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Advances in Molecular and Genomic Profiling of Health and Performance Traits in Horses

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Abstract

Molecular and genomic technologies have significantly transformed equine research by enabling accurate and comprehensive profiling of health status and performance-related traits in horses. The integration of advanced molecular tools has shifted traditional approaches from phenotype-based assessment to precise genotype-driven evaluation, thereby improving the efficiency of disease diagnosis, genetic selection, and overall herd management. This short communication provides an overview of key molecular and genomic techniques widely applied in equine science, including polymerase chain reaction (PCR), next-generation sequencing (NGS), single nucleotide polymorphism (SNP) genotyping, and emerging multi-omics approaches such as transcriptomic and proteomics.

PCR-based techniques remain essential for rapid and sensitive detection of infectious and genetic diseases, while NGS technologies have revolutionized genome-wide analysis by enabling high-throughput sequencing, gene discovery, and identification of functional genetic variants. SNP genotyping has further contributed to understanding genetic diversity, parentage verification, and marker-assisted as well as genomic selection for economically important traits such as endurance, speed, and disease resistance. In addition, omics technologies provide deeper insights into gene expression patterns, metabolic pathways, and complex biological interactions that influence equine health and performance.

The integration of bioinformatics tools has enhanced the analysis and interpretation of large-scale genomic datasets, facilitating accurate identification of candidate genes and biological markers. These advancements support the development of precision veterinary medicine, allowing customized health management strategies and improved breeding decisions. Moreover, genomic profiling plays a crucial role in early disease detection, monitoring of hereditary disorders, and conservation of valuable equine genetic resources. Despite these advancements, several challenges hinder the widespread adoption of genomic technologies in routine veterinary practice, particularly in developing regions. High costs, requirement of specialized infrastructure, limited technical expertise, and lack of awareness among stakeholders remain significant constraints. Nevertheless, continuous technological innovations and decreasing sequencing costs are expected to improve accessibility and applicability in the near future.

Overall, molecular and genomic profiling holds immense potential to enhance equine health, welfare, and productivity. Its integration into research, clinical practice, and breeding programmers will play a pivotal role in advancing sustainable equine management and precision veterinary science.

Introduction

Genomic profiling has emerged as a transformative approach in veterinary science, enabling comprehensive characterization of animal genomes and facilitating the identification of genetic variations associated with economically important traits, disease susceptibility, adaptation, and evolutionary processes [1–4]. Rapid advancements in molecular biology, high-throughput sequencing technologies, and computational genomics have shifted research focus from single-gene analysis to genome-wide investigations, thereby enhancing the precision and scope of veterinary research [2–5].

These developments have significantly improved our understanding of the molecular mechanisms governing animal health, productivity, reproduction, and disease resistance, ultimately supporting evidence-based decision-making in veterinary practice and livestock management [1–4].

Historically, animal breeding programmers relied primarily on phenotypic selection and pedigree records to improve desirable traits [6, 7]. While effective to a certain extent, these approaches often lack the resolution needed to dissect complex traits influenced by multiple genes and environmental interactions [6–8]. The advent of molecular marker systems, such as restriction fragment length polymorphisms (RFLPs), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs), microsatellites or simple sequence repeats (SSRs), and single nucleotide polymorphisms (SNPs), marked a significant milestone in genetic research [8–11]. These tools enabled more precise evaluation of genetic diversity, parentage verification, quantitative trait loci (QTL) mapping, and marker-assisted selection in animal populations.

Subsequently, the development of advanced DNA sequencing technologies revolutionized veterinary genomics. First-generation sequencing methods laid the groundwork, while next-generation sequencing (NGS) and third-generation long-read sequencing platforms enabled rapid, high-throughput, and cost-effective genome analysis [12–16]. These technologies facilitate a wide range of applications, including whole-genome sequencing, transcriptome profiling, epigenetic studies, metagenomics, and structural variant detection. Their integration into veterinary science has significantly enhanced diagnostic accuracy, genetic evaluation, and research efficiency [13–16].

In parallel, advances in bioinformatics have played a crucial role in managing and interpreting large-scale genomic datasets. Computational tools and databases enable sequence alignment, variant identification, gene annotation, and pathway analysis, thereby providing deeper insights into gene function and biological processes [17–20]. The integration of multi-omics approaches, combining genomics, transcriptomic, proteomics, and metabolomics, further strengthens our understanding of complex traits and host–pathogen interactions in animals.

In veterinary medicine, genomic profiling has become an indispensable tool for improving livestock productivity, enhancing disease resistance, diagnosing inherited disorders, and monitoring infectious disease outbreaks [2–5, 21]. The incorporation of genomic information into breeding programmers through genomic selection has enabled more accurate prediction of breeding values, leading to accelerated genetic improvement [22, 23]. Additionally, genomic surveillance of pathogens has improved epidemiological tracking and disease control strategies, while comparative genomics has provided insights into evolutionary relationships among domestic animals and wildlife species [24–26].

The effectiveness of genomic profiling depends on a series of critical steps, including proper sample collection, high-quality nucleic acid extraction, robust molecular techniques, advanced sequencing platforms, and reliable bioinformatics analysis [17–20, 27]. Each component contributes to the generation of accurate and reproducible data, making the selection of appropriate tools and methodologies essential for achieving specific research objectives.

In equine science, molecular and genomic profiling has gained increasing importance for evaluating health status, disease susceptibility, and performance traits. Traits such as endurance, speed, musculoskeletal strength, and adaptability are influenced by complex genetic factors that can now be studied using advanced genomic tools. The integration of genomic data into equine management and breeding programmers allows for improved selection strategies, early disease detection, and enhanced welfare outcomes. This short communication highlights the key molecular and genomic techniques applied in horses and emphasizes their role in advancing precision veterinary medicine and sustainable equine production systems.

Molecular Techniques and Marker-Based Genomic Profiling in Equine Science

Molecular techniques play a fundamental role in equine genomic profiling by enabling precise detection of pathogens, identification of genetic variations, and assessment of traits associated with health and performance. Among these, polymerase chain reaction (PCR) and its variants, particularly real-time PCR (qPCR), are widely used due to their high sensitivity, specificity, and rapid turnaround time [28, 29]. These techniques are routinely applied in the diagnosis of infectious diseases such as equine influenza, equine herpesvirus infections, and parasitic infestations. In addition, PCR-based assays are employed for detection of genetic mutations and inherited disorders in horses. Microsatellite markers have also been extensively utilized for parentage verification, breed characterization, and evaluation of genetic diversity in equine populations [30, 31]. Recent advancements in molecular diagnostics have further improved detection accuracy, making these tools highly valuable under field conditions where early diagnosis is critical for effective disease management [32, 33].

A crucial prerequisite for successful genomic analysis is the collection of appropriate biological samples and the extraction of high-quality nucleic acids. Commonly used samples in equine studies include whole blood, hair follicles, buccal swabs, tissue biopsies, semen, and fecal material, depending on the research objectives [34, 35]. The extracted DNA or RNA must be free from contaminants such as proteins, salts, and inhibitors that can affect downstream applications [36]. Standard extraction techniques include phenol–chloroform extraction, salting-out procedures, silica column-based purification, and magnetic bead-based methods. Commercial kits have simplified and standardized the process, ensuring reproducibility and efficiency [36, 37]. The quality and quantity of nucleic acids are typically assessed using spectrophotometry and gel electrophoresis prior to molecular analysis.

Molecular marker systems form the backbone of genomic profiling by enabling detection of polymorphisms and mapping of economically important traits. Early marker systems such as Restriction Fragment Length Polymorphism (RFLP) were based on variations in restriction enzyme sites and required Southern blotting for detection [38, 39]. Although highly reliable and co-dominant, RFLP is labor-intensive and has largely been replaced by PCR-based techniques. Random Amplified Polymorphic DNA (RAPD) markers utilize short arbitrary primers to amplify random DNA segments and are useful for preliminary genetic diversity studies, although they suffer from limited reproducibility [40, 41]. Amplified

Fragment Length Polymorphism (AFLP), which combines restriction digestion with selective PCR amplification, provides high-resolution genomic fingerprints and has been widely used in population genetics and biodiversity studies [42, 43].

Microsatellites or Simple Sequence Repeats (SSRs), also known as Short Tandem Repeats (STRs), consist of repeating nucleotide motifs and are highly polymorphic and co-dominant in nature [44, 45]. These markers have been extensively applied in parentage verification, linkage mapping, and population genetic studies in horses. However, with the advent of high-throughput technologies, their use in large-scale genomic studies has declined.

Currently, Single Nucleotide Polymorphisms (SNPs) represent the most widely used molecular markers in veterinary genomics due to their abundance, stability, and suitability for automation [46, 47]. SNPs serve as the foundation for genome-wide association studies (GWAS), genomic selection, and estimation of genomic breeding values. High-density SNP arrays, such as the Axiom Equine Genotyping Array, enable simultaneous analysis of thousands to millions of loci, thereby facilitating comprehensive genomic analysis in horses and other livestock species [48, 49]. These technologies have significantly accelerated genetic improvement programmers, disease gene identification, and precision breeding strategies.

Overall, the integration of molecular techniques with advanced marker systems has greatly enhanced the efficiency and accuracy of equine genomic profiling. These tools provide a strong foundation for disease diagnosis, genetic improvement, and sustainable equine management.

4. Genomic Tools and High-Throughput Technologies

The emergence of high-throughput genomic technologies has significantly advanced equine research by enabling large-scale and precise analysis of genetic variation. Among these, next-generation sequencing (NGS) platforms have revolutionized genomic profiling by facilitating comprehensive analysis of entire genomes and transcriptomes [50–53]. Techniques such as whole genome sequencing (WGS), whole exome sequencing (WES), and RNA sequencing (RNA-seq) allow the identification of genes and regulatory elements associated with health, disease susceptibility, and performance traits in horses [51–54], as illustrated in Fig. 1. These NGS methods enable large-scale detection of genetic variations and functional elements in equine populations.

Next-generation sequencing (NGS) methods, including WGS, WES, and RNA-sea, enable large-scale detection of genetic variations. Single nucleotide polymorphism (SNP) genotyping arrays are widely used for detecting genome-wide variation, studying population structure, and implementing marker-assisted and genomic selection strategies [55–57]. These tools have enabled the identification of genetic markers linked to economically important traits such as racing ability, endurance capacity, coat colour, fertility, and inherited disorders [50, 58–60]. The integration of genomic data into breeding programmers has improved selection accuracy, enhanced genetic gain, and reduced the prevalence of hereditary diseases in equine populations.

5. PCR-Based Techniques

Polymerase chain reaction (PCR) remains a cornerstone of molecular diagnostics and genomic profiling due to its sensitivity, specificity, and rapid turnaround time [61–62]. It enables exponential amplification of specific DNA sequences from minimal template material, making it indispensable in veterinary genetics.

Several PCR variants have been developed to address diverse research and diagnostic needs:

5.1 Conventional PCR

Conventional PCR involves cyclic denaturation, primer annealing, and extension using thermostable DNA polymerase to amplify target DNA sequences [63].

5.2 Multiplex PCR

Multiplex PCR allows simultaneous amplification of multiple targets in a single reaction using multiple primer sets, increasing efficiency and reducing costs [64].

5.3 Reverse Transcription PCR (RT-PCR)

RT-PCR converts RNA into complementary DNA (cDNA) prior to amplification and is widely used for gene expression studies and detection of RNA viruses [65].

5.4 Quantitative Real-Time PCR (qPCR)

qPCR enables real-time monitoring of DNA amplification using fluorescence signals, allowing accurate quantification of nucleic acids. Adherence to MIQE guidelines ensures reproducibility and reliability [66].

5.5 Digital PCR (dPCR)

Digital PCR partitions samples into numerous micro-reactions, enabling absolute quantification of nucleic acids without standard curves and providing high sensitivity for detecting low-abundance targets. The dMIQE guidelines standardize reporting for improved reproducibility [67].

Collectively, PCR-based techniques are widely applied in pathogen detection, mutation screening, gene expression analysis, and validation of genomic findings in horses.

6. DNA Sequencing Technologies

DNA sequencing technologies form the foundation of modern genomic profiling by enabling precise determination of nucleotide sequences and comprehensive analysis of genetic variation [68,69]. Advances in sequencing technologies have significantly improved throughput, accuracy, and cost-effectiveness.

Sequencing platforms are broadly categorized into three generations:

1. **First-generation sequencing (Sanger sequencing):**
   Highly accurate but low-throughput, primarily used for validation and small-scale studies [18].
2. **Second-generation sequencing (Next-Generation Sequencing, NGS):**
   Enables massively parallel sequencing, facilitating whole-genome, transcriptome, and metagenomics analyses [70-72].
3. **Third-generation sequencing (Long-read sequencing):**

Technologies such as SMRT and nanopore sequencing provide long reads, enabling improved genome assembly, detection of structural variants, and epigenetic analysis [73].

These sequencing approaches have transformed equine genomics by enabling the discovery of novel genes, identification of disease-associated variants, and improved understanding of complex traits. Furthermore, they support applications in precision medicine, comparative genomics, and advanced breeding strategies.

7. Bioinformatics and Data Integration

The large volume of data generated by high-throughput genomic technologies necessitates the use of advanced bioinformatics tools for efficient analysis, management, and interpretation. Bioinformatics integrates computational algorithms, statistical models, and biological databases to transform raw genomic data into meaningful biological insights [74–75]. Key analytical processes include sequence alignment, genome assembly, variant detection, and functional annotation of genes and regulatory elements, as illustrated in Fig. 2. High-throughput genomic data are analyzed through these processes, supported by public databases such as NCBI, Ensemble, and UCSC.

High-throughput genomic data are analyzed through alignment, assembly, variant detection, and annotation, supported by public databases (NCBI, Ensembl, UCSC). Multi-omics integration enables biomarker discovery, precision medicine, and improved breeding strategies. Public databases and software platforms such as NCBI, Ensemble, and the UCSC Genome Browser facilitate storage, retrieval, and comparative analysis of genomic data [76–77]. Variant discovery approaches enable the identification of single nucleotide polymorphisms (SNPs), insertions/deletions (intel's), and structural variations, which are essential for understanding genetic diversity and disease susceptibility.

Furthermore, the integration of multi-omics data—including genomics, transcriptomic, proteomics, and metabolomics—provides a comprehensive systems-level understanding of biological processes influencing equine health and performance [78–79]. Such integrative approaches enhance the identification of biomarkers, gene networks, and molecular pathways, thereby supporting precision veterinary medicine and informed decision-making in breeding and disease management.

8. Applications in Equine Health and Performance

Genomic profiling has become a powerful tool for improving equine health, performance, and management. It plays a critical role in early disease diagnosis, identification of genetic disorders, and the implementation of preventive and control strategies [80–81]. Techniques such as genome-wide association studies (GWAS) and sequencing have enabled the identification of genes associated with inherited conditions and complex diseases in horses, as illustrated in Fig. 3. These genomic approaches also support performance trait selection and the conservation of genetic diversity.

Genomic approaches support disease diagnosis, identification of genetic disorders, performance trait selection, and conservation of genetic diversity. In addition, genomic tools support the selection of horses with superior athletic traits, including speed, endurance, adaptability, and resilience. For example, genetic variants in performance-related genes have been linked to racing ability and muscle development, facilitating more accurate selection in breeding programmers [82–83].

Genomic profiling also contributes significantly to conservation genetics by maintaining genetic diversity and reducing inbreeding in indigenous and rare horse breeds [84]. Molecular markers and SNP-based analyses are widely used for parentage verification, breed characterization, and population structure analysis, ensuring the sustainability and preservation of valuable equine genetic resources.

9. Challenges and Future Perspectives

Despite the rapid advancement of genomic technologies, several challenges continue to limit their widespread adoption in veterinary practice, particularly in equine science. One of the primary constraints is the high cost associated with genomic analyses, including next-generation sequencing (NGS), high-density SNP arrays, and advanced bioinformatics infrastructure [85, 86]. Although sequencing costs have decreased over time, the overall expenses related to sample processing, data storage, and computational analysis remain substantial, making these technologies less accessible in low-resource settings and developing countries.

Another significant limitation is the lack of technical expertise required to perform and interpret genomic analyses. Veterinary practitioners often face challenges in integrating complex genomic data into routine clinical decision-making due to insufficient training in bioinformatics and molecular genetics [87]. Additionally, the shortage of skilled personnel capable of managing large-scale genomic datasets further restricts the practical implementation of these technologies. Infrastructure-related issues, such as limited access to high-performance computing systems, sequencing platforms, and reliable internet connectivity, also hinder the adoption of genomic tools in field conditions [88].

Data management and standardization present further challenges in veterinary genomic profiling. The enormous volume of data generated through high-throughput technologies necessitates robust data storage systems, standardized analytical pipelines, and efficient data-sharing frameworks [89]. Inconsistent data formats, lack of harmonized protocols, and limited interoperability among databases can impede data integration and comparative analyses across studies and species. Moreover, ensuring

data security and privacy, particularly for commercially valuable breeding information, remains a critical concern.

Ethical considerations also play an important role in the application of genomic technologies. Issues related to genetic manipulation, ownership of genomic data, and potential misuse of genetic information must be carefully addressed [90]. In equine breeding, there is ongoing debate regarding the ethical implications of selecting animals based solely on genetic merit, which may lead to reduced genetic diversity and unintended health consequences. Therefore, the development of ethical guidelines and regulatory frameworks is essential to ensure responsible use of genomic technologies in veterinary science.

Looking ahead, future research should focus on developing cost-effective, rapid, and user-friendly genomic tools that can be applied directly in field conditions. Portable sequencing technologies and point-of-care diagnostic platforms have the potential to revolutionize veterinary diagnostics by enabling real-time genomic analysis in remote locations [91]. Furthermore, the integration of artificial intelligence (AI) and machine learning (ML) with genomic data is expected to significantly enhance predictive accuracy, disease diagnosis, and breeding decisions [92]. AI-driven models can analyses complex multi-omics datasets, identify patterns, and predict phenotypic outcomes with greater precision than traditional methods.

The adoption of multi-omics approaches, combining genomics with transcriptomic, proteomics, metabolomics, and epigenetics, is another promising direction for future research. Such integrative analyses provide a comprehensive understanding of biological systems and enable the identification of robust biomarkers for health, disease, and performance traits [93]. Additionally, advancements in genome-editing technologies, particularly CRISPR–Cas systems, offer new opportunities for functional validation of genes and potential therapeutic interventions, although their application in animals requires careful ethical consideration [94].

In conclusion, while genomic technologies hold immense potential to transform equine health management, breeding, and research, overcoming current challenges is essential for their broader adoption. Continued technological innovation, capacity building, infrastructure development, and establishment of ethical and regulatory frameworks will be critical in realizing the full potential of genomic profiling in veterinary medicine. The integration of advanced computational tools and emerging biotechnologies is expected to drive the next generation of precision veterinary science, ultimately improving equine health, welfare, and productivity.

Conclusion

In conclusion, the title *“Advances in Molecular and Genomic Profiling of Health and Performance Traits in Horses”* aptly reflects the significant progress achieved in equine genomics and its growing impact on veterinary science. Molecular and genomic techniques have become indispensable tools for understanding the complex genetic architecture underlying equine health and performance. The

transition from conventional molecular marker-based methods to advanced high-throughput sequencing technologies has revolutionized the field, enabling rapid, accurate, and large-scale genomic analyses at unprecedented resolution.

These technological advancements have broadened the scope of applications in equine research and practice, including early disease detection, identification of hereditary disorders, and the development of precision medicine strategies. Moreover, genomic profiling has become a cornerstone in modern breeding programs, allowing for the selection of horses with enhanced athletic ability, disease resistance, and environmental adaptability. Such improvements not only increase productivity but also promote animal welfare and sustainability.

The availability of diverse genomic platforms offers flexibility in addressing different research and clinical needs. While traditional markers remain useful for fundamental applications such as parentage testing and breed characterization, next-generation and third-generation sequencing technologies provide comprehensive insights into genome structure and function. The careful selection of appropriate tools based on specific objectives and available resources is essential for maximizing their effectiveness.

Importantly, the integration of genomic technologies with bioinformatics and multi-omics approaches has transformed equine genomics into a highly interdisciplinary field. This holistic framework enables a deeper understanding of the molecular mechanisms that govern health, disease, and performance traits. However, challenges such as high costs, limited technical expertise, and infrastructure constraints continue to hinder widespread adoption, particularly in developing regions.

Looking forward, continued technological innovation, improved accessibility, and collaborative research efforts are expected to further expand the role of genomic profiling in equine science. With responsible implementation, these advances hold great promise for enhancing equine health, welfare, and productivity, while contributing to the broader goals of sustainable livestock management and veterinary medicine.

Declarations

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Ethics approval and consent to participate

This Brief Report is based exclusively on previously published literature and does not involve original research involving live animals, animal experimentation, biological sample collection, or human participants. Therefore, ethical approval from an Institutional Animal Ethics Committee (IAEC) and informed consent were not required for this study.

Statement of informed consent

Informed consent was obtained from all individual participants included in the study. The respondents were informed about the purpose of the study, and their participation was voluntary.

Declaration of Helsinki is not appropriate

For a literature-only horse genomics Brief Report; it is primarily associated with research involving human participants.

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Conflict of Interest

The authors declare no conflict of interest.

Consent to Publish

Consent to Publish declaration: not applicable.

Author contributions

All authors contributed to the conception, literature review, interpretation of the available evidence, and preparation and revision of the manuscript. All authors approved the final manuscript.

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References

1. Dekkers JCM. Application of genomics tools to animal breeding. Curr Genomics. 2012;13:207–12.
2. Rothschild MF, Ruvinsky A. The Genetics of the Pig. 2nd ed. CAB International; 2011.
3. Andersson L. Genetic dissection of phenotypic diversity in farm animals. Nat Rev Genet. 2001;2:130–8.
4. Hayes BJ, et al. Genomic selection in animals: applications and challenges. Nat Rev Genet. 2009;10:381–91.
5. Meuwissen TH, Hayes BJ, Goddard ME. Prediction of total genetic value using genome-wide dense marker maps. Genetics. 2001;157:1819–29.
6. Falconer DS, Mackay TFC. *Introduction to Quantitative Genetics*. 4th ed. Longman; 1996.
7. Bourdon RM. Understanding Animal Breeding. 2nd ed. Prentice Hall; 2000.

8. Williams JGK, et al. DNA polymorphisms amplified by arbitrary primers. Nucleic Acids Res. 1990;18:6531–5.
9. Vos P, et al. AFLP: a new technique for DNA fingerprinting. Nucleic Acids Res. 1995;23:4407–14.
10. Tautz D. Hypervariability of simple sequences. Nucleic Acids Res. 1989;17:6463–71.
11. Vignal A, et al. A review on SNP and other types of molecular markers. Genet Sel Evol. 2002;34:275–305.
12. Sanger F, et al. DNA sequencing with chain-terminating inhibitors. PNAS. 1977;74:5463–7.
13. Metzker ML. Sequencing technologies: the next generation. Nat Rev Genet. 2010;11:31–46.
14. van Dijk EL, et al. Ten years of next-generation sequencing technology. Trends Genet. 2014;30:418–26.
15. Goodwin S, et al. Coming of age: ten years of next-generation sequencing. Nat Rev Genet. 2016;17:333–51.
16. Logsdon GA, et al. Long-read sequencing advances. Nat Rev Genet. 2020;21:597–614.
17. Mount DW. Bioinformatics: Sequence and Genome Analysis. 2nd ed. Cold Spring Harbor; 2004.
18. Lesk AM. Introduction to Bioinformatics. Oxford University Press; 2014.
19. Kulski JK. Next-generation sequencing—overview of the history. Methods Mol Biol. 2016;1354:3–60.
20. Stephens ZD et al. Big data in genomics. PLoS Biol. 2015;13.
21. Georges M, et al. Genomics in livestock improvement. Nat Rev Genet. 2019;20:135–56.
22. Goddard ME, Hayes BJ. Genomic selection. J Anim Breed Genet. 2007;124:323–30.
23. VanRaden PM. Efficient methods to compute genomic predictions. J Dairy Sci. 2008;91:4414–23.
24. Woolhouse ME, Gowtage-Sequeria S. Host range and emerging diseases. Emerg Infect Dis. 2005;11:1842–7.
25. Pybus OG, Rambaut A. Evolutionary analysis of viruses. Nat Rev Genet. 2009;10:540–50.
26. Ellegren H. Genome sequencing and population genomics. Trends Ecol Evol. 2014;29:51–63.
27. Sambrook J, Russell DW. Molecular Cloning: A Laboratory Manual. 3rd ed. Cold Spring Harbor; 2001.
28. Mullis K, Faloona F. Specific synthesis of DNA in vitro via PCR. Methods Enzymol. 1987;155:335–50.
29. Mackay IM. Real-time PCR in the microbiology laboratory. Clin Microbiol Infect. 2004;10:190–212.
30. Bowling AT, Clark RS. Microsatellite markers in horses. Anim Genet. 1988;19:153–65.
31. Cunningham EP, Dooley JJ. Microsatellites and parentage testing. Anim Genet. 1999;30:337–45.
32. OIE. Manual of Diagnostic Tests for Terrestrial Animals. 2019.
33. Sambrook J, Russell DW. *Molecular Cloning: A Laboratory Manual*. 2001.
34. Green MR, Sambrook J. DNA isolation methods. Cold Spring Harb Protoc. 2017.
35. Wilson K. Preparation of genomic DNA. Curr Protoc Mol Biol. 2001.
36. Tan SC, Yiap BC. DNA extraction methods. J Biomed Biotechnol. 2009;2009:574398.
37. Gallagher SR, Desjardins PR. Quantitation of DNA and RNA. Curr Protoc Mol Biol. 2006.

38. Botstein D, et al. RFLP in genetic mapping. Am J Hum Genet. 1980;32:314–31.
39. Southern EM. Detection of DNA fragments. J Mol Biol. 1975;98:503–17.
40. Williams JGK, et al. RAPD markers. Nucleic Acids Res. 1990;18:6531–5.
41. Hadrys H, et al. RAPD reliability. Mol Ecol. 1992;1:55–63.
42. Vos P, et al. AFLP technique. Nucleic Acids Res. 1995;23:4407–14.
43. Mueller UG, Wolfenbarger LL. AFLP applications. Trends Ecol Evol. 1999;14:389–94.
44. Tautz D. SSR markers. Nucleic Acids Res. 1989;17:6463–71.
45. Ellegren H. Microsatellite evolution. Nat Rev Genet. 2004;5:435–45.
46. Vignal A, et al. SNP markers review. Genet Sel Evol. 2002;34:275–305.
47. Morin PA, et al. SNP applications. Trends Ecol Evol. 2004;19:208–16.
48. McCue ME, et al. Equine SNP genotyping arrays. Anim Genet. 2012;43:617–25.
49. Orlando L, et al. Equine genomics advances. Science. 2013;339:1288–93.
50. Metzker ML. Sequencing technologies—the next generation. Nat Rev Genet. 2010;11:31–46.
51. van Dijk EL, Auger H, Jaszczyszyn Y, Thermes C. Ten years of next-generation sequencing technology. Trends Genet. 2014;30:418–26.
52. Goodwin S, McPherson JD, McCombie WR. Coming of age: next-generation sequencing technologies. Nat Rev Genet. 2016;17:333–51.
53. Logsdon GA, Vollger MR, Eichler EE. Long-read sequencing applications. Nat Rev Genet. 2020;21:597–614.
54. Wade CM, Giulotto E, Sigurdsson S, et al. Genome sequence of the horse. Science. 2009;326:865–7.
55. Morin PA, Luikart G, Wayne RK. SNPs in genetics and conservation. Trends Ecol Evol. 2004;19:208–16.
56. Meuwissen THE, Hayes BJ, Goddard ME. Genomic selection using dense markers. Genetics. 2001;157:1819–29.
57. Hayes BJ, Bowman PJ, Chamberlain AJ, Goddard ME. Genomic selection review. J Dairy Sci. 2009;92:433–43.
58. Petersen JL, Mickelson JR, Rendahl AK, et al. Genetic variation in horses. PLoS Genet. 2013;9:e1003211.
59. Hill EW, Gu J, Eivers SS, et al. MSTN gene and performance. PLoS ONE. 2010;5:e8645.
60. McCue ME, McCoy AM, Valberg SJ, et al. Genomic analysis in horses. BMC Genomics. 2010;11:113.
61. Mullis K, Faloona F. PCR method. Methods Enzymol. 1987;155:335–50.
62. Saiki RK, Scharf S, Faloona F, et al. DNA amplification. Science. 1985;230:1350–4.
63. Edwards MC, Gibbs RA. Multiplex PCR development. Genome Res. 1994;3:S65–75.
64. Bustin SA. RT-PCR and gene expression analysis. J Mol Endocrinol. 2000;25:169–93.
65. Bustin SA, Benes V, Garson JA, et al. MIQE guidelines. Clin Chem. 2009;55:611–22.

66. Huggett JF, Foy CA, Benes V, et al. Digital PCR guidelines (dMIQE). Clin Chem. 2013;59:892–902.
67. Sanger F, Nicklen S, Coulson AR. DNA sequencing method. PNAS. 1977;74:5463–7.
68. Heather JM, Chain B. History of sequencing. Genomics. 2016;107:1–8.
69. Eid J, Fehr A, Gray J, et al. Real-time DNA sequencing. Science. 2009;323:133–8.
70. Mount DW. Bioinformatics: Sequence and Genome Analysis. 2nd ed. Cold Spring Harbor; 2004.
71. Lesk AM. Introduction to Bioinformatics. Oxford University Press; 2019.
72. Baxevanis AD, Bader GD, Wishart DS. Bioinformatics: A Practical Guide. Wiley; 2020.
73. Sayers EW, Beck J, Bolton EE, et al. Database resources of NCBI. Nucleic Acids Res. 2021;49:D10–7.
74. Cunningham F, Allen JE, Allen J, et al. Ensembl 2022. Nucleic Acids Res. 2022;50:D988–95.
75. Kent WJ, Sugnet CW, Furey TS, et al. UCSC Genome Browser. Genome Res. 2002;12:996–1006.
76. Hasin Y, Seldin M, Lusis A. Multi-omics approaches. Genome Biol. 2017;18:83.
77. Karczewski KJ, Snyder MP. Integrative omics. Nat Rev Genet. 2018;19:299–310.
78. Subramanian I, Verma S, Kumar S, et al. Multi-omics data integration. Brief Bioinform. 2020;21:1112–24.
79. Andersson LS, Larhammar M, Memic F, et al. Mutations in DMRT3 affect locomotion in horses. Nature. 2012;488:642–6.
80. McGivney BA, Browne JA, Fonseca RG, et al. Exercise genomics in horses. BMC Genomics. 2010;11:113.
81. Velie BD, Hamilton NA, Wade CM. Heritability of racing performance. Anim Genet. 2015;46:23–30.
82. Hill EW, Gu J, McGivney BA, et al. MSTN gene and performance traits. PLoS ONE. 2010;5:e8645.
83. Toro MA, Fernández J, Caballero A. Genetic diversity conservation. Genet Sel Evol. 2009;41:2.
84. FAO. Molecular Genetic Characterization of Animal Genetic Resources. FAO Animal Production and Health Guidelines; 2011.
85. Mardis ER. DNA sequencing technologies: 2006–2016. Nat Protoc. 2017;12:213–8.
86. Wetterstrand KA. DNA sequencing costs: data from NHGRI Genome Program. Nat Methods. 2021.
87. Attwood TK, Blackford S, Brazas MD, et al. Bioinformatics training challenges. Brief Bioinform. 2019;20:1003–13.
88. Stephens ZD, Lee SY, Faghri F, et al. Big data challenges in genomics. PLoS Biol. 2015;13:e1002195.
89. Marx V, Biology. The big challenges of big data. Nature. 2013;498:255–60.
90. Knoppers BM. Ethics in genomics. Nat Rev Genet. 2014;15:75–6.
91. Quick J, Loman NJ, Duraffour S, et al. Real-time portable genome sequencing. Nature. 2016;530:228–32.
92. Libbrecht MW, Noble WS. Machine learning in genomics. Nat Rev Genet. 2015;16:321–32.
93. Eraslan G, Avsec Ž, Gagneur J, Theis FJ. Deep learning in genomics. Nat Rev Genet. 2019;20:389–403.

94. Doudna JA, Charpentier E. CRISPR-Cas9 genome editing. Science. 2014;346:1258096.

Figures

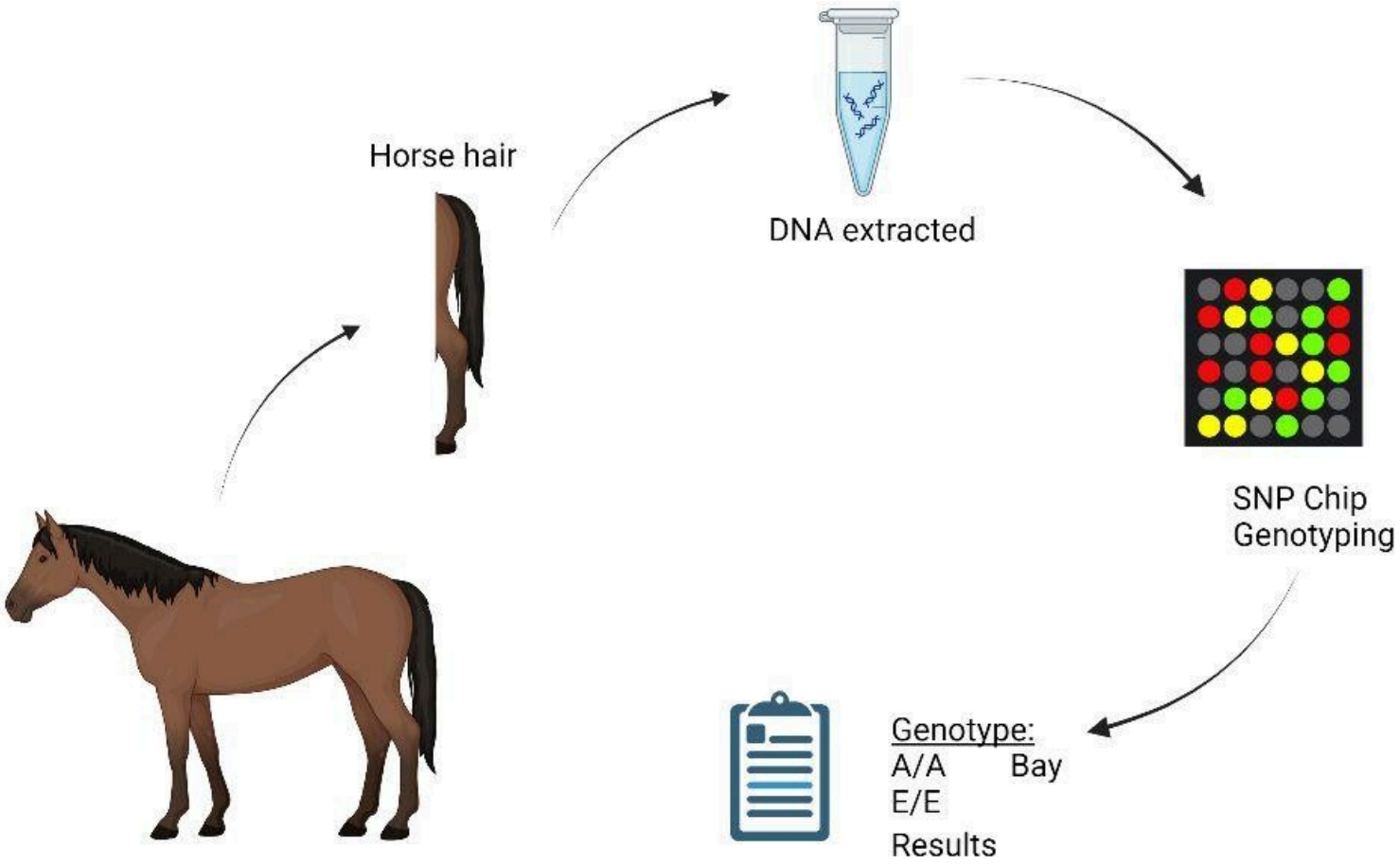


Figure 1

Overview of genomic tools in equine research.

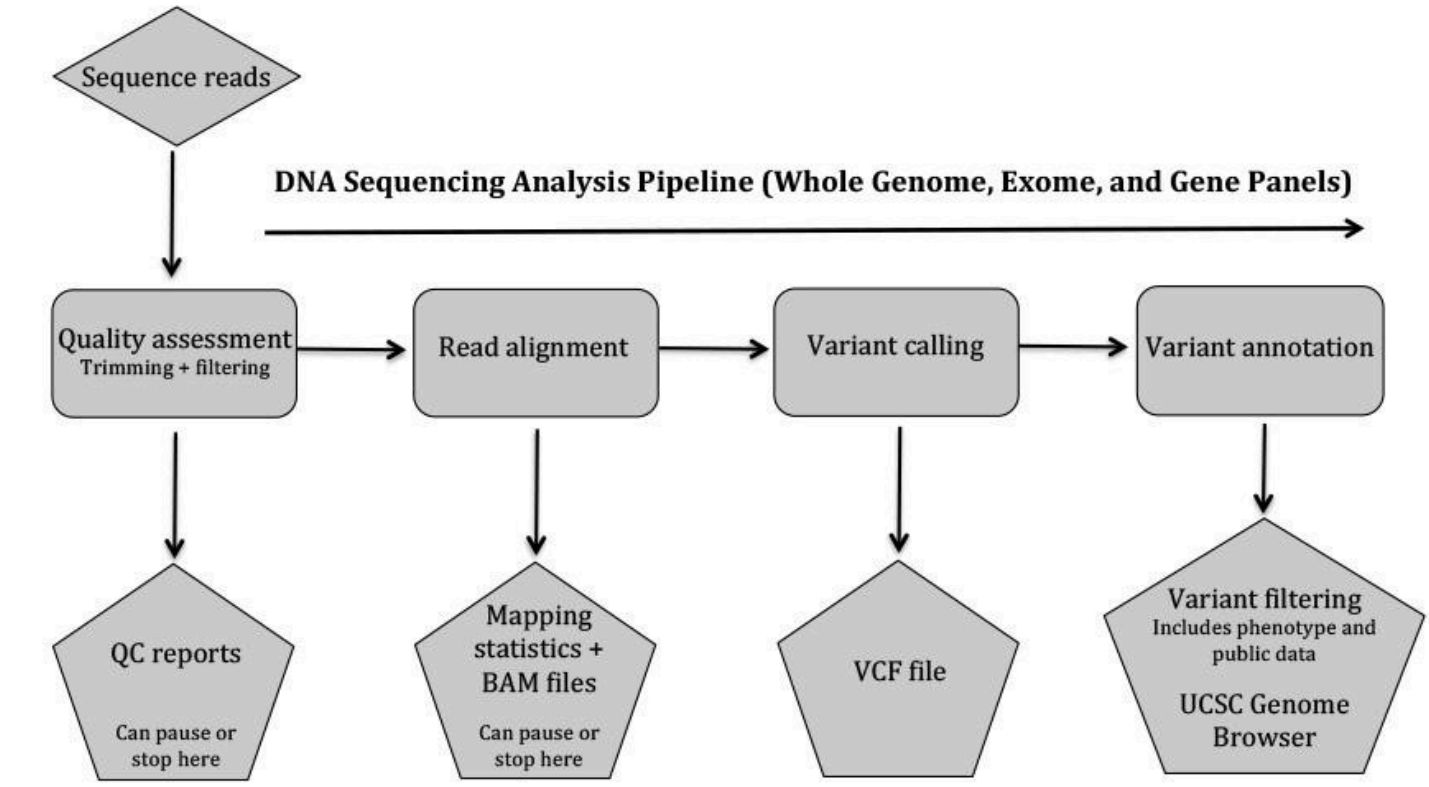


Figure 2

Bioinformatics and data integration in equine research.

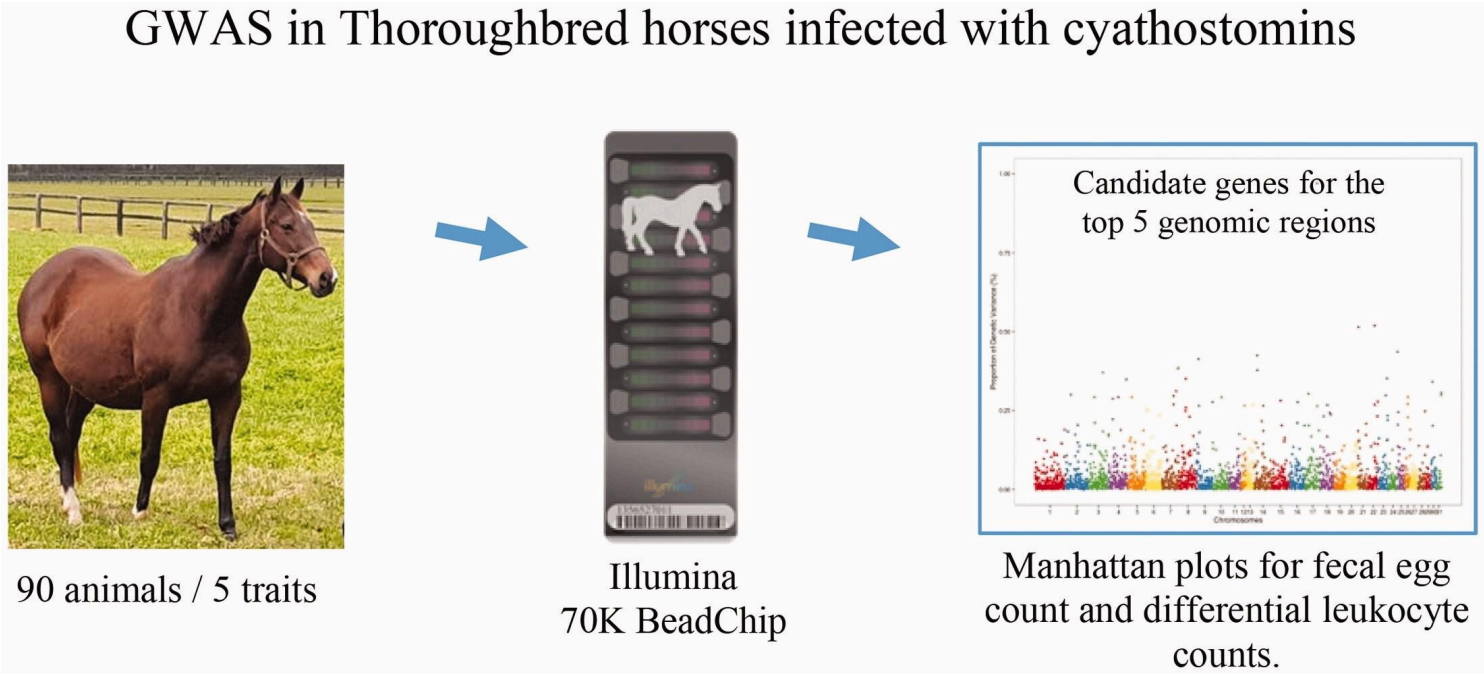


Figure 3

Applications of genomic tools in equine health and performance.