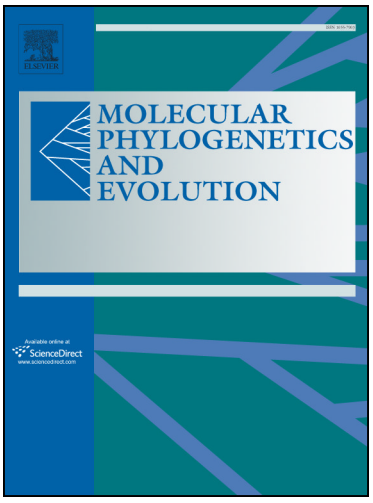

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Eliran Avni, Sagi Snir

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TOXIC GENES PRESENT A UNIQUE PHYLOGENETIC SIGNATURE

ELIRAN AVNI[1,a] AND SAGI SNIR[1,b]

[1] *Dept. of Evolutionary Biology, University of Haifa, Haifa 31905, Israel*

[a] eavni05@campus.haifa.ac.il

[b] Corresponding author: ssagi@research.haifa.ac.il

1. ABSTRACT

Horizontal gene transfer (HGT) is a major part of the evolution of Archaea and Bacteria, to the extent that the validity of the Tree of Life concept for prokaryotes has been seriously questioned. The patterns and routes of HGT remain a subject of intense study and debate. It was discovered that while several genes exhibit rampant HGT across the whole prokaryotic tree of life, others are lethal to certain organisms and therefore cannot be successfully transferred to them. We distinguish between these two classes of genes and show analytically that genes found to be toxic to a specific species (*E. coli*) also resist HGT in general. Several tools we employ show evidence to support that claim. One of those tools is the *quartet plurality distribution* (QPD), a mathematical tool that measures tendency to HGT over a large set of genes and species. When aggregated over a collection of genes, it can reveal important properties of this collection. We conclude that evidence of toxicity of certain genes to a wide variety of prokaryotes are revealed using the new tool of quartet plurality distribution.

2. BACKGROUND

Most microbial genomes have experienced extensive gene mobility between lineages during their evolution, a phenomenon known as horizontal gene transfer (HGT). This process has been critical in shaping microbial genome evolution both in terms of functional repertoires and of genome architecture [10, 17, 25, 26, 29, 31]. Many HGT events result in a gene being copied from the donor genome to the recipient genome, and this process can be mediated by integration of viruses (bacteriophages), transposable elements, or integrative plasmids, often by non-homologous recombination.

keywords: Quartet Plurality; Horizontal Gene Transfer; Gene Toxicity.