

Evolution and epidemiology of global populations of nursery-associated *Agrobacterium*

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Agrobacterium tumefaciens is unique in that it can facilitate the interkingdom transfer of DNA and genetically modify its plant host. While *Agrobacterium* has been coopted for use in the genetic modification of plants, it is also a major pathogen, causing crown gall disease in the nursery, orchard, and vineyard industries. Pathogenicity in *Agrobacterium* is the result of two components. First is the Ti plasmid, which carries virulence genes and the transferred T-DNA region. The second component is the chromosome of *Agrobacterium*, which comprises diverse bacterial lineages and multiple species-level groups. The Ti plasmid can be transferred from strain to strain, diversifying the pathogen and complicating efforts to understand its epidemiology. This system provides an opportunity to study transmission of plasmids and their impact on disease persistence and spread. However, the movement of plasmids, and diversity of chromosomal lineages, means that conventional methods of using whole genome SNPs to track outbreaks are not sufficient, and new techniques must be developed. Additionally, Ti plasmids, like *Agrobacterium*, are genetically diverse and represent multiple plasmid types. Using a framework of >200 sequenced *Agrobacterium* genomes isolated from around the world, and a previously developed model of Ti plasmid types, we modelled their epidemiology. Key to this study was that we first separately analyzed plasmids and strain. Combining results revealed links between nurseries, potential horizontal transfer of the plasmid between strains within nurseries, global spread of plasmids, and long-term persistence of plasmids in the agricultural system. Agricultural practices have the potential to promote the diversification of pathogens and the emergence of new pathogen lineages.

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