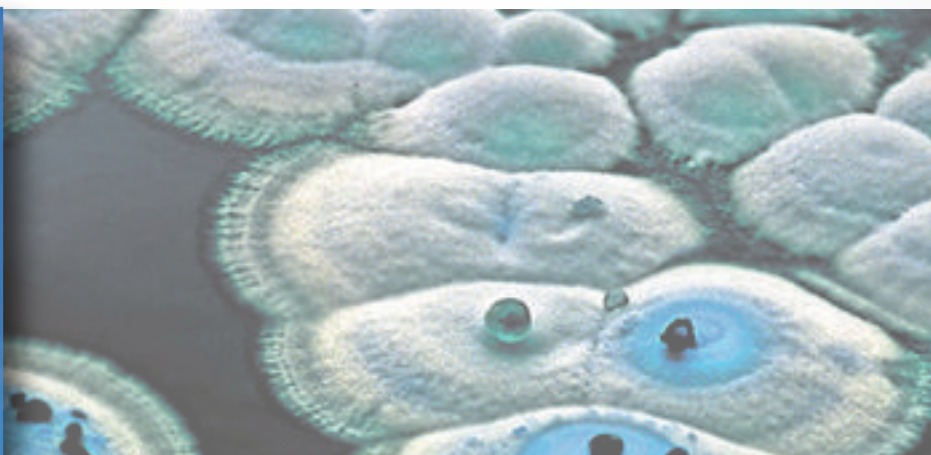


Biomolecular Characterization of Streptomyces differentiation and its relationship with Secondary Metabolite Production



PROJECT DETAILS

Funding Programme:
7th Framework Programme
(FP7)

Sub-Programme:
IDEAS-ERC

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280304;
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118

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60 Months (from 2012-01-01
to 2016-12-31)

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€ 1.341.985

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€ 1.341.985

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http://cordis.europa.eu/projects/rcn/101544_en.html

PROJECT DESCRIPTION

Streptomyces is a gram positive bacterium characterized by a complex developmental cycle. It is considered as a multicellular prokaryotic model that includes programmed cell death and sporulation. Streptomyces are very important in industry, since they produce two thirds of clinically relevant secondary metabolites. Streptomyces and other bacteria with complex life cycles represent the evolutionary origin of some of the protein domains involved in the most important eukaryotic signalling pathways.

The classical Streptomyces developmental cycle focused in the sporulation. Industrial fermentations are mainly produced in liquid cultures (large bioreactors), conditions in which there is not sporulation, and it was traditionally considered that there was no differentiation. During his predoctoral training, A. Manteca re-evaluated Streptomyces development in solid sporulating cultures, laying the foundation of a new research line about Streptomyces differentiation totally independent to the investigations of his PhD supervisor (Streptomyces nucleases). During his postdoctoral training, he continued working in this emerging research line analyzing the relation between differentiation and secondary metabolite production, reporting the first study in which antibiotic production could be associated with hyphae differentiation in liquid. Later, he focused in the proteomic analysis of Streptomyces differentiation, creating the most complete database about proteome variations associated with hyphae differentiation.

The main objective of this project will be characterizing the biomolecular pathways behind Streptomyces differentiation, and their homologies and differences with eukaryotic signalling pathways. We will use the innovative developmental model elaborated by us and the information about the proteome differences during Streptomyces differentiation, to perform large scale mutagenesis and exhaustive phenotypic/bioinformatic characterization of these mutants.

PROJECT PARTNERS

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