

Recent advances in phytoplasma research: from classification, multi-locus genotyping to pathogen-host interactions

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Phytoplasmas are a large group of phloem-inhabiting, cell wall-less bacteria responsible for numerous plant diseases worldwide. Having descended from a low G+C, Bacillus/Clostridium-like progenitor, the phytoplasma clade has evolved into diverse lineages in adaptation to a broad range of ecological niches including insect vectors. To date, 37 'Candidatus Phytoplasma' species have been formally described, and an additional 13 potentially new species have been suggested. Based on collective restriction profiles of 16S rRNA gene sequences, 32 phytoplasma groups and more than 120 subgroups have been delineated. To facilitate identification of known and new phytoplasma strains, an interactive online tool has been devised for rapid classification and taxonomic assignment of diverse phytoplasma strains. A constellation of phytoplasmal genes with different degrees of sequence conservation have been identified as additional molecular markers for finer differentiation of closely-related phytoplasma lineages.

Despite the enormous genomic and biological diversity of phytoplasmas, there are interesting common features that unite phytoplasmas. One such unifying feature is the presence of phage-based genomic islands or sequence

variable mosaics (SVMs) in all phytoplasma genomes studied thus far. We postulate that recurrent attacks by ancestral phages, integrations of phage genomes, and subsequent acquisitions of horizontally transferred genes have shaped the genomic islands, and possibly enabled phytoplasmas' transkingdom parasitism. Another common feature shared by diverse phytoplasmas is their ability to induce similar symptoms on affected plants. Such symptoms include witches'-broom growth and abnormal floral development. We found that development of these disease symptoms was linked to derailment of the genetically preprogrammed destiny of meristem cells. Such stem cell fate modifications included premature floral meristem termination, suppressed floral meristem initiation, delayed vegetative-to-inflorescence meristem conversion, and repetitive initiation of lateral vegetative meristems. Based on our findings, we hypothesize that reprogramming of meristem fate may represent a unifying mechanism underlying common disease symptoms induced by diverse phytoplasmas.