Biocontrol of *Pectobacterium*: Genomic of the biological agent *Rhodococcus erythropolis* R138

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Abstract

Pectobacterium is a pathogenic agent of the potato plant and tuber of which the virulence is regulated using quorum sensing signals. *Rhodococcus erythropolis* R138 has been isolated from the potato rhizosphere because of its capacity to degrade quorum sensing signals. Hence, *R. erythropolis* R138 seems to be an interesting candidate as a biological control agent. The use of this bacterium as an alternative to chemical products needs its genome sequencing in order to develop molecular tools allowing to follow the *Rhodococcus* population in the field and to increase our knowledge of its mode of action.

In this work, the *R. erythropolis* R138 genome has been obtained using the 454-Roche and Illumina sequencing and finalized using cloning and Sanger method. The genome assembling contains 43 contigs from 2kb to 1300kb belonging to 6 scaffolds for a total length of 6700kb. Four scaffolds can be link together corresponding to the circular chromosome. The two others of 84kb and 247kb in length can't be related to any other scaffold implicating the possible presence of two plasmids in *R.erythropolis* R138.
Comparison of the *R. erythropolis* R138 genome with that of different *R. erythropolis* isolates (two from NCBI database and 5 obtained by Hiseq2000 sequencing), revealed R138-specific sequences from 10kb to 53kb in length which can be used to design strain specific molecular markers. Of these 16 R138-specific sequences, twelve belong to a single scaffold of the circular chromosome and four sequences are localized on the putative plasmid scaffolds. Primers for the 16 sequences were designed and the specificity of the amplification fragments was verified.
Finally, the *R. erythropolis* R138 genome sequence will allow to develop functional approaches using transcriptomic or proteomic tools in order to identified the implicated genes in the antagonism in conditions closed to the natural infection. We developed an *in situ* pathosystem allowing to co-inoculate both the antagonist and the pathogen on potato tuber. Thus the triple interaction host/antagonist/pathogen will be taken into account.