BACTERIAL GENOMICS

Adapt to plants

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Plant–bacteria interactions are important for agricultural production and plant conservation due to their profound effects on plant growth and productivity. Plant-associated genes that evolved in bacteria over hundreds of millions of years of adaptation are important for such interactions. However, these genes remain poorly understood. Using a comparative genomics approach, Asaf Levy, from the US Department of Energy Joint Genome Institute, Isai Salas Gonzalez, from the University of North Carolina at Chapel Hill, and their colleagues identified plant-associated (and root-associated) genes and tried to characterize their functions.

The researchers sequenced 484 genomes of bacterial isolates from the roots of Brassicaceae, poplar and maize; these sequences were then combined with existing publicly available bacterial genomes, resulting in a data set of 3,837 genomes.

Of these, 1,160 genomes are plant-associated. Compared with non-plant-associated bacteria, plant-associated bacteria displayed a genomic expansion of carbohydrate metabolism and transport genes, and shrinkage of mobile elements. Thousands of putative plant-associated gene clusters were identified by comparing phylogenetically related genomes isolated from different environments and then validated by computational and experimental approaches. For example, two genes were experimentally shown to control bacterial colonization. Some plant-associated gene clusters captured known plant-associated operons, such as those related to root nodulation and gibberellin biosynthesis, whereas others captured novel putative plant-associated operons, such as those that encode the novel type VI effector Hyde protein that kills other plant-associated bacteria and may mediate competition among plant-associated microorganisms. The co-occurrence of many plant-associated gene clusters in multiple distant taxa suggests inter-taxon horizontal gene transfers have taken place.

Hundreds of plant-associated domains were identified as being reproducibly enriched in multiple bacterial taxa, 64 of which mimicked plant domains. In many cases, these domains showed a high homology with proteins from plant-associated oomycetes and fungi, indicating convergent evolution or horizontal gene transfer between evolutionarily distant microorganisms — probably driven by similar selective forces.

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