Genome-Scale Metabolic Reconstruction of Actinomycetes for Antibiotics Production - DTU Orbit (25/02/2019)

**Genome-Scale Metabolic Reconstruction of Actinomycetes for Antibiotics Production**

Systems biology approaches are increasingly applied to explore the potential of actinomycetes for the discovery and optimal production of antibiotics. In particular, genome-scale metabolic models (GEMs) of various actinomycetes are reconstructed at a faster rate in recent years, which has opened avenues to study interaction between primary and secondary metabolism at systems level, and to predict gene manipulation targets for overproduction of important antibiotics. Here, the status of actinomycetes’ GEMs and their applications for designing antibiotics-overproducing strains are presented. Despite advances in the practice of GEM reconstruction, actinomycetes’ GEMs still remain incomplete in describing a full set of biosynthetic pathways of secondary metabolites. As to the GEM-based strategies, various simulation methods are deployed to better describe secondary metabolism by introducing changes in constraints and/or objective function as well as by using omics data. Gene manipulation targeting algorithms developed for metabolic engineering of model organisms have also been actively applied to actinomycetes for the antibiotics production. Further consideration of computational resources dedicated to secondary metabolites in addition with automated GEM reconstruction tools will further upgrade GEMs of actinomycetes for antibiotics discovery and development.

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