Characterization of the *Agrobacterium* plasmids by next-generation sequencing

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Agrobacteria are bacteria living in various ecological niches, e.g. the rhizosphere of numerous plants. They are able to transfer a fragment of their genomic DNA, the T-DNA, to the plant cell. The expression of T-DNA genes in the infected plant cells leads to the formation of the crown gall tumor or the hairy root overgrowth. Tumor and hairy root formation is associated with the presence of the Ti and Ri plasmids, respectively. Both Ti and Ri plasmids are transmissible by conjugation to soil agrobacteria that become virulent upon reception. Aside from genes involved in the formation of the overgrowths, T-DNAs also harbor genes that encode the synthesis of opines, which are growth substrates specific for the inciting agrobacteria.

Within this context, we investigated the genetic diversity of strains isolated from various places worldwide, including Tunisia. Bioinformatic analysis of MySeq-sequenced genomes led to the generation of 54 full plasmid sequences and 7 partial plasmid sequences still under contig form. Comparative genomics permitted the characterization of a wide plasmid diversity, particularly within the T-DNA regions. This study is the first to describe a set of over 60 genomes sequences of agrobacteria belonging to both the *Agrobacterium* and the *Rhizobium* genera.

Key words: agrobacteria, plasmid, T-DNA, NGS