

# Comparative genomic analysis and constraint-based analysis of genome-scale metabolic models of the genus *Clostridia*

Vijayanand S. Moholkar<sup>1</sup>, Karan Kumar<sup>1</sup>, and Lepakshi Barbora<sup>1</sup>

<sup>1</sup>Indian Institute of Technology Guwahati

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## Abstract

In recent years, bacteria from genus *Clostridia* have attracted attention of research community because of their biofuel production capabilities. Present study reports comparative genomic (CG) analysis of 48 genomes of solventogenic and saccharolytic *Clostridia*. We have focused on central carbon metabolism and general stress response in the analysis. Comprehensive summaries on comparison of general genome features, COG categories, CDSs of the energy, catabolic, and sporulation pathways are given. Furthermore, we have proposed two new genome-scale metabolic (GSM) models *iKK848* and *iKK1425* for *Clostridium pasteurianum* DSM 525 = ATCC 6013 and *Clostridium acetobutylicum* ATCC 824, respectively. These GSM models are most comprehensive in that they account for the largest number of reactions, metabolites, and genes as compared to previous models. Model quality and metabolic flux optimization for biomass growth using *iKK1425* and *iKK848* are compared with previous literature. Our models had the highest quality score of 61% and 77%.

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