

Accepted Manuscript

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PII: S2452-0144(18)30084-0
DOI: doi:[10.1016/j.genrep.2018.07.002](https://doi.org/10.1016/j.genrep.2018.07.002)
Reference: GENREP 288
To appear in: *Gene Reports*
Received date: 13 February 2018
Revised date: 22 June 2018
Accepted date: 2 July 2018

Please cite this article as: Tulika Bhardwaj, Pallavi Somvanshi , A computational approach using mathematical modeling to assess the peptidoglycan biosynthesis of *Clostridium botulinum* ATCC 3502 for potential drug targets. Genrep (2018), doi:[10.1016/j.genrep.2018.07.002](https://doi.org/10.1016/j.genrep.2018.07.002)

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A computational approach using Mathematical modeling to assess the peptidoglycan biosynthesis of *Clostridium botulinum* ATCC 3502 for potential drug targets

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Abstract

C.botulinum ATCC 3502 is an obligate rod-shaped spore forming anaerobe causing food poisoning cases worldwide. The increased burden of sporadic hospital outbreaks reflects the pandemicity caused by this pathogen. Several attempts to control the disease surveillance, emergence of antibiotic resistant strains plagued the defense provided by the drugs. Peptidoglycan biosynthesis of *C.botulinum* ATCC 3502 is targeted to identify potential drug targets due to presence of no functional homolog in host (*Homo sapiens*). The role of peptidoglycan is to provide strength, fragility and protection to bacterial cells; therefore, it is considered as an attractive target for drug target identification. This study involves systematic exploration of targeted pathway by performing metabolic pathways analysis in two phases (1) mathematical modeling (2) elementary mode analysis (EM). Performing stoichiometric and kinetic modeling discerns the steady state conditions of the system to scrutinize elementary nodes with well-defined objective function. The study identifies Mur ligase enzymes (*murA*, *murB*, *murC*, *murD*), D-alanine-D-alanine ligase and glutamate racemase potential therapeutic targets for drug discovery. Further, the quantitative analysis characterized their potential in causing the pathogenicity. Physicochemical characterization and subcellular localization analysis assist in understanding biological activity of identified elementary nodes under different environmental conditions

Keywords: Food poisoning, *Clostridium botulinum* ATCC 3502, metabolic reconstruction, mathematical modeling, elementary mode analysis, subcellular localization, physico chemical characterization.

Introduction

The inflation rate of food poisoning cases is contributed by the busy and hectic lifestyle of urban population cases globally. The perceived convenience in availability and preparation associated

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