

SECTION C. BREEDING PROGRAMMES

1. Introduction

This section updates the state of the art in livestock breeding strategies presented in the Second Report on the State of the World's Animal Genetic Resources (SoW-AnGR), focusing on developments since 2015. Over the past decade, the most advanced animal breeding programmes have shifted from phenotype- and pedigree-based selection toward the use of high-precision molecular and digital tools. This transformation has been driven by advances in genomics, genome editing, multi-omics, artificial intelligence and precision phenotyping, often used in concert to enhance efficiency and sustainability. A major milestone has been the widespread adoption of genomic selection, particularly in dairy cattle, enabled by declining genotyping costs, high-density single nucleotide polymorphism (SNP) chips and genotype imputation (Meuwissen *et al.*, 2016). At the same time, next-generation sequencing and genome-wide association studies (GWAS) have deepened understanding of trait biology, while multi-omics approaches have expanded insights into gene regulation and physiological processes. Technological progress has also extended to genome editing, particularly methods based on clustered regularly interspaced short palindromic repeats (CRISPR), and to reproductive technologies such as artificial insemination (AI), *in vitro* fertilization and embryo production, embryo transfer and genomic pre-screening. In parallel, precision livestock farming has transformed phenotyping through automated sensors, imaging and environmental monitoring systems, generating large datasets. The integration of these data through cloud computing and artificial intelligence supports more precise genetic evaluation and management, contributing to the development of data-driven and integrated breeding systems. (cross reference to phenotyping study)

This chapter aims to review the main innovations in animal breeding and genetics over the past decade, with particular attention to how they have been integrated into breeding programmes across the major livestock species. It then provides a global overview of current capacities, followed by a more detailed analysis of stakeholder involvement, as well as educational, research and institutional capacities, breeding activities and policies, and regional perspectives. Finally, the chapter assesses changes over the past two decades and discusses their implications to identify key priorities for the future development of breeding strategies.

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2. State of the art

2.1. Scientific and technological advances

This section provides a brief insight on the technological advances that have occurred over the last ten years, and that are relevant for breeding programmes, independently from their actual integration in breeding programmes. The methodological developments, applications and limitations of these technologies are discussed in greater detail in the section investigating molecular biotechnologies in the chapter dedicated to technologies ([Cross-reference to Technology chapter](#)).

Genomic selection

Compared to the first SoW-AnGR, genomic selection is no longer an emerging strategy but a well-established, routinely applied method in both private and public breeding programmes (VanRaden, 2020). Its expansion has been driven by declining genotyping costs, advances in computational methods, and strong empirical evidence of effectiveness. Genotyping is now widely applied, including to productive females in dairy systems, as SNP panel costs have fallen to a few tens of euros per animal (Mäntysaari *et al.*, 2020). Methods such as imputation of unknown genomic information, improved statistical models (e.g. single-step GBLUP), and enhanced computing infrastructure have increased efficiency and reduced costs (Teng *et al.*, 2022).

Over the past decade, genomic selection (GS) has consistently shown higher prediction accuracy, shorter generation intervals and increased genetic gain compared with pedigree-based selection (Guinan *et al.*, 2023). These gains stem from the ability of genomic markers to capture Mendelian sampling and track realized allele sharing at the individual level (VanRaden, 2008). As a result, selection decisions can be made earlier and more reliably on animals lacking phenotypic data, encouraging wider adoption even among smaller breeding programmes (Bonifazi *et al.*, 2026; Mancin *et al.*, 2025).

Technically, GS can be implemented through different models. Genomic best linear unbiased prediction (GBLUP) uses genomic relationships instead of pedigree-based ones, while SNP-BLUP estimates marker effects directly; both are theoretically equivalent under standard assumptions (Miształ & Legarra, 2017). Genomic information can also be integrated using two-step or single-step (ss) approaches, with the latter (ssGBLUP) now widely preferred due to higher accuracy (Legarra *et al.*, 2009; Christensen & Lund, 2010; Cesarani *et al.*, 2022). In practice, method choice depends largely on data structure and computational considerations.

Bayesian SNP-regression methods have been less widely adopted than expected, as their advantages over simpler approaches diminish with large datasets (Habier *et al.*, 2013). Similarly, whole-genome sequence data have provided only limited gains in prediction accuracy relative to dense SNP panels, while increasing complexity and costs (Van Binsbergen *et al.*, 2015; Pocrnic *et al.*, 2024).

Despite its benefits, GS poses challenges. Accelerated genetic gain may lead to unfavourable correlated responses in fitness, health and resilience if these traits are not adequately included in breeding goals (Miształ & Lourenco, 2024). Shorter generation intervals further amplify these risks, requiring greater emphasis on robustness traits to ensure long-term sustainability. Computational challenges remain, particularly for large-scale evaluations, although emerging methods are addressing these constraints (Miształ & Gowane, 2025).

Omics technologies

“Omics” data refers to large-scale molecular measurements, genomic, transcriptomic, proteomic and metabolomic, that describe the biological layers underlying trait expression in livestock, including productivity, health, reproduction, product quality and resilience (Verardo *et al.*, 2023). While genomics

remains the foundation of modern breeding, increasing attention is being given to post-genomic disciplines (e.g. transcriptomics, proteomics, metabolomics, epigenomics and microbiomics), which capture dynamic biological processes that respond to environmental conditions. These layers help bridge the gap between genotype and phenotype by explaining how genetic information is translated into biological functions (Dall’Olio *et al.*, 2025; Rezvani *et al.*, 2025). As costs decline and technologies mature, their application in livestock research is expanding rapidly.

Omics approaches offer practical advantages, including early detection of disease or stress, improved understanding of complex traits, and the potential use of proxy phenotypes for traits that are difficult to measure directly (Nuñez *et al.*, 2025; Wadood *et al.*, 2025). They can also contribute to refining genetic evaluations by capturing biological variation not explained by traditional models, although large-scale implementation remains constrained by cost and operational complexity (Magro *et al.*, 2025). Current efforts therefore focus on using omics data as reference standards to calibrate more scalable proxies.

Genome editing

Genome editing (Cross-reference to thematic study) refers to the targeted modification of DNA sequences using tools such as CRISPR/Cas9, zinc-finger nucleases, and TALENs, which introduce precise breaks in the genome to enable the deletion, insertion, or alteration of genes (Petersen, 2017). Widely applied in livestock since its first use in mammalian systems in 2013, it allows direct testing of gene function and has been used to improve traits such as disease resistance (e.g. PRRS-resistant pigs), productivity, animal welfare (e.g. hornless cattle), and environmental adaptation (Burkard *et al.*, 2017; Carlson *et al.*, 2016). Despite its potential, large-scale adoption remains limited by technical challenges such as off-target effects and dissemination constraints, as well as regulatory uncertainty and low consumer acceptance. As a result, its most promising applications are currently those that improve animal health and welfare, although significant barriers still hinder widespread commercial implementation (Rodriguez-Villamil *et al.*, 2024).

Reproductive technologies

Reproductive technologies are central to genetic improvement because they influence generation interval, selection intensity and the ability to disseminate superior genetics (Falconer & Mackay, 1996). By increasing the number of offspring from selected animals and accelerating the spread of elite genotypes, these technologies enhance the rate of genetic gain and act as key enablers of modern breeding programmes (Mueller & Van Eenennaam, 2022; Menchaca *et al.*, 2023). Their role is particularly important in cattle, where naturally low reproductive rates constrain genetic progress. Artificial insemination, combined with semen cryopreservation, has been the most influential technology, enabling widespread use of elite sires across herds and countries. Its impact has been further amplified by GS, which allows early identification and rapid deployment of superior young bulls, significantly reducing generation intervals.

Additional technologies, such as embryo transfer, *in vitro* embryo production, ovum pick-up and sexed semen, have expanded the exploitation of elite female genetics and improved reproductive management. However, their impact has generally been more limited than AI due to higher costs, technical requirements and variable biological efficiency. Advanced approaches such as multiple ovulation and embryo transfer (MOET) and cloning offer theoretical benefits but remain constrained by economic, technical and societal factors. Overall, the effectiveness of reproductive technologies depends on their integration into breeding systems and their cost-effectiveness under practical conditions, with AI and genomics remaining the dominant drivers of genetic progress in livestock.

Large scale phenotyping

Large-scale phenotyping involves the high-throughput, systematic collection of detailed phenotypic data across large livestock populations, enabled by precision livestock farming technologies such as sensors, wearable devices, imaging systems and omics tools (Berckmans, 2017; Rutten *et al.*, 2013). This shift from sporadic measurements to continuous data streams has expanded the range of traits that can be monitored, including feed efficiency, behaviour, health status, resilience and disease susceptibility. From a breeding perspective, it improves the detection of genetic variation in complex traits, enhances genomic prediction accuracy, and supports the inclusion of functional traits related to robustness, welfare and environmental efficiency in selection programmes (Goddard and Hayes, 2007; Mrode *et al.*, 2019). The development of big data and artificial intelligence offers significant potential to further advance large-scale phenotyping (see Box 2C1).

Box 2C1 Use of artificial intelligence for animal breeding

Artificial intelligence has achieved major advances across fields such as medical imaging, climate modelling and natural language processing, yet its application in animal breeding remains limited, with most uses still experimental rather than routine. In this domain, artificial intelligence applications can be grouped into three areas: automated phenotyping, improved predictive models, and decision support for selection and mating (Morota *et al.*, 2026). To date, the most successful applications are in phenotyping; in contrast, improvements in genetic prediction accuracy are more limited, partly because existing genomic models are already highly optimized and artificial intelligence methods can be computationally demanding (Hamadani *et al.*, 2024). Artificial-intelligence-based decision support, such as defining breeding objectives, building selection indices and balancing production, welfare and sustainability traits, remains underdeveloped and rarely implemented in practice.

In principle, artificial intelligence could integrate genomic, economic and environmental data to guide breeding decisions and balance short- and long-term objectives. However, its practical use is constrained by the need for stable selection indices and by the difficulty of formalizing breeder expertise and farm-specific priorities (Cole, 2025). Moreover, artificial intelligence methods have not consistently outperformed classical genomic models, partly due to benchmarking issues, limited interpretability and high computational requirements (Chafai *et al.*, 2023; Montesinos-López *et al.*, 2025). While some gains have been reported for traits with non-linear or non-additive effects, these remain context-specific (Abdollahi-Arpanahi *et al.*, 2020).

The most mature application of in animal breeding is digital phenotyping. By processing images, sensor data and other high-throughput information, artificial intelligence can generate proxy traits for behaviour, health, welfare and performance (Neethirajan & Kemp, 2021; Rohan *et al.*, 2024). This is especially valuable for traits that are difficult or costly to measure directly, enabling large-scale, automated phenotyping. Deep learning is particularly effective in this context, supporting applications such as behaviour recognition, carcass evaluation and health monitoring from sensor or spectral data (Fuentes *et al.*, 2022; Menezes *et al.*, 2024). Overall, compared with genomic prediction and decision-making, digital phenotyping remains the most practical and rapidly advancing application of artificial intelligence in animal breeding (Morota *et al.*, 2026).

However, their implementation faces important challenges. Lack of data standardization across farms and technologies can introduce biases and limit comparability, while high infrastructure and operational costs may restrict adoption, particularly in low-resource systems. In addition, managing and analysing large, complex datasets requires advanced computational tools and expertise, and the biological interpretation of proxy traits derived from sensors remains difficult. As a result, fully realizing the benefits of large-scale phenotyping depends on coordinated efforts in data harmonization, methodological development and investment, ensuring its effective contribution to sustainable livestock production systems. The topic of phenotyping is further investigated in the chapter “*Animal phenotyping challenges and solutions*” (crossreference).

Database management and data storage

The rapid growth of data-intensive research has made database management a central component of scientific infrastructure. Modern biological research relies on large, heterogeneous datasets from sequencing, sensors and monitoring systems, requiring scalable, secure and interoperable platforms for storage, processing and reuse (Wilkinson *et al.*, 2016). Key challenges include the exponential increase in data volumes, which often exceeds storage and processing capacity, and the need for advanced infrastructures such as cloud computing and high-performance systems. However, these solutions raise issues related to cost, governance, and unequal access to resources (Stephens *et al.*, 2015; Marx, 2013).

Effective database design is therefore critical for ensuring efficiency, sustainability and data reuse. Standardized metadata, efficient data architectures and adherence to FAIR principles (i.e. findable, accessible, interoperable, and reusable) can improve interoperability and reduce redundancy, but balancing performance, scalability, cost and data security remains complex (Wilkinson *et al.*, 2016). As a result, database management is increasingly viewed not as technical support but as a strategic investment essential for ensuring reproducibility, transparency and long-term value in scientific research.

2.2. Integration of technological advances into breeding programmes

The following section examines how the advances outlined above have been integrated into breeding strategies and programmes over the past decade. It focuses primarily on the five major livestock species, dairy and beef cattle, sheep and goats, pigs, and chickens, and on high-input production systems. These systems, characterized by intensive management and significant investments in technology, nutrition and genetics, are more likely to adopt and operationalize such innovations. While their primary objective remains maximizing output per animal and per unit of land, increasing attention is also being given to health, welfare, sustainability and resilience. Advances and challenges specific to low-input systems are addressed separately in the chapter “*Establishing and scaling up breeding programmes in challenging environments*” (crossreference), which provides a more detailed analysis of contexts where resource constraints limit the uptake of these technologies.

Dairy and beef cattle

The cattle breeding sector has undergone profound transformation over the past two decades, driven by the rapid integration of GS, reproductive biotechnologies, precision livestock farming and, more recently, genome editing tools. Among these, GS has become the backbone of modern breeding programmes. Introduced commercially in the late 2000s, with the first bovine SNP chips in 2007 and routine genomic evaluations starting shortly thereafter, GS is now widely implemented in dairy cattle (Guinan *et al.*, 2023) and increasingly applied in beef populations (VanRaden, 2020). Its impact has been particularly strong in international transboundary dairy breeds, where large reference populations and well-established recording systems have supported high prediction accuracy (see Box 2C2). By enabling the early selection of genomically tested animals, GS has replaced traditional progeny testing, substantially reducing generation intervals and costs. As a result, rates of genetic gain in dairy cattle have approximately doubled, while generation intervals have been halved (Wiggans *et al.*, 2017). Initially focused on production traits, GS has progressively expanded to include health, fertility, longevity and feed efficiency, reflecting broader breeding objectives.

Box 2C2. Impact of genomic selection on US dairy cattle

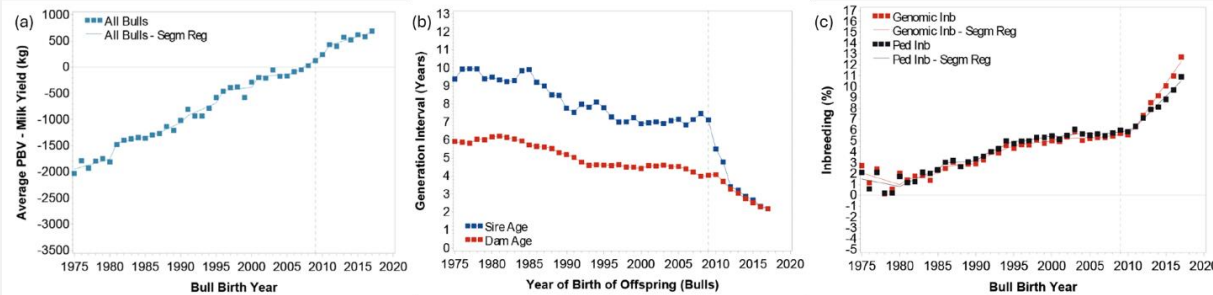
Early theoretical work on genomic selection (GS) predicted that, by increasing the accuracy of estimated breeding values through improved capture of Mendelian sampling, its application would enable higher rates of genetic gain while simultaneously reducing the rate of inbreeding compared with conventional selection methods (Daetwyler *et al.*, 2007). After more than 15 years of implementation in dairy cattle, it is therefore pertinent to assess the extent to which these expectations have been realized in practice.

Guinan *et al.* (2023) analyzed trends in genomic predicted breeding values (PBV) for Ayrshire, Brown Swiss, Guernsey, Holstein and Jersey cattle populations in the United States. Their analysis was based on a large dataset comprising 154 008 bulls and over 33 million cows born since 1975, allowing the estimation of long-term genetic trends in both sexes.

A central finding of the study is the substantial acceleration of genetic gain following the adoption of genomic selection. Across breeds, rates of genetic improvement in economically important traits increased markedly compared with the pre-genomic era. This effect was particularly pronounced in Holstein and Jersey populations, where genetic gain rose by up to 192 percent compared with the pre-genomic period. This stronger response is also consistent with the earlier implementation of official genomic evaluations in these breeds: in the United States, such evaluations were released in 2009 for Holstein, Jersey and Brown Swiss, in 2013 for Ayrshire and in 2016 for Guernsey. The early evaluations were based on multibreed BLUP followed by single-breed estimation of SNP effects, which helps explain why Holstein and Jersey benefited earlier and more strongly over the period considered. The interpretation of long-term trends should also take into account that selection indices changed over time. Although production traits remained central, some functional traits, such as daughter pregnancy rate and livability, were introduced later, and the relative emphasis assigned to traits in the index evolved progressively. Genetic trends therefore reflect not only the effects of genomic selection itself, but also changing breeding objectives and selection pressures.

Another major impact of GS identified in the study is the significant reduction in generation intervals. By allowing selection decisions to be made on young animals without waiting for progeny testing, genomic tools have shortened the time between generations for both sires and dams. This reduction has been a critical driver of increased rates of genetic gain, as it allows faster turnover of elite genetics within populations.

However, the impact of GS on inbreeding trends has been more variable across breeds. In particular, Holstein populations have experienced a marked increase in inbreeding, likely driven by strong selection intensity combined with decrease in generation interval. This highlights that, in practice, the expected reduction in inbreeding is not automatically achieved, and underscores the importance of explicitly incorporating measures of inbreeding or genetic diversity into selection objectives and breeding programme design in order to balance short-term genetic gain with the long-term sustainability of animal genetic resources.



Estimates of annual genetic change derived from segmented regressions of predicted breeding values (PBV) on birth year for milk yield (a); generation intervals for sires and dams (b); and pedigree-based (Ped) and genomic inbreeding (Inb) (c) in U.S. Holstein cattle.
Adapted from Guinan et al. (2023) under Creative Common License

Although adoption in beef cattle has been slower, GS has demonstrated clear benefits, particularly for traits that are difficult or expensive to measure, such as feed efficiency and meat quality. Its wider implementation has been facilitated by methodological advances, notably single-step genomic BLUP (ssGBLUP), which integrates genomic, pedigree and phenotypic data into a unified evaluation framework (Legarra *et al.*, 2009). This approach has been especially important for smaller or local populations, where limited reference data previously constrained prediction accuracy. Complementary tools such as genotype imputation have further reduced costs by allowing low-density genotyping to be extrapolated to higher densities, enabling broader adoption across breeds and production systems. These developments have supported the expansion of GS to local breeds and to developing-country contexts, although challenges remain in building sufficiently large and representative reference populations.

At the same time, GS has been complemented by other genetic and genomic approaches. Marker-assisted selection continues to be used for traits influenced by major genes, such as milk composition, while whole-genome sequencing and genome-wide association studies have improved the identification of causal variants and selection signatures. Emerging initiatives, including the development of cattle pangenomes, aim to better capture genetic diversity across breeds and enhance the accuracy of genomic predictions. More recently, genome editing technologies, particularly CRISPR-based methods, have opened new possibilities for targeted trait improvement, including disease resistance, thermotolerance and polledness. While some applications have reached advanced stages, the widespread use of genome editing remains constrained by technical, regulatory and societal factors, and its role in commercial breeding systems is still evolving.

Reproductive technologies have continued to play a central role in amplifying the impact of genetic progress. Artificial insemination remains the most widely used tool, enabling the global dissemination of elite genetics, particularly when combined with GS. Other technologies, such as embryo transfer, in vitro fertilization and sexed semen, have further increased selection intensity and enabled more efficient use of both male and female genetic resources. New breeding strategies, such as beef-on-dairy systems, are expanding rapidly, allowing producers to increase the value of dairy-derived calves while optimizing herd structure and improving overall system efficiency (Berry, 2021). Together, these reproductive innovations have strengthened the link between genetic evaluation and practical dissemination.

Parallel advances in precision livestock farming have transformed phenotyping, moving from periodic measurements to continuous, high-resolution data collection. The use of automated milking systems, wearable sensors, imaging devices and digital monitoring tools now allows detailed recording of production, health, behaviour and environmental responses (Berckmans, 2017). Coupled with advances in artificial intelligence (see Box 2C1) and data analytics, these technologies generate large datasets that enhance the estimation of breeding values and enable earlier and more accurate selection decisions. They also support the integration of functional traits into breeding programmes, including animal welfare, robustness and environmental efficiency.

In this context, breeding objectives have evolved significantly. While productivity remains important, increasing emphasis is placed on sustainability, resilience and reduced environmental impact. Traits such as feed efficiency, methane emissions and resource use efficiency are now being incorporated into selection indices. Similarly, resilience is receiving growing attention, with efforts to develop novel indicators based on production variability or behavioural responses and to account for genotype–environment interactions in genetic evaluations. Reaction norm models and other approaches are increasingly used to identify genotypes that perform consistently across diverse environmental conditions, including under heat stress or variable feeding regimes.

Advances in multi-omics technologies are also contributing to a deeper understanding of complex traits. The integration of genomics, transcriptomics, metabolomics and microbiomics is helping to bridge the gap between genotype and phenotype, allowing a more precise characterization of biological processes

underlying production, health and adaptation. These approaches support the development of more refined selection strategies, although their routine use in large-scale breeding programmes remains limited by cost and complexity.

Finally, the acceleration of genetic gain associated with GS has raised concerns about the increase in inbreeding and the potential loss of genetic diversity. This has led to the wider adoption of management strategies such as optimal contribution selection, which aims to maximize genetic gain while controlling the rate of inbreeding (Fleming *et al.*, 2018). Maintaining genetic diversity is increasingly recognized as essential for long-term sustainability, particularly in the context of changing environments and emerging challenges. Overall, the cattle breeding sector is characterized by the integration of multiple technological innovations within increasingly complex and data-driven systems, enabling significant gains in productivity while progressively addressing broader objectives related to resilience, welfare and sustainability.

Sheep and goats

The technological advances that have transformed cattle breeding over the past decade have also influenced sheep and goat genetic improvement, although their adoption has generally been slower and more heterogeneous due to the specific characteristics of small ruminant production systems. The sequencing of sheep and goat genomes in the early 2010s enabled the development of SNP chips and the introduction of genomic tools within breeding programmes (Jiang *et al.*, 2014). Genomic selection (GS), now widely established in cattle, has progressively been implemented in sheep and goats, though at a more limited scale. This slower adoption reflects structural constraints, including smaller population sizes, higher genotyping costs relative to animal value, and more limited availability of large, well-phenotyped reference populations (Rupp *et al.*, 2016). Nevertheless, GS has been applied since the 2010s, initially in dairy sheep breeds and later extended to traits such as milk production, meat quality, disease resistance and adaptation to environmental stressors (Mucha *et al.*, 2022). The introduction of single-step GBLUP (ssGBLUP), which integrates genomic, pedigree and phenotypic information, has been particularly important in improving prediction accuracy under conditions of limited data and is now widely used in routine evaluations (Legarra *et al.*, 2009; Lourenco *et al.*, 2020).

Alongside GS, marker-assisted selection (MAS) continues to play a significant role in small ruminants, especially for traits controlled by major genes or quantitative trait loci. Notable examples include the PrP gene for scrapie resistance and casein genes affecting milk composition in goats (Rupp *et al.*, 2016). Advances in genomic analyses, including genome-wide association studies and the detection of selection signatures, have improved the identification of genes underlying economically important traits, such as growth, fibre production and environmental adaptation. While genome editing techniques such as CRISPR/Cas9 have been explored in experimental settings to modify traits like muscle growth or disease resistance, their practical use remains limited by technical challenges, regulatory uncertainty and societal concerns (Lee *et al.*, 2020). Compared to cattle, the application of advanced reproductive technologies in sheep and goats remains more restricted, with artificial insemination and oestrus synchronization being the most widely used methods. More complex techniques, such as embryo transfer or in vitro fertilization, are still largely confined to research or high-value applications due to cost and variable efficiency.

Recent developments in precision livestock farming are beginning to transform phenotyping in small ruminants, enabling improved monitoring of production, health and behavioural traits through sensors and automated systems (Brito *et al.*, 2021). These technologies support the growing emphasis on functional traits, including resilience, welfare and adaptation to climate change. Indeed, breeding objectives are increasingly incorporating traits related to parasite resistance, heat tolerance and overall robustness, reflecting the need for animals to perform under more variable environments (Mucha *et al.*, 2022). Approaches such as the analysis of genotype–environment interactions are also gaining importance, helping to identify animals better adapted to specific production conditions. At the same time, the acceleration of genetic gain raises concerns about inbreeding, prompting the adoption of strategies such as optimal contribution selection to balance progress and genetic diversity.

Overall, sheep and goat breeding has made significant progress over the past decade through the gradual integration of genomic tools, improved phenotyping and evolving breeding objectives. However, key challenges remain, including the need to expand reference populations, reduce costs and strengthen data integration. Future developments are likely to rely increasingly on the combination of genomics, precision phenotyping and emerging multi-omics approaches, supported by advanced data analytics, to enable more precise and sustainable breeding strategies.

Pigs

Pig breeding has largely maintained the pyramidal structure described in previous SoW-AnGR reports, with genetic improvement concentrated in nucleus populations composed of specialized sire and dam lines. Sire lines are selected primarily for growth, carcass traits, meat quality and robustness, while dam lines focus on reproductive performance. Crossbreeding between these lines generates commercial animals, maximizing heterosis, particularly for low-heritability traits such as litter size and piglet survival. This structure is implemented by both national breeding organizations and highly integrated private companies, which have rapidly adopted modern technologies. Among these, GS (GS) has become a standard tool in commercial pig breeding, supported by SNP chips and imputation strategies that reduce costs while maintaining accuracy (Mote & Rothschild, 2020). Since its implementation in the early 2010s, GS has substantially increased genetic gain, by more than 35% overall and over 50% for low-heritability traits, through improved accuracy of breeding value estimation and better control of inbreeding (Knol *et al.*, 2016). Advances in whole-genome sequencing and GWAS have further enabled the identification of key genes affecting production and reproduction, such as ESR, MC4R and IGF2, supporting both genomic and marker-assisted selection approaches.

Genome editing has emerged as a complementary innovation, offering the potential for targeted trait improvement, such as disease resistance (e.g. PRRS-resistant pigs through CD163 editing) and improved feed efficiency. Although experimental results are promising, large-scale application remains limited by technical, regulatory and societal constraints, and GS remains the dominant approach in practice (Hickey *et al.*, 2016). Reproductive technologies continue to play a central role in disseminating genetic progress, with artificial insemination, particularly post-cervical AI, widely adopted in commercial systems. Emerging techniques such as in vitro embryo production are improving but remain less widely applied. Precision livestock farming (PLF) technologies are now extensively integrated into pig production, enabling real-time monitoring of growth, feeding behaviour, health and welfare through automated feeders, sensors and imaging systems (Brito *et al.*, 2021). These data streams support more accurate phenotyping and selection, particularly for complex traits.

However, rapid genetic progress has also revealed trade-offs, notably on animal welfare. Selection for productivity traits has been associated with negative correlated responses, such as reduced piglet birth weight, increased mortality and behavioural issues (Turner *et al.*, 2024). As a result, breeding goals are increasingly incorporating welfare, robustness and resilience traits. Advanced approaches, including models accounting for maternal and social (indirect) genetic effects (IGEs), as well as GWAS analyses, are being explored to better capture these complex traits, although their routine implementation remains challenging. Resilience and adaptation to climate change have also become key priorities, with increasing emphasis on heat tolerance, genotype–environment interactions and precision nutrition strategies tailored to specific production conditions (Dekkers, 2025). These approaches require large datasets and are often better implemented at commercial rather than nucleus level due to the environmental variability that can be found in commercial farms.

In parallel, sustainability considerations are reshaping breeding objectives, with growing emphasis on feed efficiency, reduced emissions and overall system robustness. Modern breeding programmes increasingly allocate a substantial proportion of selection indices to health and functional traits, supported by genomic and phenotypic data (Brito *et al.*, 2021). At the same time, the rapid increase in genetic gain has heightened concerns about inbreeding and loss of genetic diversity, prompting the adoption of strategies such as optimal contribution selection to balance progress with long-term sustainability. Finally, the integration of multi-omics approaches, including transcriptomics,

metabolomics and microbiomics, is opening new perspectives for understanding the biological basis of complex traits and improving prediction models. Overall, pig breeding has become a highly technology-driven sector, combining genomic tools, advanced reproduction, precision phenotyping and data analytics to enhance productivity, resilience and sustainability, while addressing emerging challenges related to welfare and genetic diversity.

Poultry

The poultry breeding sector continues to be characterized by a highly structured and vertically integrated “breeding pyramid,” dominated by a small number of multinational companies controlling nucleus, multiplication and commercial levels. Genetic improvement is concentrated in elite pure lines (sire and dam lines), with progress disseminated through successive multiplication tiers to produce commercial hybrids. This structure enables the rapid diffusion of innovations and has facilitated faster and more uniform adoption of advanced technologies compared to other livestock species. Over recent decades, breeding goals have evolved from a primary focus on growth rate, egg production and feed efficiency toward a more balanced emphasis that also includes disease resistance, welfare, resilience and environmental sustainability.

Genomic selection is now firmly established as the core tool of poultry breeding programmes, supported by the early availability of a reference genome and the development of high-density SNP arrays (Meuwissen *et al.*, 2016; Saxena & Kullori, 2018). Dense genotyping is typically applied at the nucleus level, while low-density panels combined with imputation are used for large populations, allowing cost-effective genomic evaluation at scale. GS has improved selection accuracy, by up to 30–50 percent for key traits, while reducing generation intervals and accelerating genetic gain. It is particularly valuable for traits that are difficult to measure directly on selection candidates, such as meat quality in broilers or egg production in males. The use of single-step GBLUP (ssGBLUP) further enhances accuracy by integrating genomic, pedigree and phenotypic data, including information from non-genotyped animals, while reducing selection bias (Misztal *et al.*, 2020). In addition, genomic data support genome-wide association studies and the identification of quantitative trait loci, enabling more precise targeting of traits such as growth, reproduction and disease resistance.

Genome editing technologies, particularly CRISPR/Cas9, have demonstrated substantial potential in poultry research. Applications include the development of resistance to viral diseases such as avian leukosis and avian influenza, modification of egg proteins to reduce allergenicity, and potential improvements in growth and meat quality (Liao *et al.*, 2026). Innovative concepts such as editing primordial germ cells offer the possibility of rapidly introducing targeted traits into breeding populations. However, despite promising experimental results, commercial implementation remains limited due to regulatory constraints and societal concerns. Reproductive technologies also play a role, although artificial insemination is primarily restricted to higher tiers of the breeding pyramid (and widely used in species such as turkey), while advanced techniques such as germline modification remain largely experimental.

Precision livestock farming (PLF) technologies are increasingly integrated into poultry systems, enabling large-scale automated phenotyping. Unlike in cattle or pigs, monitoring is often performed at flock level rather than individual level, due to the high density of poultry production systems. Environmental sensors, acoustic monitoring, imaging technologies and automated feeding systems provide continuous data on growth, health, behaviour and environmental conditions (Brocklehurst *et al.*, 2025; Maharjan & Liang, 2020). These tools are widely applied in commercial operations and support early disease detection, improved welfare management and optimized production efficiency. At the breeding level, more detailed phenotyping, sometimes including individual-level data, is used to enhance the accuracy of selection.

Breeding objectives in poultry have broadened considerably in recent years. While productivity traits remain central, increasing emphasis is placed on welfare and robustness, partly in response to negative correlated effects of intense selection (e.g. skeletal disorders or behavioural issues). Models incorporating indirect genetic effects (IGEs) and social interactions have shown promise in improving

traits such as survival and reducing harmful behaviours, and are increasingly being integrated into breeding strategies in leading companies (Ellen *et al.*, 2014). Similarly, resilience and adaptation to environmental stressors, including heat stress, are gaining importance, with research focusing on genotype–environment interactions and the identification of adaptive genes.

Advances in genomics and multi-omics approaches are further enhancing the understanding of complex traits. Studies integrating transcriptomics, metabolomics and microbiomics are identifying biological pathways underlying production, immunity and adaptation. These approaches are particularly relevant for improving disease resistance and feed efficiency, and for identifying biomarkers that could support precision selection in the future. Although their routine application in commercial breeding remains limited, they are increasingly used in research and are expected to contribute to future innovations.

In conclusion, poultry breeding has been rapidly reshaped by the integration of genomic technologies, precision phenotyping and emerging biotechnologies. The sector’s highly centralized structure has enabled fast adoption of innovations, resulting in substantial gains in productivity and efficiency. At the same time, breeding objectives are evolving toward a more holistic approach that integrates welfare, resilience and sustainability. Future progress will depend on further advances in data integration, cost-effective technologies and the responsible deployment of emerging tools such as genome editing, while maintaining genetic diversity and addressing societal expectations.

Conclusion

Overall, the integration of technological advances into breeding programmes has proceeded unevenly across species, with the most rapid and comprehensive uptake occurring in highly structured commercial sectors such as cattle, pigs and poultry. Genomic selection, advanced reproductive technologies and large-scale phenotyping are now central components of many breeding systems, while genome editing, multi-omics and artificial intelligence remain at earlier stages of operational use. At the same time, breeding objectives are broadening beyond productivity to include health, welfare, resilience and environmental sustainability. Table 2C1 summarizes the main innovations integrated into breeding programmes across the principal livestock species and highlights both common trends and species-specific patterns.

Table 2C1. Comparative summary of innovations in animal breeding and genetics in the main livestock species (cattle, sheep and goats, pigs, poultry)

Innovation Area	Cattle	Pigs (Swine)	Sheep & Goats	Poultry
1. Genomic Selection (GS)	Widely implemented; high-density and low-cost SNP panels (e.g., BovineSNP50, BovineHD). Used for milk yield, fertility, feed efficiency, and methane reduction.	Fully integrated in breeding companies (PorcineSNP60). Used for feed efficiency, reproduction, and carcass traits.	Expanding; SNP panels (OvineSNP50, GoatSNP50) and low-density chips for smallholders. Focus on milk yield, fiber, disease resistance.	Rapid adoption; high-density SNP arrays (600K). Used for egg yield, growth, and disease resistance.
2. Genome Editing (CRISPR, TALENs, ZFNs)	Used for disease resistance (bTB, trypanosomiasis), welfare (polled cattle), and	Highly advanced; PRRS-resistant pigs (CD163 knockout) a major success. Work on	Applied for fecundity (<i>BMP15</i> , <i>GDF9</i>), fiber traits, and	Experimental use; avian influenza-resistant chickens,

	productivity (<i>MSTN</i> , <i>SLICK</i> genes).	ASF, muscle growth, and feed efficiency.	disease resistance (scrapie, mastitis).	thermotolerant lines, elimination of male chick culling.
3. Marker-Assisted Selection (MAS)	<i>DGATI</i> , <i>CSN2</i> (milk), <i>BoLA-DRB3</i> (disease), <i>Leptin</i> (growth).	<i>RYR1</i> , <i>IGF2</i> , <i>MC4R</i> , <i>PRLR</i> (growth, litter size, meat quality).	<i>FecB</i> (Booroola), <i>CSN1S1</i> , <i>DRB1</i> (milk, resistance).	<i>MHC</i> , <i>GHR</i> , <i>PRL</i> , <i>MC1R</i> (disease, growth, plumage).
4. Reproductive and Biotechnological Advances	AI, IVF, ET, OPU-IVF, sexed semen; genomic embryo screening.	AI with genomic boars, IVF, cloning, embryo cryopreservation.	AI, ET, OPU-IVF, sexed semen; conservation of indigenous breeds.	AI in elite flocks, germ cell cryopreservation, surrogate host and sexing technologies.
5. Precision Phenotyping & Sensor Technologies	Wearables, 3D imaging, automatic milking sensors, health and heat monitoring.	Automated feeders, sound sensors, weight tracking, behavior cameras.	Smart collars, automated weighing, thermal sensors, IoT-based monitoring.	Vision systems, sound analysis, IoT welfare sensors, AI-based behavior tracking.
6. Sustainable & Climate-Smart Breeding	Focus on feed efficiency, methane reduction, heat tolerance (<i>SLICK</i> gene).	Selection for nutrient efficiency, low emissions, heat tolerance.	Adaptation to drought and heat; resilience breeding using indigenous genetics.	Feed efficiency, nitrogen reduction, heat-tolerant alleles (<i>Naked Neck</i> , <i>Frizzle</i>).
7. Functional Genomics & Multi-Omics Integration	Integration of genomics, transcriptomics, proteomics, metabolomics, and microbiomics.	Multi-omics for gut microbiome, immunity, and feed efficiency.	Multi-omics for fertility, disease resistance, and fiber quality.	Multi-omics for immunity, egg quality, and microbiome research.
8. Artificial Intelligence & Big Data	Predictive modeling for genomic breeding values; inbreeding management.	AI-driven health monitoring, mating optimization, and decision support.	AI for selection, disease detection, and community breeding program management.	AI for real-time welfare monitoring, egg grading, and flock management.
9. Sustainability & Ethics	Focus on welfare, biodiversity, and traceability via blockchain.	Regulations on gene-edited pigs; emphasis on ethics and transparency.	Community-based breeding programs (CBBPs) integrating genomics.	Welfare and transparency central; elimination of male chick culling under development.
10. Industry Adoption Level	Mature and globally standardized (especially dairy).	Very high adoption in commercial systems.	Moderate adoption, growing in developing regions.	Extremely high adoption and integration, led by global breeding companies.

3. Global overview

For each of the main livestock species covered in the reporting questionnaire, most countries indicated that at least one breeding programme exists (Table 2C1). In the 2025 reporting round, the reported presence of breeding programmes is high across all seven species categories, with world values generally in the low-to-high 90 percent range. In contrast to the more uneven pattern reported in the Second SoW-AnGR, where programme presence tended to be more higher in cattle particularly, the current results suggest a more consistently high level of reported programme presence across cattle, small ruminants, pigs and chickens (FAO, 2015).

As in earlier assessments, these figures need to be interpreted carefully. The indicator captures whether a country reported the existence of at least one breeding programme for a given species. It does not indicate how many breeds are covered, how widely the programme operates, or how effective it is. Nor does it show whether all the core elements of a breeding programme are in place. As noted in the previous report, some activities reported by countries as breeding programmes may not fully correspond to breeding programmes in the strict sense of the term (FAO, 2015).

The regional breakdown (Table 2C2) shows that breeding programmes for the main livestock species are widely reported in most regions. Asia reports breeding programmes for all seven species categories in all reporting countries. A similarly high level of reported programme presence is seen in the Southwest Pacific, although based on only two reporting countries. Latin America and the Caribbean also shows uniformly high values, with 100 percent reported for all cattle categories and pigs, and slightly lower values for sheep, goats and chickens. Africa records high values across all species, but remains below the world average for some categories, particularly chickens and sheep. Europe also reports generally high levels of programme presence, although values for sheep and goats are somewhat lower than for most other regions. The Near East shows complete reporting for all species except pigs, for which no breeding programmes were reported. North America reports breeding programmes for all species except multipurpose cattle, which were not reported as having a breeding programme.

Compared with the 2014 results presented in the Second SoW-AnGR, the 2025 results (Figure 2C1) show a generally higher reported presence of breeding programmes across most species and regions, with the increase being especially marked for sheep, goats, pigs and chickens in Africa and for several non-cattle species in other regions. However, some region–species combinations continue to show little change or remaining gaps, indicating that breeding programme presence is still not uniform across production systems.

Table 2C2. Proportion of countries reporting the existence of breeding programmes - regional breakdown

Regions	Number of countries	Dairy cattle	Beef cattle	Multipurpose cattle	Sheep	Goats	Pigs	Chickens
		%						
Africa	35	97	100	93	91	94	94	88
Asia	14	100	100	100	100	100	100	100
Southwest Pacific	2	0	100	100	100	100	100	100
Europe	31	93	93	92	90	89	96	96
Latin America and the Caribbean	17	100	100	100	93	93	100	87
Near East	11	100	100	100	100	100	0	100
North America	2	100	100	0	100	100	100	100
World	112	97	95	95	93	94	97	93

Note: The figures and bars represent the number of countries indicating the presence of breeding programmes (at least one) as a proportion of the number of countries reporting the presence of the respective species.

Source: Country reports, 2025.

For species outside the “big five”, reported programme presence remains more variable (Table 2C3). However, the results suggest that breeding programmes are reported for a wider set of species than in the previous reporting round, with particularly high values reported for horses (93) and Bactrian camels (89), buffaloes (88), managed bees and deer (82 each), while several other species show moderate values (e.g. rabbits 77 percent; turkeys 66 percent; ducks 65 percent; pigeons 54 percent etc).

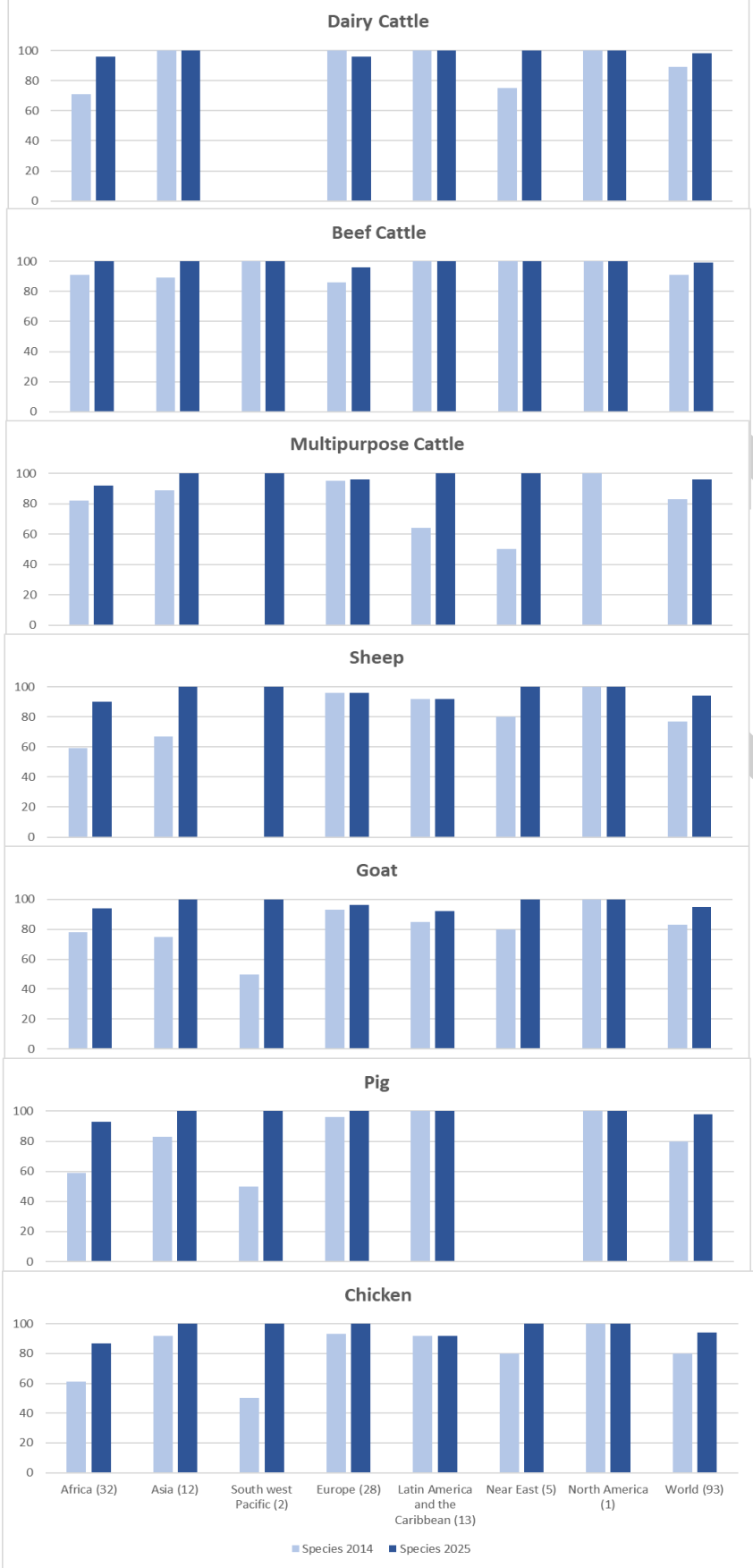
559 **Table 2C3. Proportion of countries reporting the existence of breeding programmes**

Species	Number of countries reporting presence	Percentage of countries with breeding programmes (at least one)
Cattle (specialized dairy)	100	97
Cattle (specialized beef)	87	98
Cattle (multipurpose)	85	95
Sheep	105	93
Goats	105	94
Pigs	93	97
Chickens	102	93
horses	82	93
managed bee	67	82
ducks	52	65
rabbits	53	77
asses	40	60
geese	36	64
turkeys	32	66
buffaloes	32	88
pigeons	26	54
guinea fowls	27	63
quails	23	70
dromedaries	26	85
ostriches	18	50
muscovy ducks	14	50
deer	11	82
bactrian camels	9	89
guinea pigs	6	67
yaks	6	100
alpacas	6	83
llamas	5	100
mithun	2	50

Source: Country reports, 2025.

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Figure 2C1: Comparison of the proportion of countries reporting the existence of breeding programmes for the main livestock species, by region, 2014 and 2025.



Note: For comparability, the results are based only on the 93 countries that reported in both rounds. Countries that reported in only one round were excluded from the comparison.

Source: Country reports, 2025.

4. Stakeholder involvement

Breeding programmes need stable institutional arrangements if they are to function over time. Depending on the species, production system and national context, the lead role may be taken by public institutions, private-sector actors, non-governmental organizations (NGOs), livestock keepers acting collectively, or a combination of these. Table 2C4 summarizes the stakeholder groups that countries reported as operating breeding programmes, that is, taking the main organizational role in their implementation. For this analysis, the non-public categories are distinguished as national commercial companies, external commercial companies, breeders' associations or cooperatives, NGOs and livestock keepers organized at community level. At world level, breeders' associations or cooperatives and governments are the stakeholder groups most often reported as operators of breeding programmes. Livestock keepers organized at community level and national commercial companies are also reported relatively often, while external commercial companies, NGOs and other actors are less prominent. Compared with the previous reporting round, the results point to a wider range of organizational models. In particular, breeder organizations, community-level structures and commercial companies appear more frequently in the current results than in the earlier report (Country reports, 2025).

The regional pattern remains uneven. In Europe and North America, breeders' associations are the most prominent operators, whereas in Africa, Asia and the Near East the reported role of government remains stronger. Latin America and the Caribbean stands out for the relatively important role of both breeders' associations and commercial companies. In the Southwest Pacific, livestock keepers organized at community level are reported more often than any other stakeholder group. NGOs are reported as operators in several regions, but usually less often than governments, breeders' associations, community-level groups and commercial companies.

Table 2C4. Extent of involvement of different stakeholder groups as operators of breeding programmes

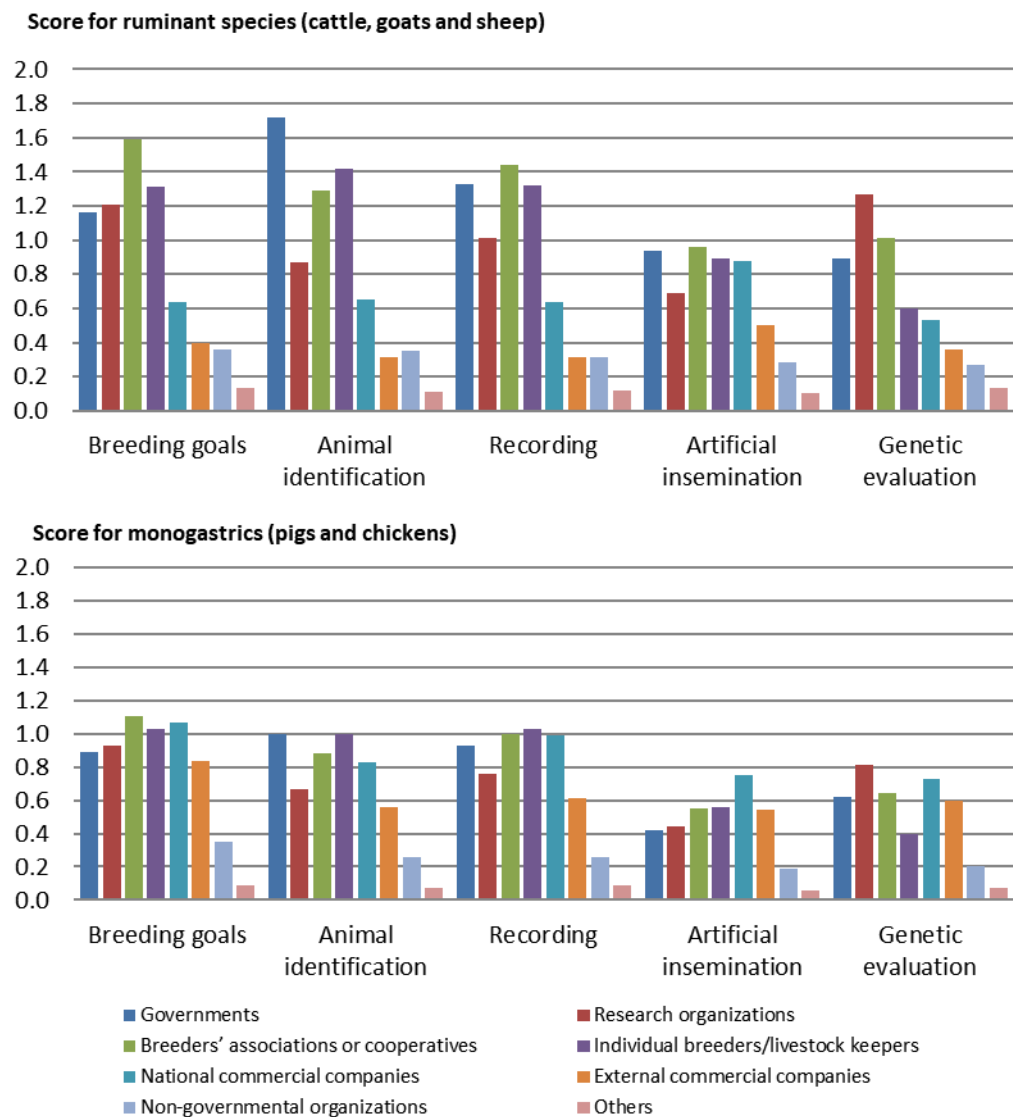
Regions	Number of countries	Government	Livestock keepers organized at community level	Breeders' associations or cooperatives	National commercial companies	External commercial companies	NGOs	Others
%								
Africa	35	70	61	60	34	16	32	16
Asia	14	93	74	54	54	43	28	3
Southwest Pacific	2	64	79	0	0	0	36	0
Europe	31	25	4	77	25	20	12	5
Latin America & the Caribbean	17	58	39	74	60	49	29	16
Near East	11	65	56	47	56	20	24	20
North America	2	0	21	93	57	57	43	57
World	112	56	43	66	41	27	25	13

Note: The figures refer to the percentage of countries (among those reporting the respective species) in which the respective stakeholder group operates breeding programmes averaged over seven species/categories, i.e. the "big five" species (cattle, sheep, goats, pigs and chickens), with the three categories of cattle breeds (dairy, beef and multipurpose) treated separately. Source: Country reports, 2025.

Whichever stakeholder group leads a breeding programme, a number of functions need to be in place. These include defining breeding goals, identifying animals, recording performance, providing artificial insemination services and carrying out genetic evaluation. Together, these functions can be regarded as the main building blocks of breeding programmes. Some of them may also serve wider livestock-sector purposes. Animal identification, for example, can contribute to disease control and livestock administration, while recording can support herd or flock management (FAO, 2015). Countries were therefore asked not only whether these activities existed, but also which stakeholder groups were involved in carrying them out. The reported scores for stakeholder involvement in these activities are summarized in Figure 2C2 for ruminants and monogastrics. In general, governments, research organizations, breeders' associations and individual breeders or livestock keepers are reported as the main actors across most activities. In ruminants, governments are especially prominent in animal

identification, breeders’ associations in breeding goals and recording, and research organizations in genetic evaluation. In monogastrics, commercial companies play a more visible role than in ruminants, especially in breeding goals, recording and artificial insemination. NGOs remain relatively less involved across the activities shown.

Figure 2C2. Stakeholder involvement in breeding-related activities in ruminants and monogastrics – global averages

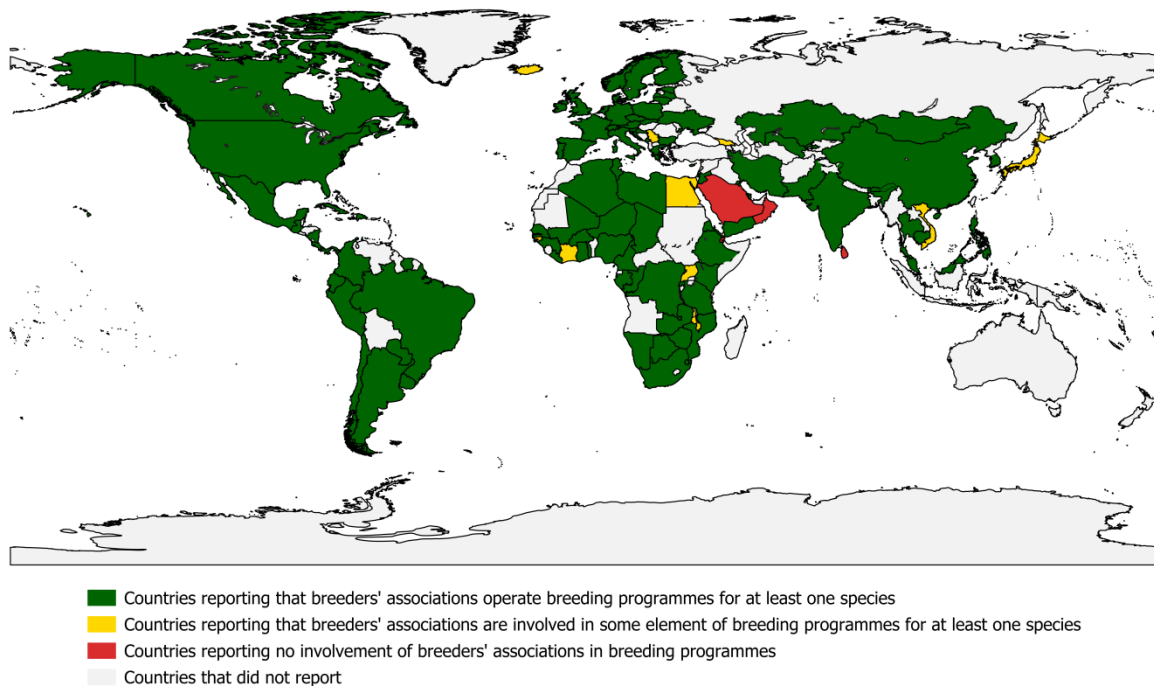


Note: Countries provided scores (at species level) for the level of stakeholder involvement in each activity. Answering the question was optional (the number of responses varied from species to species). The scores were converted into numerical values (none = 0; low = 1; medium = 2; high = 3). The figures shown are global averages for the respective groups of species. Source: Country reports, 2025.

Figure 2C3 shows the distribution of countries in which breeders’ associations are reported either as operators of breeding programmes or as participants in one or more breeding-programme elements. The map suggests that breeders’ associations are involved in breeding activities in a large share of reporting countries, and in many of these countries they are reported as taking an operational role rather than only contributing to specific elements. Compared with the previous reporting round, this points to a broader reported role for breeders’ associations, including in parts of Africa, Asia and the Near East where their role appeared more limited before (FAO, 2015; Country reports, 2025). As with the earlier report,

630 however, the distinction between operating a breeding programme and being involved in some of its
 631 elements may not have been understood in exactly the same way by all reporting countries.

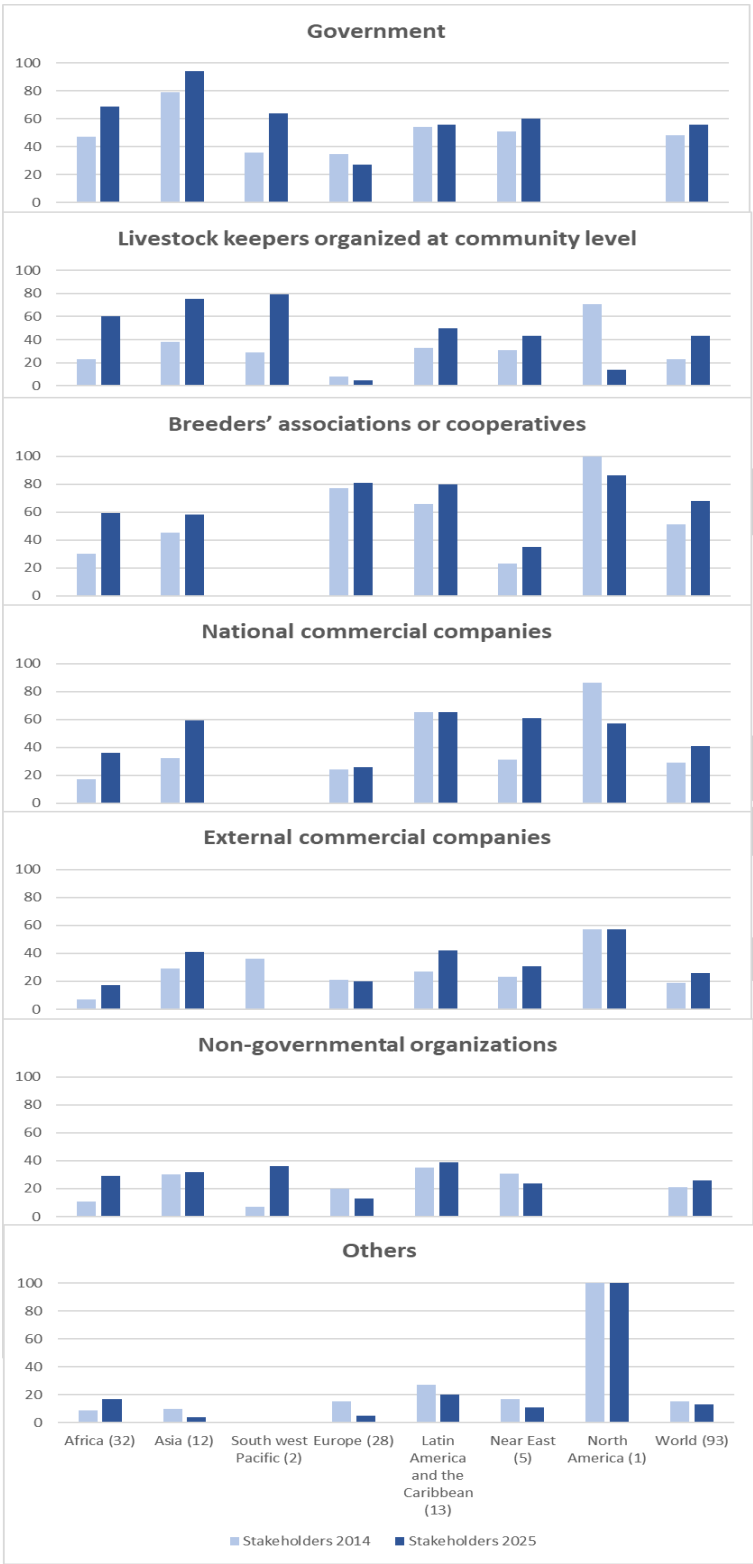
632 **Figure 2C3. Involvement of breeders' associations in breeding programmes and elements of**
 633 **breeding programmes**



634
 635 *Source: Country reports, 2025.*
 636

637 The comparison between 2014 and 2025 points to a broader mix of stakeholder groups being reported
 638 as operators of breeding programmes in many regions. Increases are particularly visible for
 639 governments, livestock keepers organized at community level, breeders' associations or cooperatives,
 640 and national commercial companies. The change is especially noticeable in Africa and Asia for
 641 community-level structures and breeder organizations. At the same time, the overall regional pattern
 642 remains similar, with breeders' associations most prominent in Europe and North America, and
 643 governments continuing to play a stronger role in Africa, Asia and the Near East (Figure 2C4). NGOs
 644 and other actors remain less frequently reported in most regions.
 645

646 **Figure 2C4: Comparison of the reported proportion of countries in which different stakeholder**
 647 **groups operate breeding programmes for the main livestock species, 2014 and 2025**



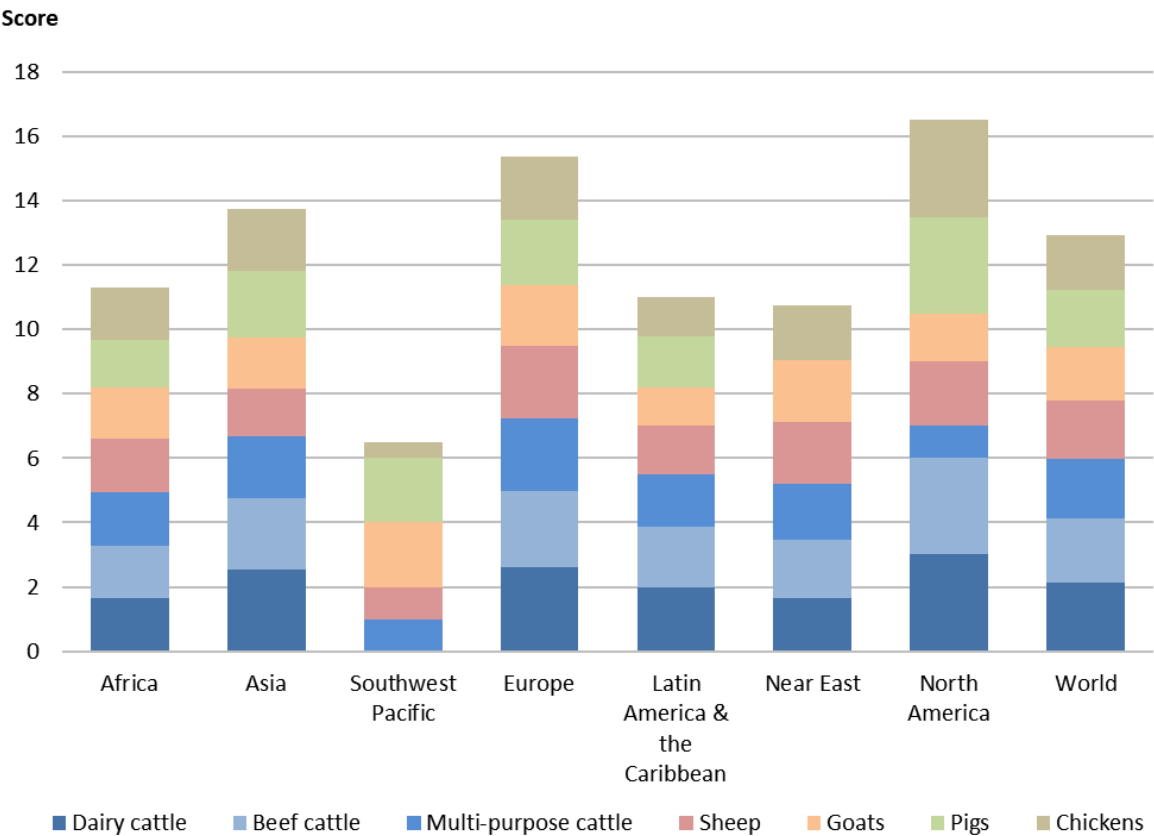
Note: For comparability, the results are based only on the 93 countries that reported in both rounds. Countries that reported in only one round were excluded from the comparison.

Source: Country reports, 2025.

5. Educational, research and organizational capacities

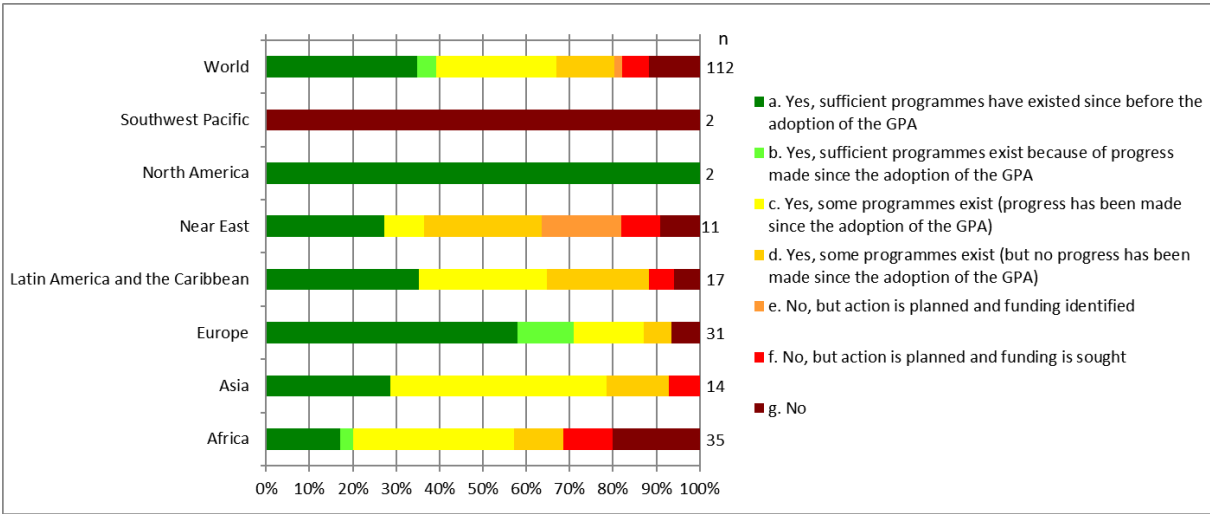
The development and operation of breeding programmes depend on technical knowledge, institutional support and effective organization among the stakeholders involved. In many countries, limited knowledge and weak service provision continue to constrain breeding activities. General information on education and training in the field of animal genetic resources is discussed in Part 3, Section A. Countries were also asked, more specifically, to score the state of education and training in the field of animal breeding. The responses are summarized in Figure 2C5. The results indicate that the provision of training in animal breeding remains uneven across regions. North America and Europe report the highest overall levels, while Africa, the Near East and, in particular, the Southwest Pacific report lower levels of provision. The world total also remains well below the potential maximum, indicating that substantial gaps in training capacity persist across species and regions. Asia records intermediate-to-high scores, while Latin America and the Caribbean is below Asia and Europe but above the lowest-scoring regions.

Figure 2C5. State of training in the field of animal breeding



Note: Each country provided a score for the level of provision with respect to each species. The scores were converted into numerical values (none = 0; low = 1; medium = 2; high = 3) and an average score calculated for the respective species × region combinations (countries where the respective species was not reported to be present were excluded from the calculations). The length of each bar corresponds to the cumulative average scores across all species for the respective region. The maximum potential score is 21 (3×7).
Source: Country reports, 2025.

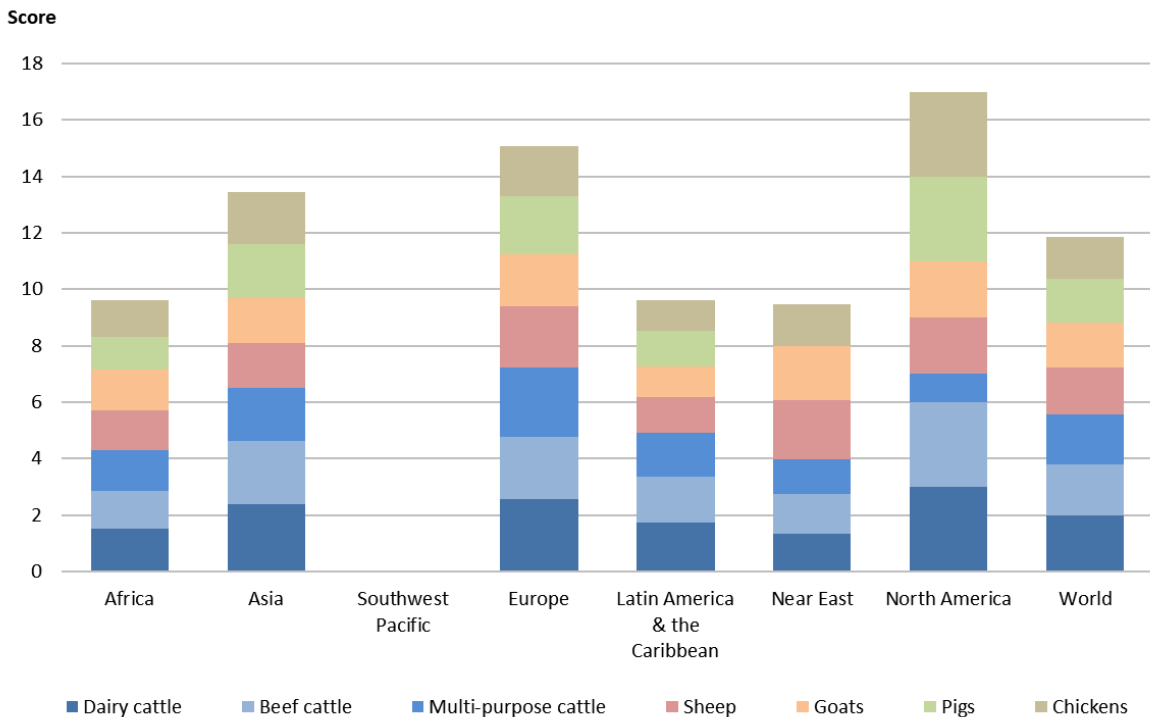
Figure 2C6. State of implementation of training and technical support programmes for the breeding activities of livestock-keeping communities



Note: The country-report questionnaire required countries to respond to the following question: “Have training and technical support programmes for the breeding activities of livestock-keeping communities been established or strengthened in your country?”
Source: Country reports, 2025.

A similar picture is seen from the responses on the implementation of training and technical-support programmes for the breeding activities of livestock-keeping communities (Figure 2C6). Europe and North America report the strongest implementation status, while Africa and the Near East show a larger share of countries reporting only partial provision or no provision. The Southwest Pacific stands out as the region with the lowest in this regard. At global level, the results suggest that many countries have made some progress, but full and adequate provision remains far from universal.

Figure 2C7. State of research in the field of animal breeding



Note: Each country provided a score for the level of provision with respect to each species. The scores were converted into numerical values (none = 0; low = 1; medium = 2; high = 3) and an average score calculated for the respective species × region combinations (countries where the respective species was not reported to be present were excluded from the

calculations). The length of each bar corresponds to the cumulative average scores across all species for the respective region. The maximum potential score is 21 (3×7).
Source: Country reports, 2025.

Countries were also asked to report on the state of research activities in the field of animal breeding. The responses are summarized in Figure 2C7. As in the case of training, the reported level of research activity remains substantially below the maximum possible score of 21, indicating important gaps in research capacity across species and regions. Scores are highest in North America and Europe, followed by Asia, while Africa, Latin America and the Caribbean, and the Near East report lower levels. This pattern suggests that research capacity remains clustered in a limited number of regions, with possible implications for the coverage of different production systems and species.

A comparison of the 2014 and 2025 scores (Table 2C5) indicates that the state of research slightly improved in all regions but Southwest Pacific, with the largest increase reported by Near East, and smaller increases reported in Europe, Latin America and the Caribbean and North America. The pattern for training is relatively similar, with the largest increase reported by Near East, and Europe and Latin America and the Caribbean reporting no improvement. In general, the comparison suggests some improvement since the previous reporting round, but also confirms that progress has been uneven across regions.

Table 2C5. Comparison of regional scores for the state of training and research in the field of animal breeding, 2014 and 2025

	Number of countries	Research			Training		
		2014	2025	Δ	2014	2025	Δ
Africa	32	1.0	1.3	0.4	1.2	1.6	0.4
Asia	12	1.6	2.0	0.4	1.8	2.0	0.3
Southwest Pacific	2	0.3	0.0	-0.3	0.9	1.1	0.2
Europe	28	2.1	2.2	0.0	2.2	2.2	0.0
Latin America and the Caribbean	13	1.3	1.4	0.1	1.6	1.6	0.0
Near East	5	1.3	1.8	0.6	1.2	1.8	0.6
North America	1	2.4	2.6	0.1	2.3	2.6	0.3
World	93	1.5	1.7	0.2	1.6	1.9	0.2

Note: This comparison is based on the country reports of 93 countries that reported for both the second and third SoW-AnGR reports. Scores range from 0 to 3, where 0 = none, 1 = low, 2 = medium, and 3 = high.

For comparability, the results are based only on the 93 countries that reported in both rounds. The colour scale ranges from yellow (−0.3, indicating a slight decline in the state of research or training) to average green (+0.66, indicating a slight to average improvement in the state of research or training).
Source: Country reports, 2014, 2025.

Breeding programmes depend not only on technical knowledge and institutional support, but also on the extent to which livestock keepers are organized to participate in breeding activities. Countries were therefore asked to report on the level of livestock-keeper organization with respect to animal breeding, taking into account the various elements of breeding programmes. The responses are summarized in Table 2C6. The highest scores are reported in North America and Europe, while Africa reports the lowest overall levels. Asia and Latin America and the Caribbean show intermediate values, whereas the Near East is generally slightly below these regions. The Southwest Pacific shows a mixed pattern, with very low or zero scores for some species and relatively high scores for others. At world level, average scores range from 1.5 for goats and chickens to 1.9 for dairy cattle, indicating that the organization of livestock keepers for breeding remains moderate rather than strong in most regions.

Table 2C6. Level of organization of livestock keepers with respect to animal breeding activities

Regions	Dairy cattle	Beef cattle	Multi-purpose cattle	Sheep	Goats	Pigs	Chickens
Africa	1.1	1.0	1.0	1.2	1.2	1.1	1.2
Asia	1.9	1.9	1.4	1.3	1.2	1.7	1.9
Southwest Pacific		0.0	1.0	1.0	3.0	2.0	0.0
Europe	2.8	2.6	2.6	2.5	2.1	2.3	1.8
Latin America & the Caribbean	1.9	1.8	1.5	1.4	1.3	1.5	1.4
Near East	1.6	1.2	1.4	1.5	1.4		1.5
North America	3.0	3.0	2.0	3.0	2.5	3.0	3.0
World	1.9	1.8	1.6	1.7	1.5	1.7	1.5

Note: Each country provided a score for the level of organization with respect to each species. The scores were converted into numerical values (none = 0; low = 1; medium = 2; high = 3). The figures shown in the table are average scores for the countries of the respective region.

Source: Country reports, 2025.

6. Breeding methods and activities

An overview of the status of breeding programmes is presented above (Subsection 2). This subsection looks more closely at the extent to which the main elements of breeding programmes are being implemented and at the types of programmes reported to be in operation, in particular the prevalence of programmes involving cross-breeding. Countries were asked to indicate, separately for exotic and locally adapted breed populations, whether breeding goals had been defined and whether the following activities were being implemented: animal identification, pedigree recording, performance recording, artificial insemination, genetic evaluation using the classic approach, genetic evaluation including genomic information, and management of genetic variation. The findings are presented in Table 2C7 (regional breakdown) and Table 2C8 (species breakdown).

Table 2C7. Level of implementation of breeding-programme elements and techniques - regional breakdown

Regions	Number of national breed populations		Animal identification (%)		Pedigree recording (%)		Performance recording (%)		Artificial insemination (%)	
	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted
Africa	709	765	48	50	26	34	31	33	37	35
Asia	360	1078	42	72	37	57	28	27	29	28
Southwest Pacific	10	22	80	23	10	0	0	0	50	0
Europe	1369	1463	82	106	64	85	68	99	44	35
Latin America & the Caribbean	690	314	66	64	48	45	52	45	48	49
Near East	137	220	74	48	51	28	39	28	47	18
North America	57	264	37	100	36	68	37	77	37	76
World	3332	4126	65	79	48	60	51	58	41	35
Regions	Number of national breed populations		Breeding goal defined (%)		Genetic evaluation (classic approach) (%)		Genetic evaluation including genomic information (%)		Management of genetic variation (%)	
	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted
Africa	709	765	45	43	16	28	7	6	15	26
Asia	360	1078	31	42	19	26	8	3	13	18
Southwest Pacific	10	22	20	0	0	0	0	0	0	0
Europe	1369	1463	82	73	50	46	23	22	37	59
Latin America & the Caribbean	690	314	36	43	25	40	16	34	16	7
Near East	137	220	47	34	35	27	23	5	28	30
North America	57	264	37	78	36	56	36	23	0	11
World	3332	4126	57	54	33	36	17	14	24	33

Note: The figures refer to the proportion of breeds (national breed populations) belonging to the big five species (cattle, goats, sheep, pigs and chickens) covered by the respective breeding-programme elements and techniques. They provide no indication of population coverage within breeds.

Source: Country reports, 2025.

Table 2C8. Level of implementation of breeding-programme elements and techniques - species breakdown

Species	Number of national breed populations		Animal identification		Pedigree recording		Performance recording		Artificial insemination	
	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted
	(%)									
Dairy cattle	301	198	74	83	58	63	62	73	70	89
Beef cattle	641	511	86	81	62	61	71	69	77	68
Multipurpose cattle	175	486	89	100	47	100	65	100	70	52
Sheep	702	997	79	81	60	54	63	62	30	24
Goats	329	589	63	75	46	47	49	47	32	23
Pigs	372	455	67	76	47	63	51	56	53	46
Chickens	812	890	28	50	26	44	17	26	5	10
Species	Number of national breed populations		Breeding goal defined		Genetic evaluation (classic approach)		Genetic evaluation including genomic information		Management of genetic variation	
	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted
	(%)									
Dairy cattle	301	198	51	74	44	61	24	40	31	44
Beef cattle	641	511	66	65	44	52	29	29	32	37
Multipurpose cattle	175	486	62	41	30	32	21	18	23	33
Sheep	702	997	57	59	45	42	20	12	25	39
Goats	329	589	47	48	28	28	12	10	23	32
Pigs	372	455	52	59	37	46	18	25	29	38
Chickens	812	890	55	48	12	17	3	10	11	21

Note: The figures refer to the proportion of breeds (national breed populations) covered by the respective breeding-programme elements and techniques. They provide no indication of population coverage within breeds.

Source: Country reports, 2025.

The figures presented in the tables indicate that important gaps remain in the implementation of breeding-programme elements. Basic activities such as animal identification, pedigree recording and performance recording are more widely reported than the more advanced elements, but none of them approaches full coverage across reported breed populations. As in the previous report, the implementation of genetic evaluation, especially evaluation including genomic information, remains much less widespread than the more basic programme components (FAO, 2015; Country reports, 2025). The regional breakdown shows that Europe and North America generally report the highest levels of coverage for the core programme elements, while Africa, Asia and the Near East tend to report lower levels for several activities. Artificial insemination is a partial exception to this pattern, with relatively high reported coverage in some regions outside Europe and North America. The Southwest Pacific shows a highly uneven pattern across elements, reflecting the small number of reported breed populations in the region. At world level, locally adapted populations are reported more often than exotic populations for several of the basic elements, including animal identification, pedigree recording and performance recording (Country reports, 2025).¹ This pattern may reflect, in part, the fact that some exotic populations benefit from breeding work carried out outside the reporting country, while locally adapted populations depend more directly on national or local action.²

The species breakdown shows that the highest reported coverage for most programme elements is found in cattle populations, particularly dairy and beef cattle. Multipurpose cattle also show relatively high coverage for several activities, especially among locally adapted populations. Sheep, goats and pigs are generally at intermediate levels, while chickens tend to have the lowest reported coverage across most activities. Artificial insemination is most widely reported in cattle populations and is much less common in sheep, goats and chickens. Breeding goals are reported for a substantial share of populations, but far from all, especially in some locally adapted populations. Management of genetic variation and the use of genomic information remain limited in most species, although locally adapted dairy cattle, beef cattle

¹ Results for the Southwest Pacific should be interpreted with caution because they are based on a very small number of reported national breed populations.

² Some locally adapted breeds are present in more than one country. However, international exchange of improved breeding animals and germplasm is dominated by a limited number of widely used transboundary breeds. For local breeds confined to one country, importing genetic material is generally not an option for straight-breeding improvement.

and pig populations show somewhat higher reported coverage than many other categories (Country reports, 2025).

Countries were also asked to indicate the prevalence of breeding programmes involving straight/pure-breeding only and those involving both straight/pure-breeding and cross-breeding. The responses are summarized in Tables 2C9a and 2C9b. As in the case of the overview figures presented above, the results should be interpreted with some caution, because the term “breeding programme” may have been applied by countries to activities of varying scope and structure (FAO, 2015; Country reports, 2025).

Table 2C9a. Proportion of breeds reported to be subject to breeding programmes applying straight/pure-breeding and cross-breeding

Regions	Dairy cattle (%)		Beef cattle (%)		Multipurpose cattle (%)		Sheep (%)		Goats (%)		Pigs (%)		Chickens (%)	
	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted
Africa	64	70	82	65	90	37	49	56	59	62	47	58	31	42
Asia	46	37	26	8	45	16	20	16	86	7	45	25	27	10
Southwest Pacific	n/r	n/r	0	0	100	0	50	0	0	100	150	25	0	0
Europe	38	30	37	19	34	10	25	12	27	8	44	29	15	20
Latin America and the Caribbean	44	45	46	38	85	91	42	55	63	40	39	40	54	45
Near East	54	42	17	50	38	70	16	62	19	52	n/r	n/r	40	11
North America	0	95	0	61	0	0	0	95	0	82	0	74	0	100
World	49	55	48	46	65	27	28	28	53	29	49	37	25	24

Table 2C9b. Proportion of breeds reported to be subject to breeding programmes applying straight/pure-breeding only

Regions	Dairy cattle (%)		Beef cattle (%)		Multipurpose cattle (%)		Sheep (%)		Goats (%)		Pigs (%)		Chickens (%)	
	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted	Exotic	Locally adapted
Africa	45	52	35	48	52	29	35	56	30	35	33	39	35	30
Asia	38	126	12	82	85	84	34	80	28	91	28	81	19	91
Southwest Pacific	n/r	n/r	0	0	0	0	50	0	0	0	0	0	33	0
Europe	51	88	69	86	70	325	72	79	85	92	54	72	65	59
Latin America and the Caribbean	12	51	27	44	43	48	16	46	17	21	31	21	8	9
Near East	38	33	17	50	0	17	16	32	19	42	n/r	n/r	28	24
North America	0	45	0	39	0	0	89	5	0	18	0	26	0	0
World	40	68	46	59	54	122	54	68	44	67	39	62	42	60

"n/r" means that no breed was reported under a breeding programme while 0 means that no breed was reported under cross-breeding

Note: n/a indicates that no breed belonging to the respective species and breed category is reported from the respective region. The term “breeds” in the heading refers to national breed populations.

Source: Country reports, 2025.

The tables show that both straight/pure-breeding and programmes involving cross-breeding are reported across all regions and species, although their relative prevalence varies considerably. At world level, programmes involving both straight/pure-breeding and cross-breeding are reported relatively often for cattle, goats and pigs, while straight/pure-breeding only is also widely reported, particularly for locally adapted populations. In several regions, especially Africa, Latin America and the Caribbean, and the Near East, locally adapted populations are frequently reported as being included in programmes that combine straight/pure-breeding with cross-breeding. This suggests that cross-breeding remains an important feature of breeding strategies in many production systems. At the same time, the tables do not show how systematically these strategies are designed or implemented, nor the extent to which their impacts are monitored.

7. Breeding policies

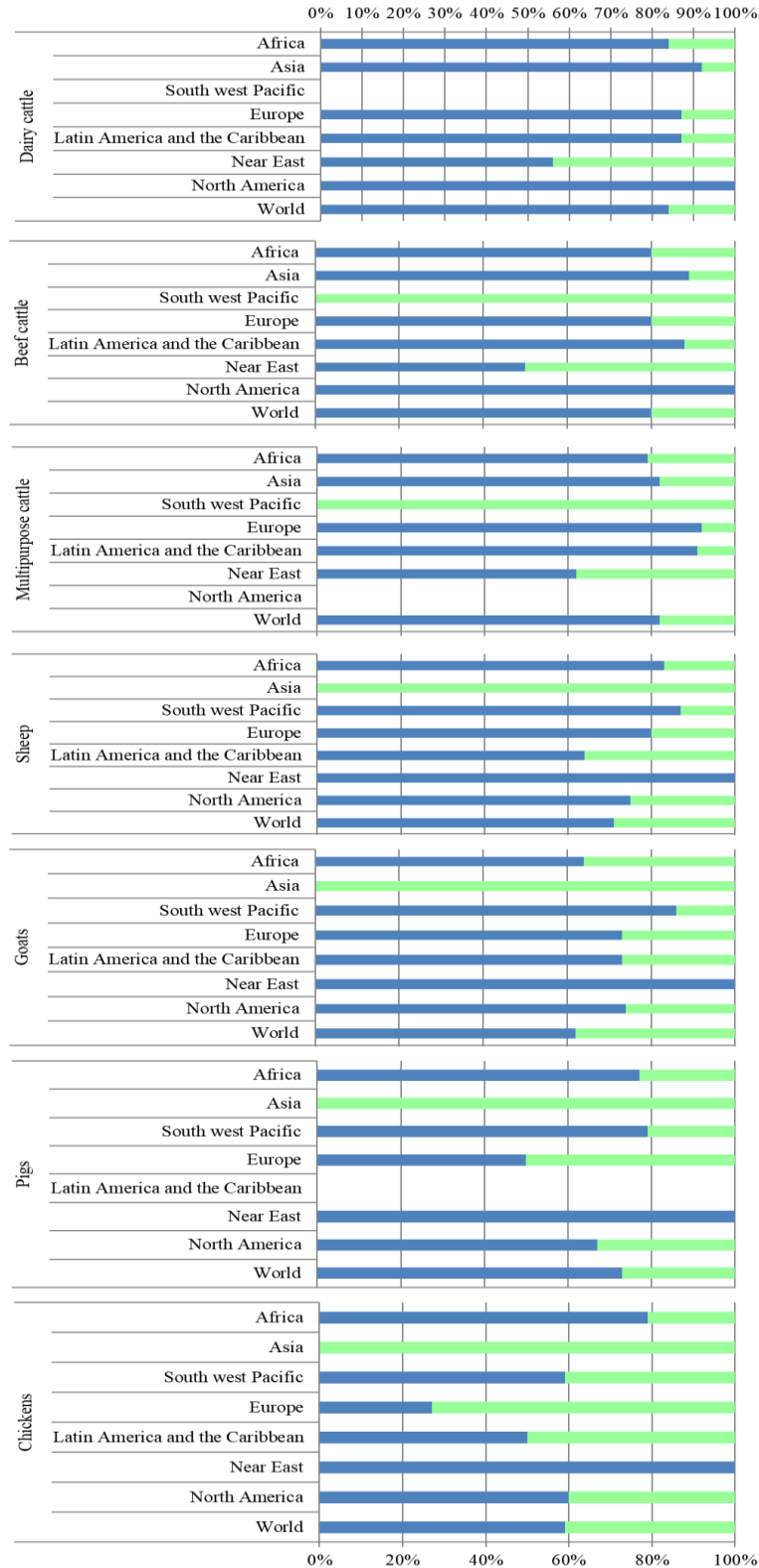
A majority of countries report that they have policies or programmes in place to support breeding programmes or influence their objectives (Figure 2C8). The current results show that this combined presence of breeding programmes and supporting policies or programmes is most widespread in cattle, particularly dairy, beef and multipurpose cattle, while coverage is generally lower in sheep, goats, pigs and especially chickens. In all species, some countries also report breeding programmes in the absence of supporting policies or programmes, while cases in which policies or programmes are reported without breeding programmes are limited or absent in most region-species combinations.

As in the previous reporting round, there are clear regional differences. North America reports full coverage for most species, while Asia and Europe also show broad coverage across several cattle

categories. Latin America and the Caribbean reports relatively strong coverage in cattle, but more mixed patterns in sheep, goats, pigs and chickens. In Africa, the proportion of countries reporting both breeding programmes and supporting policies or programmes is relatively high in cattle and lower in some of the other species. In the Near East, coverage is uneven across species, with stronger reporting in sheep, goats, pigs and chickens than in some cattle categories. The Southwest Pacific continues to show a narrow and uneven pattern, reflecting the small number of reporting countries and the limited scale of breeding activity in the region.

The reported policies and programmes vary in their objectives and in the extent to which they appear to shape breeding practice. In some countries, they mainly provide a general framework for identification, recording, genetic improvement and dissemination of breeding material. In others, they are more directly linked to specific strategies, including the use of exotic breeds, cross-breeding or support for locally adapted breeds. As noted elsewhere in this section, the consequences of such policies depend greatly on how well they are designed and implemented. In particular, where the use of exotic germplasm and cross-breeding is promoted without adequate safeguards, there is a risk of erosion of locally adapted breeds. National breeding policies and programmes are discussed further in the regional overviews below. This is consistent with the Global Plan of Action for Animal Genetic Resources, which calls for long-term sustainable-use policies and breed development strategies that maintain genetic diversity, and with more recent evidence showing that breeding policies are most effective when they are linked to organized recording, clear breeding objectives and sustained stakeholder support (FAO, 2007; Haile *et al.*, 2023).

Figure 2C8. Proportion of countries reporting breeding programmes and policies supporting breeding programmes



Note: Proportions refer to the proportion of countries reporting the respective species, i.e. countries not reporting the respective species are excluded from calculations.
Source: Country reports, 2025.

8. Regional overviews

8.1. Africa

Breeding programmes in Africa continue to rely heavily on the public sector, although the current results indicate a broader institutional mix than in the previous reporting round. Governments remain the most frequently reported operators of breeding programmes in the region, but livestock keepers organized at community level and breeders' associations are also now reported relatively often. Even so, the regional pattern across the earlier sections of this chapter suggests that organizational capacity, training and research support remain weaker in Africa than in most other regions, and this is reflected in the generally lower coverage of several breeding-programme elements (Country reports, 2025).

Breeders' associations still appear to play a smaller role in much of Africa than in Europe or North America, although their importance is increasing in some countries. The country reports suggest considerable diversity within the region. South Africa reports a relatively advanced role for breed societies in setting standards and supporting recording and evaluation, while Rwanda indicates that breeders' associations participate in livestock-sector coordination and contribute, albeit on a limited scale, to breeding-goal setting, animal identification, recording and artificial insemination. In several other countries, however, public institutions still carry most breeding functions and breeder participation remains weak. Constraints reported by countries repeatedly include limited funding, weak recording systems, shortage of technical personnel and low farmer participation in organized breeding activities. At the same time, community-based breeding programmes have become one of the most important alternatives to centralized or import-based models in African smallholder systems (Tebourbi *et al.* 2024). Evidence from eastern and southern Africa indicates that such programmes have been used to improve local breeds while maintaining adaptation to local conditions, especially in small ruminants, but that their continuity depends on sustained data recording, advisory support, governance and market linkages (Haile *et al.* 2023; Belay *et al.* 2024)

Cross-breeding with exotic breeds remains widely reported across the region, often as part of efforts to raise milk or meat output rapidly. The current results suggest, however, that breeding strategies in Africa are not limited to cross-breeding alone: locally adapted populations are also reported to have substantial coverage for several programme elements, especially animal identification and performance recording. This points to growing recognition that improvement of local breeds and better organization of livestock keepers are both needed if breeding programmes are to become more sustainable in African production systems (Country reports, 2025).

8.2. Asia

Breeding programmes in Asia remain strongly influenced by the public sector, and the current results confirm high reported programme presence for the main livestock species across the region. Governments are the most frequently reported operators, but livestock keepers organized at community level, breeders' associations and national commercial companies are also reported to play substantial roles. This suggests that, while public institutions remain central, implementation models are diverse and vary widely across subregions and species (Country reports, 2025).

The country reports confirm this diversity. India reported a coordinated involvement of government, research institutions and non-governmental organisations, which jointly deliver AI and animal health services, design breeding and conservation programmes, and provide advisory support through a nationwide network of animal husbandry agencies (Box 2C3). Bhutan reports that the Department of Livestock and research organizations are involved in all major breeding functions, but also notes that

animal recording and genetic evaluation are still carried out only on a small scale. Malaysia reports that most ruminant nucleus farms are government managed, whereas poultry and pig breeding are largely handled by the private sector and depend heavily on imported parent and grandparent stock. Mongolia reports species-specific breeding strategies that combine improvement and conservation objectives for native breeds. Together, these examples support the view of a region where public leadership is strong, but actual breeding arrangements vary greatly across countries and livestock sectors (Country reports, 2025). In parts of Asia, especially where rapid increases in livestock output are a policy priority, cross-breeding with imported high-output germplasm continues to play a major role. At the same time, the current results show that the region reports relatively strong organizational, training and research capacities compared with most developing regions, which may partly explain the widespread reporting of breeding programmes and programme elements. Even so, the challenge of organizing breeding activities among large numbers of smallholders remains important in many countries, particularly where breeder organizations are still weak or fragmented (Country reports, 2025).

Box 2C3. India: continued public investment in indigenous bovine breeding

India illustrates the strong public-sector role that still characterizes much of Asia's breeding landscape. The Rashtriya Gokul Mission continues under the broader livestock-development framework and supports the development and conservation of indigenous bovine breeds through progeny testing, pedigree selection, genomic selection and support to semen stations. A 2024 government release reported that, in Gujarat, progeny testing was being implemented for Gir cattle and Mehsana buffaloes, while pedigree selection covered Kankrej cattle and Jaffarabadi and Banni buffaloes. These features are consistent with the current chapter results, which show a strong role for governments and structured public support in Asian breeding programmes.

Source: India, Ministry of Fisheries, Animal Husbandry & Dairying (2024)

8.3. Southwest Pacific

The Southwest Pacific continues to show a sharp contrast between highly developed breeding systems in large livestock-exporting countries and much more limited breeding activity in the smaller island states. In the current results, the region is represented by very few reporting countries and very small numbers of national breed populations, and this is reflected in the uneven regional pattern across programme elements and capacity indicators. In practical terms, this means that the region combines cases where breeding programmes are long established and technically sophisticated with others where breeding activities remain limited, government-led or focused mainly on importation and dissemination of exotic genetic material (Country reports, 2025). For example, the country reports indicate that Tonga uses government stations and imported superior stock to avoid inbreeding and improve local populations, especially in pigs and poultry. The Cook Islands notes that breeding activities depend heavily on government support and external inputs, and that technical personnel, infrastructure and continuity of funding remain major constraints. This is consistent with the current data, which suggest that livestock-keeper organization and programme-element coverage in the region are highly variable depending on the activity considered. This uneven pattern also suggests that, in the smaller island countries, multiplication, dissemination and carefully managed cross-breeding may be more common than complete breeding schemes covering all programme elements. In such settings, independent national breeding programmes may not always be the most practical approach (Country reports, 2025).

8.4. Europe

Europe remains the region in which breeders' associations or cooperatives are most strongly reported as operators of breeding programmes. The current results also show high levels of training, research and

livestock-keeper organization, together with relatively high coverage of many breeding-programme elements. Governments appear to play more of a supervisory, regulatory or support role than a direct operational role in many countries, while breeder organizations, research bodies and private breeding companies together provide the main institutional framework for programme delivery (Country reports, 2025). In the country reports, Austria reports that breeders' associations issue official ear tags or microchips, breeders register animals in national central databases, and data, including genomic information in some species, feed into breeding-value estimation. Ireland reports that breed societies manage herd books and breeding strategies, while government oversees compliance and supports national databases and research. These examples fit closely with the broader regional pattern of breeder-led implementation supported by strong technical infrastructure and public oversight. Commercial companies remain especially important in pigs and poultry, and in some dairy sectors, while breeder organizations continue to be central for many cattle, sheep and goat breeds. At the same time, the region still includes some countries where breeding activities are less developed and where the organizational role of breeders' associations is weaker. As in the previous report, imported genetics continue to shape parts of the livestock sector, but many countries also maintain explicit conservation or support measures for local breeds, especially where these remain important for marginal environments or specialized products (Country reports, 2025).

8.5. Latin America and the Caribbean

In Latin America and the Caribbean, breeding programmes continue to be implemented through a relatively diverse set of institutional arrangements. The current results show comparatively strong roles for breeders' associations and commercial companies, alongside government involvement and, in some contexts, community-level organization. This makes the region more mixed institutionally than Africa, Asia or the Near East. As in earlier assessments, the Caribbean generally appears less developed than Central and South America in terms of programme coverage and capacity, while much of mainland Latin America reports stronger breeder organizations, more active research support and broader private-sector participation (Country reports, 2025).

The country reports show this diversity clearly. Argentina reports organized genetic-evaluation programmes for major cattle breeds led by breeders' associations with technical support from INTA and universities, and also describes a public-private bee improvement programme based on locally adapted material. Costa Rica reports that its National Genetic Evaluation Programme for purebred cattle is led by the livestock corporation with technical support from research institutions and breeders' associations. Panama, by contrast, reports the absence of a clear national genetic-improvement programme and notes that research bodies, associations and producers often carry much of the practical work. These differences illustrate the wide range of institutional arrangements through which breeding activities are being implemented in the region. Cross-breeding remains widely used across the region, especially in cattle. At the same time, the current results suggest that breeding-programme elements are more widely implemented in several cattle categories than in small ruminants or chickens, and that commercial companies play a particularly important role in some species. Public research institutions also continue to be important, especially in genetic evaluation and technical support (Country reports, 2025). Peru provides a recent example of breeding support for a non-major but regionally important species. AGRO RURAL reported in January 2025 that, through its alpaca genetic-improvement project, 222 male breeding alpacas were acquired in 2024 and 11 000 technical assistance visits were carried out for producers in high-Andean regions. Government information also links the programme to broader efforts to improve fibre quality, productivity and producer support in Arequipa, Puno, Cusco, Huancavelica, Ayacucho, Pasco and Junín. This fits the wider Latin American pattern of mixed public, technical and producer support for breeding activities, including in species outside the main cattle, pig and poultry sectors (Peru, Programa de Desarrollo Productivo Agrario Rural, 2025).

8.6. North America

North America continues to report highly developed breeding systems, strong livestock-keeper organization and the highest or near-highest regional scores for training and research. The current results also show very high programme presence across most of the main livestock species and very high coverage of many breeding-programme elements, especially in cattle. Breeders' associations and commercial companies remain especially prominent, while governments appear less important as direct operators than in most other regions (Country reports, 2025).

In the country report, the United States states that breeding decisions are made largely by individual breeders, breed associations and commercial actors, while breed associations support pedigree, phenotype and genotype recording and breeding-value estimation. Canada likewise reports defined roles for breed organizations, third-party evaluators, commercial AI providers and government, although some sectors still face cost and scale constraints. These observations fit the broader view of highly developed but mostly industry-led breeding systems in the region. The region also remains at the forefront of genomic tools in livestock breeding. In the United States, GS in dairy cattle has been associated with a doubling of the rate of genetic gain and the use of evaluations for more than 50 traits (Wiggins & Carrillo, 2022). In Canada, Lactanet reported in 2024 that the country had completed 15 years of GS and that its database had exceeded 8 million genotypes (Sweett, 2024). These developments fit well with the current chapter results, which show North America among the strongest regions for research, training and advanced programme elements.

8.7. Near and Middle East

The country reports indicate that breeding programmes in the Near East are characterized by strong public-sector involvement and are mainly found in a limited number of species and activities. Governments are still the most frequently reported operators, and programme activity appears to be concentrated in a limited number of species, notably sheep and goats (Country reports, 2025). For example, Oman reports that the ministry plays the leading role in policy, breeding support and the distribution of improved males for sheep and goats, while also planning molecular characterization and breed databases. Jordan highlights that the lack of farm-level record keeping remains a key constraint to scaling breeding programmes nationally. Current efforts focus on an elite Awassi nucleus flock at NARC, supplying improved genetics to producers, alongside AI-based dissemination using elite sire semen. Recent studies also indicate growing interest in more structured breeding strategies for Awassi sheep and Shami goats, including improved data systems, performance recording and systematic genetic dissemination (CGIAR, 2024; Al-Atiyat *et al.*, 2026). In Iran, government led programmes have largely supported improvement of indigenous breeds (see Box 2C4). Together, these examples point to a region in which breeding efforts remain strongly public-sector led, with persistent gaps in recording, farmer participation and broader institutional coordination.

Box 2C4. Capacity building for the indigenous Khuzestani buffalo: from breeding nucleus to adoptable intensive farming systems

In the hot lowlands of Khuzestan, where water buffaloes have supported rural livelihoods for generations, a valuable indigenous genetic resource has remained largely underutilized. To address this gap, a project established the first structured buffalo breeding nucleus in the region, specifically designed for the Khuzestani buffalo and adapted to local environmental and management conditions.

The programme integrates genetic improvement with a practical, intensive production system suited to real farm conditions. Genetic progress is driven by systematic performance recording and phenotypic selection over four consecutive years, covering milk production and body weight traits at different ages. A multi-trait selection index targets growth performance (average daily gain), milk yield (270-day milk yield), milk components (fat and protein yields), and quality attributes (fat and protein percentages).

(Karimi *et al.*, 2026). Herds are evaluated every six months, breeding catalogues are compiled for all animals, and sires are selected based on the overall index. Together, these herds form an integrated breeding network aimed at the sustainable improvement of the Khuzestani buffalo.

The breeding network currently comprises a 300-head nucleus herd at Safiabad and two participating farmer herds, one with approximately 100 animals (with plans to expand to 500) and another with about 60 animals. Efforts are ongoing to attract additional farmers and investors to further expand the network and accelerate dissemination of improved genetics. To date, the programme has achieved an estimated annual genetic gain of +57 kg in 270-day milk yield, along with increases of +2.134 kg in milk protein yield and +5.553 kg in milk fat yield, indicating balanced improvement in both milk quantity and quality.



In parallel, the project developed and validated a low-cost intensive milking management system. By separating calves from their dams during milking, while ensuring adequate milk intake, calves achieved an average additional body weight gain of 24.6 kg during their first year. Early weaning at three months enabled farmers to market all subsequent milk production. This approach improved calf growth and welfare while significantly increasing farm revenues.

By aligning genetic improvement with practical management and economic feasibility, the project has established a scalable, farmer-driven model. Its uptake by independent producers demonstrates its potential to enhance sustainable breeding programmes, support the conservation of indigenous genetic resources, and strengthen rural livelihoods across Khuzestan.

Provided by Mahmoud Amiri Roudbar, Alireza Jolazadeh

9. Changes since 2005

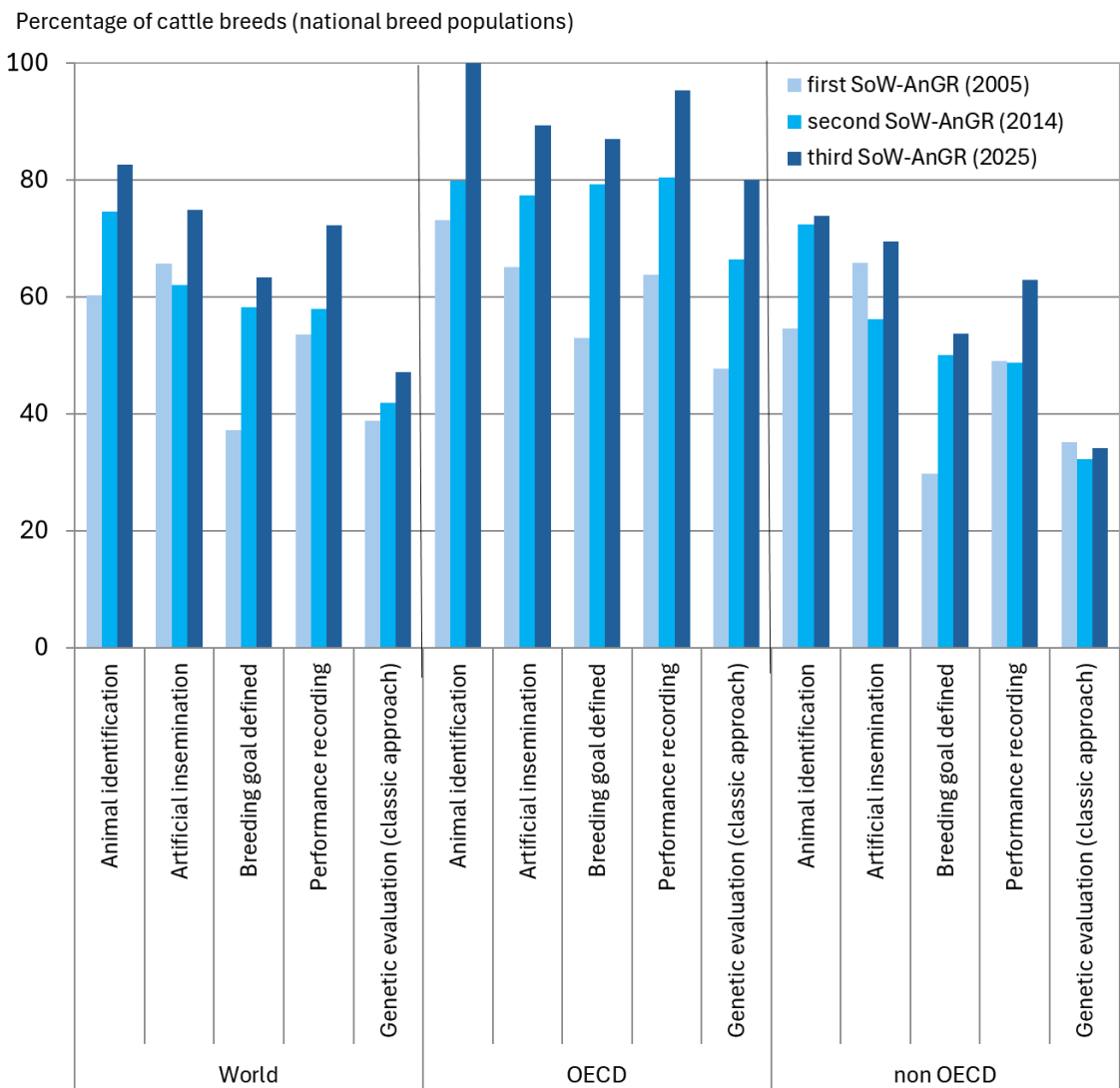
As noted in the introduction to this section, not all of the information presented in this chapter is directly comparable across reporting rounds. However, comparable information is available for a set of key breeding-programme elements in cattle, allowing broad comparison across the first, second and third SoW-AnGR reporting processes. The results are presented in Figure 2C9. Because the first reporting process was not based on a structured questionnaire,³ directly comparable figures are available only for

³ During the first SoW-AnGR process, countries were provided with predefined tables or “tabulation tools”, intended to facilitate the collection and analysis of information during the preparation of their country reports. Some countries included the completed tables in their country reports, while others did not.

a limited number of countries.⁴ At world level, the clearest gains between 2014 and 2025 are seen in animal identification, breeding goals defined, performance recording and genetic evaluation (classic approach). Artificial insemination also increased overall, although less strongly than some of the other activities. This suggests that, over time, breeding programmes for cattle have become more structured, with wider use of the basic organizational and technical elements needed for systematic genetic improvement.

The figure also points to differences between OECD and non-OECD countries. In OECD countries, coverage was already relatively high in 2005 and increased further in 2014 and again in 2025, with particularly strong gains in breeding goals defined, performance recording and genetic evaluation (classic approach). In non-OECD countries, progress is also evident across most activities, especially in animal identification, breeding goals defined and performance recording. However, the increase in genetic evaluation (classic approach) remains more limited than for the more basic programme elements. This pattern suggests that, while substantial progress has been made in establishing the foundations of breeding programmes, expanding the coverage of genetic evaluation remains an important next step, especially outside the OECD group.

Figure 2C9. Implementation of breeding tools in cattle (2005, 2014 and 2025)



Note: The figure is based on information reported by 33 countries (9 OECD and 24 non-OECD) that provided comparable information in the first, second and third SoW-AnGR reporting processes. The figures represent the percentage of cattle breeds

⁴ The comparison presented in Figure 2C8 is based on information reported by 33 countries, comprising 9 OECD countries and 24 non-OECD countries, that provided comparable information across the first, second and third SoW-AnGR reporting processes.

1092 *(national breed populations) in which the respective tools are used. Note that they may be used only in part of the population*
 1093 *within these breeds.*

1094

1095

1096 10. Conclusions and priorities

1097

1098 Breeding programmes are widely reported, but the reported coverage of key breeding-programme
 1099 elements indicates that, in many cases, these programmes are still only partially developed. Important
 1100 gaps remain in breeding goals, recording, genetic evaluation and the management of genetic variation,
 1101 and the presence of a breeding programme does not necessarily imply the existence of a fully organized
 1102 system for genetic improvement. At the same time, as discussed in section 2, the integration of
 1103 technological advances into breeding programmes has progressed rapidly in some sectors, especially in
 1104 highly structured commercial systems, but remains uneven across species and production contexts.

1105

1106 The organization and implementation of breeding programmes continue to differ markedly across
 1107 regions. In Africa, Asia and the Near East, governments remain the most frequently reported operators,
 1108 although community-level structures, breeders' associations and commercial companies are also visible
 1109 in some countries. In Europe and North America, breeding programmes are more often led by breeders'
 1110 associations and commercial companies, supported by stronger technical infrastructure, livestock-
 1111 keeper organization and research capacity. Latin America and the Caribbean remains more mixed, with
 1112 breeder organizations, commercial companies, public institutions and, in some cases, community-based
 1113 structures all contributing to programme delivery.

1114

1115 In many developing countries, however, several of the conditions needed for effective and sustainable
 1116 breeding programmes remain only partly in place. Livestock-keeper organization, training, research
 1117 support and recording systems are still weak in many contexts, limiting the transition from policy
 1118 ambition or isolated breeding activities to programmes that operate systematically and at sufficient scale.
 1119 This also constrains the uptake of newer tools such as GS, precision phenotyping and advanced data
 1120 management, which depend on stronger technical and institutional foundations. At the same time, a
 1121 number of countries report progress in breeder organization, community-based breeding approaches and
 1122 wider implementation of programme elements, suggesting that some of the institutional barriers
 1123 identified in earlier assessments are beginning to be addressed, albeit unevenly.

1124

1125 Many countries report policies or programmes intended to improve livestock breeding, and in a number
 1126 of developing countries these still place strong emphasis on the use of exotic breeds and cross-breeding
 1127 as a way of rapidly increasing output. Such strategies can offer clear short-term advantages, but their
 1128 success depends on planning, monitoring and the existence of complementary breeding-programme
 1129 elements. Where these conditions are weak, there is a risk that the use of exotic germplasm contributes
 1130 to the erosion of locally adapted breeds rather than to sustainable genetic improvement. At the same
 1131 time, many countries increasingly recognize the importance of locally adapted breeds, particularly in
 1132 the context of climate change, disease pressure and the continuing importance of low-input and small-
 1133 scale production systems. Improving these breeds through well-designed breeding programmes
 1134 therefore remains an important priority, but wider progress will depend on stronger local institutions,
 1135 better data systems and sustained stakeholder support.

1136

1137 The evidence also suggests that some progress has been made since previous reporting rounds in the
 1138 implementation of several key programme elements, particularly animal identification, breeding goals
 1139 and performance recording. Even so, major gaps remain in all developing regions, and the expansion of

1140 more advanced elements, especially genetic evaluation including genomic information, remains uneven.
1141 Moreover, the available figures reflect coverage across breeds and do not show how much of each breed
1142 population is actually covered by the activity in question. This means that the practical reach of many
1143 reported activities may still be limited.

1144

1145 As in earlier assessments, the development of effective national breeding strategies remains challenging.
1146 Countries must often balance short-term production goals against longer-term needs related to resilience,
1147 adaptation and the maintenance of genetic diversity. This underlines the continuing importance of better
1148 breed characterization and stronger information on production environments, as well as closer
1149 monitoring of livestock-sector trends and drivers of change. Without such information, it remains
1150 difficult to assess the relative merits of different breeding approaches or to design strategies that are both
1151 productive and sustainable.

1152

1153 Specific priorities will necessarily vary across countries and production systems. Nevertheless, the
1154 information provided in the current reporting round suggests a number of broad priorities: strengthening
1155 capacity at all levels, from livestock keepers to technical personnel and policy-makers; improving
1156 animal identification, recording and genetic evaluation systems; reinforcing livestock-keeper
1157 organization and breeder participation; ensuring that breeding policies are better linked to
1158 implementation; and designing breeding strategies that make more effective use of locally adapted
1159 genetic resources while managing the risks associated with indiscriminate cross-breeding. Future
1160 strategies will also need to give greater attention to resilience, health, welfare and environmental
1161 sustainability alongside productivity. In many countries, greater and more sustained involvement of
1162 livestock keepers remains one of the most important conditions for progress.

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