

Pan-reactome analysis of multiple *Streptomyces* strains using genome-scale metabolic models

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Streptomyces is a prominent source of novel natural products with medicinal and industrial values. Among various approaches of systems biology, genome-scale metabolic models (GEMs) have shown to be effective in predicting comprehensive metabolic phenotypes in terms of fluxes in a target cell. In this study, GEMs were reconstructed for a total of 242 *Streptomyces* strains through an automatic pipeline, and pan-reactome analysis was conducted using the 242 GEMs to characterize important metabolic phenotypes of these *Streptomyces* species. Pan-reactome analysis revealed innate diversity of metabolic contents of the *Streptomyces* species, especially those associated with biosynthesis of secondary metabolites. Metabolic phenotypes examined using the 242 *Streptomyces* GEMs include growth capability under a wide range of media conditions, gene essentiality, and biosynthetic capability of secondary metabolite precursors. GEMs reconstructed for the 242 *Streptomyces* strains and insights from the pan-reactome analysis will serve as a useful source for our better understanding of this important group of bacteria.