CHAPTER 52

TECHNOLOGY
APPLIED SCINCES & HUMANITIES

Doctoral Theses

01. RAVI KUMAR
Cloning, Expression, and Characterization of Xylose Tolerant GH43 β-xylosidase from Thermophilic Fungus Thermothelomyces thermophilus BJA.
Supervisors: Dr. Shilpa Sharma and Prof. T. Satyanarayana
Th 29277

Abstract

A recombinant β-xylosidase from a thermophilic filamentous fungus, Thermothelomyces thermophilus BJA was cloned, expressed, and comprehensively characterized to evaluate its potential in industrial xylan hydrolysis. The enzyme displayed high thermostability, broad substrate specificity, and efficient catalytic activity under alkaline and elevated temperature conditions, making it well suited for biomass conversion processes. Structural modeling confirmed the conserved five-bladed β-propeller fold typical of GH43 enzymes, while computational analysis provided mechanistic insights into substrate binding and catalytic residues. Experimental assays demonstrated that the recombinant β-xylosidase synergized effectively with commercial cellulase preparations, reducing oligosaccharide accumulation and enhancing monosaccharide yields. Building on this enzymatic foundation, the study explored lignoellulosic biomass (LCB) pretreatment and saccharification. Paddy straw and sugarcane bagasse were subjected to physicochemical and biocatalyst-assisted pretreatments, which improved hemicellulose accessibility. Integration of the recombinant β-xylosidase into enzyme cocktails significantly increased sugar release compared to commercial formulations alone. Solid-state and submerged fermentation trials with wild fungal strains further highlighted complementary enzyme profiles, underscoring the value of multi-enzyme systems. Together, these findings demonstrate that thermostable β-xylosidase from T. thermophilus BJA can play a pivotal role in overcoming biomass recalcitrance and driving efficient lignocellulose saccharification. By combining enzyme engineering, pretreatment strategies, and computational insights, this work advances bioconversion technologies and contributes to sustainable bioenergy production within the global bioeconomy. Keywords: β-xylosidase, thermophilic fungi, lignocellulosic biomass, enzymatic hydrolysis, biomass pretreatment, glycoside hydrolase, hemicellulose, bioconversion, thermostability, enzyme synergy.

Contents

1. Introduction 2. Theoretical background 3. Materials and methods 4. Results and discussion 5. Summary and conclusion. Bibliography and appendices.

02. VERMA (Varsha)

Molecular Studies on Biosynthesis of Antimicrobial Metabolites in Streptomyces Chrestomyceticus Strain ADP4.

Supervisors: Prof. A. K. Dubey and Prof. Medicherla K. Mohan

Th 29379

Abstract

Streptomyces chrestomyceticus strain ADP4 is a soil isolate with very potent and broad-spectrum antimicrobial activity. This study employed an integrated polyphasic, genomic, transcriptomic, metabolomic, and systems biology approach to elucidate the molecular basis of antimicrobial metabolite biosynthesis and identify novel therapeutic candidates. A comprehensive phenotypic and molecular characterization of strain ADP4 was done by understanding morphological, physiological, biochemical and genetic parameters. The genome was sequenced and assembled, with a genome size of 9.64 MB and 8,378 coding regions. Comparative genomic and phylogenomic analyses identified Streptomyces chrestomyceticus NPDC045757 as the closest relative while revealing unique genomic features of strain ADP4. Genome mining identified 51 putative biosynthetic gene clusters (BGCs), demonstrating its remarkable biosynthetic capacity. Comparative genome analysis revealed eight strain-specific hypothetical proteins. Among those, HP2 is an active peptide with possible anti-viral activity, underscoring its potential as a novel therapeutic drug. The structural validation, peptide-protein molecular docking and MD simulation suggested strong antiviral potential of HP2 against HIV, SARS-CoV and HCV. This represented the first report of antiviral potential in S. chrestomyceticus spp. To investigate nutrient-dependent regulation of secondary metabolites, strain ADP4 was cultivated in complex media (CDH, HiM, and SB) and an optimized chemically defined medium (MM). Strain ADP4 supported One Strain–Many Compounds (OSMAC) approach, demonstrating media composition (condition)-dependent changes in growth, pigment and antimicrobial activity profile. To address this, complete metabolome and transcriptome differential analyses across conditions were performed, revealing differential expression along with uniquely expressed metabolites and genes. Correlation of transcriptomic and metabolomic data with genome-mined BGCs showed that most biosynthetic gene clusters were preferentially expressed in MM medium, supporting its suitability for BGC-specific expression. Further functional network analysis of putative BGCs and WGCNA correlation between metabolite profile with expressed secondary metabolite-associated genes and transcription factors (TFs), resulted in hub genes. These hub genes were further integrated to form a combined network, resulting in potential gene regulatory switches. Overall, this study provides a comprehensive multi-omics framework for understanding antimicrobial metabolite biosynthesis in S. chrestomyceticus ADP4 and establishes this strain as a promising source of novel antimicrobial and antiviral therapeutics.

Contents

1. Introduction and objectives 2. Literature review 3. Materials and method 4. Results and discussion 5. Summary. 6. Bibliography. Appendices.