

Mining *Streptomyces* genome for thiopeptide biosynthetic pathway

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Abstract: The genus *Streptomyces* comprises of filamentous gram positive eubacteria that undergoes differentiation during their complex life cycle. The *Streptomyces* genome has a linear DNA molecule of approximately 8×10^6 bp with a very high G + C content of about 73%. Many species belonging to this genus produce antibiotics and others molecules with biological activities.¹

The whole genome sequencing of a linear chromosome of *Streptomyces* sp B1, a *Citrus* endophyte was performed and provide approximately 8 millions of base pairs subdivided in 584 contigs. The antiSMASH² platform allowed to identify 66 biosynthetic clusters to production of secondary metabolites, among them t1-PKS, NRPS, terpene synthases, thiopeptides and others hybrid clusters.

The unknown gene cluster (Figure 1A) that encodes for enzymes of a putative thiopeptide antibiotic is now under in investigation to explore his biosynthetic potential.

To investigate it deletion strategies (Figure 1B) is getting place in our studies aiming to reconstruct the pathway of these thiopeptide and eventually lead to the production of new compounds.

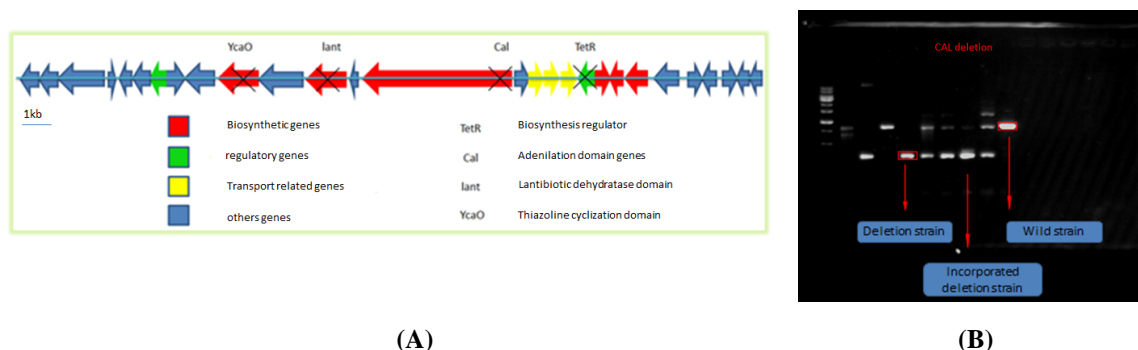


Figure: A) A putative thiopeptide-lanthipeptide-NRPS-t1PKS gene cluster predicted from antiSMASH. B) The deletion experiment provide the disrupt of CAL domain.

References:

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- [2] Medema, M. H.; *et al.*; antiSMASH: rapid identification, annotation and analysis of secondary metabolite biosynthesis gene clusters in bacterial and fungal genome sequences. 2011 *Nucleic Acids. Res.* 39, W339 – W346.