

The great *Agrobacterium* bestiary and its hidden ecological adaptations.

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Even if *Agrobacterium* is given as causing crown gall, this is the Ti plasmid that is the real causative agent of the disease, agrobacteria being just plasmid vehicles. The forms of agrobacterium initially non-pathogenic may become pathogenic following the acquisition of a Ti plasmid. Hence, studying the biodiversity of agrobacteria, including non-pathogenic forms, is of paramount importance to understand the crown gall epidemiology.

A.tumefaciens is not a valid species name. Thus, we'll firstly show how phylogeny and evolution studies allow the re-examination of the taxonomy of *Agrobacterium* spp. This will include the genus in the frame of its controversial inclusion into *Rhizobium* spp., and those of numerous bona fide species delineated by genome similarities (1).

Agrobacterial populations are diverse with several species co-existing in the same biotopes. According to the competitive exclusion principle, the coexistence of species depending on the same resource is unexpected, implying that evolutionary forces are driving the fixation of adaptive differences for specialized micro-niches. In a second step, we'll thus show how ancestral genome reconstruction and reverse ecology approaches permitted us to unmask the hidden ecological micro-niches that allow species to evade inter-specific competition and make species able to co-exist (2).

(1) Ramírez-Bahena M-H, Vial L, Lassalle F, Diel D, Chapulliot D, Daubin V, Nesme X, Muller D (2014). Single acquisition of protelomerase gave rise to speciation of a large and diverse clade within the *Agrobacterium/Rhizobium* supercluster characterized by the presence of a linear chromid. *Mol. Phyl. Evol.* 73:202-207.

(2) Lassalle F, Campillo C, Vial L, Baude J, Costechareyre D, Chapulliot C, Shams M, Abrouk D, Lavire C, Oger-Desfeux C, Hommais F, Guéguen L, Daubin V, Muller D, Nesme X (2011). Genomic species are ecological species as revealed by comparative genomics in *Agrobacterium tumefaciens*. *Genome Biol. Evol.* 3:762–781.