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Lateral gene transfer highlight the tree of life

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Bacteria and Archaea integrate foreign DNA into their genomes via the phenomenon known as lateral gene transfer. Now widely accepted as a key driver of prokaryotic evolution, lateral gene transfer presents evolutionary biologists with a fundamental problem: Can a tree-like view of relationships among species adequately represent histories in which unrelated species commonly exchange genetic material? Sophie Abby et al. [(pp. 4962-4967) <http://www.pnas.org.gate1.inist.fr/content/109/13/4962.abstract>] investigated whether lateral transfer blurs information in phylogenetic trees. The authors used Pruniera computer program they developed to locate lateral gene transfer to examine 16 bacterial and archaeal phyla, representing 12,000 gene families distributed in 336 genomes. The authors found that for most phyla, lateral gene transfer represents a robust phylogenetic signal within the pattern of a species' diversification, and that the signal is unique to the gene family being studied. Furthermore, the history of lateral gene transfer, the authors report, contains previously overlooked information related to pinpointing the root of a species tree. The findings demonstrate that explicitly modeling lateral gene transfer can yield a more complete picture of evolution, using techniques that integrate phylogenetic information from thousands of gene families and reveal explicit evolutionary scenarios for these families, according to the authors.