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Pangenomics in domestic animals: From genomic diversity to precision breeding and conservation

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ABSTRACT

Rapid advances in genome sequencing have transformed livestock genomics from marker-based analysis toward comprehensive characterization of genome-wide variation. However, most genomic studies remain anchored to a single linear reference genome, which may incompletely represent genetic diversity across breeds, populations and geographic regions. This limitation is particularly important in domestic animals, where domestication, artificial selection, breed formation, migration and environmental adaptation have generated extensive genomic diversity. Pangenomics provides an alternative framework by integrating multiple high-quality genome assemblies to represent conserved, variable and non-reference genomic sequences within a species. In addition to single-nucleotide variants and small insertions/deletions, pangenomic approaches facilitate characterization of structural variants, copy-number variation, presence/absence variation, alternative haplotypes, novel genes and regulatory sequences. Long-read sequencing, haplotype-resolved assembly and graph-based genome representations have accelerated pangenome development in livestock. Pangenomic resources are now available or emerging for cattle, pigs, goats, chickens and water buffalo, providing new opportunities to investigate breed diversity, domestication, adaptation and economically important traits. Integration with genome-wide association studies, quantitative trait loci, population-genetic analyses and functional multi-omics can facilitate prioritization of biologically relevant variants. Pangenomics may also contribute to genomic selection, breed identification, genetic purity assessment, conservation and climate-resilient breeding. However, its practical value for routine breeding requires representative sampling, standardized analytical frameworks, rigorous validation and direct comparison with conventional genomic prediction. This review summarizes the principles, technologies, livestock applications, challenges and future prospects of pangenomics, with particular emphasis on precision breeding and conservation.

Keywords: Conservation, Domestic animals, Genomic selection, Livestock breeding, Pangenome, Structural variation

1. Introduction

Genomic technologies have transformed animal breeding by enabling genome-wide association studies (GWAS), quantitative trait locus mapping, genomic selection, population-structure analysis and high-resolution characterization of genetic diversity (Goddard *et al.*, 2009; Hayes *et al.*, 2010; Georges *et al.*, 2019; Daetwyler *et al.*, 2014; Gong *et al.*, 2023) [1, 2, 3, 4, 5]. These approaches have accelerated genetic improvement for production, reproduction, health and functional traits. Nevertheless, most analyses rely on a single linear reference genome representing one genomic configuration.

A linear reference genome provides a standardized framework for read alignment, variant calling, gene annotation and comparative genomics, but it cannot fully represent the diversity present across breeds and populations. Divergent haplotypes, insertions, deletions, duplications, inversions and other structural variants (SVs) may be poorly represented or completely absent from the reference (Ho *et al.*, 2020; Bickhart *et al.*, 2014; Sherman *et al.*, 2020; Sedlazeck *et al.*, 2018) [6, 7, 8, 9]. Consequently, conventional reference-based analyses can underrepresent biologically relevant genomic variation.

This limitation is particularly important in domestic animals because livestock populations have experienced domestication, directional selection, breed formation, migration, genetic drift and adaptation to contrasting environments. Indigenous and locally adapted breeds may therefore contain genomic sequences and structural alleles that are poorly represented in global reference genomes.

Pangenomics addresses this limitation by integrating multiple genome assemblies into a species-level representation. Rather than defining one genome as the complete genomic template, a pangenome represents conserved and variable sequences across a population or species (Gong *et al.*, 2023; Rhie *et al.*, 2021; Paten *et al.*, 2017; Garrison *et al.*, 2018) [5, 10, 11, 12]. Recent livestock studies demonstrate that pangenomic re

sources can reveal extensive previously uncharacterized sequence and structural variation in cattle, pigs, goats, chickens and buffalo (Zhou *et al.*, 2022; Li *et al.*, 2023; Jiang *et al.*, 2023; Leonard *et al.*, 2024; Bian *et al.*, 2024; Rice *et al.*, 2023; Clop *et al.*, 2012; Rosen *et al.*, 2020; Yang *et al.*, 2026; Naval-Sánchez *et al.*, 2018; Arshad *et al.*, 2025) [13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23].

The objective of this review is to summarize the conceptual basis, technologies, analytical approaches and applications of pangenomics in domestic animals and to evaluate its potential contribution to precision breeding, breed identification, genetic conservation and climate-resilient livestock production.

2. From linear reference genomes to pangenomes

A linear reference genome provides a standardized coordinate system for read alignment, variant discovery, gene annotation and comparative genomics. However, reads containing highly divergent sequences may align poorly to a reference that lacks the corresponding haplotype. This can result in reference bias and reduced detection of non-reference sequence and complex structural variation.

A pangenome expands this framework by incorporating genomic sequences from multiple individuals. It can be represented as a collection of assemblies, multiple sequence alignments or a genome graph (Rhie *et al.*, 2021; Paten *et al.*, 2017; Garrison *et al.*, 2018) [10, 11, 12]. Graph-based references represent alternative genomic paths and can therefore accommodate multiple haplotypes within a common framework.

The conceptual transition can be summarized as:

Single reference genome → multiple genomes → pangenome → graph-based representation → population-scale genotyping → functional and phenotypic interpretation.

For livestock, this transition is particularly valuable because breed diversity is substantial and many indigenous populations remain poorly represented in global reference resources.

3. Components of a livestock pangenome

A pangenome can be broadly divided into three components: the core genome, the variable genome and the non-reference genome. The core genome consists of sequences shared among most or all sampled individuals and generally provides the conserved genomic backbone of the species. The variable genome includes sequences and alleles that differ among breeds, populations or individuals. Variation may involve SNPs, small indels, structural variants, copy-number variants and alternative haplotypes.

The non-reference component consists of sequences absent from the selected linear reference genome. These regions may include genes, regulatory elements, repetitive sequences and breed- or population-specific sequences. Importantly, discovery of a sequence or variant does not establish its biological function. Functional interpretation requires complementary evidence from transcriptomics, epigenomics, proteomics, phenotype association or experimental validation.

4. Types of pangenomic variation

Pangenomic analysis extends beyond conventional SNP discovery. Single-nucleotide variants and small insertions/deletions remain important for population genetics and trait mapping. Structural variants include insertions, deletions, inversions, duplications and complex rearrangements and can affect gene structure, dosage and regulation (Ho *et al.*, 2020; Bickhart *et al.*, 2014; Sherman *et al.*, 2020; Sedlazeck *et al.*, 2018) [6, 7, 8, 9].

Copy-number variants alter the number of copies of genomic segments and may influence gene dosage and phenotypic variation (Clop *et al.*, 2012) [19]. Presence/absence variants represent genomic sequences or genes present in some individuals but absent in others. Non-reference sequences may also contain novel genes or previously unannotated regulatory elements. Together, these variant classes provide a more complete representation of livestock genomic diversity than SNP-focused approaches alone.

5. Technologies enabling livestock pangenomics

5.1 Long-read sequencing

PacBio HiFi and Oxford Nanopore sequencing provide long DNA reads capable of spanning repetitive and structurally complex genomic regions. These technologies substantially improve detection of large insertions, deletions, inversions and complex SVs (Ho *et al.*, 2020; Sedlazeck *et al.*, 2018) [6, 9].

5.2 Haplotype-resolved assembly

Haplotype-resolved assemblies distinguish homologous chromosomes and preserve allelic differences. This is particularly important for heterozygous structural variation and complex genomic regions.

5.3 Chromosome-level assembly

Chromosome-level and near-complete assemblies provide improved genomic continuity and facilitate accurate comparative analysis and gene annotation (Rhie *et al.*, 2021) [10].

5.4 Genome graphs

Genome graphs provide a flexible representation of alternative genomic sequences and haplotypes. Variation graph approaches allow reads to be mapped against multiple possible genomic paths rather than a single linear sequence (Paten *et al.*, 2017; Garrison *et al.*, 2018) [11, 12].

6. Construction and analysis of livestock pangenomes

A robust livestock pangenome requires representative biological sampling followed by high-quality genome sequencing and assembly.

A typical workflow is:

Representative sampling → high-molecular-weight DNA extraction → long-read sequencing → haplotype-resolved assembly → assembly quality control → genome alignment → variant discovery → pangenome/graph construction → population-scale genotyping → functional annotation → association analysis → independent validation.

Sampling is particularly important because a pangenome constructed exclusively from closely related animals may underestimate genomic diversity. Therefore, breed, geographic origin, ancestry, environmental adaptation and conservation status should be considered during sample selection. Population-scale short-read or long-read datasets can subsequently be genotyped against the pangenome. Functional annotation and association analyses can then be used to prioritize candidate variants.

7. Pangenomics across domestic animal species

7.1 Cattle

Cattle currently represent one of the most advanced livestock systems for pangenomic research. (Zhou *et al.*) [13] developed a global cattle pangenome using 898 cattle representing 57 breeds and identified approximately 83 Mb of non-reference sequence together with extensive structural variation. (Leonard *et al.*) [16] demonstrated the utility of pangenome-derived SVs for molecular phenotype mapping in cattle, showing that pangenomic genotypes can expand analyses beyond conventional SNP variation.

(Gao *et al.*) [28] characterized breed-specific structural variation and novel sequences in Holstein and Jersey cattle, highlighting the value of breed-specific pangenomic resources. (Yang *et al.*) [21] developed a Holstein pangenome from 40 phased haploid assemblies and characterized 93,059 SVs in 1,571 cattle. Large-scale imputation enabled the analysis of pangenome-derived SVs in 50,299 bulls and identified 1,225 SV–trait associations across 43 complex traits.

(Zhao *et al.*) [29] identified 80,328 high-quality SVs in 2,929 cattle and integrated these variants with transcriptomic data to investigate SV–gene regulatory relationships. These studies illustrate the progression from pangenome construction and SV discovery to population-scale genotyping and functional interpretation.

7.2 Pig

Pig pangenomics has revealed substantial structural and sequence diversity. (Jiang *et al.*) [15] constructed a pangenome from 11 long-read genomes and identified approximately 206 Mb of novel sequence and 183,352 non-redundant SVs. Li *et al.* [14] expanded the resource using 250 pigs representing 32 breeds and identified 308.3 Mb of non-reference sequence and 3,438 novel genes. These studies demonstrate that pig pangenomics can reveal gene-content and structural variation associated with genetic diversity and adaptation.

7.3 Goat

(Bian *et al.*) [17] developed a graph-based goat pangenome using representative breeds and population-scale samples. Approximately 113 Mb of autosomal novel sequence was identified, and several structural variants showed signatures associated with domestication and adaptation. Goat pangenomics is therefore promising for investigating adaptation to diverse production environments and identifying genomic variation associated with locally important traits.

7.4 Sheep

Sheep have substantial genetic diversity across production systems, but sheep pangenomic resources remain less developed than those of cattle and pigs. Functional annotation studies have identified regulatory elements associated with domestication (Naval-Sánchez *et al.*, 2018) [22]. However, functional annotation should not be confused with pangenome construction.

Future sheep pangenomes should deliberately include indigenous and locally adapted populations to improve representation of adaptation-related genomic diversity.

7.5 Chicken

(Rice *et al.*) [18] developed a pangenome graph from 30 chicken genomes and demonstrated improved genotyping of large and complex SVs. The graph reduced reference bias when analyzing diverse wild and domestic chickens. This framework may be particularly useful for studying production traits, disease susceptibility, domestication and environmental adaptation in poultry.

7.6 Water buffalo

Water buffalo are particularly important for South Asian livestock production. (Arshad *et al.*) [23] developed a comprehensive buffalo pangenome using 12 assemblies and 711 global samples and identified more than 140 Mb of additional sequence. The study revealed extensive population-specific structural variation, providing an important foundation for buffalo breed characterization, population genetics, adaptation and conservation. For India, such resources could be particularly valuable for breeds including Murrah, Jaffarabadi, Bhadawari, Surti and Pandharpuri.

8. Functional interpretation of pangenomic variation

Pangenomics substantially expands the number of candidate variants available for biological investigation. However, the presence of a variant does not establish its function. Functional prioritization can integrate gene annotation, RNA sequencing, eQTL and sQTL analyses, chromatin accessibility, DNA methylation, transcription-factor binding, proteomics, metabolomics and tissue-specific regulatory annotations.

FAANG initiatives provide an important framework for functional annotation of livestock genomes (Andersson *et al.*, 2015) [27]. Pangenomic variants overlapping genes, promoters, enhancers or tissue-specific regulatory elements can be prioritized for further investigation. Such analyses should be described as functional prioritization or interpretation rather than proof of mechanism unless supported by experimental evidence.

9. Pangenome-based trait discovery

Conventional GWAS is largely dominated by SNPs and small indels. Pangenomic association studies can additionally include SVs, CNVs, PAVs and alternative haplotypes.

A practical framework is:

Pangenome → variant discovery → population genotyping → GWAS/QTL/selection analysis → functional annotation → independent validation.

Recent cattle studies demonstrate the feasibility of integrating pangenome-derived SVs with large-scale phenotype datasets (Leonard *et al.*, 2024; Yang *et al.*, 2026; Zhao *et al.*, 2026) [16, 21, 29]. Nevertheless, statistical association should not automatically be interpreted as causality. Functional assays and independent populations remain important for validating candidate variants.

10. Pangenomics and genomic selection

Genomic selection traditionally uses dense SNP markers to estimate genomic breeding values (Meuwissen *et al.*, 2001; VanRaden, 2008; Meuwissen *et al.*, 2013) [24, 25, 26]. Because SVs and PAVs may not be adequately tagged by conventional SNP panels, pangenomics provides an opportunity to broaden the genomic information used for prediction. However, pangenomics should not be assumed to improve genomic prediction automatically. The appropriate approach is empirical comparison of SNP-only, SNP-plus-SV, whole-genome sequence and pangenome-informed prediction models.

Evaluation should include prediction accuracy, bias, calibration, computational requirements and performance across breeds and generations. Large-scale SV imputation in dairy cattle (Yang *et al.*, 2026) [21] represents an important technical step toward such evaluation, but association and imputation results alone do not establish superior genomic selection performance.

11. Breed identification and genetic purity

Breed identification traditionally relies on SNP panels, microsatellites, PCA, admixture analysis and genomic relationships. Pangenomics can complement these methods by incorporating breed-enriched SVs, population-specific PAVs, private sequences, differentiated haplotypes and breed-specific gene-content variation.

A practical strategy would involve reference population development, pangenome construction, identification of breed-enriched variants, marker prioritization, assay development and independent validation. Machine-learning methods such as random forests, support vector machines and gradient boosting may subsequently be evaluated for breed classification. For Indian buffaloes, this approach could provide an additional genomic layer for breed identification and genetic-purity assessment.

12. Pangenomics for genetic conservation

Conservation programmes traditionally emphasize heterozygosity, inbreeding, effective population size and SNP diversity. Pangenomics can extend these assessments by identifying rare structural variants, population-specific sequences, private haplotypes, PAVs and gene-content differences. This may be particularly important for indigenous livestock breeds that are poorly represented in international reference genomes. However, conservation value should not be inferred from variant number alone. Allele frequency, population history, functional annotation and adaptive relevance should also be considered.

13. Pangenomics and climate-resilient livestock breeding

Heat stress, disease pressure, feed scarcity and water limitation are major challenges for livestock production. Indigenous breeds may contain genomic variation associated with adaptation to local environments. Pangenomics provides an opportunity to investigate sequence and structural variants associated with heat tolerance, disease response, feed efficiency, reproductive resilience, drought adaptation and environmental fitness.

Because adaptation is generally polygenic and environment-dependent, candidate variants should be evaluated using accurate phenotyping, genotype-by-environment analysis and independent validation.

14. Multi-omics and artificial intelligence

Pangenomics describes genomic diversity, whereas transcriptomics, epigenomics, proteomics and metabolomics provide complementary biological information. Integration of these datasets can help connect genomic variation with gene expression, regulatory activity, molecular phenotypes and observable traits.

Recent cattle work linking pangenomic SVs with gene regulation illustrates this approach (Zhao *et al.*, 2026) [29]. The scale of pangenomic datasets also creates opportunities for machine learning in breed classification, ancestry prediction, SV classification, phenotype prediction, genomic prediction, candidate-variant prioritization and conservation planning. However, population structure, relatedness and data leakage can artificially inflate model performance. Independent validation and ancestry-balanced datasets are therefore essential.

15. Relevance to Indian livestock

India possesses exceptional livestock genetic diversity. Indigenous cattle include Sahiwal, Gir, Tharparkar, Rathi and Red Sindhi, while important buffalo populations include Murrah, Jaffarabadi, Bhadawari, Surti and Pandharpuri. Many of these populations have evolved under distinctive environmental and management conditions. Their genomic diversity may therefore contain valuable variation related to adaptation, disease response, fertility and production.

An Indian livestock pangenome could support breed identification, genetic-purity assessment, structural variant discovery, population differentiation, adaptation studies, genomic selection, conservation and climate-resilient breeding. A long-term objective could be the development of compact pangenome-informed marker panels that translate high-resolution sequence information into affordable assays for routine livestock genetic-resource management.

16. Sampling considerations

Sampling is one of the most important determinants of pangenome quality. A representative design should consider breed identity, geographic origin, pedigree, population size, production system, environmental exposure, admixture, conservation status and genetic relatedness.

For breed-specific pangenomes, unrelated animals with well-documented ancestry should be prioritized. Species-level resources should deliberately include major breeds, geographically distinct populations and rare indigenous populations. Pangenomes should also be considered dynamic resources that can be expanded as additional genomes become available.

17. Challenges and limitations

Despite rapid progress, several challenges remain.

Long-read sequencing and high-quality haplotype-resolved assemblies remain more expensive than conventional genotyping. Graph construction, SV discovery, graph indexing and population-scale genotyping require substantial computational resources.

Different SV callers and analytical pipelines may produce different variant catalogues, complicating comparisons among studies. Accurate population-scale genotyping of complex SVs remains challenging, particularly when only short-read data are available.

Functional annotation also lags behind sequence discovery. Finally, a larger variant catalogue does not automatically produce greater genetic gain. The incremental value of pangenome-derived information must be demonstrated through rigorous validation and breeding evaluation.

18. Future perspectives

Future livestock pangenomes are likely to become increasingly population-scale, haplotype-resolved, graph-based and multi-omics integrated. Large reference populations containing pangenomic genotypes and high-quality phenotypes will allow more rigorous testing of SV-informed genomic prediction. Pangenome-wide association analyses may expand conventional GWAS to include SVs, CNVs and PAVs.

Functional pangenomics will increasingly connect structural variation with tissue-specific gene expression, chromatin accessibility and other molecular phenotypes. For conservation, pangenomes may help identify rare genomic components that are poorly captured by conventional SNP panels and improve prioritization of animals for germplasm preservation.

19. Pangenome-assisted breeding framework

A practical pangenome-assisted breeding programme can be organized into ten stages:

1. Representative sampling
2. Long-read sequencing
3. Haplotype-resolved assembly
4. Pangenome construction
5. Comprehensive variant discovery
6. Population-scale genotyping
7. Trait association analysis
8. Functional integration
9. Independent validation
10. Breeding or conservation implementation

The final objective should not simply be a larger genomic variant catalogue, but a validated genomic resource that provides measurable value for animal improvement and genetic-resource management.

Table 1. Major applications of pangenomics in domestic animals

Application	Conventional approach	Added value of pangenomics	Potential outcome
Variant discovery	SNPs and indels	SVs, CNVs, PAVs and non-reference sequences	Comprehensive variant catalogue
Breed characterization	SNP panels, PCA and admixture	Breed-enriched SVs and private sequences	Breed identification and genetic-purity assessment
Trait mapping	SNP-GWAS/QTL	Complex genomic variants	Expanded candidate discovery
Functional genomics	Reference-based annotation	Alternative genes and regulatory sequences	Functional prioritization
Genomic selection	SNP arrays	Potential inclusion of informative SVs	Pangenome-informed prediction after validation
Disease genetics	Candidate genes/SNPs	Structural and gene-content variation	Candidate discovery
Adaptation	SNP selection scans	Population-specific sequences and SVs	Climate-resilience studies

(continued on next page)

Application	Conventional approach	Added value of pangenomics	Potential outcome
Conservation	SNP diversity	Rare structural and non-reference variation	Germplasm prioritization
Multi-omics	Linear reference	Alternative genomic contexts	Genome-to-phenome analysis
Precision breeding	Limited marker sets	Broader genomic information	Validated marker development

Table 2. Representative pangenomic resources in domestic animals

Species	Study	Resource	Major finding
Cattle	Zhou <i>et al.</i> [13]	898 cattle; 57 breeds	~83 Mb non-reference sequence; extensive SV diversity
Cattle	Leonard <i>et al.</i> [16]	16 HiFi haplotype-resolved assemblies	Pangenome-derived SVs for molecular phenotype mapping
Cattle	Gao <i>et al.</i> [28]	28 Holstein and Jersey cattle	Breed-specific SVs and novel sequences
Cattle	Yang <i>et al.</i> [21]	1,571 cattle and 50,299 bulls	93,059 SVs; large-scale SV imputation and trait associations
Cattle	Zhao <i>et al.</i> [29]	2,929 cattle	80,328 high-quality SVs; SV–gene regulation
Pig	Jiang <i>et al.</i> [15]	11 long-read genomes	~206 Mb novel sequence; 183,352 SVs
Pig	Li <i>et al.</i> [14]	250 pigs; 32 breeds	308.3 Mb non-reference sequence; 3,438 novel genes
Goat	Bian <i>et al.</i> [17]	Representative breeds and population-scale samples	~113 Mb novel sequence; adaptation-associated SVs
Chicken	Rice <i>et al.</i> [18]	30 genome assemblies	Complex SV genotyping and reduced reference bias
Water buffalo	Arshad <i>et al.</i> [23]	12 assemblies; 711 samples	> 140 Mb additional sequence; population-specific SV signatures

Table 3. Pangenome-assisted breeding framework

Stage	Major activity	Representative approaches	Expected output
1	Representative sampling	Breed, geography, pedigree and phenotype	Representative population panel
2	Genome sequencing	PacBio HiFi/ONT	High-quality genomic data
3	Haplotype resolution	Phasing and de novo assembly	Haplotype-resolved genomes
4	Pangenome construction	Whole-genome alignment and graph methods	Pangenomic reference
5	Variant discovery	SNP, indel, SV, CNV and PAV detection	Comprehensive variant catalogue
6	Population genotyping	Graph genotyping and imputation	Population-scale genotypes
7	Trait association	GWAS, QTL and selection analyses	Candidate loci
8	Functional integration	RNA-seq, eQTL, epigenomics and proteomics	Functionally prioritized variants
9	Validation	Independent populations and functional assays	Validated candidate markers
10	Implementation	Genomic prediction, marker assays and conservation	Practical breeding applications

20. Conclusion

Pangenomics represents a major shift from a single-reference view of livestock genomes toward a more inclusive representation of genomic diversity. By integrating multiple high-quality genome assemblies, pangenomic resources can capture non-reference sequences, structural variants, copy-number variation, presence/absence variation and alternative haplotypes that may be underrepresented in conventional SNP-based analyses. Recent studies in cattle, pigs, goats, chickens and water buffalo demonstrate the increasing maturity of this field and its value for investigating genetic diversity, domestication, adaptation and complex traits. In cattle, recent work has progressed from pangenome construction and structural variant discovery to breed-specific graph references, large-scale SV imputation, trait association and gene-regulation analysis.

The principal value of pangenomics is therefore the expansion of the genomic search space. Its practical breeding value, however, must be demonstrated rather than assumed. Future studies should prioritize representative sampling, standardized SV analysis, population-scale genotyping, functional multi-omics, independent validation and direct comparison with established genomic prediction approaches.

For India, pangenomes representing indigenous cattle and buffalo breeds could be particularly valuable for breed identification, genetic-purity assessment, conservation and climate-resilient breeding.

Pangenomics should therefore be viewed not as an endpoint, but as genomic infrastructure for more inclusive and biologically informed livestock improvement.

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References

- Goddard ME, Hayes BJ. Mapping genes for complex traits in domestic animals. *Nat Rev Genet.* 2009;10:381–391.
- Hayes B, Goddard M. Genome-wide association and genomic selection in animal breeding. *Genome.* 2010;53:876–883.
- Georges M, Charlier C, Hayes B. Harnessing genomic information for livestock improvement. *Nat Rev Genet.* 2019;20:135–156.

4. Daetwyler HD, Calus MPL, Pong-Wong R, de los Campos G, Hickey JM. Genomic prediction in animals and plants: simulation of common issues and identification of beneficial strategies. *Nat Genet.* 2014;46:858–865.
5. Gong Y, Li Y, Liu X, Ma Y, Jiang L. A review of the pangenome: how it affects our understanding of genomic variation, selection and breeding in domestic animals? *J Anim Sci Biotechnol.* 2023;14:73.
6. Ho SS, Urban AE, Mills RE. Structural variation in the sequencing era. *Nat Rev Genet.* 2020;21:171–189.
7. Bickhart DM, Liu GE. The challenges and importance of structural variation detection in livestock. *Front Genet.* 2014;5:37.
8. Sherman RM, Salzberg SL. Pan-genomics in the human genome era. *Nat Rev Genet.* 2020;21:243–254.
9. Sedlazeck FJ, Lee H, Darby CA, Schatz MC. Piercing the dark matter: bioinformatics of long-range sequencing and mapping. *Nat Rev Genet.* 2018;19:329–346.
10. Rhie A, McCarthy SA, Fedrigo O, Damas J, Formenti G, Koren S, *et al.* Towards complete and error-free genome assemblies of all vertebrate species. *Nature.* 2021;592:737–746.
11. Paten B, Novak AM, Eizenga JM, Garrison E. Genome graphs and the evolution of genome inference. *Genome Res.* 2017;27:665–676.
12. Garrison E, Sirén J, Novak AM, Hickey G, Eizenga JM, Dawson ET, *et al.* Variation graph toolkit improves read mapping by representing sequence diversity. *Nat Biotechnol.* 2018;36:875–879.
13. Zhou Y, Yang L, Han X, Han J, Hu Y, Li F, *et al.* Assembly of a pangenome for global cattle reveals missing sequences and novel structural variations, providing new insights into their diversity and evolutionary history. *Genome Res.* 2022;32:1585–1601.
14. Li Z, Liu X, Wang C, Li Z, Jiang B, Zhang R, *et al.* The pig pangenome provides insights into the roles of coding structural variations in genetic diversity and adaptation. *Genome Res.* 2023;33:1833–1847.
15. Jiang YF, Wang S, Wang CL, Xu RH, Wang WW, Jiang Y, *et al.* Pangenome obtained by long-read sequencing of 11 genomes reveal hidden functional structural variants in pigs. *iScience.* 2023;26:106119.
16. Leonard AS, Mapel XM, Pausch H. Pangenome-genotyped structural variation improves molecular phenotype mapping in cattle. *Genome Res.* 2024;34:300–309.
17. Bian P, Li J, Zhou S, Wang X, Gong M, Guo X, *et al.* A graph-based goat pangenome reveals structural variations involved in domestication and adaptation. *Mol Biol Evol.* 2024;41:msae251.
18. Rice ES, Alberdi A, Alfieri J, Athrey G, Balacco JR, Bardou P, *et al.* A pangenome graph reference of 30 chicken genomes allows genotyping of large and complex structural variants. *BMC Biol.* 2023;21:267.
19. Clop A, Vidal O, Amills M. Copy number variation in the genomes of domestic animals. *Anim Genet.* 2012;43:503–517.
20. Rosen BD, Bickhart DM, Schnabel RD, Koren S, Elisk CG, Tseng E, *et al.* De novo assembly of the cattle reference genome with single-molecule sequencing. *GigaScience.* 2020;9:giaa021.
21. Yang L, Wang J, Kuhn K, Li W, Zanton G, Neupane M, *et al.* Pangenome-based structural variant imputation enables large-scale genotype-phenotype studies in dairy cattle. *Nat Commun.* 2026;17:8281.
22. Naval-Sánchez M, Nguyen Q, McWilliam S, Porto-Neto LR, Tellam R, Vuocolo T, *et al.* Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of domestication. *Nat Commun.* 2018;9:859.
23. Arshad F, Jayaraman S, Talenti A, Owen R, Mohsin M, Mansoor S, *et al.* A comprehensive water buffalo pangenome reveals extensive structural variation linked to population-specific signatures of selection. *GigaScience.* 2025;14:giaf099.
24. Meuwissen THE, Hayes BJ, Goddard ME. Prediction of total genetic value using genome-wide dense marker maps. *Genetics.* 2001;157:1819–1829.
25. VanRaden PM. Efficient methods to compute genomic predictions. *J Dairy Sci.* 2008;91:4414–4423.
26. Meuwissen T, Hayes B, Goddard M. Accelerating improvement of livestock with genomic selection. *Annu Rev Anim Biosci.* 2013;1:221–237.
27. Andersson L, Archibald AL, Bottema CDK, Brauning R, Burton J, Churchill GA, *et al.* Coordinated international action to accelerate genome-to-phenome research in livestock. *Genome Biol.* 2015;16:57.
28. Gao Y, Yang L, Kuhn K, Li W, Zanton G, Bowman M, *et al.* Long read and preliminary pangenome analyses reveal breed-specific structural variations and novel sequences in Holstein and Jersey cattle. *J Adv Res.* 2026;79:137–150.
29. Zhao P, Peng C, Gao Y, Dai S, Yang L, He J, *et al.* Pangenome graph reveals the structural variation landscape in 2929 cattle samples and its impact on gene regulation. *Genomics Proteomics Bioinformatics.* 2026.
30. Liu GE. Exploring cattle structural variation in the era of long reads, pangenome graphs, and near-complete assemblies. *J Anim Sci Biotechnol.* 2025;16:158.
31. Ashraf H, Doerr D, Ebler J, Marschall T. Building and applying pangenome references to capture genetic diversity. *Nat Rev Genet.* 2026.

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