Characterization of a MarR repressor involved in *Agrobacterium* fitness *in Planta*

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Agrobacterium tumefaciens is a bacterial species complex well known to be responsible of crown gall disease when they harbor the Ti (Tumor inducing) plasmid. However, agrobacteria that do not contain Ti plasmid are non-pathogenic cells, living in soil and in the rhizosphere of numerous plants. Rhizosphere is a complex environment influenced by plant roots, that exudate compounds like sugar, carboxylic acid or phenolic compounds. Some of these molecules show antimicrobial activities, some other can be used either as carbon sources by microorganism, or signals involved in plant-microbe interactions.

Genomic comparison between *Agrobacterium* species permit to identify 7 genomic regions shared by all *A. fabrum* species members (genomic species G8 of the *A. tumefaciens* complex) and absent from other agrobacteria (i.e. 7 species specific regions) (Lassalle *et al* 2011). Those regions are thought involved in plant-bacteria commensal or pathogen interactions. We studied one of this species specific regions (SpG8-1b) annotated as a putative hydroxycinnamicacid degradation region (HCA). We showed that it encodes an original pathway for the degradation of HCAs (Campillo *et al* 2014). A MarR regulator (FerR sub-family) was annotated in SpG8-1b region, suggesting that it is involved in regulation of HCA degradation. By molecular means (deletion mutant, transcriptional fusion, gel-shift) we studied the expression of HCA degradation genes and showed that this MarR regulator is a repressor of SpG8-1b gene expression. Competition analyses and *in planta* expression studies revealed a role for the regulation of HCA degradation in *A. fabrum* adaptation to plants.

Lassalle et al.(2011). Genomic species are ecological species as revealed by comparative genomics in *Agrobacterium tumefaciens*. *GBE*3:762–781

Campilloet al.(2014). Analysis of hydroxycinnamic acids degradation in *Agrobacterium fabrum* reveals a CoA-dependent, beta-oxidative deacetylation pathway. *AEM* 80 (11):3341-3349