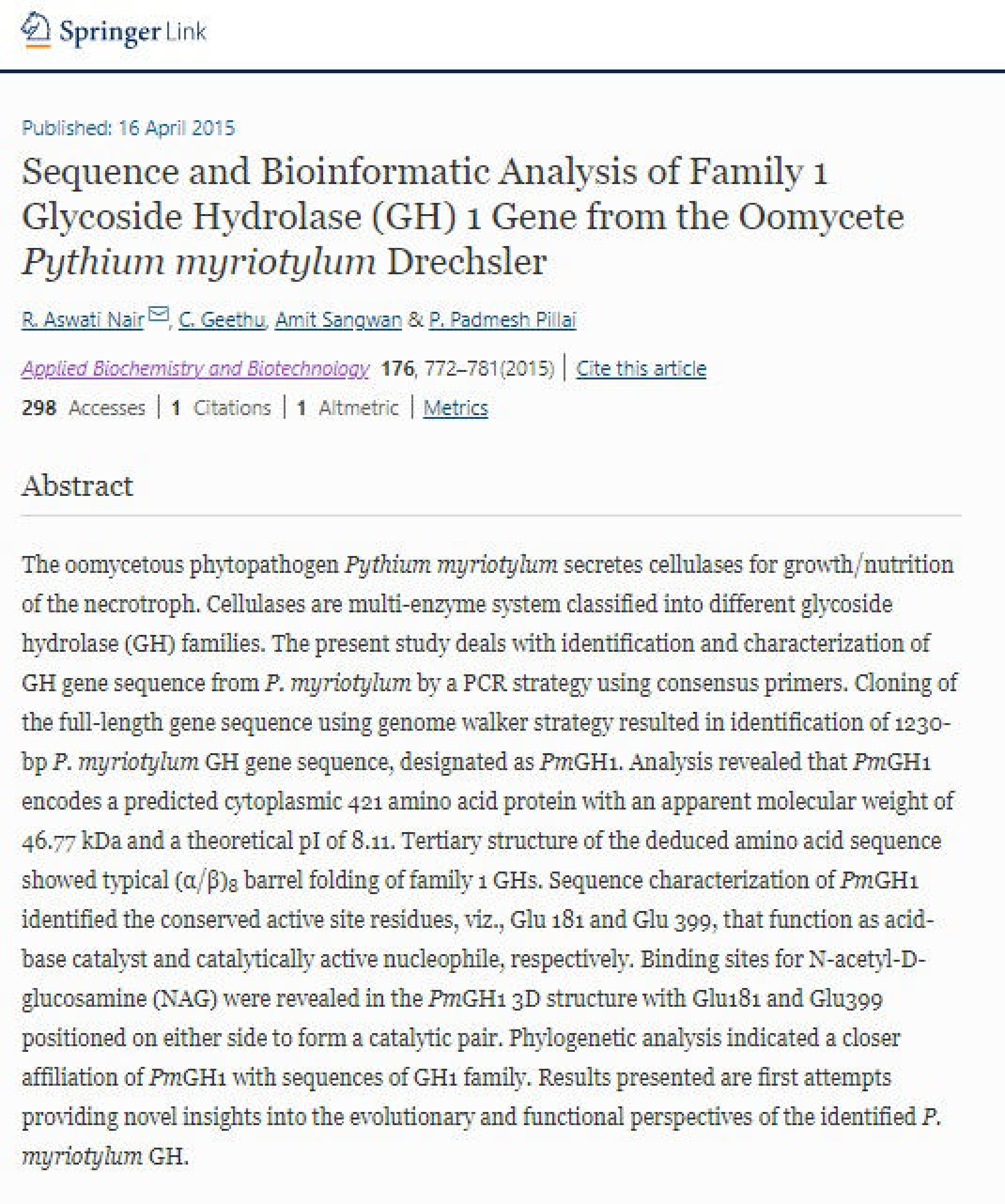

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Sequence and Bioinformatic Analysis of Family 1 Glycoside Hydrolase (GH) 1 Gene from the Oomycete *Pythium myriotylum* Drechsler

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Abstract

The oomycetous phytopathogen *Pythium myriotylum* secretes cellulases for growth/nutrition of the necrotroph. Cellulases are multi-enzyme system classified into different glycoside hydrolase (GH) families. The present study deals with identification and characterization of GH gene sequence from *P. myriotylum* by a PCR strategy using consensus primers. Cloning of the full-length gene sequence using genome walker strategy resulted in identification of 1230-bp *P. myriotylum* GH gene sequence, designated as *Pm*GH1. Analysis revealed that *Pm*GH1 encodes a predicted cytoplasmic 421 amino acid protein with an apparent molecular weight of 46.77 kDa and a theoretical pI of 8.11. Tertiary structure of the deduced amino acid sequence showed typical $(\alpha/\beta)_8$ barrel folding of family 1 GHs. Sequence characterization of *Pm*GH1 identified the conserved active site residues, viz., Glu 181 and Glu 399, that function as acid-base catalyst and catalytically active nucleophile, respectively. Binding sites for N-acetyl-D-glucosamine (NAG) were revealed in the *Pm*GH1 3D structure with Glu181 and Glu399 positioned on either side to form a catalytic pair. Phylogenetic analysis indicated a closer affiliation of *Pm*GH1 with sequences of GH1 family. Results presented are first attempts providing novel insights into the evolutionary and functional perspectives of the identified *P. myriotylum* GH.