Review of: "Darwin, Gödel, Luria, Delbrück: Biomedical, Mathematical, and Metamathematical Perspectives on Attributes and Consequences of Random Somatic Mutations Subject to Selection"

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Potential competing interests: No potential competing interests to declare.

Review of: *Darwin, Gödel, Luria, Delbrück: Biomedical, Mathematical, and Metamathematical Perspectives on Attributes and Consequences of Random Somatic Mutations Subject to Selection* by Greenspan and Han

The paper is intended for “a special issue of Axioms” which is a journal concerned with various aspects of mathematics. Their aim is to “further our understanding of the diverse mechanisms underlying phenotypic change,” and there is reference to “*The Long Reach of the Gene”* as set out by Dawkins, who focuses on “genes” and regards Darwin’s great question (the origin of species) as less important.

As reviewer Wolyniac notes, there are “myriad of ways in which phenotypic alteration may take place by direct or indirect means” and the authors discuss some interesting examples. After all this, they concede “some complexities inherent in DNA sequences” such as “the ability of a nucleotide or stretch of nucleotides of varying length to embody more than one type of information.” Here they “are not prepared to offer definitive answers.” However, their mathematician readers might have been told that Chargaff in the 1950s distinguished a factor of taxonomic importance (base composition) from base order, which provides the details. The former can now be seen as the “accent” or “dialect” of DNA that acts at a higher level (e.g. answering Darwin’s question) than the latter (e.g., determining the nature of the genes).

Thus, there are two levels of information. The authors write with approval of the “founders of population genetics, Ronald Fisher and Sewall Wright” and their followers, many of whom appear unaware of the enormous advances that were being made by biochemists and molecular biologists while theoretical population geneticists debated the so-called “modern synthesis.” A key observation is that a high GC% species has fundamental units (k-mers) enriched in those two bases (e.g., GAC, TCG, CGC), whereas a low GC% species has less of these bases (e.g., GAA, TCT, AAT, CTA). Laboratory scientists have joined forces with historians to help us understand this.