

Genome Duplication and Gene Loss in Eels: Unraveling the Mysteries of Vertebrate Genome Dynamics

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The paper "The hagfish genome and the evolution of vertebrates" authored by Ferdinand Marlétaz, Jeramiah J. Smith, Daniel S. Rokhsar, and others was published in *Nature* on January 23, 2024. The authors are affiliated with the Department of Genetics at University College London, the Department of Molecular and Cell Biology at the University of California, Berkeley, and the University of Tokyo, among others. In this study, the research team explored the genome of the jawless vertebrate, the hagfish, revealing the complex history of early vertebrate evolution and the functional role of whole genome duplication. By analyzing the chromosome-level genome sequence of the brown hagfish (*Eptatretus atami*), the study presents an overview of vertebrate genome evolution, including autotetraploidization that occurred in the early Cambrian period followed by subsequent whole-genome polyploidization events. Additionally, the study discovered gene-programmed deletion phenomena occurring during the early developmental stages of hagfish. These findings provide a framework for further research into the evolution of jawless and jawed vertebrates.

1 Interpretation of Experimental Data

The study utilized high-resolution genome sequencing and phylogenetic analysis to reveal the phylogenetic relationships and genomic architectures of eels, lampreys, and jawed vertebrates. The results show significant collinearity between eel chromosomes and lamprey chromosomes, indicating that eel chromosomes are generally formed by the fusion of multiple lamprey chromosomes. Integrated analysis of gene trees and species trees supports that the vertebrate ancestor underwent one round of whole-genome duplication (1RV), followed by independent polyploidization events in jawed vertebrates and jawless fish (2RJV and 2RCY, respectively). Additionally, the eel genome exhibits significant gene loss, particularly genes related to eye and skeletal development, which explains the simplification of its body structure. The study also found that eels undergo gene-programmed deletion during early developmental stages, with these genes exhibiting different expression patterns in germ cells and somatic cells, revealing their critical roles in eel reproduction and development.

Figure 1 displays the phylogenetic relationships and genomic collinearity architectures of eels, lampreys, and jawed vertebrates. Figure 1a shows a photograph of a brown eel. Figure 1b, based on a phylogenetic tree of 176 selected genes, displays the evolutionary relationships among chordates including jawless and jawed vertebrates. Figure 1c presents karyotype diagrams of chromosomes from eels, lampreys, and sturgeons, revealing their relationships with the ancestral chordate chromosome groups (CLGs A1, A2, and B-Q). Figure 1d, through collinearity analysis, shows that eel chromosomes are generally the result of multiple lamprey chromosomes fusing together, providing significant insights into the genomic structures of eels and lampreys.

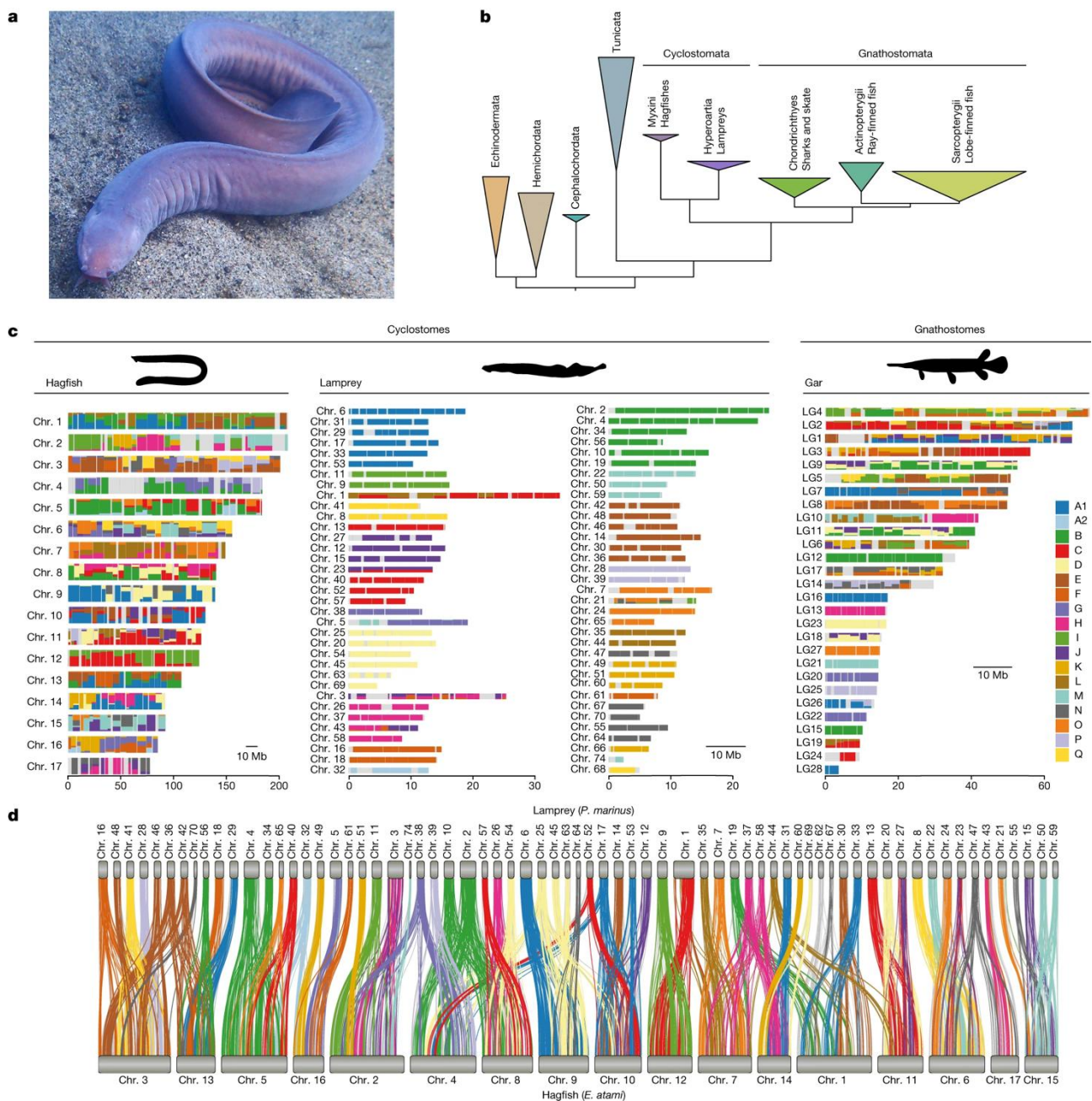


Figure 1 Phylogenetic relationships and synteny architecture of cyclostomes and gnathostomes

Figure 4 demonstrates the functional impacts of whole genome duplication (WGD) and gene loss in vertebrates. Figure 4a lists key gene families associated with neural crest cells (NCC), showing their duplication patterns in 1RV and 2RV, supporting the hypothesis that NCC predates 1RV. Figure 4b displays the functional annotation enrichment of gene retention patterns across different vertebrate species, revealing different retention patterns of genes related to the central nervous system (CNS) and organ development after genome duplication. Figure 4c compares gene expression patterns among eels, lampreys, and amphioxus, highlighting the lowest expression specificity in eels. Figure 4d shows the loss of gene families in vertebrates and other deuterostomes, emphasizing significant gene loss in eels. Figure 4e displays the functional enrichment of gene families lost in eels, particularly noting the simplification of the visual and hormonal systems. Figure 4f presents two alpha-keratin gene clusters on chromosomes 14 and 4 of eels and their expression in different tissues, highlighting the unique gene expression patterns in the eel's mucous glands.

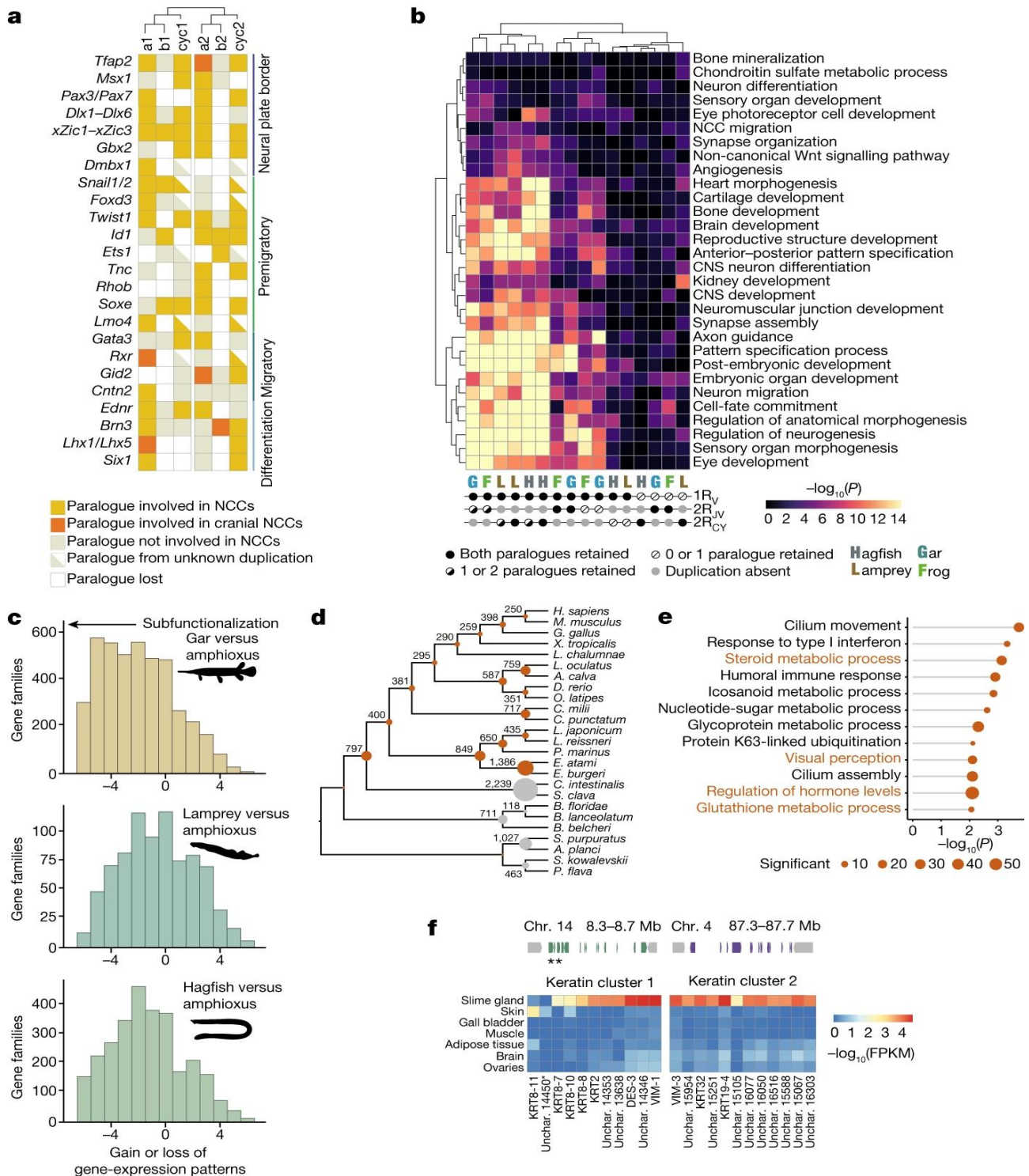


Figure 4 Functional effects of vertebrate WGD and gene loss in vertebrates

2 Insights of Research Findings

The study, through high-resolution sequencing and analysis of the eel genome, has revealed key events in the early evolution of vertebrates. The genomic structures of eels and lampreys highlight significant differences in their collinearity and chromosomal fusion, supporting their monophyletic grouping. These results suggest that eel chromosomes are typically the result of multiple lamprey chromosomes fusing together, offering a new perspective on the evolution of vertebrate genomes. The study also found multiple whole-genome duplication events during early vertebrate evolution. The first whole-genome duplication (1RV) occurred in the vertebrate ancestor, followed by independent polyploidization events in jawed vertebrates and jawless fish (2RJV and

2RCY), which profoundly impacted the complexity and diversity of vertebrate genomes. The eel genome exhibits extensive gene loss, particularly genes related to eye and skeletal development, explaining the simplification of its body structure. Additionally, gene-programmed deletion phenomena occurring during the early developmental stages of eels reveal the critical roles of these genes in eel reproduction and development. Overall, this study provides important insights into the early evolution and genome dynamics of vertebrates through an in-depth analysis of the eel genome. These findings not only reveal genomic structural differences between eels and lampreys but also provide new data to understand the complex evolutionary processes of vertebrate genomes.

3 Evaluation of the Research

This study, through high-quality genome assembly and comprehensive phylogenetic analysis, has significantly advanced our understanding of the early evolution of vertebrates and genome polyploidization events. The findings reveal notable differences in genomic structure between eels and lampreys, providing crucial evidence for the phylogenetic relationships between jawless and jawed vertebrates. The research also uncovered whole-genome duplication events experienced by vertebrate ancestors and their impact on genome structure and function, which is of great importance for understanding the complexity and diversity of vertebrate genomes. Additionally, the extensive gene loss and programmed deletion phenomena observed in the eel genome during its evolutionary process offer a new perspective on the genomic dynamics of jawless fish. However, despite the valuable data provided by the study, further research is needed to reveal more details about the functional and evolutionary aspects of the eel genome. Overall, this study provides a solid foundation for understanding the genomic evolution of vertebrates.

4 Concluding Remarks

This study, through high-resolution sequencing and detailed analysis of the brown eel genome, has revealed key genomic events in the early evolution of vertebrates. The research found that vertebrate genomes have undergone multiple whole-genome duplications, which have profoundly impacted the complexity and diversity of the genome. The first whole-genome duplication occurred during the vertebrate ancestor period, followed by independent polyploidization events in jawed vertebrates and jawless fish. These polyploidization events shaped the basic architecture of existing vertebrate genomes. Additionally, eels experienced extensive gene loss during their genomic evolution, particularly genes related to eye and skeletal development, explaining the simplification of their body structure. The study also revealed that eels eliminate specific genes in germ cells through gene-programmed deletion during early development, a mechanism that is significant in jawless fish. Overall, this study provides new perspectives and a solid data foundation for understanding the early genomic evolution of vertebrates, advancing our deep understanding of vertebrate genome dynamics and evolutionary processes.

5 Access Original Paper

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