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Molecular Mechanisms Underlying Mammalian Trait Evolution

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Abstract This study systematically reviews the molecular mechanisms underlying mammalian trait evolution, revealing the significant roles of genetic mutations, natural selection, genetic drift, gene flow, and epigenetic modifications in trait evolution. It delves into the roles of genomic innovations such as transcription factors and their regulatory networks, non-coding RNAs, differential gene expression, gene duplication and divergence, horizontal gene transfer, genome rearrangements, as well as key molecular pathways such as signaling pathways, metabolic pathways, and sensory adaptation-related pathways. Through case studies on the evolution of fur and skin pigmentation, mammalian teeth and dietary adaptations, and reproductive strategies and mechanisms, the concrete manifestations of genomic innovation and environmental adaptation in trait evolution are demonstrated. The study also discusses the application of high-throughput sequencing technologies, comparative genomics and phylogenetics, functional genomics, and gene editing technologies (such as CRISPR/Cas9) in evolutionary research, emphasizing the impact of the environment on gene expression and trait evolution. These findings provide profound insights into evolutionary biology and related fields.

Keywords Mammals; Trait evolution; Molecular mechanisms; Gene regulation; Epigenetics

1 Introduction

Mammalian trait evolution encompasses a wide array of complex characteristics, including behaviors, physiological adaptations, and morphological changes. These traits have evolved through intricate genetic and molecular mechanisms, often in response to environmental pressures and ecological niches. For instance, the transition of mammalian species to marine environments has led to convergent evolution in traits such as muscle physiology and sensory systems, driven by parallel shifts in evolutionary rates of specific genes (Foote et al., 2015; Chikina et al., 2016). Similarly, the evolution of longevity in mammals has been linked to genetic changes in pathways related to cell cycle, DNA repair, and immunity, highlighting the role of molecular constraints in shaping lifespan traits (Kowalczyk et al., 2020).

Understanding the molecular mechanisms underlying mammalian trait evolution is crucial. It provides insights into the genetic basis of adaptation and the connection between genotype and phenotype (Pardo-Díaz et al., 2015). This knowledge can elucidate how specific genetic changes contribute to the development of complex traits, such as the cognitive abilities observed in certain fish species, which may offer parallels to mammalian brain evolution (Schartl et al., 2013). Additionally, identifying the molecular events that drive phenotypic changes can inform our understanding of human-specific traits and their evolutionary origins, as seen in the loss of regulatory DNA sequences that correlate with unique human anatomical features (McLean et al., 2011). Moreover, a comprehensive understanding of these mechanisms can aid in predicting evolutionary responses to environmental changes and in identifying potential targets for medical and conservation efforts.

This study is to synthesize current knowledge on the molecular mechanisms driving the evolution of mammalian traits. By integrating findings from various studies, this study aims to identify common genetic pathways and molecular events that have contributed to the diversification of mammalian species. We desire to uncover patterns of positive selection, gene duplication, and regulatory changes that have facilitated the adaptation of mammals to diverse environments and lifestyles. Through this comprehensive analysis, the study excepts to provide a cohesive understanding of how molecular changes drive phenotypic evolution in mammals, offering insights that are both scientifically valuable and practically relevant.

2 Evolutionary Framework

2.1 Overview of mammalian evolutionary history

Mammalian evolution is marked by significant diversification and adaptation events that have shaped the vast array of species we see today. The emergence of the six-layered neocortex in reptilian ancestors of mammals represents a fundamental evolutionary landmark, enabling the remarkable sensory, motor, and cognitive abilities of mammals (Franchini, 2021). The evolutionary history of mammals also includes the divergence of major lineages such as placentals, marsupials, and monotremes, each adapting uniquely to their environments (Figure 1) (Brawand et al., 2011; Franchini, 2021). Additionally, the study of marine mammals from different orders has provided insights into convergent evolution, where similar phenotypic traits have evolved independently in response to aquatic environments (Foote et al., 2015).

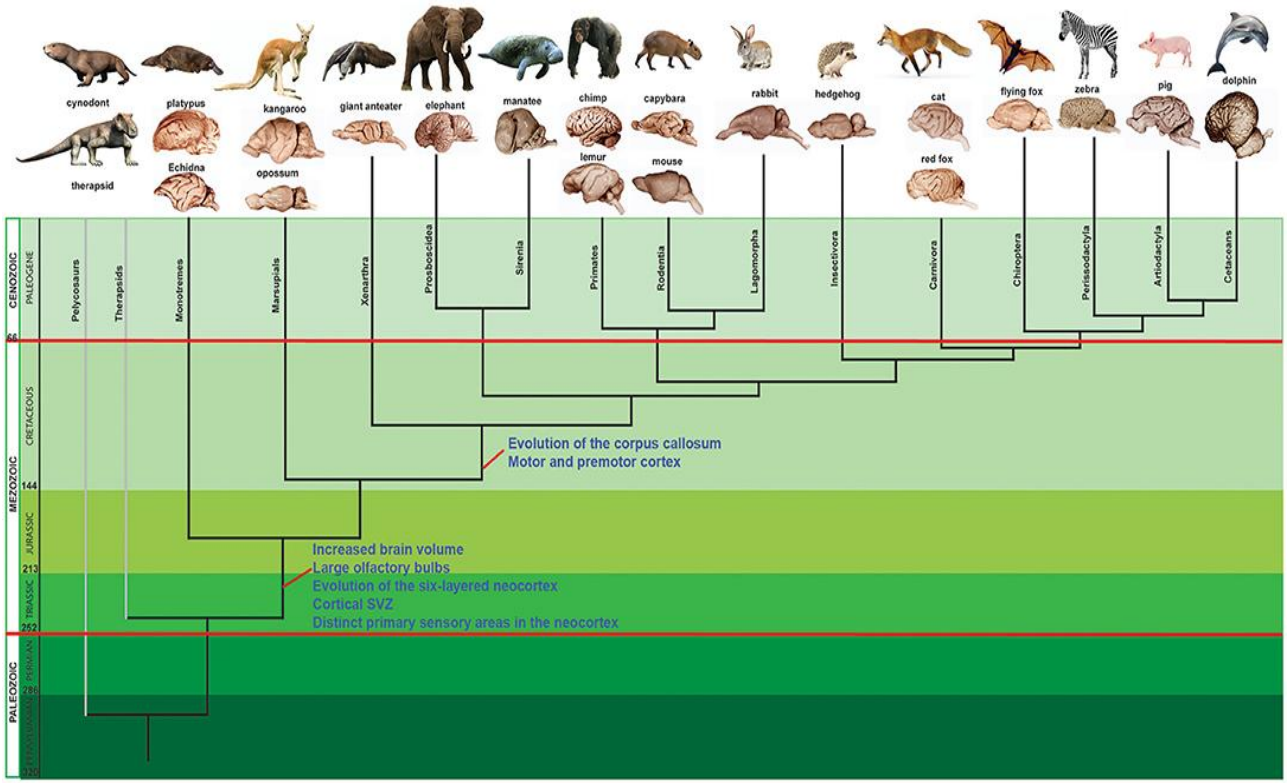

Figure 1 Phylogenetic tree of mammalian evolution (Adopted from Franchini, 2021)

Image caption: The schematic phylogenetic tree has been based on phylogenetic trees built by Goffinet (2017) and Rowe (2017). Red lines mark the mass extinction events. In every lineage two examples of lissencephalic and gyrencephalic brains are shown. Extinct lineages show examples of species that have been described from fossils specimens (Adopted from Franchini, 2021)

2.2 Key evolutionary milestones and speciation events

Several key milestones have punctuated mammalian evolution. The diversification of the neocortex in different mammalian lineages, particularly its expansion in primates, has been crucial for the development of complex behaviors and cognitive functions. The sequencing of the platyfish genome has revealed evolutionary stability in chromosomes and identified genes associated with viviparity and cognition, highlighting instances of parallel evolution and positive selection (Schartl et al., 2013). Furthermore, the study of gene expression evolution across mammalian organs has shown that selective pressures have shaped the transcriptome differently across tissues and lineages, contributing to the unique biology of various mammals.

2.3 Importance of genetic diversity in trait evolution

Genetic diversity plays a critical role in the evolution of mammalian traits. Differences in gene regulation, rather than protein-coding sequences, are often responsible for species-specific traits (Hernando-Herraez et al., 2015)1. The evolution of gene expression levels, influenced by selective pressures, has been a major driver of phenotypic diversity among mammals (Chen et al., 2018; Sun et al., 2020). Additionally, the identification of loci of adaptive

evolution through a combination of DNA, RNA, and functional methodologies has been essential in understanding the genetic basis of adaptive traits (Pardo-Díaz et al., 2015). The complexity of trait evolution is further underscored by the interplay between direct and maternal genetic effects, which vary throughout the developmental stages of an organism.

3 Molecular Basis of Trait Evolution

3.1 Genetic mutations and natural selection

Genetic mutations serve as the fundamental source of genetic variation, which is essential for the process of natural selection. Natural selection acts on these variations, favoring traits that enhance survival and reproduction. The mutation rate itself is subject to evolutionary pressures, with natural selection often pushing mutation rates down to a lower limit set by the power of random genetic drift (Lynch, 2010; Lynch et al., 2016). This drift-barrier hypothesis suggests that while natural selection aims to improve replication fidelity, the ultimate limits are determined by genetic drift. Additionally, the accumulation of deleterious mutations due to relaxed purifying selection can significantly shape life-history traits (Cui et al., 2019).

3.2 Role of genetic drift and gene flow

Genetic drift, the random fluctuation of allele frequencies, plays a crucial role in the evolution of traits, especially in small populations where its effects are more pronounced. It can lead to the fixation of neutral or even deleterious mutations, thereby influencing the genetic architecture of populations. Gene flow, on the other hand, introduces new genetic material into populations, which can either constrain or facilitate adaptive evolution.

3.3 Epigenetic modifications and their impact

Epigenetic modifications, such as DNA methylation, histone modification, and RNA-associated silencing, can alter gene expression without changing the underlying DNA sequence. These modifications can have significant morphological, physiological, and ecological consequences and are heritable across generations, suggesting their importance in evolution (Wang et al., 2017). Furthermore, environmental factors can induce epigenetic changes that are transmitted across generations, providing a mechanism for the inheritance of acquired traits (Chen et al., 2016). This neo-Lamarckian concept integrates with neo-Darwinian evolution, suggesting that epigenetic mechanisms can directly influence phenotypic variation and thus impact natural selection (Skinner, 2015).

4 Gene Regulation and Expression

4.1 Transcription factors and regulatory networks

Transcription factors (TFs) are pivotal in controlling gene expression, determining cellular functions, and responses to environmental stimuli. The human genome contains approximately 1 391 sequence-specific DNA-binding transcription factors, which are crucial for various biological processes (Vaquerizas et al., 2009). These factors interact with cis-regulatory DNA elements to modulate gene expression, and their interactions can diverge rapidly across evolutionary distances, contributing to phenotypic diversity (Wilson and Odom, 2009). The interplay between TFs and other regulatory elements, such as microRNAs (miRNAs), forms complex regulatory networks that coordinate gene expression on a genome-wide scale. These networks are essential for understanding the mechanisms of transcriptional evolution and the emergence of new phenotypes.

4.2 Non-coding RNAs in gene regulation

Non-coding RNAs (ncRNAs), including long non-coding RNAs (lncRNAs) and microRNAs (miRNAs), play significant roles in gene regulation. LncRNAs are transcribed from thousands of loci in mammalian genomes and can influence the expression of nearby genes through various mechanisms, including enhancer-like activity, transcriptional processes, and RNA splicing (Engreitz et al., 2016). Cis-acting lncRNAs, in particular, modulate gene expression based on their transcription sites, contributing to the fine-tuning of spatial and temporal gene expression programs (Gil and Ulitsky, 2019). MiRNAs, on the other hand, regulate gene expression post-transcriptionally by binding to target mRNAs, often in the 3' untranslated regions, and are integral to the regulatory networks involving TFs (Martinez and Walhout, 2009). The evolution of these ncRNAs and their binding sites is crucial for understanding the broader regulatory mechanisms that drive phenotypic diversity.

4.3 Mechanisms of differential gene expression

Differential gene expression is a fundamental mechanism underlying phenotypic variation within and between species. This process is regulated at multiple levels, including transcriptional and post-transcriptional stages. Transcriptional regulation involves the interaction of TFs with DNA, which can be influenced by chromatin structure and the presence of cis-regulatory elements. Post-transcriptional regulation, mediated by miRNAs and other ncRNAs, adds another layer of control by modulating mRNA stability and translation. Advances in RNA sequencing have enabled high-resolution analysis of gene expression variation, revealing the impact of genetic variation on transcription, splicing, and allele-specific expression (Pickrell et al., 2010). These insights highlight the complexity of gene regulatory networks and the importance of integrating multiple regulatory mechanisms to fully understand the evolution of gene expression (Chen and Rajewsky, 2007).

5 Genomic Innovations

5.1 Gene duplication and divergence

Gene duplication is a fundamental mechanism that provides raw genetic material for evolutionary innovation. It allows for the emergence of novel functions, facilitating adaptive evolutionary changes. Recent studies have shown that gene duplications can lead to dynamic changes in tissue expression preferences, contributing to specific organ functions during vertebrate evolution (Guschanski et al., 2017). Additionally, RNA-based gene duplication has been identified as a significant source of new functional gene copies, shedding light on the evolutionary origin and biology of sex chromosomes. The “one-to-two-to-four” rule in vertebrates highlights the importance of genome duplications in the evolution of novel gene functions. Overall, gene duplication plays a crucial role in the evolution of genomes and organisms by providing the genetic material necessary for the development of new functions.

5.2 Horizontal gene transfer

Horizontal gene transfer (HGT) is another significant mechanism driving genomic innovation. Unlike gene duplication, which primarily increases gene dosage, HGT introduces new functions by transferring genes between different species. This process has been shown to be the predominant factor in the expansion of protein families in prokaryotes, even in those with large genomes (Treangen and Rocha, 2011). HGT allows for the rapid acquisition of new biochemical capabilities, contributing to the diversification of protein families and the evolution of biological systems.

5.3 Genome rearrangements and their evolutionary significance

Genome rearrangements, including chromosomal breakages and reconfigurations, are key drivers of evolutionary change. These rearrangements can introduce genetic variation, which serves as a substrate for natural selection. For instance, nonallelic homologous recombination (NAHR) and nonhomologous end-joining (NHEJ) are mechanisms responsible for recurrent and nonrecurrent rearrangements, respectively, in the human genome (Lupski and Stankiewicz, 2005). Segmental duplications, or low-copy repeats (LCRs), are often associated with these rearrangements and can stimulate NAHR, leading to evolutionary changes analogous to base pair mutations. The presence of segmental duplications at syntenic breakpoints in the human and mouse genomes supports a nonrandom model of chromosomal evolution, indicating that specific regions are predisposed to both small-scale duplications and large-scale rearrangements. Furthermore, the alignment of conserved genomic sequences in the presence of rearrangements and horizontal transfer has revealed the mosaic nature of genomes, with lineage-specific segments and conserved regions shuffled among different genomes. These findings underscore the evolutionary significance of genome rearrangements in generating genetic diversity and driving the evolution of complex traits.

6 Key Molecular Pathways

6.1 Signaling pathways involved in trait development

Signaling pathways play a crucial role in the development and evolution of mammalian traits. Hormone-signaling pathways, for instance, are pivotal in regulating cellular physiology and gene expression, which underlie phenotypic traits. These pathways respond to environmental stimuli, mediating developmental stage-specific

phenotypic plasticity. This plasticity allows organisms to adapt their phenotypes in response to environmental variations (Lema, 2014; Sharma et al., 2018). Additionally, the IGF1 pathway has been identified as being under increased evolutionary constraint in long-lived mammals, indicating its significant role in trait development related to longevity (Chen et al., 2018; Kowalczyk et al., 2020).

6.2 Metabolic pathways influencing physiological traits

Metabolic pathways are integral to the physiological adaptations observed in mammals. For example, lipid metabolism pathways have been shown to undergo convergent evolutionary changes in marine mammals, facilitating their adaptation to aquatic environments. These changes include both adaptive evolution and loss of function in genes related to muscle physiology and sensory systems (Chikina et al., 2016). Furthermore, pathways related to cell cycle, DNA repair, and cell death are under increased evolutionary constraint in long-lived mammals, highlighting their importance in maintaining physiological traits that contribute to extended lifespan.

6.3 Pathways related to sensory adaptations

Sensory adaptations in mammals are driven by specific molecular pathways that have undergone significant evolutionary changes. The phototransduction pathway, which is crucial for visual perception, has evolved under non-random selective pressures. Central proteins in this pathway, such as G proteins and retinoid cycle chaperones, are more evolutionarily constrained, while peripheral proteins like ion channels have experienced relaxed selective pressures. Positive selection signals have been detected in genes such as the short-wave opsin (OPN1SW) in hominids, indicating adaptive changes in vision (Invergo et al., 2013). Similarly, genes involved in the development and function of the mammalian inner ear have shown signatures of positive selection, contributing to the unique hearing capacities of mammals. For instance, the genes *STRIP2* and *ABLIM2* have been identified as crucial for auditory function, with mutations leading to cochlear neuropathy in mice (Pisciottano et al., 2019). Additionally, the loss of regulatory DNA sequences near genes involved in neural function has been linked to sensory adaptations in humans, such as the loss of sensory vibrissae and penile spines (McLean et al., 2011; Endo et al., 2020).

7 Case Studies of Trait Evolution

7.1 Evolution of fur and skin pigmentation

The evolution of fur and skin pigmentation in mammals is a complex process influenced by both genetic and environmental factors. Mammalian colors and color patterns are among the most diverse traits in nature, driven by variations in pigment type and distribution. These variations have distinct developmental bases and are influenced by factors such as background matching, signaling, and physiological needs (Caro and Mallarino, 2020). Research on marine mammals has shown that genes related to skin and connective tissue have undergone adaptive evolution, further illustrating the genetic mechanisms behind pigmentation changes (Chikina et al., 2016).

7.2 Adaptations in mammalian teeth and diet

Mammalian teeth and diet have co-evolved to meet the dietary needs of different species. The *Peromyscus* genus of rodents, for example, exhibits significant diversity in reproductive strategies and dietary adaptations, which are likely driven by local environmental conditions and plasticity in phenotypic traits (Wilsterman and Cunningham, 2022). Marine mammals also provide a compelling case for studying dietary adaptations. Genes associated with lipid metabolism and sensory systems have shown accelerated evolutionary rates, suggesting adaptations to a marine diet that includes high-fat content and different sensory requirements compared to terrestrial diets. These genetic changes are indicative of the broader evolutionary pressures that shape mammalian teeth and dietary adaptations.

7.3 Evolutionary rates and lifespan phenotypes

Kowalczyk et al. (2020) proposed a novel approach to identify associations between protein evolutionary rates and continuous phenotypes across mammalian phylogeny (Figure 2). They treated absolute and relative lifespans as quantitative traits and demonstrated that these lifespan traits influence the evolutionary constraints of hundreds of genes. Specifically, the study found that genes associated with the cell cycle, DNA repair, cell death, the IGF1 pathway, and immunity are under increasing evolutionary constraint in large, long-lived mammals.

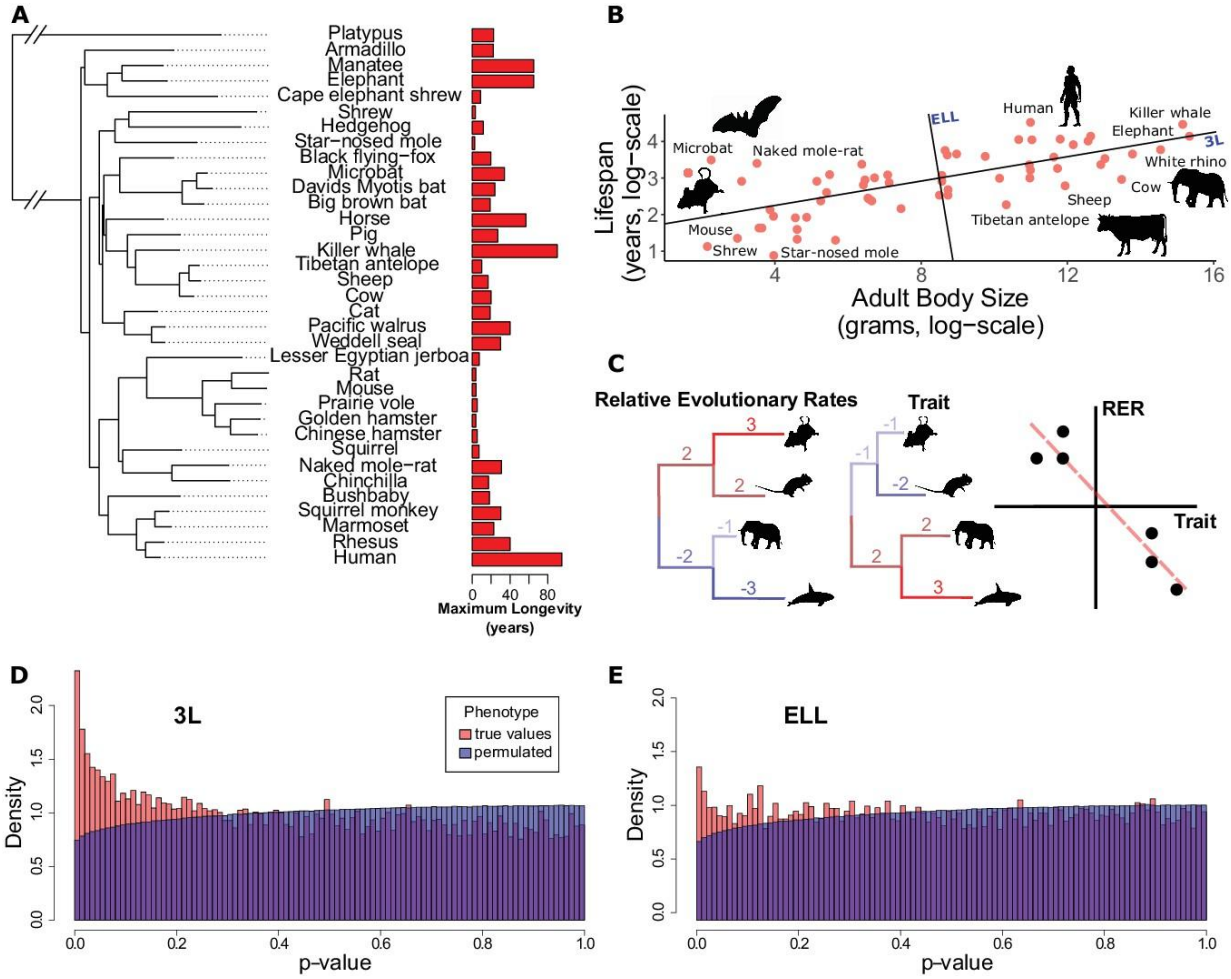

Figure 2 Many genes have evolutionary rates correlated with longevity phenotypes as demonstrated by analysis with RERconverge (Adopted from Kowalczyk et al., 2020)

Image caption: (A) A subset of species used for this analysis alongside their maximum longevity values. Lifespan varies widely across mammals independent of phylogeny. (B) Mammal body size and maximum lifespan values for 61 species. Lines represent the 3L phenotype and the ELL phenotype. (C) RERconverge pipeline to find correlation between relative evolutionary rates of genes and change in lifespan phenotypes. (D and E) Distribution of p-values from correlations between evolutionary rates of genes and change in the 3L and ELL phenotypes indicate an enrichment of significant correlations (Adopted from Kowalczyk et al., 2020)

7.4 Evolution of reproductive strategies and mechanisms

Reproductive strategies in mammals are highly diverse and have evolved to maximize reproductive success in varying environmental contexts. The *Peromyscus* genus serves as an excellent model for studying this diversity, with species exhibiting different reproductive phenologies and litter investments that are likely locally adaptive (Wilsterman and Cunningham, 2022). The platyfish, although not a mammal, offers insights into the evolution of viviparity (live birth), a trait that has independently evolved in several mammalian lineages. Genes associated with viviparity in the platyfish show signatures of positive selection, suggesting similar genetic mechanisms may be at play in mammals (Schartl et al., 2013). Furthermore, marine mammals have undergone convergent evolution in reproductive traits, with genes related to reproductive physiology showing adaptive changes to support life in aquatic environments (Foote et al., 2015).

8 Molecular Techniques in Evolutionary Studies

8.1 Advances in genomics and sequencing technologies

The advent of high-throughput sequencing technologies has significantly advanced our understanding of genomics and evolutionary biology. Next-generation sequencing (NGS) techniques have enabled the rapid sequencing of entire genomes, providing comprehensive data on genetic variation across a wide range of organisms. This genomic revolution has facilitated the annotation of genomes, allowing researchers to link genetic sequences with

functional and clinical relevance (Schulze and Lammers, 2020). The integration of these sequencing technologies with bioinformatics tools, such as the Molecular Evolutionary Genetics Analysis (MEGA) software, has further enhanced our ability to reconstruct evolutionary histories, estimate rates of molecular evolution, and infer selective forces shaping the evolution of genes and genomes.

8.2 Comparative genomics and phylogenetics

Comparative genomics and phylogenetics play a crucial role in understanding the evolutionary relationships between species. By comparing DNA and protein sequences, researchers can infer phylogenetic trees, estimate evolutionary distances, and test evolutionary hypotheses. The development of user-friendly computational tools, such as MEGA, has made it easier to perform these analyses, thereby expanding the scope of molecular evolutionary studies. These methods have been instrumental in identifying conserved genetic elements and understanding the genetic basis of adaptation and speciation (Ansai and Kitano, 2022).

8.3 Functional genomics and gene editing

Functional genomics aims to understand the roles of genes and their interactions by perturbing the flow of genetic information from DNA to RNA to protein. The CRISPR/Cas9 system has emerged as a powerful tool in this field, allowing precise and efficient genome editing across a wide range of organisms. This technology has revolutionized functional genomics by enabling researchers to create genetic knockouts, transgenics, and other forms of gene manipulation with unprecedented ease and accuracy (Bono et al., 2015; Hartenian and Doench, 2015). The CRISPR/Cas9 system has been applied to study gene function in non-model organisms, investigate the genetic basis of adaptive traits, and explore the roles of specific genes in development and disease (Chen et al., 2014; Gilles and Averof, 2014; Ahmad et al., 2018). The versatility of CRISPR/Cas9 extends to various applications, including targeted gene knock-out, gene knock-in, precise gene replacement, and chromosomal rearrangement. These techniques have been used to conduct functional analyses of naturally occurring genetic variations, providing insights into the genetic basis of reproductive isolation and adaptive traits in natural populations.

9 Integrating Genomic and Environmental Data

9.1 Environmental influences on gene expression

Environmental factors play a significant role in shaping gene expression, which in turn affects various organism-level traits. Functional genomics has provided new insights into how these environmental inputs influence gene regulation. For instance, research has shown that the social and physical environment can impact health, reproduction, and survival across mammalian species by altering gene expression patterns (Snyder-Mackler and Lea, 2018). Additionally, studies on genotype-by-environment interactions (GxE) in Simmental cattle have revealed that environmental variables significantly contribute to phenotypic variance in growth traits, highlighting the importance of understanding these interactions for predicting population vulnerability to climate change (Braz et al., 2020).

9.2 Adaptation to climate and habitat changes

Adaptation to changing climates and habitats is a critical aspect of mammalian evolution. Research has shown that species inhabiting variable environments tend to maintain a higher proportion of small-scale duplication (SSD) genes, which are essential for adapting to novel environments and surviving environmental changes (Tamate et al., 2014). In the context of climate change, phenotypic plasticity and microevolution are the primary mechanisms through which mammals adapt. However, most observed phenotypic changes in wild mammal populations have been attributed to plasticity rather than evolutionary changes (Boutin and Lane, 2013). Studies on US beef cattle have also provided evidence of local adaptation to different environmental conditions, with numerous genomic loci associated with environmental variables, indicating ongoing selection for traits that enhance survival and productivity in diverse climates (Rowan et al., 2021).

9.3 Role of ecological interactions in trait evolution

Ecological interactions are fundamental in shaping trait evolution in mammals. For example, the adaptation of marine mammals to aquatic environments has involved convergent evolution in genes associated with

thermoregulation, such as *NFIA* and *SEMA3E*, which help limit heat loss and enhance survival in aquatic habitats (Yuan et al., 2021). Additionally, the loss of certain protein-coding genes has been linked to morphological, physiological, and metabolic adaptations in both aquatic and flying mammals, suggesting that gene loss can be an important evolutionary mechanism (Sharma et al., 2018). The study of polygenic traits has also highlighted the role of gene expression differentiation in local adaptation, demonstrating that ecological interactions can drive significant evolutionary changes even in the absence of coding-sequence variation (Margres et al., 2017).

10 Future Directions and Emerging Trends

10.1 Insights from synthetic biology and evolutionary engineering

Synthetic biology is revolutionizing our understanding of gene expression and its evolutionary implications. By constructing artificial genetic systems, researchers can experimentally test evolutionary hypotheses and explore the evolutionary paths not taken by natural organisms. This approach allows for a deeper investigation into whether observed gene network architectures evolved due to selective pressures or non-adaptive forces (Bayer, 2010). Additionally, advancements in synthetic biology tools, such as CRISPR/Cas9 and programmable genetic circuits, are enabling precise control over cellular behaviors, which is crucial for studying complex regulatory networks and their evolutionary significance (Black et al., 2017; Mathur et al., 2017). These tools are expanding our understanding of gene function and regulation.

10.2 Potential of personalized genomics in understanding trait evolution

The integration of personalized genomics into evolutionary biology holds significant promise for elucidating the molecular mechanisms underlying trait evolution. By leveraging RNA-seq data across multiple mammalian species, researchers can model gene expression evolution and identify pathways under different selective pressures (Chen et al., 2018). This approach can also be applied to individual patients, allowing for the detection of deleterious expression levels and providing insights into the genetic basis of disease susceptibility and trait variation.

10.3 Ethical considerations in evolutionary research

As evolutionary research continues to advance, it is imperative to address the ethical considerations associated with these studies. The manipulation of genetic material, particularly in the context of synthetic biology and personalized genomics, raises concerns about unintended consequences and the potential for misuse. Ethical guidelines must be established to ensure that research is conducted responsibly and that the benefits of these technologies are realized without compromising safety or ethical standards. Additionally, the study of human evolution through epigenetic modifications, such as DNA methylation, necessitates careful consideration of privacy and consent, especially when dealing with sensitive genetic information (Hernando-Herraez et al., 2015). Researchers must navigate these ethical challenges to foster public trust and ensure the responsible advancement of evolutionary biology.

11 Concluding Remarks

This study systematically reviews the molecular mechanisms underlying mammalian trait evolution, revealing the significant roles of genetic mutations, natural selection, genetic drift, gene flow, and epigenetic modifications in trait evolution. It delves into the roles of genomic innovations such as transcription factors and their regulatory networks, non-coding RNAs, differential gene expression, gene duplication and divergence, horizontal gene transfer, genome rearrangements, as well as key molecular pathways such as signaling pathways, metabolic pathways, and sensory adaptation-related pathways. Additionally, through case studies, the study illustrates specific instances of fur and skin pigmentation evolution, mammalian teeth and dietary adaptations, and reproductive strategies and mechanisms evolution. The study concludes by discussing the application of high-throughput sequencing technologies, comparative genomics and phylogenetics, functional genomics, and gene editing technologies (such as CRISPR/Cas9) in evolutionary research, emphasizing the impact of the environment on gene expression and trait evolution.

These findings have profound implications for evolutionary biology and related fields. They enhance our understanding of how gene regulatory networks and gene expression changes drive phenotypic diversity. Simultaneously, advances in synthetic biology and personalized genomics provide new tools and methods for studying evolutionary processes and adaptation mechanisms, helping to unravel the complex genetic and environmental interactions. Case studies demonstrate the concrete manifestations of genomic innovation and environmental adaptation in trait evolution, providing scientific evidence for biodiversity conservation and species management. Furthermore, these studies also promote advancements in medical biology and agricultural sciences, such as disease susceptibility research, crop improvement, and animal breeding.

Despite significant progress, many unresolved questions and future research directions remain in the study of the molecular mechanisms of mammalian trait evolution. For instance, further exploration is needed into the complexities of gene regulatory networks, especially the interactions and regulatory mechanisms in different genomic contexts. Additionally, the specific roles of epigenetic modifications in long-term evolution require in-depth study, particularly how environmental information is transmitted across generations and affects phenotypic changes. Moreover, although gene editing technologies like CRISPR/Cas9 have achieved tremendous success in functional genomics research, their application in non-model organisms and complex polygenic trait studies needs further refinement and optimization. Addressing these issues will help to comprehensively reveal the molecular basis of mammalian trait evolution, driving the further development of evolutionary biology.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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