
Genomic diversity of *Dickeya* species associated to potato

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Abstract

Blackleg and soft rot diseases caused by soft rot enterobacteria provoke important losses in potato production worldwide and are the cause of up to one third of the rejections of seed tubers lots in Europe. Modifications in the structure of pathogenic bacterial populations causing blackleg disease have been observed these last decades with the emergence of two *Dickeya* species – *D. dianthicola* and *D. solani*. To tackle the putative genetic traits involved in this emergence, we undertook both intra- and inter-species genomic comparisons. While *D. solani* appeared to be mostly clonal (Khayri et al, 2015), *D. dianthicola* strains are more diverse. Both species harbour more than 3,000 interspecific common genes including the virulence genes characterized in the model *D. dadantii* 3937 strain. Each species also possesses hundreds of specific genes that are often regrouped in genomic regions that may present signatures of horizontal transfer. To deepen our comparison of the two *Dickeya* species, we performed a transcriptomic analysis of one strain of each species after growth either in rich medium or on potato tubers. Several genes included in species-specific genomic regions were activated on tubers pointing to a possible role in interactions with plants. Interestingly, a few hundreds genes common to both species, including virulence genes, presented different expression profiles in the two species suggesting different adaptations to similar environmental conditions.

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