

The Latest Genomic Research Unravels the Mystery of Primate Species Evolution

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Abstract This article provides a review of a recently published research paper titled “Phylogenomic Analyses Provide Insights into Primate Evolution”. The study utilized extensive genomic data analysis to investigate the origin and evolutionary processes of primates, constructing a high-resolution phylogenetic tree of primate species and proposing several significant new insights. This review first outlines the main contents of the research, including the timing of primate species origin, the origin of human chromosome 8, the rapid evolution of primate brains, and the adaptive variations in certain genes. Next, the innovative aspects of the study are analyzed, such as its data scale and the utilization of molecular clocks, emphasizing its important contributions to deepening our understanding of the origin and evolution of primates. Lastly, this review suggests that further research should involve multiple evidence verification and functional experiments to enhance our explanatory power of complex evolutionary mechanisms. Overall, this is a groundbreaking study that provides valuable references for exploring the origins of primates and humans.

Keywords Primates; Genome; Origin; Evolution

For a long time, the origin and evolution of primates have been of great interest to humans. Primates represent a highly evolved branch of mammals, exhibiting a high degree of complexity in their morphology and behavior (Mueller and Thalmann, 2000). Humans are among the primates, so exploring the genomes, origins, and social evolution of primates will not only help answer questions about human origins but also provide valuable insights into the evolutionary history of unique human physical characteristics, thus greatly enhancing our understanding of ourselves (Fleagle, 2013). However, currently, only 23 representative non-human primate genomes have been published, with 72% of genera still unsequenced, leading to significant gaps in knowledge.

Recently, there has been a breakthrough in this situation as Chinese scientists published a research paper titled “Phylogenomic Analyses Provide Insights into Primate Evolution” (Shao et al., 2023). Using rich genomic data, they conducted an in-depth analysis of primate evolution and proposed many new insights. There are over 500 species of primates, classified into 16 families and 79 genera. This study covered 50 primate species from 14 families and 38 genera, including New World monkeys and prosimians, which were less studied in previous research. The study included 27 new high-quality primate genome sequences, providing more accurate genetic information and allowing for a more comprehensive and in-depth understanding of primate evolution. The researchers constructed a high-resolution phylogenetic tree of primate species by analyzing genomic data and fossil time data, estimating the evolutionary times of all internal nodes.

This article will provide a systematic review of the research paper, starting with an overview of the research content, followed by an analysis of the paper’s innovations and contributions, and its own insights into future research directions, in order to help readers gain a comprehensive and accurate understanding of the study and inspire further research in this field.

1 Overview of the Research Content

This research constructed a large-scale genomic dataset covering 50 primate species and reconstructed a high-resolution phylogenetic tree of primate species, delving into the evolutionary history of primates. The research revealed that the most recent common ancestor of all primates appeared approximately 68.29 to 64.95

million years ago, near the end of the Cretaceous-Paleogene mass extinction event. This suggests that the mass extinction event may have influenced the origin of primates (Shao et al., 2023).

Furthermore, the study also reconstructed the evolutionary history of primate karyotypes, finding that the karyotypes are relatively conserved. It corrected the historical hypothesis of the origin of human chromosome 8 (Figure 1). The study utilized more primate species at the chromosomal level to address previous biases caused by insufficient data. The research revealed that human chromosome 8 corresponds to two chromosomes in prosimians. Therefore, the researchers speculated that the common ancestor of hominoids and all primate ancestors had two chromosomes, which fused into one chromosome after the appearance of Catarrhini, eventually evolving into human chromosome 8.

In terms of brain evolution, there is evidence of positive selection for some genes related to brain development in primate species, which may have driven the increase in brain size from prosimians to humans (Figure 2). The study also identified certain non-coding regions that experienced accelerated evolution at four key evolutionary nodes in primates (ancestors of hominoids, catarrhines, great apes, and humans), potentially playing a role in optimizing brain development by regulating the expression of brain-related genes. These findings enrich our understanding of the molecular mechanisms underlying brain evolution.

The researchers also explored adaptive variations in certain genes related to skeletal development, digestive systems, and other functions within specific primate lineages. Additionally, the loss of tails in apes may be associated with mutations in key gene regulatory regions (Figure 3). Overall, this study has significantly advanced our understanding of the evolutionary history of primate species, providing valuable clues for the origin of humans.

2 Innovations and Contributions

2.1 Innovations of the research

This research constructed the most extensive and comprehensive genomic dataset of primate species to date, encompassing genomic information from 50 primate species. Leveraging this large-scale dataset, the researchers established a high-resolution phylogenetic tree of primate species and made corrections to some existing controversies.

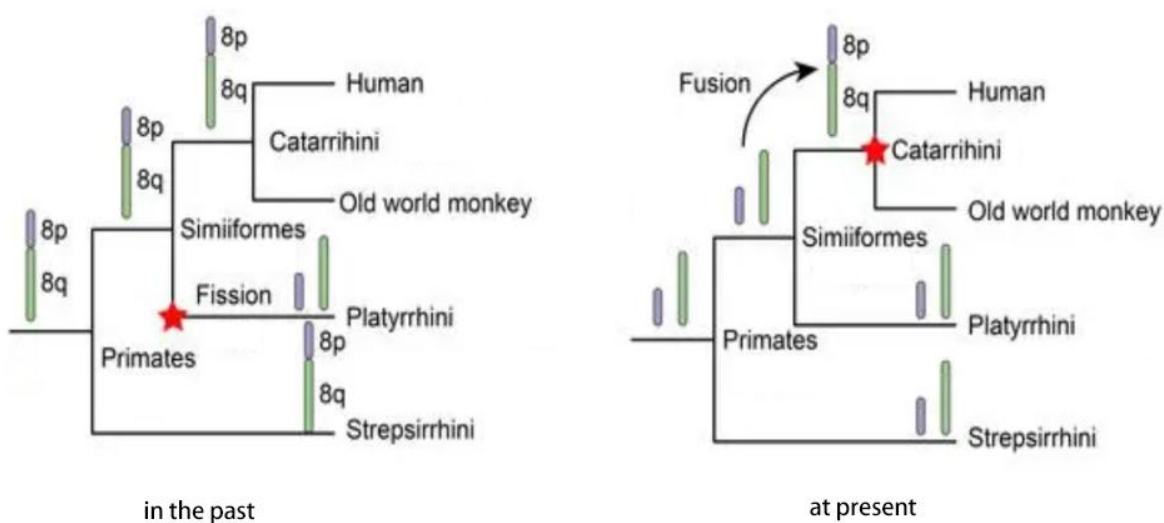


Figure 1 Different hypotheses of human Chromosome 8 in the process of primate origin (photo created: Shao et al., 2023)

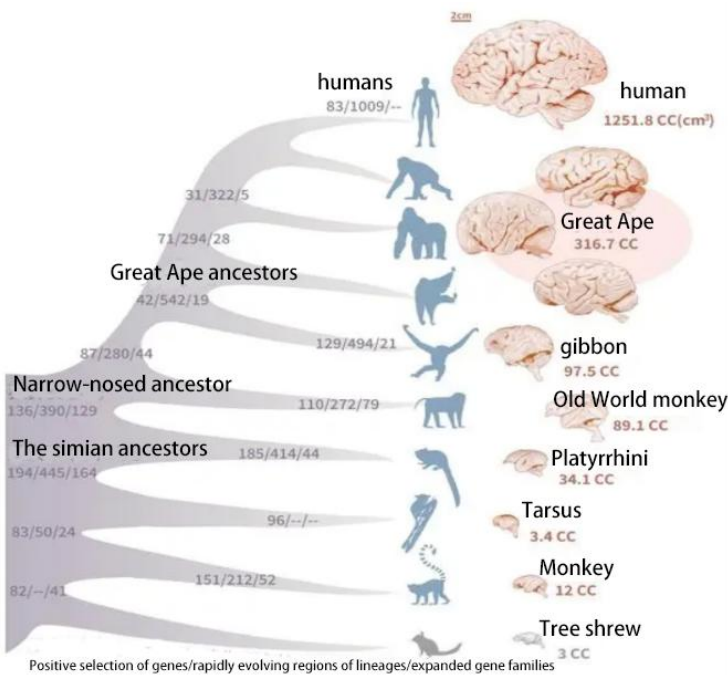


Figure 2 Evolution of brain size of primate species and genomic changes in the process (photo created: Shao et al., 2023)

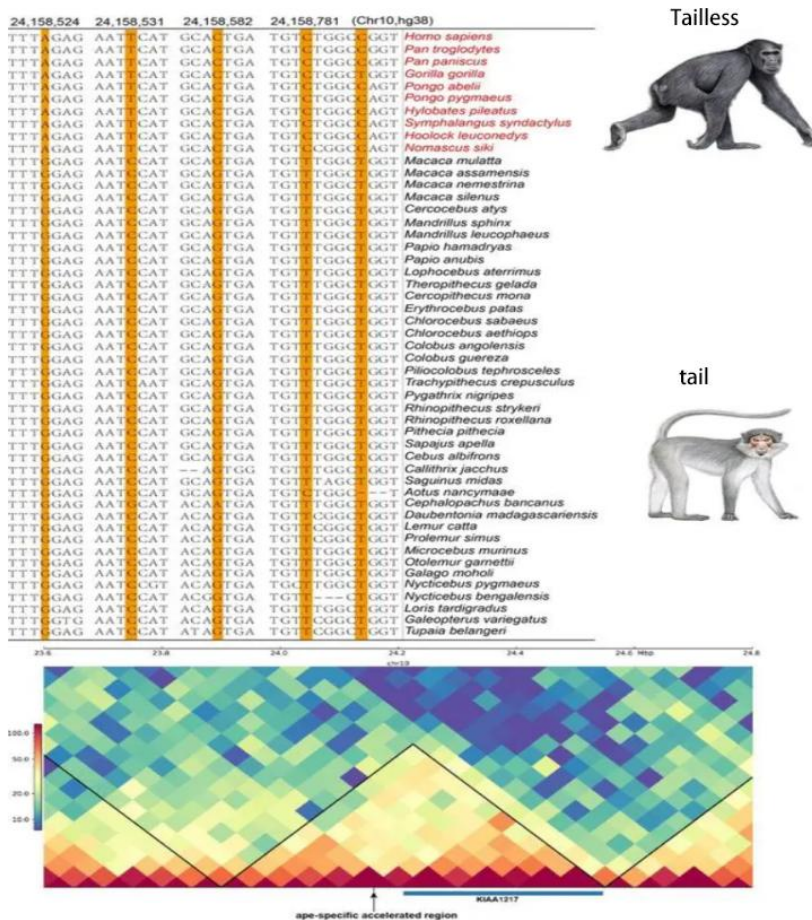


Figure 3 The rapid evolution of the regulatory region of the KIAA1217 gene in apes may cause it to lose its tail (photo created: Shao et al., 2023)

During this research, the researchers also employed molecular clock analysis for the first time to estimate the emergence time of all major primate evolutionary branches. Furthermore, they compared these estimates with paleoclimatic data, revealing the role of climate change in driving primate evolution. These aspects represent the pioneering innovations of this research.

2.2 Contributions to the research field

This research established the most comprehensive and accurate evolutionary framework of primate species to date, providing a clearer understanding of the origin and evolutionary history of primates. Particularly, for the first time, it determined the emergence time of primate clades, laying an empirical foundation for studying the origin of primates and humans.

Additionally, by analyzing positive selection genes and other factors, this research revealed some genetic mechanisms that may have driven the evolution of key adaptive traits in primates, such as the role of brain development-related genes in the evolution of intelligence. This offers clues for understanding the emergence of unique characteristics in hominoids at the molecular level.

In summary, this research, with its vast amount of data and extensive coverage, constructed a high-resolution phylogenetic tree of primate species and proposed numerous new evolutionary inferences, making significant contributions to advancing research in this field. Particularly, by uncovering the association between positively selected genes and adaptive traits, it has expanded our understanding of molecular mechanisms, providing valuable references for a deeper comprehension of the origin and evolution of primates.

3 Future Research Directions

This research primarily inferred the evolutionary relationships of primates based on genomic data and genetic information, providing new insights into the origin and evolutionary history of primates. However, there are certain limitations to relying solely on genetic information for phylogenetic analysis, and it requires validation from multiple lines of evidence to improve the accuracy of the inferences.

For instance, validation from a morphological perspective can be achieved by collecting more fossil specimens and comparing them with the evolutionary timeframe constructed in this research. Fossil records can provide independent morphological evidence (Marshall, 2019), helping to test the results obtained from genomic analysis. Additionally, further functional validation experiments are necessary to verify the some newly discovered possible mechanisms that promote primate evolution, such as gene optimization related to brain development, which will enhance the explanatory power and persuasiveness of these discoveries.

In subsequent research, expanding the samples is also essential. More primate species, especially those of rare species, can be included to provide a more comprehensive comparative basis. Moreover, comparing the primate genomes with those of other mammals will better elucidate the connections between primates and other species.

In conclusion, this research has opened up a new era of investigating primate evolution using genomic data. However, it is essential to recognize the limitations of this approach. By incorporating fossil specimens and more diverse samples, we can gain a more systematic and comprehensive understanding of the complex origin and evolutionary history of primates. This will be a key focus for future research in this field.

4 Conclusion

Exploring the origin and evolution of primate species is a crucial step in addressing the significant scientific question of human origins and an important pathway for understanding ourselves. The research paper titled “Phylogenomic Analyses Provide Insights into Primate Evolution” employs systematic genomic analysis methods to uncover important new insights into the origin and evolutionary history of primates.

The research constructs a high-quality genomic dataset, establishes the evolutionary timeframe of primates, and proposes potential genetic mechanisms driving key adaptive traits. It significantly contributes to and guides the deepening of our scientific understanding of the origin and evolutionary history of primates. However, it is

important to recognize the limitations of relying solely on one research approach. In future research, it is necessary to collect more fossil evidence, expand the sample ranges, and conduct functional validations to enhance our explanatory power of complex evolutionary history.

In conclusion, this groundbreaking research opens a new window for understanding primates and the origins of humans. It warrants further long-term exploration and extension in subsequent research endeavors.

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