

Peer Review

Review of: "Micro- and Macroevolution: A Continuum or Two Distinct Types of Change?"

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DeJong and Degens present an ambitious theoretical contribution that reframes the long-standing micro–macroevolution debate through a systems-theoretical and mathematical lens. By distinguishing **first-order evolution** (parameter change within an existing state–vector space) from **second-order evolution** (expansion of the dimensionality of that space), the authors offer a formalized, genotype-based reinterpretation of evolutionary change. The conceptual clarity of mapping genes and regulatory elements onto vector dimensions—and expression levels onto parameters—is one of the paper’s central strengths. This move allows the authors to operationalize their distinction using measurable genomic properties (e.g., DNA length expansion) rather than relying solely on phenotype-based interpretations.

The simulation of “digital amoebae” effectively illustrates the alternation between parameter optimization and dimensional expansion, providing an intuitive visualization of punctuated growth patterns. The discussion thoughtfully situates the framework within existing debates on evolutionary novelty (e.g., Erwin, Wagner, Müller & Newman), and the authors appropriately moderate earlier claims by presenting their model as a contribution to, rather than a final resolution of, the controversy.

However, several issues merit careful consideration. First, equating second-order evolution strictly with code expansion (DNA length increase) may oversimplify the molecular basis of novelty; gene duplication, regulatory rewiring, exon shuffling, and network reconfiguration can generate substantial phenotypic innovation without necessarily increasing total genome size. Second, the assertion that first- and second-order evolution cannot form a continuum rests heavily on definitional boundaries, and some evolutionary biologists may argue that dimensional expansion itself often emerges incrementally from parameter changes (e.g., duplication followed by divergence). Third, while the genotype-based framing reduces certain subjective aspects of phenotype classification, the identification of “dimensions” (genes

or regulatory elements) still involves interpretative decisions regarding function and boundary definition.

Overall, the manuscript is conceptually rigorous, clearly structured, and intellectually provocative. It does not overturn the prevailing view that macroevolution builds upon microevolutionary processes, but it provides a mathematically explicit framework that sharpens the conceptual distinction between adaptive variation within an existing genetic architecture and the emergence of novel genetic architecture. As such, it represents a stimulating and valuable contribution to theoretical evolutionary biology, particularly in discussions of evolutionary novelty, systems dynamics, and genotype–phenotype mapping.

Declarations

Potential competing interests: No potential competing interests to declare.