

# Two new studies confirm the 'endogenosymbiosis' hypothesis

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Endogenosymbiosis, such as the capacity of "gene carriers" (viruses, retrovirus and bacteriophages) to share parts of their genomes in an endogenous symbiotic relationship with their hosts, was proposed in 2015 by Roberto Cazzolla Gatti, Ph.D., associate professor in ecology and biodiversity at the Tomsk State University (Russia), in a paper uploaded to bioRxiv and published in March of this year in the journal *Biologia*.

This hypothesis emerged after the idea of endosymbiosis proposed by Lynn Margulis in 1967 to explain another process that drives the expansion of the diversity of life on our planet.

Dr. Cazzolla Gatti argued in his hypothesis that "the main likely cause of the evolution of sexual reproduction, parasitism, also represents the origin of biodiversity." In other words, he suggested that sexual reproduction acts as a conservative system against the inclusion of new genetic variations into cells' DNA (supported by the DNA repair systems) and instead, the evolution of species can take place only when this preservative system fails to contrast the inclusion within the host genome of hexogen parts of DNA (and RNA) coming from obliged "parasitic" elements (viruses and phages) that establish a symbiosis with their hosts. "As two parallel evolutionary lines, [sexual reproduction](#) seems to preserve what the endogenosymbiosis moves to diversify. Following the former process, the species can adapt slowly and indefinitely to the external factors, adjusting themselves, but not 'creating' novelty. The latter process, instead, leads to the speciation due

to sudden changes in genes sequences," Cazzolla Gatti wrote.

This idea challenges the canonical natural selection models based on the gradualism of the mutation-adaptation pattern, providing more support to the punctuated equilibrium theory proposed by Jay Gould and Eldredge.

Now, two independent studies recently published on *eLife* have empirically confirmed Cazzolla Gatti's hypothesis and gave it the status of a new [evolutionary theory](#).

Dr. Jamie E. Henzy and Dr. Welkin E. Johnson from Boston College has demonstrated that the complex evolutionary history of a family of antiviral genes called "interferon-induced proteins with tetratricopeptide repeats" has been shaped by continuous interactions between mammalian hosts and their many viruses.

And Dr. David Enard and colleagues from Stanford University estimate that viruses have driven close to 30 percent of all adaptive amino acid changes in the part of the human proteome conserved within mammals. Their results suggest that viruses are among the most dominant drivers of evolutionary change across mammalian and human proteomes.

"Not only can organelles be symbiotic with other cells," argues Dr. Cazzolla Gatti, "but entire pieces of genetic material coming from symbiotic parasites can be included in the host DNA, changing the gene expression and addressing the speciation process."

Previously, it was estimated that 7 to 8 percent of the entire human genome carries about 100,000 pieces of DNA from endogenous retroviruses. But currently, researchers believe this is an underestimation and that the quantity of the endogenous genetic material coming from external sources could be much higher and a more significant driver of

evolution.

**More information:** David Enard et al. Viruses are a dominant driver of protein adaptation in mammals, *eLife* (2016). [DOI: 10.7554/eLife.12469](https://doi.org/10.7554/eLife.12469)

Jamie E Henzy et al. Phylogenetic sleuthing reveals pair of paralogous genes, *eLife* (2016). [DOI: 10.7554/eLife.17224](https://doi.org/10.7554/eLife.17224)

Roberto Cazzolla Gatti. A conceptual model of new hypothesis on the evolution of biodiversity, *Biologia* (2016). [DOI: 10.1515/biolog-2016-0032](https://doi.org/10.1515/biolog-2016-0032)

A new idea on the evolution of biodiversity doi: [dx.doi.org/10.1101/019828](https://dx.doi.org/10.1101/019828)

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