Evolution and epidemiology of global populations of nursery-associated Agrobacterium

Alexandra Weisberg 1, Edward Davis II 1, Javier Tabima 1, Melodie Putnam 1, Marilyn Miller 1, Michael Belcher 1, Niklaus Grünwald 1,2, Walt Ream 3, Erh-Min Lai 3, Chih-Horng Kuo 3, Joyce Loper 1,2, Jeff Chang 1

1 Oregon State University, Corvallis, USA; 2 Agricultural Research Service, Corvallis, USA; 3 Academia Sinica, Taipei, Taiwan

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.

AUTHORS’ INFO

Alexandra Weisberg, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA. Scopus: 5636735170

Edward Davis II, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA. Scopus: 55328495700

Javier Tabima, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA. Scopus: 37262084000
AUTHORS’ INFO

Melodie Putnam, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331. Scopus: 7005638450

Marilyn Miller, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA. Scopus: 57223801124

Michael Belcher, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA. Scopus: 57200333901

Niklaus Grünwald, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA; Horticultural Crops Research Laboratory, US Department of Agriculture, Agricultural Research Service, Corvallis, OR 97331, USA. Scopus: 57581518400

Walt Ream, Department of Microbiology, Oregon State University, Corvallis, OR, 97331, USA. Scopus: 6603918074

Erh-Min Lai, Institute of Plant and Microbial Biology, Academia Sinica, Taipei 11529, Taiwan. Scopus: 36110147800

Chih-Horng Kuo, Institute of Plant and Microbial Biology, Academia Sinica, Taipei 11529, Taiwan. Scopus: 35076199500

Joyce Loper, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA; Horticultural Crops Research Laboratory, US Department of Agriculture, Agricultural Research Service, Corvallis, OR 97331, USA. Scopus: 7006458001

Jeff Chang, Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, 97331, USA. Scopus: 7601552801