Zits, Grapes, and Frank Zappa

In a striking case of pathogen transfer involving the bacterium responsible for human acne, *Propionibacterium acnes*, Campisano et al. (2014) report on a new type of *P. acnes* that exploits grapevines, dubbing it *P. acnes*-type Zappae. They named the bacterium after the Italian term “zappa,” meaning hoe, as well as a tribute to eclectic composer Frank Zappa, who once wrote of “sand-blasted zits” in one of his most famous satirical songs “Jewish Princess” from his controversial 1979 “Sheik Yerbouti” album.

“This bacteria is so unconventional in its behavior, and its new habitat is so unexpected that we thought of Frank Zappa. Indeed, at the time we were discovering it, we were both playing a Zappa album in our cars,” say authors Andrea Campisano and Omar Rota-Stabelli.

The bacterium was first discovered by the research team via a 16S rDNA gene-based microbiome analysis gathered from the stems of plants sampled from multiple sites throughout northeast Italy.

The bacterium colonizes bark tissues and the pith, where the bacterium can localize intracellularly. Thus, compared with being a bane to millions of teenage faces, *P. Zappae* has adapted to an entirely new intracellular ecological niche in grapevines.

The research team also investigated the evolutionary history of *P. Zappae* by using two marker genes, recA and tly. Remarkably, their results support a human origin for the *P. Zappae* bacterium. Their data also suggest a loss of function of recA, a protein essential for the repair of DNA, which means that *P. Zappae* must rely on its grapevine host for survival. Finally, they estimate the emergence of *P. Zappae* around 7,000 years ago, an age highly compatible with the first domestication of the grapevine and a time when human-intensive practices, such as the grafting and pruning of vines, may have led to the transfer to its new host.

This is the first evidence ever of human to plant obligate transfer and gives new perspective of bacteria host transfer between humans and domesticated plants. The significance of *P. Zappae* and its influence on plant growth and health will be continued in future studies.

Reference

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Man’s Best Friend Equally Adapted to High Altitudes of Tibet

As humans have expanded into new environments and civilizations, dogs, man’s best friend, have been a faithful companion at their sides. Now, with DNA sequencing technology readily available to examine the dog genome, scientists are gaining new insights into canine evolution.

In a recent study, Li et al. (2014) explored the genetic basis of high-altitude adaptation of Tibetan mastiffs, which were originally domesticated from the Chinese native dogs of the plains. The authors examined genome-wide mutations (called single nucleotide polymorphisms or SNPs) of 32 Tibetan mastiffs, and compared them with 20 Chinese native dogs and 14 gray wolves. Overall, they identified more than 120,000 SNPs, and in their analysis, narrowed these down to 16 genes that have undergone positive selection in mastiffs, with 12 of these relevant to high-altitude adaption.

These candidate genes have been shown to be involved in energy production critical to high-altitude survival under low oxygen conditions. Similar categories showing selective signatures have been observed in other high-altitude animals, suggesting that “independently, genes can be adaptively evolved to yield similar phenotypic adaptive responses,” said Li et al. (2014).

One hypoxia-inducible factor, called EPAS1, has also been found in hypoxia adaptation in Tibetans, supporting the possibility of convergent evolution occurring between dogs and humans, though the authors caution that much more work needs to be done for a full comparison of high-altitude adaptation. For future studies, the authors will explore using whole-genome sequences from individual Tibetan mastiffs to gain better
insights into high-altitude adaptations and canine evolution.

Reference

New Software Tool Automates and Improves the Accuracy of Phylogenetic Inference from Next-Generation Sequencing Data

To reconstruct phylogenetic trees from next-generation sequencing data using traditional methods requires a time-consuming combination of bioinformatic procedures including genome assembly, gene prediction, orthology identification, and multiple alignment. As a consequence, more recently, scientists have relied on a simpler method where short-sequence reads from each species are aligned directly to the genome sequence of a single reference sequence.

Bertels et al. (2014) not only show that this simpler method can lead to significant errors and biases in phylogeny reconstruction but also have developed a new online tool called REALPHY (reference sequence alignment-based phylogeny builder) that automatically reconstructs evolutionary trees from data generated by next-generation sequencing data in a way that avoids these errors and biases. Applying this new method to several collections of bacterial genomes, the authors show that the method is at least as accurate, and often more accurate, than the traditional methods.

“We hope that REALPHY will make it easier to reconstruct phylogenies from whole genome sequences, so people can focus on solving biological problems instead of dealing with technical issues,” said Frederic Bertels (Bertels et al. 2014) of the University of Basel, Switzerland.

The software is simple enough for biologists without much bioinformatics expertise to use. REALPHY is available through a web server (http://realphy.unibas.ch/fcgi/realphy, last accessed March 19, 2014), allowing for the fast and automated generation of multiple sequence alignments from a variety of genome sequence data formats (e.g., Illumina sequences, draft genomes, fully sequenced genomes) and the automated reconstruction of phylogenies from these alignments.

Reference