

THINKING LATERALLY ABOUT GENOMES

MARK A. RAGAN^{1,2}
m.ragan@uq.edu.au

¹*The University of Queensland, Institute for Molecular Bioscience, 306 Carmody Rd,
St Lucia, Brisbane, Queensland 4072, Australia*

²*Australian Research Council Centre of Excellence in Bioinformatics*

Keywords: lateral genetic transfer; horizontal genetic transfer; genome evolution; network of life

Abstract

Perhaps the most-surprising discovery of the genome era has been the extent to which prokaryotic and many eukaryotic genomes incorporate genetic material from sources other than their parent(s). Lateral genetic transfer (LGT) among bacteria was first observed about 100 years ago, and is now accepted to underlie important phenomena including the spread of antibiotic resistance and ability to degrade xenobiotics. LGT is invoked, perhaps too readily, to explain a breadth of awkward data including compositional heterogeneity of genomes, disagreement among gene-sequence trees, and mismatch between physiology and systematics. At the same time many details of LGT remain unknown or controversial, and some key questions have scarcely been asked. Here I critically review what we think we know about the existence, extent, mechanism and impact of LGT; identify important open questions; and point to research directions that hold particular promise for elucidating the role of LGT in genome evolution.

Evidence for LGT in nature is not only inferential but also direct, and potential vectors are ubiquitous. Genetic material can pass between diverse habitats and be significantly altered during residency in viruses, complicating the inference of donors. In prokaryotes about twice as many genes are interrupted by LGT as are transferred intact, and about 5Short protein domains can be privileged units of transfer. Unresolved phylogenetic issues include the correct null hypothesis, and genes as units of analysis. Themes are beginning to emerge regarding the effect of LGT on cellular networks, but I show why generalization is premature. LGT can associate with radical changes in physiology and ecological niche. Better quantitative models of genome evolution are needed, and theoretical frameworks remain to be developed for some observations including chromosome assembly by LGT.