors, machine learning, and artificial intelligence, new phenotypes will become more cost-effective and accessible for broader use. Gene editing, if it gains consumer acceptance, will increase in significance.

However, there are still many technical issues to address, such as undesirable off-target mutations and pleiotropic effects (Pozzebon et al., 2024), as well as the need for regulatory frameworks governing the technology's use. In near future, more rapid implementation of more advanced technologies may widen the discrepancy between Global North and South in both management of breeds and the way the breed concept is considered.

Not only will the concept of breed continue to be debated, but also the use of genomic methods and the accompanying legal framework will continue to be discussed by experts and the public.

Appendix – Survey statements

PHENOTYPE/BREED CONCEPT (7 statements)

- The phenotypic appearance of an animal is sufficient to determine the breed identity.
- The animals of one breed have an agreed set of distinguishable phenotypic characteristics which are reliably replicated in their offspring.
- The animals of a breed have specific adaptation/unique traits for a particular environment
- The animals of a breed share a common production system or are found in a similar environment
- It is not appropriate to use coat color and pattern only to distinguish breed populations that are otherwise genetically very similar
- “Breed” is a cultural construct, defined by a group of persons with a common interest.
- Within a breed, the development of extreme characteristics detrimental to the health and welfare of the animal must be prohibited.

REGISTRATION/RECOGNITION (9 statements)

- An established breed must have a written herd book (paper or electronic format) with at least three generations of ancestors.
- The oral history of a breed is equivalent to a written herd book.
- For registration, community or breeding organization needs to justify that the animals are different from other populations and have been kept in that production environment for a long time
- The establishment of a breed can be initiated by a large-enough group of enthusiasts/farmers/breeders who collectively define it as such, even without research on the unique identity of the new breed.
- In order to achieve international recognition, a breed must be officially registered at the national level, in accordance with the laws, rules, and regulations of the country where the breed is established.
- Only breeds that are formally registered in a national legal system may be registered in DAD-IS.
- There is a need for an internationally recognized set of criteria for defining breeds.
- Owners of animals of the same breed have to be organized in a breeders’ association.
- Registered breeds need to be kept pure by avoiding mating with animals of different types/breeds.

GENOTYPE/GENOMICS (5 statements)

- In the era of genomics, the concept of “breed” is outdated.
- To establish breed authenticity, genomic data must be utilized to ensure sufficient genetic distance between members of this breed and other similar breeds.
- Efforts should be made to find out whether separate breeds in different countries with very similar phenotype are genetically distinct enough to call them different breeds.
- Breed assignment based on genetic differentiation using genetic markers (microsatellite or SNP) is possible.
- Genomic monitoring of breeds for purity, diversity and genetic load (harmful mutations) should be routinely performed.

CROSSBREEDING/COMPOSITE BREEDS (4 statements)

- Crossbreeding of two or more established breeds is a valid strategy to create a new breed.
- For a new composite/synthetic breed to be accepted by national or DAD-IS systems, at least 3 generations of inter se mating of crossbreds must have passed.
- Composite breeds should be genomically monitored to ensure the intended composition based on their parental breeds.

- Rather than creating new breeds, emphasis should be placed on maximizing the utilization of existing breeds through dedicated efforts.

GENE EDITING (5 statements)

- Gene editing and use of gene edited animals must follow national regulations.
- Gene editing of a few variants does not change breed identity.
- Animals of a breed, whose germ lines have been genetically engineered, must be declared by the owners.
- Routine genomic monitoring for known edits within a breed needs to be performed.
- Gene editing and use of gene edited animals must follow of the access and benefit sharing rules of the Nagoya protocol

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