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## EDITED BY

John Maxwell Halley,  
University of Ioannina, Greece

## REVIEWED BY

Diogo Mayrinck,  
Rio de Janeiro State University, Brazil

## \*CORRESPONDENCE

Alexis Marchesini

✉ alexis.marchesini@cnr.it

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# Commentary: Biological recycling theory: a cyclic network framework for evolutionary innovation and recovery

Alexis Marchesini<sup>1,2\*</sup>

<sup>1</sup>Research Institute on Terrestrial Ecosystems (IRET), National Research Council of Italy (CNR), Terni, Italy, <sup>2</sup>NBFC, National Biodiversity Future Center, Palermo, Italy

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## A Commentary on:

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## 1 Introduction

Macroevolutionary patterns such as biodiversity recovery after mass extinctions and evolutionary radiations driven by biological novelties are central questions in evolutionary biology (Erwin, 2008; Benton, 2010). Mechanisms such as mutation, selection, recombination, and hybridization provide well-established explanations for genetic and phenotypic innovation. Recently, Mesallum (2025) introduced the Biological Recycling Theory (BRT), proposing that evolution operates through a “cyclic network” rather than a purely tree-like process of descent with modification. In this view, alleles lost from extinct populations/species may persist in environmental DNA (eDNA) reservoirs and be later reintroduced into genomes through processes such as horizontal gene transfer (HGT), and recombination. While conceptually intriguing, BRT conflates processes of different nature and scope, extending microbial mechanisms to all life without a solid empirical foundation. This commentary evaluates BRT’s conceptual soundness, highlighting its major flaws (Table 1) and suggesting directions for future research.

## 2 Conceptual overreach and theoretical inconsistencies of BRT

BRT combines established processes like balancing selection, cryptic variation, and HGT into a single, problematic “recycling” mechanism.

TABLE 1 Summary of major conceptual, methodological, and empirical flaws in the Biological Recycling Theory (BRT).

Flaw category	Criticism	Rationale
Conceptual overreach	Congflation of distinct mechanisms	BRT erroneously combines intra-lineage processes (balancing selection, cryptic variation) with inter-lineage processes (HGT) into a single, universal “recycling” mechanism, ignoring vast differences in their scope and applicability.
	Indiscriminate generalization	The theory commits a category error by applying principles of microbial network evolution to eukaryotic macroevolution, which is dominated by vertical descent and is not governed by continuous environmental DNA recycling.
Methodological weaknesses	Unrealistic simulations	Agent-based models use arbitrary parameters, low replication, and oversimplified genetics (binary alleles), producing outcomes that reflect model assumptions rather than biological reality.
	Misleading innovation metric	Equating “novel genotype combinations” in a simulation with real-world phenotypic or ecological innovation is a invalid proxy that overstates the model’s findings.
Empirical implausibility	eDNA degradation	eDNA degrades rapidly and, even under ideal preservation conditions, ancient DNA is highly fragmented and damaged: the preservation of complete, functional alleles over macroevolutionary timescales is highly implausible.
	Cellular & genomic barriers	Multicellular eukaryotes lack mechanisms for the routine uptake, germline integration, and functional expression of ancient eDNA.
	Lack of genomic evidence	Comparative genomics shows no signatures of random environmental DNA integration, only evidence for vertical descent, introgression, and gene duplication.

Balancing selection maintains polymorphisms within lineages (Charlesworth, 2006), not across extinction boundaries, and cryptic genetic variation is an intragenomic reservoir, not a transgenerational recycling system (Paaby and Rockman, 2014). In contrast, HGT is a recognized evolutionary force in prokaryotes and some protists (Lorenz and Wackernagel, 1994). While HGT’s occurrence in multicellular eukaryotes is acknowledged, it remains a more limited phenomenon (Soucy et al., 2015; see point 4). Crucially, there is no compelling evidence for functional HGT from ancient eDNA into complex multicellular eukaryotes. The unifying metaphor of “alleles circulating through time and space” thus collapses mechanisms that differ profoundly in frequency and scope.

3 Methodological limitations of the simulation model

The agent-based simulations used to support BRT are elegant but biologically unrealistic. Mesallum (2025) simulated scenarios where the “full BRT” model produced faster recovery after extinctions. However, methodological concerns undermine these conclusions: (a) arbitrary parameters: probabilities for DNA uptake and mutation rates are not empirically grounded; (b) low replication: only three replicates per scenario were run, limiting statistical confidence; (c) simplistic genotype definition: binary alleles and additive fitness fail to capture genetic complexity like epistasis and pleiotropy; (d) misleading innovation proxy: counting unique genotype combinations does not equate to phenotypic innovation (Wagner, 2011). The outcomes reported by the author thus reflect model assumptions rather than emergent properties of real evolution.

4 Empirical implausibility of environmental DNA recycling

The core BRT premise, i.e. that eDNA acts as a long-term reservoir of functional alleles, conflicts with empirical evidence.

DNA persistence: DNA degrades rapidly due to chemical and enzymatic processes. Its persistence in the environment can range from days/years for extracellular eDNA in water (Harrison et al., 2019) up to ~2–2 Myr in exceptional cold, stable, clay-rich sediments (Kjær et al., 2022). However, even under ideal conditions, ancient DNA is highly fragmented and damaged (Willerslev and Cooper, 2005), rendering the preservation of complete, functional alleles over geological timescales highly implausible. Furthermore, even if well preserved, a released ancient allele would degrade rapidly, making its uptake and functional integration into a living organism infinitesimally rare (except perhaps for microorganisms under particular conditions).

Cellular and genomic barriers: for heritable change, an ancient allele must be taken up by germline cells and integrated into the genome without deleterious effects. While bacteria can freely exchange genetic material with their environment, multicellular eukaryotes show no evidence of routinely integrating environmental eDNA into their genomes. Although it is true that documented cases of HGT in plants and animals are increasingly common, they are not ubiquitous but rather context-specific. Most importantly, they typically involve direct cellular contact (e.g., in parasitism or symbiosis) or vectors like viruses (Keeling and Palmer, 2008; Mariault et al., 2025), not the scavenging of free, ancient eDNA proposed by BRT. Critically, even if integration occurred, an allele from a distantly related extinct organism (e.g., a dinosaur) would be functionally incompatible with the gene regulatory network of a living species (e.g., a modern mammal).

Genomic signatures: evidence from comparative genomics reveal clear signatures of vertical descent, introgression, and duplication, but no evidence for the systematic genomic integration of exogenous eDNA sequences in eukaryotic organisms.

## 5 The problem of scale and generalization

Cyclic genetic exchange is already a recognized model for microbial evolution, where HGT is rampant (Doolittle and Baptiste, 2007). However, this does not extend to eukaryotic evolution, which is largely vertical and shaped by mutation, recombination and hybridization. By proposing a universal framework that conflates microbial gene flow with eukaryotic macroevolution, BRT commits a category error. Evolutionary mechanisms must be interpreted within their cellular, phylogenetic and ecological contexts.

## 6 Framing and epistemic caution

The rhetorical framing of BRT as a replacement for the “*tree of life*” can lead to a misrepresentation of evolutionary theory. Tree-like descent remains a robust model, even when augmented by networks for specific cases. Moreover, relying on the “recycling” analogy without empirical evidence may inadvertently promote an “*eternal return*” view of evolution, which is not only problematic under the perspective of biodiversity conservation, but also risks acquiring theological overtones, confusing to the public’s understanding of how nature’s laws operate.

## 7 Perspectives and future directions

Despite its flaws, BRT highlights a genuine research frontier: the role of non-vertical genetic processes in macroevolution. Future research should focus on empirically testable questions: (1) What are the actual rates and adaptive impact of HGT across major lineages?; (2) Can genomic data distinguish ancient HGT events from introgression or duplication? (3) How can evolutionary models incorporate reticulate processes and HGT without sacrificing realism?

## 8 Conclusions

The biological recycling theory is a stimulating but scientifically fragile proposal. It fuses credible processes into an implausible evolutionary framework that lacks empirical grounding. Rather

than offering a paradigm shift, BRT could serve as a reminder that theoretical synthesis must remain constrained by mechanistic plausibility. Conceptual creativity is welcome, but without empirical anchors, it produces elegant metaphors detached from reality. The future of evolutionary theory lies in integrating genomic evidence, palaeontological data, and the biotic and abiotic drivers of evolution within realistic modelling frameworks, grounding evolutionary inference in both known biological processes and the deep-time patterns documented in the fossil record.

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