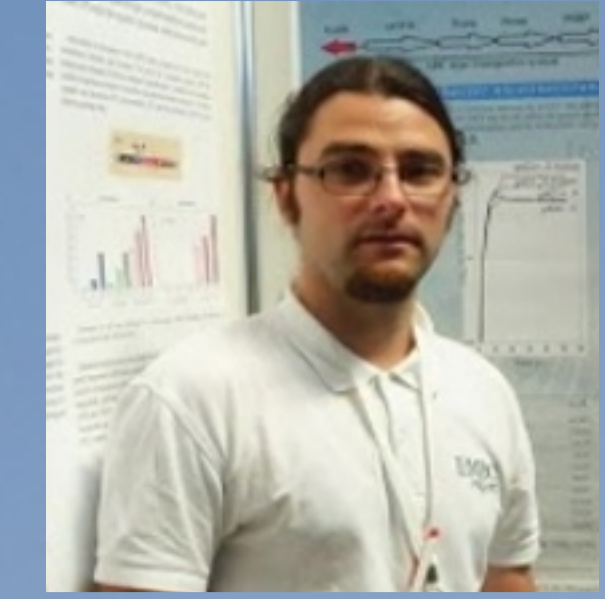


Comparative analysis of the *nic*-gene cluster within the *Arthrobacter* genus

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Introduction

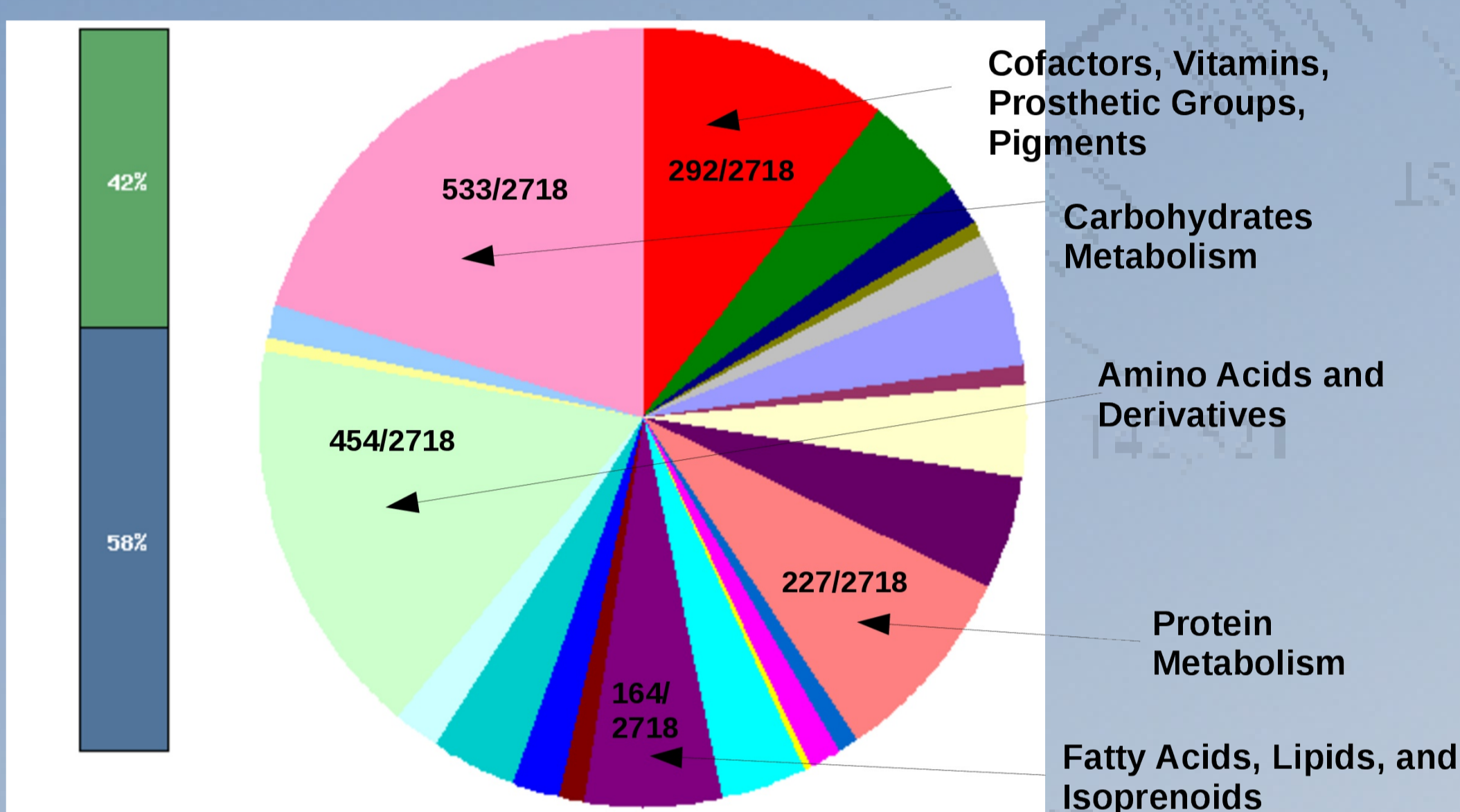
The pAO1 megaplasmid of *Arthrobacter nicotinovorans* harbors two different catabolic pathways: one for degradation of xylose (*xyl* operon) and one for nicotine degradation (*nic*-gene cluster). Our previous work has shown that the megaplasmid is responsible for spreading the nicotine degrading ability to various Gram positive soil bacteria, such as *Rhodococcus* or *Nocardioides*. The recent advances 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:NC AKKK00000000), *Arthrobacter* sp. SJCon (GI: NC AOFD00000000) and *Arthrobacter* sp. AK-YN10 (GI: NC 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.

Methods

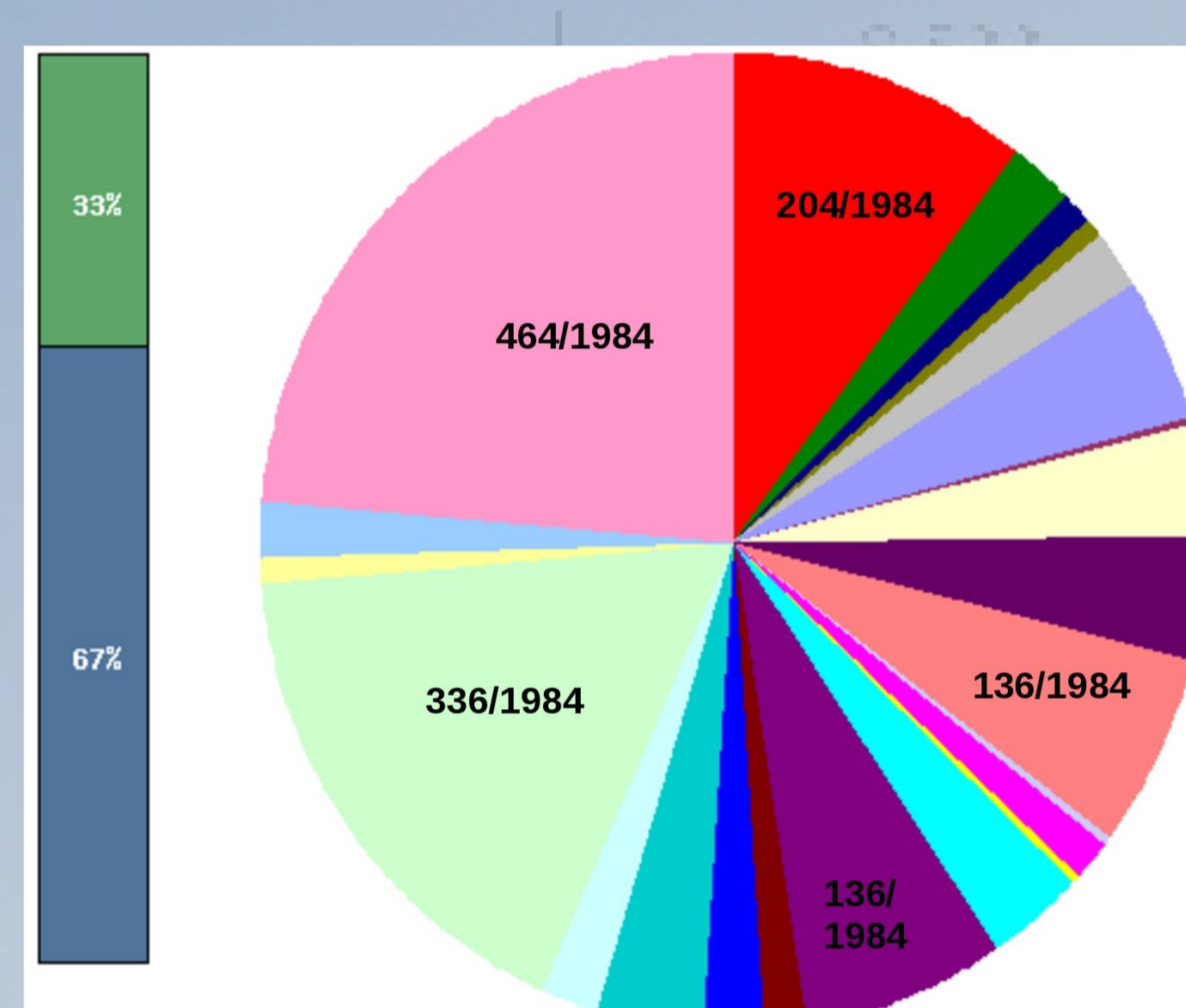
The three draft genomes of the above mentioned *Arthrobacter* strains were assembled based on five reference genomes (*Arthrobacter aurescens* TC1 (GI:NC 008711), *Arthrobacter chlorophenolicus* A6 (GI:NC 011886), *Arthrobacter arilaitensis* Re117 (GI:NC 014550), *Arthrobacter phenanthrenivorans* Sphe3 (GI:NC_015145), *Arthrobacter nitroguajacolicus* Rue61a (GI:NC_018531) by using the AlignContig module from MAUVE v.2.1.3. For each draft genome, the sequence of aligned contigs was further uploaded to the RAST server for automated annotation. The final genomes were further aligned using MAUVE, BLAST and BRIG. The *Arthrobacter* sp. AK-YN10 strain was a kind gift from Dr. Atya Kapley (National Environmental Engineering Research Institute, CSIR-NEERI, Nagpur, India) and was grown on citrate medium supplemented or not with nicotine. Nicotine resistance was assayed using the broth microdilution method. The nicotine concentration in the medium was followed by HPLC of a Bischoff dual-pump system equipped with a DAD detector and a Nucleodur RP C18ec column. An isocratic elution was employed using 1mM H₂SO₄ at a flow rate of 1 ml/min.

Metabolic profiles of the annotated *Arthrobacter* genomes

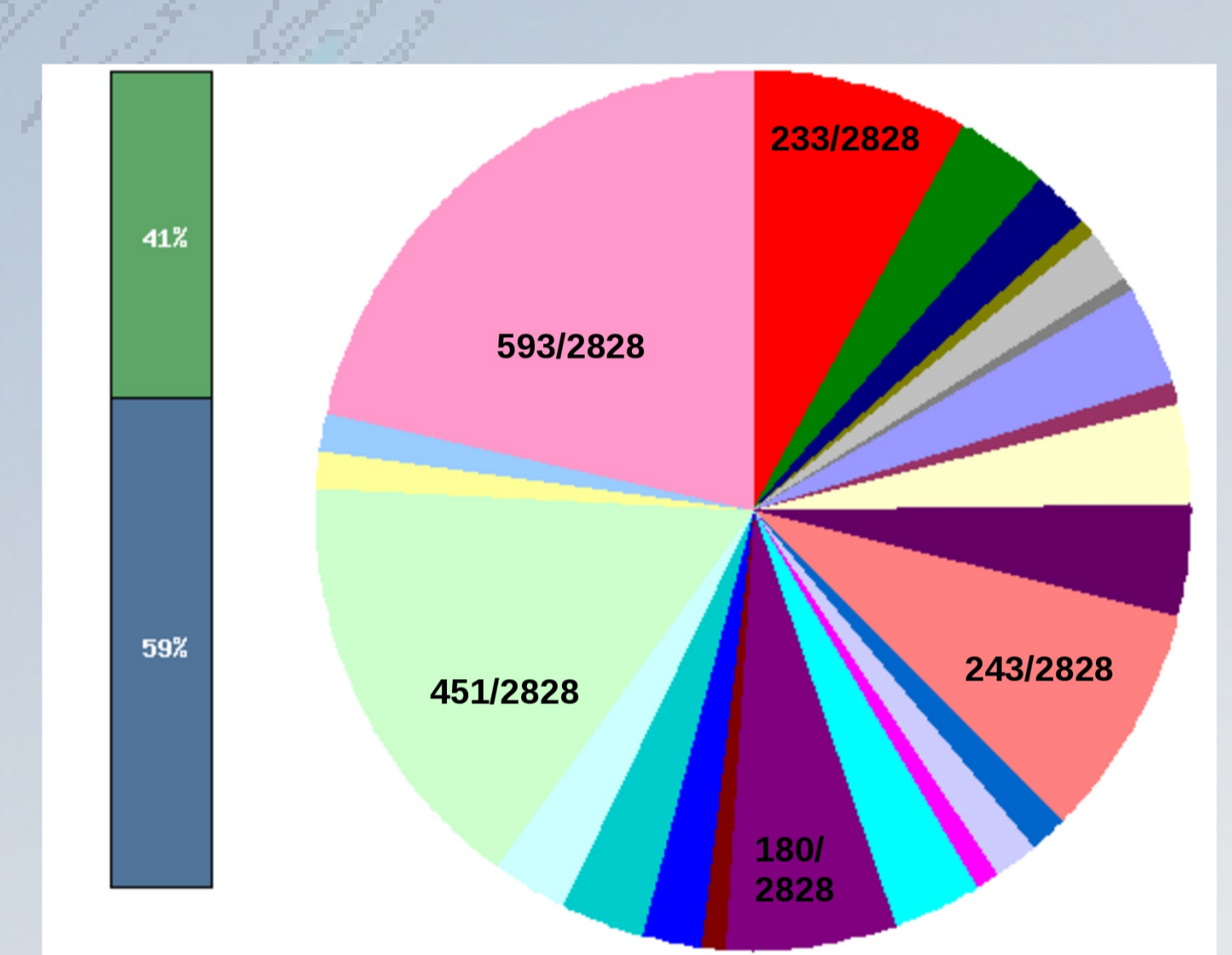
Arthrobacter sp. M2012083



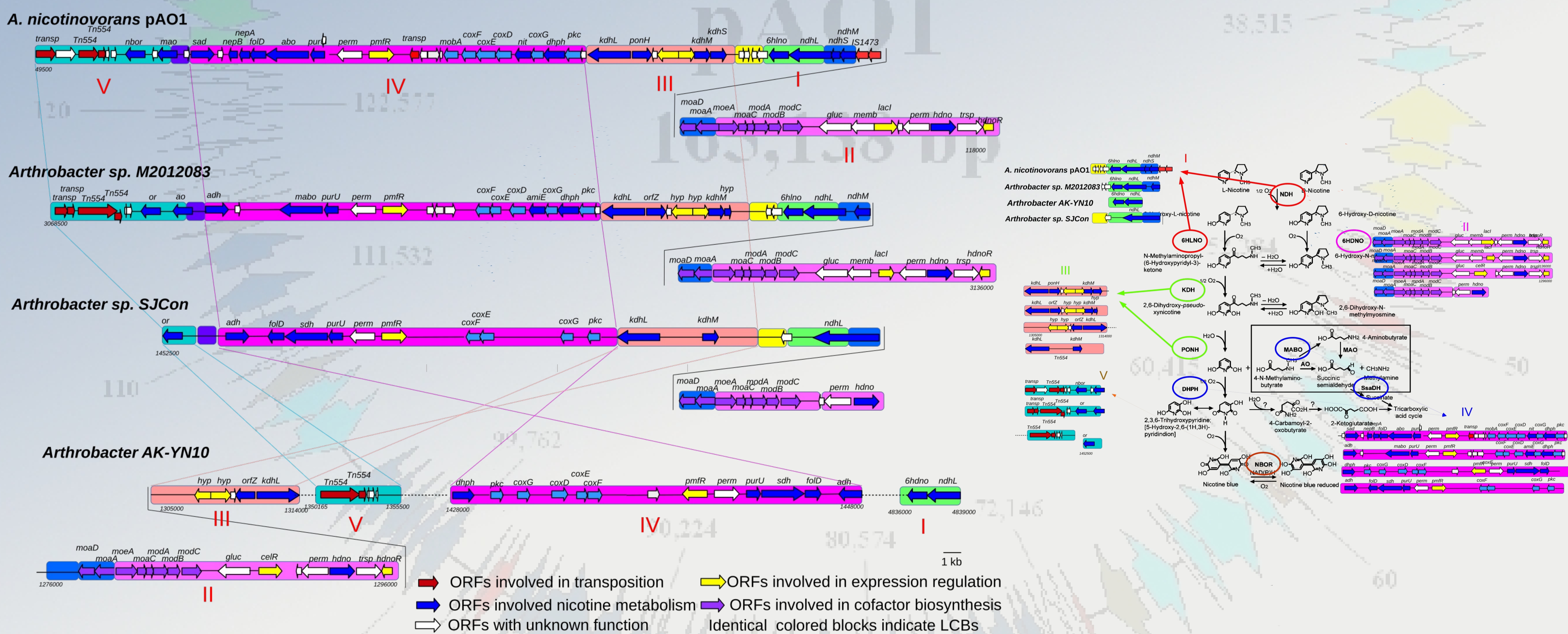
Arthrobacter sp. SJCon



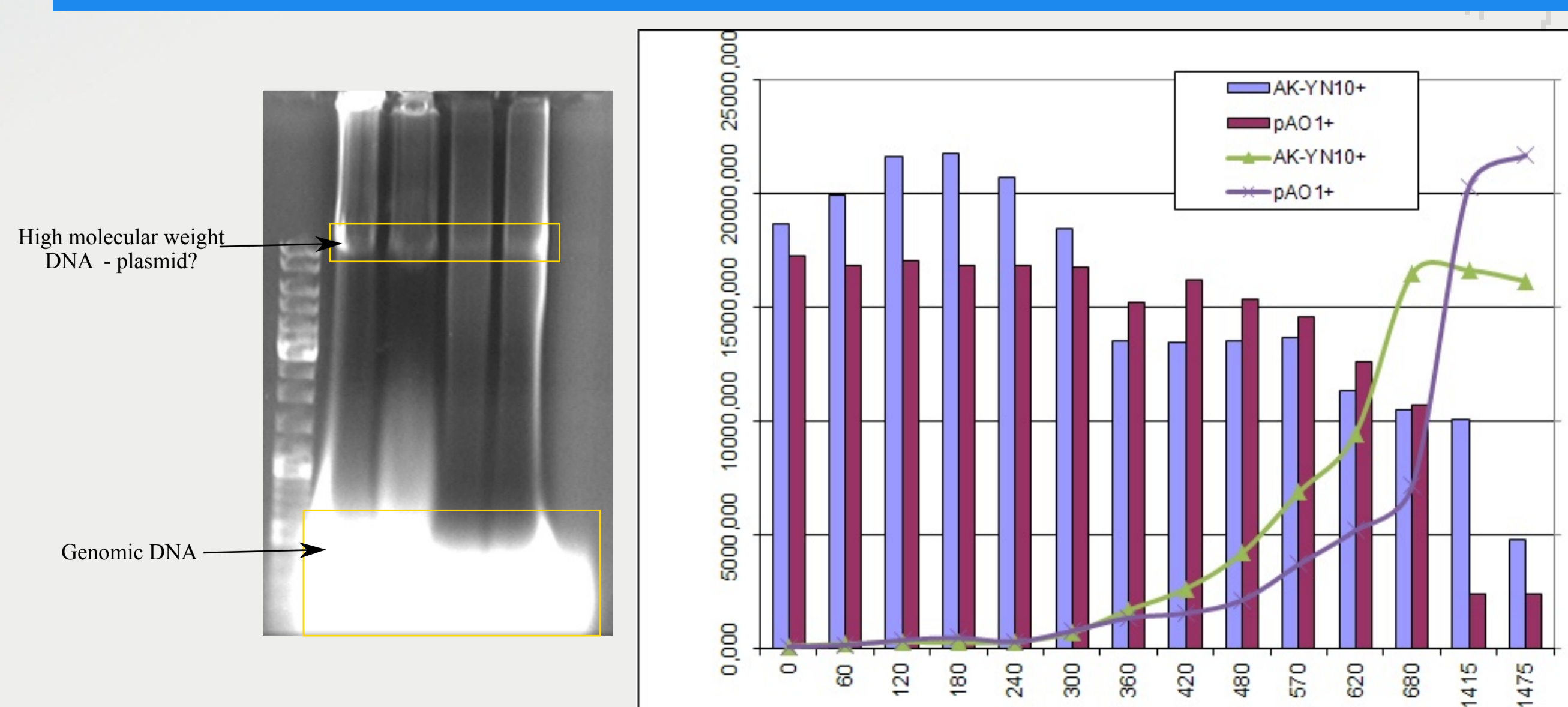
Arthrobacter AK-YN10



Nic-gene cluster consists of five modules



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

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Acknowledgements. MM was supported by the POSDRU/159/1.5/S/133652 strategic grant within the European Social Fund 2007–2013