Bioinformatic Analysis and Stability Assessment of Cold-adapted Xylanases

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Abstract: Xylanases are receiving considerable attention due to their huge applications in paper and pulp industry [1], deinking of waste paper [2], animal feeds manufacturing [1], food industry [1], biofuel production [2], pharmaceutical industry [1] and textiles [1]. They constitute approximately 75% of the markets for industrial enzymes along with other hydrolytic enzymes [3,4]. Whilst many of the xylanases used in industry are mesophilic enzymes, cold-adapted xylanases appear to be more efficient in biotechnological processes where low temperatures are required [3] such as food industry, bioremediation and textile [5]. In this study, we assessed physicochemical characteristics of 22 novel cold-adapted xylanases produced by various microorganisms using the **ExPASy's ProtParam server**. The phylogenetic tree was constructed in order to analyse phylogenetic relationship using **MEGA 7.0** and **SignalP server** used to predict the presence and location of signal peptide as well. Furthermore, secondary structure prediction, 3D structure for the selected xylanases were calculated using **SOPMA**, **PSIPRED**, **PredictProtein** and **SWISS-MODEL**. Results of this assessment suggested that *Penicillium chrysogenum FS010* and *Sphingobacterium sp. TN19* were classified as stable enzymes and demonstrated high thermostability index among fungal and bacterial sources. Both xylanases proved the presence of signal peptides and belonged to Glycosyl hydrolases family 10. Instability index and aliphatic index for xylanase produced by *Penicillium chrysogenum FS010* were 29.19 and 86.01, respectively. Whereas instability index for *Sphingobacterium sp. TN19* xylanase was 25.91 and its aliphatic index was 84.56. The very high aliphatic index of both xylanases indicated that they could be stable for a wide temperature range.

Keywords: Cold-adapted xylanase; ProtParam; Secondary structure prediction; Swiss-model; 3D structure prediction

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