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Genetic Analysis of Wild and Domestic Rabbits Using Whole-genome Sequencing

Mario Zhan*

Department of Chemistry, University of Florence, Sesto Fiorentino, Italy

Introduction

Rabbits, both wild and domestic, have been the subject of extensive genetic research due to their evolutionary adaptations, domestication processes, and agricultural significance. Whole-genome sequencing has provided an opportunity to explore the genetic diversity, population structure, and evolutionary history of rabbit breeds, shedding light on the genetic basis of domestication and the traits that differentiate wild and domestic populations. The genetic divergence between wild and domestic rabbits is a product of both natural selection and artificial selection imposed by humans. Wild rabbits, primarily represented by the European rabbit, exhibit high genetic diversity due to their adaptation to diverse environments and natural evolutionary processes. In contrast, domestic rabbits have undergone selective breeding for traits such as docility, size, fur quality, and reproductive efficiency. These selection pressures have led to reduced genetic diversity in domestic breeds compared to their wild counterparts, as seen in other domesticated species.

Description

Whole-genome sequencing of multiple wild and domestic rabbit populations enables the identification of genetic variants associated with domestication and adaptation. By analyzing genome-wide Single Nucleotide Polymorphisms (SNPs) and structural variations, researchers can pinpoint specific genomic regions that have been under selection. Studies have identified genes related to neural development and behavioral traits, which are crucial in differentiating domestic rabbits from their wild ancestors. Genes involved in brain function and neurotransmission, such as those in the glutamate and dopamine pathways, show significant differences between wild and domestic rabbits, highlighting the role of neural adaptations in domestication. Population genetic analysis further reveals the demographic history of rabbits, including past bottlenecks and expansions. The domestication of rabbits is believed to have occurred by monks in Southern France, and genomic evidence supports a strong selection for tameness and reduced flight response. This process is reflected in the reduction of genetic variation in domestic populations, particularly in regions of the genome associated with stress response and cognition. Genome-wide scans for signatures of selection have identified specific loci where domestic rabbits exhibit reduced heterozygosity, indicating selective sweeps in domesticated breeds [1].

Another key aspect of whole-genome sequencing is its ability to uncover the genetic basis of phenotypic diversity among domestic breeds. Rabbits display a wide range of coat colors, fur textures, and body sizes, many of which are the result of specific genetic mutations. The ASIP and MC1R genes, for example, play crucial roles in coat color determination, and mutations in these genes contribute to the diverse pigmentation seen in domestic breeds. Additionally, genes related to skeletal structure and muscle development have been identified, providing insights into the morphological differences between wild and domestic rabbits. Hybridization between wild and domestic rabbits is another factor that influences genetic variation. In regions where wild and domestic populations coexist, genetic introgression occurs, leading to the exchange of alleles between the groups. This gene flow can introduce beneficial traits from wild rabbits into domestic populations, potentially enhancing genetic resilience. Conversely, domestic alleles may influence wild populations, affecting their fitness and adaptability. Whole-genome sequencing allows researchers to trace these hybridization events and assess their impact on genetic diversity [2,3].

Beyond domestication and adaptation, whole-genome sequencing has implications for rabbit conservation and breeding programs. Understanding the genetic makeup of different rabbit populations helps in managing genetic resources, preserving rare breeds, and preventing the loss of valuable genetic diversity. Conservation efforts for wild rabbit populations, particularly those facing habitat loss and disease threats, can benefit from genomic studies that identify genetic markers associated with disease resistance and environmental adaptation. Future research in rabbit genomics will likely focus on integrating functional genomics, epigenetics, and transcriptomics to gain deeper insights into gene regulation and expression. Comparative genomics between rabbits and other domesticated species can also provide broader perspectives on the mechanisms underlying domestication and species evolution. The application of genome editing technologies, such as CRISPR, may further enable targeted genetic modifications to enhance desirable traits in domestic rabbits while preserving genetic integrity [4,5].

Conclusion

In conclusion, whole-genome sequencing has revolutionized our understanding of wild and domestic rabbit genetics by revealing the evolutionary, demographic, and functional aspects of their genomes. The study of genetic variation and selection in rabbits provides valuable insights into domestication, adaptation, and breed diversification, contributing to both fundamental biology and practical applications in animal breeding and conservation.

Acknowledgement

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Conflict of Interest

None.

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Address for Correspondence: Mario Zhan, Department of Chemistry, University of Florence, Sesto Fiorentino, Italy, E-mail: zhanmar@gmail.com

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