

HIGHLIGHTS

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EVOLUTION

Good arbitrations

An enduring problem in evolutionary-tree building — phylogenetics — is familiar to every parent or teacher that acts as an arbitrator between squabbling children: presented with conflicting stories from different information sources how do you decide which is true? If new genome-scale analyses of phylogenetic incongruence are any guide, perhaps all child minders need to do to resolve this dilemma is to gather enough independent versions of the story.

Antonis Rokas, Barry Williams and colleagues clearly show in their new study that large concatenated data sets can overcome the problem of conflicts — that is, incongruence — between trees that are built using single genes. On the basis of a concatenated data set of 106 genes that were unambiguously orthologous among the genomes of seven *Saccharomyces* species and a related fungus, they built a tree in which every relationship received the maximum possible level of statistical support. This is an unprecedented result for a tree with so many taxa.

Phylogeneticists dream of such trees, but in their waking lives — in which usually, at best, a few genes are available — they rarely get anywhere near these consistent levels of support. In the absence of a time machine, this tree is clearly the best possible estimate of the evolutionary relationships among these yeast species.

The authors went on to look at the question of what would be the mini-



imum number of genes that would lead to the correct tree being built with good statistical support for all relationships. By randomly resampling and concatenating variable numbers of genes from the complete data set and building trees from these, they showed that 20 genes would be sufficient.

However, the authors also showed that if the chosen genes are biased in the same direction, trees that strongly support the wrong relationships can result. This is important because one common strategy is to build trees from many genes that could be biased in the same direction: mitochondrial genes are the classic example.

These new results should raise the hopes of phylogeneticists while simultaneously raising the bar for them: the true tree is out there, but more than a few genes must be sam-

pled to be sure that you have it.

The problem remains that for most researchers a few genes are all that they have or can afford to gather. The next few years might see the falling cost of high-throughput sequencing and the availability of a more diverse range of genomes make trees that are built with 20 or more genes the norm. However, until then there will still be many who, like the parent with only two versions of a juvenile dispute to work from, will be faced with the problem of how to resolve conflict in a non-arbitrary fashion.

Nick Campbell

References and links

ORIGINAL RESEARCH PAPER Rokas, A. *et al.* Genome-scale approaches to resolving incongruence in molecular phylogenies. *Nature* **425**, 798–804 (2003)

WEB SITE

Sean Carroll's laboratory:
<http://www.molbio.wisc.edu/carroll>