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EVOLUTION

Family tree for γ -proteobacteria

The availability of whole-genome sequences for increasing numbers of related species makes studying evolutionary genetics in bacteria an attractive prospect. By comparing sequence data between species in a group, the key genomic changes that led to the diversification of different species can be identified. But the high levels of lateral gene transfer (LGT) in bacteria, by which genetic material can be transferred between distantly related species, have cast doubt on whether accurate phylogenetic trees — a crucial starting point for studies of evolutionary genetics — could ever be drawn up for bacteria. In a recent paper, Nancy Moran and colleagues have now shown that reliable bacterial phylogenetic trees can be constructed using a method that minimizes the impact of LGT events to determine taxonomic relationships among the γ -proteobacteria.

The γ -proteobacteria are a diverse group that include free-living, pathogenic and endosymbiotic members, and more complete genome sequences are available for these organisms than for any other group of bacterial species. But the γ -proteobacteria also show an extremely high tendency for LGT. The most accurate way to determine phylogenetic relationships between species is to compare the sequences of as many genes as possible that are common to all the members of the group being studied. But if this analysis includes genes that have been passed on by LGT rather than by vertical transmis-

sion from one generation to the next, the results will be skewed, making it look like certain species are more closely related than they really are.

Moran and colleagues attempted to construct a phylogenetic tree for the γ -proteobacteria using only single-copy orthologous genes — genes present in different species that have evolved from a single ancestor, but have become different from each other over time — to infer taxonomic relationships. Surprisingly, considering the high level of LGT reported for this group, they found that out of 205

such gene families analysed, 203 were consistent with the same predicted family tree. Further analysis of the only two families that disagreed with the consensus tree showed that both of these are highly likely to have undergone LGT, explaining the different phylogenies for these genes. These results indicate that single-copy orthologues only very rarely undergo LGT events and can therefore be reliably used to determine taxonomic relationships between related species. This approach provides a new method for constructing accurate phylogenetic trees for bacterial species, which will allow the changes that have driven the diversification of bacterial genomes to be determined and ultimately shed light on the processes by which new species evolve.

Louisa Flintoft



References and links

ORIGINAL RESEARCH PAPER Lerat, E., Daubin, V. & Moran, N. A. From gene trees to organismal phylogeny in prokaryotes: the case of the γ -proteobacteria. *PLoS Biol.* **1**, 1–10 (2003)

WEB SITE

Nancy Moran's laboratory:
<http://eebweb.arizona.edu/faculty/moran/lab/pages/index2.html>