

New insights into the taxonomy of agrobacteria

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Taxonomy of agrobacteria is in constant evolution. Recent studies, primarily relying on genotypic characterization, led to description of the new species and revised taxonomy of agrobacteria. Multilocus sequence analysis (MLSA) of housekeeping genes and estimation of whole-genome based average nucleotide identity (ANI) have been especially relevant in describing novel *Agrobacterium* taxa.

In this respect, recently, our groups described two novel *Agrobacterium* species, *A. arsenijevidii* and *A. nepotum* (former *Rhizobium nepotum*), which included phytopathogenic strains carrying tumor-inducing (Ti) plasmid. They belonged to *A. tumefaciens* (biovar 1), species complex composed of at least 12 genomovars, which are not all formally named. The ANI values between type strains of *A. arsenijevidii* (KFB 330T) and *A. nepotum* (39/7T), and related species and genomic species of *A. tumefaciens* complex were lower than 92%, which was below the proposed threshold (94–96%) for the species definition and therefore confirmed that they are authentic species. In addition, another plant pathogenic species related to *A. rubi* was described as *Rhizobium skierniewicense*, and now reclassified in the genus *Agrobacterium*.

Furthermore, we studied additional atypical agrobacterial strains isolated from crown gall tumors on various fruit plants and grapevine. They have been preliminary assigned as non-pathogenic by PCR analysis targeting Ti plasmid genes. Based on sequence analysis of 16S rDNA and housekeeping genes, atypical strains clustered within the genus *Agrobacterium*, with *A. rubi*, *A. skierniewicense* and *Agrobacterium* sp. strain NCPPB 1650 as their closest relatives. Thus, our results suggest additional taxonomic diversity of agrobacteria and existence of novel phylogenetic lineages.