



Genomic analysis of the biocontrol strain *Pseudomonas fluorescens* Pf29Arp with evidence of T3SS and T6SS gene expression on plant roots

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Titre	Genomic analysis of the biocontrol strain <i>Pseudomonas fluorescens</i> Pf29Arp with evidence of T3SS and T6SS gene expression on plant roots
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Auteur	Marchi, Muriel [1], Boutin, Morgane [2], Gazengel, Kévin [3], Risper, Claude [4], Gauthier, Jean-Pierre [5], Guillerme-Erckelboudt, Anne-Yvonne [6], Lebreton, Lionel [7], Barret, Matthieu [8], Daval, Stéphanie [9], Sarniguet, Alain [10]
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Résumé en anglais	<p>Several bacterial strains of the <i>Pseudomonas</i> genus provide plant growth stimulation, plant protection against pests or bioremediation. Among these bacteria, <i>P. fluorescens</i> Pf29Arp reduces the severity of take-all, a disease caused by the pathogenic fungus <i>Gaeumannomyces graminis</i> var. <i>tritici</i> (Ggt) on wheat roots. In this study, we obtained a draft genome of Pf29Arp and subsequent comparative genomic analyses have revealed that this bacterial strain is closely related to strains of the 'P. brassicacearum-like' subgroup including <i>P. brassicacearum</i> ssp. <i>brassicacearum</i> NFM421 and <i>P. fluorescens</i> F113. Despite an overall chromosomal organization similar to these strains, a number of features including antibiotic synthesis gene clusters from secondary metabolism are not found in the Pf29Arp genome. But Pf29Arp possesses different protein secretion systems including type III (T3SS) and type VI (T6SS) secretion systems. Pf29Arp is the first <i>Pseudomonas</i> sp. strain described with four T6SS clusters (cluster I, II, III and IV). In addition, some protein-coding genes involved in the assembly of these secretion systems are basally expressed during Pf29Arp colonization of healthy wheat roots and display different expression patterns on necrotized roots caused by Ggt. These data suggest a role of T3SS and T6SS in the Pf29Arp adaptation to different root environments.</p>
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Liens

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