# THE WAY TO COMPLEXITY: RETHINKING A MAJOR EVOLUTIONARY TRANSITION

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For hundreds of millions of years, life on Earth consisted of simple unicellular prokaryotes, Archaea and Bacteria. It changed with the emergence of the third domain, Eukarya. Afterwards, major transitions associated with greater complexity appeared: sexuality, multicellularity, social organization, etc. For all of this to occur, prokaryotic cells had to give rise to eukaryotic cells in a singular evolutionary event: eukaryogenesis. The endosymbiotic theory explains this and is widely accepted. However, the billions of years that have passed since the fusion of an Archaea and a Bacteria have resulted in a lack of known evolutionary intermediates during that period of time. Here, we provide new insights. Both theoretical and observational approaches have been used to quantitatively understand how protein coding gene (gene hereafter) regulatory regions were transformed to allow such an increase in complexity [1–3]. The analysis of 150 million genes and 50 million proteins revealed that gene lengths and their corresponding protein lengths follow lognormal distributions across different species. The genomic operators are equivalent to multiplicative stochastic processes in terms of gene length. In addition, in a scale-invariant relationship, we found a Taylor law: the variance of the distributions depends on their mean gene length, which is a good proxy of organismal complexity. We conclude that the eukaryotic cell emerged as a second-order phase transition. The onset of the eukaryotic cell occurred abruptly at a critical and observable point. We further propose that the transition was algorithmic in nature, led by a crisis of computational complexity encountered during the design of longer prokaryotic proteomes. With our results, we can discuss whether that transition was accidental. Nevertheless, it unlocked the path toward other major transitions that shaped life on our planet as we know it today.

## **KEYWORDS**

Computational biology, evolution, eukaryogenesis, Taylor's law, phase transition

<sup>[1]</sup> E. M. Muro, F. J. Ballesteros, B. Luque, and J. Bascompte, "The emergence of eukaryotes as an evolutionary algorithmic phase transition," *Proc. Natl. Acad. Sci. U.S.A.*, vol. 122, no. 13, e2422968122, 2025. DOI: 10.1073/pnas.2422968122.

<sup>[2]</sup> E. Ferrada, "An algorithmic constraint at the transition to complex life," Proc. Natl. Acad. Sci. U.S.A., vol. 122, no. 17, e2505484122, 2025. DOI: 10.1073/pnas.2505484122.

<sup>[3]</sup> M. Buchanan, "When life got complex," Nature Physics, vol. 21, p. 683, 2025. DOI: 10.1038/s41567-025-02905-w.

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