

Natural products genome-mining approaches for the discovery of new and old drugs

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Microbial genome sequencing has revitalized the field of natural products with relevant biological activities, such as antibiotics. Paradoxically, as it may seem, the overwhelming amount of data generated by these genome projects has hampered progress in this field.

In this talk, the main genome-mining approaches used to discover natural products genes and enzymes - feeding the drug discovery pharmaceutical programs, as well as novel biotechnological processes - that have allowed for analysis of large sets of genomic data, will be revised. In particular, a novel approach based in evolutionary principles, which was developed by our laboratory and has been used to pose testable hypothesis in the model genus *Streptomyces*, will be presented.

The main advantages of this novel approach are (i) analysis of the sequences does not depend on the most common enzymes/genes involved in natural products biosynthesis, i.e. non-ribosomal peptide synthetases (NRPSs) and polyketide synthetases (PKS); and (ii) analysis is compatible with recently and/or unfinished sequenced genome drafts. These two features, together, increase the likelihood of discovering novel natural-products biosynthetic pathways, and therefore, novel drugs, in a more efficient fashion.