Comparative analysis of the nic-gene cluster within the Arthrobacter genus

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Introduction

The pAO1 megaplasmid of Arthrobacter nicotinovorans harbors two different catabolic pathways: one for degradation of xylose (xyf operon) and one for nicotine degradation (nic-gene cluster). Our previous work has shown that the megaplasmid is responsible for spreading the nicotine degrading ability to various Gram positive soil bacteria, such as Rhodococcus or Nocardioides. The recent advance in NextGen sequencing has led to the deposition of 37 genomes and 24 plasmids belonging to the Arthrobacter genus. Interestingly, the pAO1 shows low levels of sequence similarity with the other Arthrobacter plasmids, but shares most of its nic-genes with three Arthrobacter genomes: Arthrobacter sp. M2012083 (GI: NZ_AOFD00000000) and Arthrobacter sp. AK-YN10 (GI: NZ_AVPD00000000). The current study attempts to make an evolutionary analysis of the nic-cluster taking into account only the gene arrangement and collinearity of the open reading frames.

Metabolic profiles of the annotated Arthrobacter genomes

Arthrobacter sp. M2012083

Arthrobacter sp. SJCon

Arthrobacter AK-YN10

Vic-gene cluster consists of five modules

Arthrobacter sp. M2012083

Arthrobacter sp. SJCon

Arthrobacter AK-YN10

Arthrobacter AK-YN10 can degrade nicotine

Conclusions

Within the Arthrobacter genus, the nic-gene cluster is not singular to the pAO1 megaplasmid. Three strains (Arthrobacter sp. M2012083, Arthrobacter AK-YN10, Arthrobacter sp. SJCon) have been identified here as containing the nic-gene cluster. A modular design for the nic-gene cluster can be described, each module coding for a step in the nicotine catabolic pathway. Arthrobacter AK-YN10 can degrade nicotine, but the catabolic pathway might be slightly different compared to the pAO1 encoded pathway.

References


Acknowledgments. MJF was supported by the POSDRU/159/1.5/S/133852 strategic grant within the European Social Fund 2007 – 2013