

A Plasmid from *Pectobacterium atrosepticum* is Self-Transmissible and Contributes to Virulence of the Host Bacterium.

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Aim of the study: The genomic diversity of *Pectobacterium atrosepticum*, a specialised potato pathogen, is mostly due to mobile DNA (phages, transposons and plasmids). The role of this DNA, and plasmids in particular, in *P. atrosepticum* lifestyle is poorly studied. In this study we aimed to characterise the largest known *P. atrosepticum* plasmid, pPA21A, present in *P. atrosepticum* strain 21A originally isolated in Belarus.

Material and methods: Bacterial strains used in this work were *P. atrosepticum* 21A and SCRI1043, *E. coli* XL-1 Blue and J62. *Nicotiana tabacum* Havana petit SR1 was used for hypersensitivity tests. Standard microbiological and molecular cloning techniques were used. Gentamicin resistance cassette was taken from pJQ200mp18 plasmid.

Results: The 32 kb plasmid pPA21A contains many genes without obvious relation to plasmid maintenance. The most interesting are the ones coding for the type IV secretion apparatus (could be involved in protein delivery into plant cells and/or in conjugative plasmid transfer) and two genes of putatively eukaryotic origin coding for phospholipase D and sirtuin-like protein. For further manipulations, the pPA21A plasmid was marked with a gentamicin resistance gene. pPA21A::Gm was capable of conjugative transfer with frequencies ranging from 10^{-3} to 10^{-5} , both in intraspecies and inter-genus matings. In accordance with the presence of a *lexA* regulator binding sites in front of the conjugative apparatus genes, the frequency of conjugative transfer increases when the SOS response is induced. pPA21A::Gm was conjugatively transferred into SCRI1043. This plasmid-free strain is normally unable to cause hypersensitive reaction on tobacco plants, but its variant carrying pPA21A::Gm acquired this ability, just as the original host strain of this plasmid. This report of a plasmid contributing to virulence of plant pathogenic *Pectobacterium* provides new insight into diversity of this important group of plant pathogens and their interaction with host plants.

Acknowledgements: This work is supported by the State Research Programme “Biotechnology”

Keywords: virulence, plasmid, hypersensitive reaction, conjugation.