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Purification and Characterization of a Xylanase from *Rhizopus oligosporus*

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ABSTRACT

Xylanases are promising eco-friendly candidate for many biotechnological and industrial fields including food, feed processing, biorefining and bio-intermediates production, biofuel, textile industries and paper and pulp industry as a biobleaching agent. An extracellular xylanase secreted by *Rhizopus oligosporus* produced under solid state fermentation using wheat bran was purified and characterized. The freeze-dried crude filtrate was subjected to two-step purification using ion exchange chromatography by DEAE-Sepharose and gel filtration chromatography over Sephacryl S-200. The enzyme was purified to homogeneity and showed a monomeric single protein band over SDS-PAGE of a molecular mass of about 23 kDa. The purified xylanase revealed maximum activity at 40°C and at pH 6.0 while remained active over a wide range of pH (4.5-8.0) and temperature (40–60°C). The purified enzyme showed a significant activity towards birchwood, beechwood and oat spelt xylan with Km values of 8.0, 4.7 and 3.2 mg ml⁻¹, respectively. The xylanolytic activity was stimulated by Ni²⁺ and Na⁺ ions, while it is completely inhibited by Hg²⁺.

Keywords: Xylanase, *Rhizopus oligosporus*, production, purification, characterization

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INTRODUCTION

Notwithstanding the fact that control recent advancement, enzymes are important organic polymers that catalyze particular biochemical reactions, changing over substrates into specific products [1]. Hemicellulose represents about 20–30% of lignocellulosic biomass which is the second most basic polysaccharide in nature [2]. Xylan is the fundamental part of hemicelluloses which is viewed as a noteworthy wellspring of renewable biomass[3]. Structurally xylan is a heterogeneous carbohydrate comprising of a spine of β -1, 4 connected D-xylopyranosyl units and branches consisting of O-acetyl, α -L-arabinofuranosyl and α -D-glucuronidyl residues [4]. Xylan hydrolysis is an indispensable step towards the debasement of lignocellulosic matter in nature [5]. The transformation of xylan into useful products represents to a noteworthy part of the push to accomplish prudent reasonability of the lignocelluloses biomass preparing and to produce distinctive approaches to achieve deliver chemicals and renewable energy too [6]. Subsequently, there has been developing consideration towards xylanase production.

Xylanases are a class of proteins that degrade 1, 4-xylan, a direct polysaccharide mainly present as hemicellulose in plant cell dividers, into xylose [7]. Because of the auxiliary heterogeneity of xylan, complete degradation of this heteropolysaccharide needs the synergistic activity of various xylanolytic enzymes, for example, endo-xylanase, glucuronidase, xylosidase, esterase and arabinofuranosidase [1,5]. Xylanases are subdivided inside glycoside hydrolase (GH) families into 5, 7, 8, 10, 11 and 43 [8]. They differ in their structure, mechanism activity and substrate specificity [9]. In between these, the most vital one is endo-1,4-xylanase (1, 4-D-xylan xylohydrolase, EC 3.2.1.8), which is otherwise called xylanase, and which begins the debasement of xylan into various sizes of xylooligosaccharides and xylose [10].

On other hand, xylanase degrades xylan filaments to short chains of sugar deposits which have enormous applications in industry [11]. An assortment of microorganisms can deliver xylanases including yeasts, bacteria and fungi [8,12]. Filamentous fungi are industrially potential producers of xylanase due to higher yield contrasted with yeast and bacteria [13]. Xylanases are central biocatalysts in the biorefining of hemicelluloses and they have many industrial applications (e.g. paper, textile, enhancing bread quality, clarification of juice and liquefaction of fruits and vegetables) [14]. Xylanases are have important role of modern industries, which can be utilized in paper pulp bleaching, increasing the shine of mash and culminating the absorbability of animal feed [9]. Xylanase improves juice clarification and maceration, diminishes viscosity and increases extraction yield and filtration, process performance and product quality. Additionally it diminishes the substance of non-starch polysaccharides, accordingly decreasing the intestinal consistency and enhancing the usage of proteins and starch, Therefore, it enhances the digestibility of animal feed for better nourish usage and nutritive estimation of inadequately degradable [16]. They are likewise, of modern significance, which can be utilized for illumination of organic product juices, upgrading the nutritional wholesome properties of farming silage and grains nourish [16]. On other hand, the products of xylan hydrolysis have applications in wheat flour for enhancing dough handling and the nature of baked products or for extraction of coffee and plant oils [17]. Concern with xylanases has notably expanded because of their potential applications in the food and beverage industries, feedstock betterment and the quality improvement of lignocellulosic buildups [18]. Where, xylanases are utilized to change over the polymeric xylan into fermentable sugars for the generation of ethanol and xylitol from plant biomass [19]. It enhances flexibility and quality of the mixture, in this way permitting less demanding taking care of in baking food industry. Xylanases can likewise be utilized for tailor designing of medications and changing the properties of food [9]. Treatment with xylanase does not represent any ecological danger and along these lines gives a hint of something to look forward to environmentalists [20]. Specifically, xylanases give an option eco-friendly innovation for bleaching Kraft pulp, which offers additional points of interest over genuine chemical treatments [21].

MATERIALS AND METHODS

Microorganism

Rhizopus oligosporus NRRL 2710, from Northern Regional Research Laboratory, United States Department of Agriculture, Peoria Illinois, USA was used for enzyme.

Enzyme production under solid state fermentation conditions

Sterilized 10 g of wheat bran was moistened with 10 ml of fermentation medium and incubated at $30^{\circ}\text{C} \pm 2^{\circ}\text{C}$.

Composition of fermentation medium

The fermentation medium had the following composition (g/ l dist. H₂O), NaNO₃, 9, KCl, 0.52, KH₂PO₄, 1.52, CoCl₂, 6 H₂O, 0.008; MgSO₄, 7 H₂O, 0.02; FeSO₄ 7 H₂O, 0.01; Casein hydrolysate, 1 and Oat xylan, 6 [22].

Preparation of xylan

Purified xylan was prepared from sugar cane bagasse according to Chen and Anderson [23] as follows: 10 g of bagasse were mixed with 100 ml of 8% NaOH (w/v) and autoclaved at 120°C for 30 min. The final filtrates were mixed to make a volume of 100 ml. The filtrate pH was adjusted to 5.0 with HCl. 150 ml of 95% ethanol were added, and the mixture was allowed to stand at room temperature for 24 h. The precipitate was collected and washed with 70% ethanol to remove lignin and other soluble. The precipitate was dehydrated with 95% ethanol, and the ethanol was removed by filtration and vacuum drying at 50°C. The extracted xylan from bagass was used in the fermentation for enzyme production.

Harvesting and the Extraction of the enzyme

For solid substrate fermentation, 100 ml dist. Water was added to each 10g fermented material and after shaking for 2 h, the extracted medium was filtered and kept frozen until use.

Xylanase assay

Xylanase activity was measured according to the method of Saha [24] using the 0.1 ml of 1% (w/v) solution of Birchwood xylan incubated with 0.4 ml of the appropriately diluted culture supernatant or enzyme enrichment fraction in 50 mM acetate buffer (pH 5.5) for 30 min at 40°C. The released reducing sugars were assayed using the DNS method [25]. One unit of xylanase activity was defined as the amount of the enzyme that liberated 1 μ mol of reducing sugar equivalent to xylose per min under the standard assay conditions. Protein was determined either by measuring the absorbance at 280 nm [26] or by the method of Bradford [27] using bovine serum albumin as a standard.

Purification of xylanase

Unless otherwise stated all steps were performed at 4-7°C. The crude supernatant extracellular xylanase was obtained by centrifugation at 15,000Xg for 15 min at 4°C and the supernatant was lyophilized. The lyophilized powder was dissolved in 3 ml of 50 mM acetate buffer, pH 5.5. It was loaded on a DEAE-Sephacrose column (15 X 1.6 cm i.d.) which was previously equilibrated with 50 mM acetate buffer, pH 5.5. Proteins were eluted with a stepwise gradient of NaCl ranging from 0.0 to 0.5 M NaCl in the same buffer at a flow rate of 60 ml/h. Fractions exhibiting xylanase activity were eluted with 0.05 M NaCl. The DEAE-Sephacrose fractions having the highest xylanase activities were combined, concentrated and loaded onto a Sephacryl S-200 column (100 X 1.6 cm i.d.) pre-equilibrated with 50 mM acetate buffer, pH 5.5, the fractions having the highest xylanase activity were pooled and used for enzyme characterization.

Molecular weight determination by sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)

Discontinuous reducing 0.1% (w/v) SDS-PAGE was performed according to the procedure of Laemmli [28] using 15% and 5% (w/v) acrylamide resolving and stacking gels, respectively. Samples were treated with reducing 2-mercaptoethanol containing sample buffer and boiled for 5 min prior to application to the gel. Electrophoresis was run at a constant current of 20 mA per slab at room temperature in a Mini-Gel Electrophoresis unit. Standards proteins were coresolved on gel and used to determine the subunit molecular weight. After electrophoresis, proteins in the gel were visualized by staining with Coomassie blue R-250.

Effect of temperature on xylanase activity and thermostability

The effect of temperature on xylanase activity was determined by incubating the enriched xylanase fraction in 50 mM sodium acetate buffer, pH 5.5 at various temperatures (20 to 70°C at 10°C intervals) for 30 min before assaying xylanase activity. The thermostability of xylanase was investigated by preincubating the enriched xylanase fraction at various temperatures (20 to 70°C at 10°C intervals) in the same buffer for the 30 min, cooling to 4°C followed by assaying the residual xylanase activity.

pH-optimum of xylanase

Incubating the enriched xylanase fraction in buffers of broadly similar salinity levels, but varying in pH from 3.0 to 9.0 was used to assess the pretreatment pH stability and the pH optima of xylanase. The buffers of 50 mM used were sodium citrate (pH 3.0 to 4.0), sodium acetate (pH 4.0 to 5.5), sodium phosphate (pH 5.5 to 8.0), Tris-HCl (pH 8.0 to 9.0). The enriched xylanase fraction was mixed with the above mentioned buffers plus the control (50 mM sodium acetate buffer, pH 5.5) and assayed for xylanase activity. For pH stability, the above xylanase-buffer mixtures were left for 30 min at room temperature and then adjusted back to 50 mM sodium acetate buffer, pH 5.5 and assayed for xylanase activity as described previously.

RESULTS AND DISCUSSION

Xylanase production

Xylanase was produced by *Rhizopus oligosporus* which was not reported earlier utilizing wheat bran under solid state fermentation. However, some xylanase producing strains have been beforehand reported by Paloheimo *et al.* [29] and Li *et al.* [30]. This study illustrated that the produced xylanase from *Rhizopus oligosporus* was lyophilized, purified and characterized.

Purification of *R. oligosporus* xylanase

R. oligosporus xylanase was purified to the point of homogeneity as shows in (Table 1). Purification of xylanase has been carried out by other researchers utilizing different microbial strains [31,32]. The lyophilized culture filtrate was applied onto DEAE-Sepharose column with different molarities of NaCl where only one single peak was eluted with 0.05 M NaCl (Fig.1) with a specific activity of 51.3 units/mg protein. The gel filtration chromatography was carried out for the pooled 0.05 M NaCl enzyme fraction using a column of Sephacryl S-200 where a single peak of *R. oligosporus* xylanase was eluted (Fig.2) with a specific activity of 96.7 units/mg protein. In the same line, Sharma *et al.* [33] reported that the purified alkaline xylanase from *Paenibacillus macquariensis* demonstrated one protein band on SDS-PAGE with a specific activity of 25.20 units/mg protein. While in another study of Ahmad *et al.* [34] was carried out to find xylanase from *A. niger* with the purification fold was figured to be 7.93, with 48.63% yield and a specific activity of 613.13 IU/mg.

Table 1: Purification scheme of *R. oligosporus* xylanase

Purification steps	Total activity* (Units)	Total protein	Specific Activity (Units/mg protein)	Fold Purification	Recovery (%)
Freeze-dried, culture filtrate	244	32.2	7.577	1.0	100
0.05 M Na Cl DEAE-Sepharose fraction	200	3.9	51.3	6.7	82
Sephacryl S-200 fraction	170	1.76	96.6	12.7	70

*One enzyme unit was defined as one μ mole xylose liberated per minute under standard assay conditions.

Molecular weight determination (SDS-PAGE)

The molecular weight of *R. oligosporus* xylanase was found to be 23 kDa by Sephacryl S-200 and affirmed by SDS-PAGE as a single subunit (Fig.3). The molecular weight of *R. oligosporus* xylanase less than those previously reported with molecular weights of 29 kDa for xylanase from *Hypocrea lixii* SS1 [1] and molecular weight 30 kDa for xylanase from *Aspergillus niger* [34]. A high molecular weight of 205 kDa was reported for xylanase from *Paenibacillus macerans* [35].

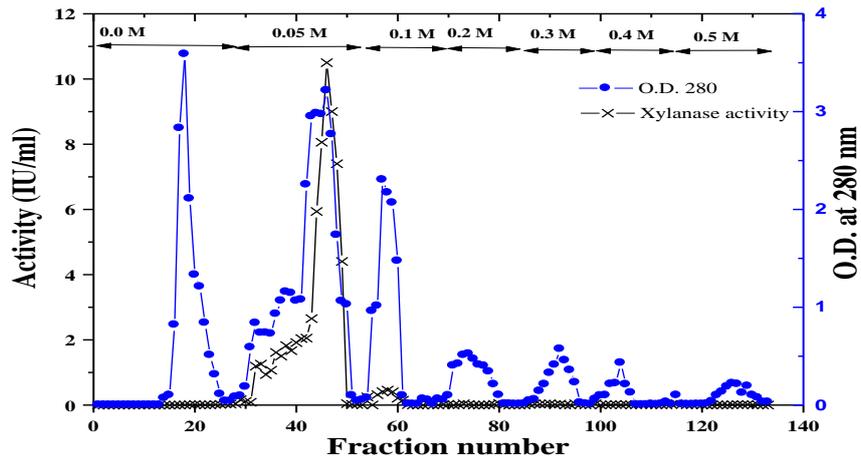


Fig 1: A typical elution profile for the chromatography of *Rhizopus oligosporus* xylanase on DEAE-Sepharose column (10 cm × 1.6 cm) previously equilibrated with 50 mM sodium acetate buffer, pH 5.5 at a flow rate of 30 ml/h and 3 ml fractions.

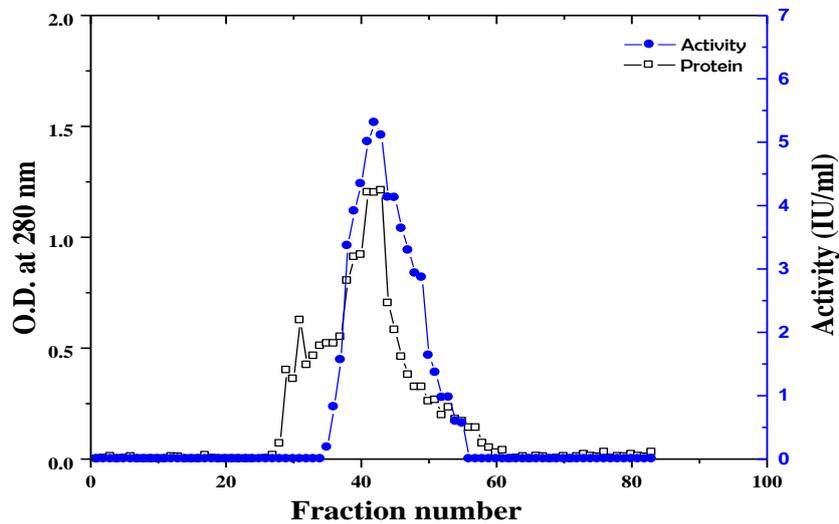


Fig 2: A Typical elution profile for *R. oligosporus* 0.05 M NaCl xylanase pooled fraction on Sephacryl S-200 column.

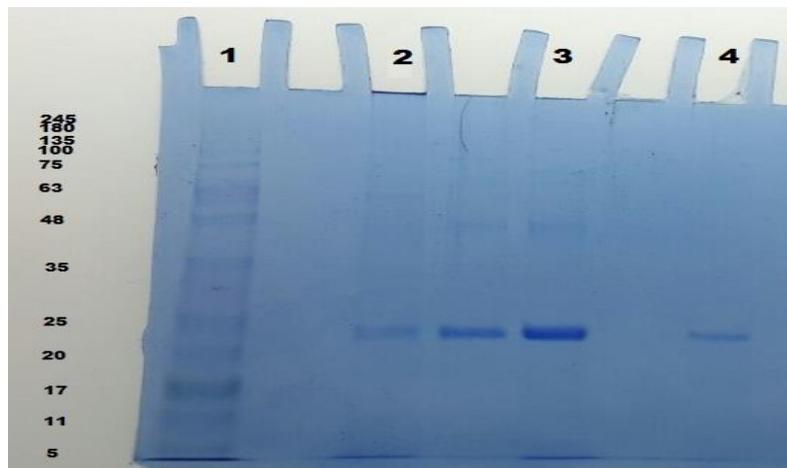


Fig 3: SDS-PAGE for molecular weight determination of *R. oligosporus* xylanase
 1- Standard proteins. 2- Crude enzyme 3- activity on ion exchange
 4-activity on gel filtration

Substrate specificity

The activity of the purified xylanase towards different substrates was assessed. Table (2) shows that the *R. oligosporus* xylanase herein was active on birchwood xylan (main substrate for assay) as 100%. Relative activity was increased to 126.6 and 129.2% toward beechwood xylan and oat spelt xylan, respectively. The enzyme was moderately active on glycogen but it has a slight activity on starch, CM-cellulose and pectin. This result was similar to xylanase from *T. inhamatum* [6], showing the inclination of the catalysts for branched and heterogeneous xylan.

Table 2: Relative activities of the purified xylanase towards different substrates

Substrate	% Relative activity
Birchwood xylan	100
Oat spelt xylan	129.2
Beechwood xylan	126.6
Pectin	13.2
Glycogen	40.8
Starch	23.2
CM-cellulose	16.3

K_m value

Determination of the apparent K_m values of *R. oligosporus* xylanase for birchwood, beechwood and oat spelt were refined through studies relating substrate concentrations to the responses speeds (Fig.4). The K_m value for oat spelt equal to 3.2 mg/ml with V_{max} of 1.7 IU ml⁻¹ min⁻¹, K_m value for beechwood were 4.7 mg/ml with V_{max} of 1.8 IU ml⁻¹ min⁻¹ while for birchwood K_m value equal to 8 mg/ml with V_{max} of 2.2 IU ml⁻¹ min⁻¹. While Silva *et al.* [6] showed that *T. inhamatum* xylanase K_m value for oat spelt was 14.5 mg/ml and for birchwood K_m value was 1.6 mg/ml.

The K_m values showed that *R. oligosporus* xylanase had higher affinity for oat spelt, beechwood than for birchwood. This result is similar to *Penicillium capsulatum* xylanase which was able to hydrolyze oat spelt substrate more efficient than birchwood [36].

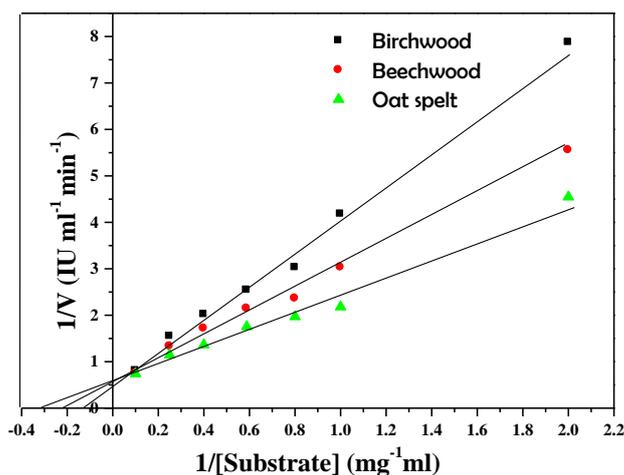


Fig 4: Lineweaver- Burk plot of *Rhizopus oligosporus* xylanase fraction with specific substrate (Birchwood, Beechwood and Oat spelt) at concentrations ranging from 0.5 mg to 10 mg.

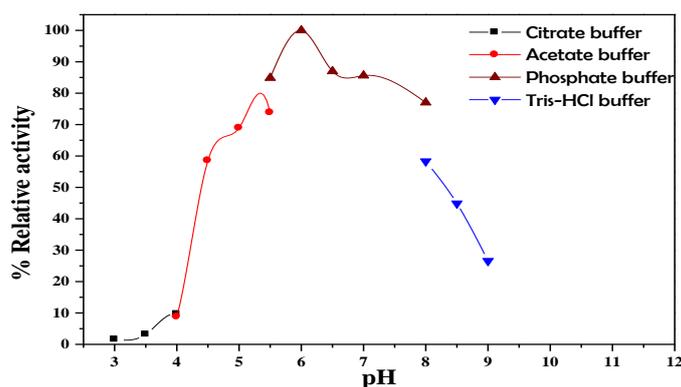


Fig 5: Effect of pH on activity of *R. oligosporus* Xylanase

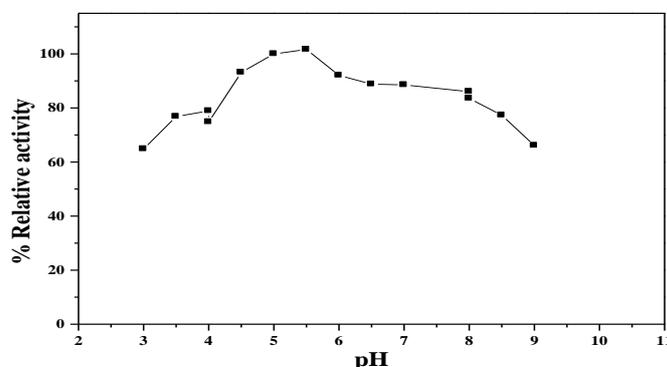


Fig 6: pH stability of *R. oligosporus* xylanase

pH of *R. oligosporus* xylanase

The activity of *R. oligosporus* xylanase was subject to pH. pH optimum of *R. oligosporus* xylanase was at pH 6.0 (Fig.5). Similar findings were also showed by Pithadiya *et al.* [15] who found that maximum xylanase production from *Bacillus circulans* was at pH 6.0. While, Lin *et al.* [37] illustrated that an optimum pH 6.5 for *Thermomyces lanuginosus*-SSBP xylanase. Also, Blanco *et al.* [38] showed a maximum activity at pH 5.5 for xylanase from a *Bacillus* species strain BP-23. This acidic xylanase is more beneficial in the textile industry than the acidic and alkaline ones because of less utilization of energy and crude material. In this way, the expense of production can be definitely diminished which thus will make it more acceptable in the market. On other hand, Irfan *et al.* [39] found an optimum pH 8.0 for production of *Bacillus* sp xylanase. However, an optimum pH 9.0 for xylanase from *Bacillus halodurans* strain KR-1 and *Bacillus* sp. strain 41M were reported [33,40], respectively.

pH stability of *R. oligosporus* xylanase

R. oligosporus xylanase was incubated at 4°C for 30 min at different pHs ranged from 3.0-9.0. The enzyme showed stability at pH 5.5 and 6.0 (Fig. 6). The residual activities were estimated under standard assay conditions. pH ranged from 4.5-8.0 was the most favorable for stability of *R. oligosporus* xylanase activity for 30 minutes. This result is in accordance with Gowdhaman *et al.* [41] who found that xylanase enzyme from *B. aerophilus* had an optimum pH for activity at 4.0 and it was stable at pH range 2.0-6.0. Xylanase with low pH optimum and good stability under acidic conditions are appropriate for food industry due to extremely low pH prevailing in the alimentary system. While in comparable study of Goswami and Rawat [42], they reported a 100% xylanase activity at pH 8.0 by *Bacillus arseniciselenatis*. While Sunny *et al.*

[43] found maximum xylanase stability from *Bacillus sp.* at pH 9.0 indicating that the enzyme was alkali stable as well as moderately acid stable.

Effect of temperature on *R. oligosporus* xylanase activity and thermostability:

Fig. (7) portray the relation between various temperatures and relative activity of *R. oligosporus* xylanase. Xylanase activity was directly proportional to increment in the temperature even to 40°C where it recorded its most optimum activity before decreasing obviously at 50°C with about 18% activity at 70°C. The ideal temperature at 40°C was like that showed of *B. Megaterium* xylanase by Irfan *et al.* [39] and from *Bacillus halodurans* by Araki *et al.* [44]. While the optimum temperature was at 45°C for *A. ficuum* AF-98 xylanase and *T. reesei* xylanase [45,46]. Comparable discoveries were furthermore reported by extreme enzyme activity from various *Bacillus species* has temperature-optima of 40–60°C [47,48]. While Monisha *et al.* [49] and Pithadiya *et al.* [15] found that *Bacillus circulans* was given greatest xylanase production at 30°C. Slightly higher optimum temperatures have been accounted for different xylanases, by strains of *Bacillus sp.* which gave most amazing yield of xylanase at optimal temperature of 45°C and 55°C [50]. In like manner Kavita *et al.* [51] reported an optimum temperature of 55°C for the purified of *Aspergillus nidulans* KK-99 xylanase. However, Dheeran *et al.* [35] found that *Paenibacillus macerans* xylanase has a wide range of enzyme activity at temperature from 40°C to 90°C and revealed an optimum activity at 60°C.

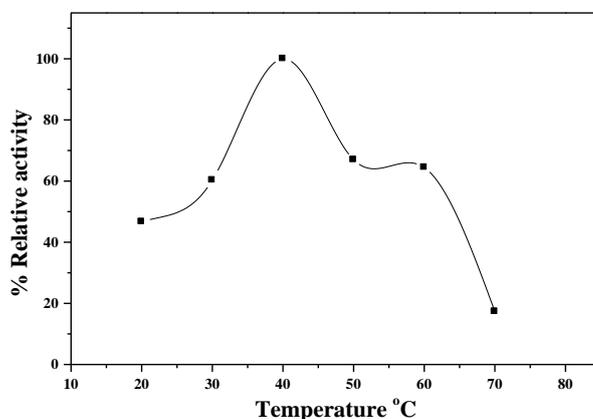


Fig 7: Effect of temperature on *R. oligosporus* xylanase

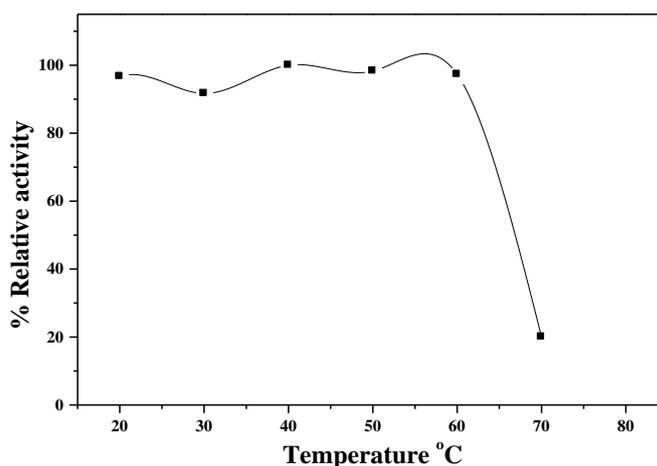


Fig 8: Thermal stability of *R. oligosporus* xylanase

Thermal stability

Thermal stability of *R. oligosporus* xylanase was estimated by keeping the protein at various temperatures extending from 20 to 70°C for 30 minutes followed by cooling in an ice bath. The residual

activities were estimated using the standard assay reaction mixture. The average of two assay experiments was taken for each point (Fig.8). The protein activity held more than 90% of its maximum activity from 40 to 60°C, while at 70°C the *R. oligosporus* xylanase activity was held only 20% of its maximum activity. In a comparable study xylanase enzyme was stable in a wide range of temperatures (40-90°C) and illustrated great thermal stability at 60°C with half life of 2 hours and could hold 80% enzyme activity up to 3 hours [42].

Effect of different metal ions on activity of *R. oligosporus* xylanase

Results regarding the effect of metal ions on xylanase activity were summarized in Table (3). It was found that Al³⁺, Co²⁺, Ba²⁺ and K⁺ has a mild inhibitory effects on xylanase activity; while, Ni²⁺ and Na⁺ ions had a weak stimulatory effects where, both Ni²⁺ and Na⁺ ions in 10 mM concentration elevated the activity to 103.5%. On other hand, the enzyme activity decreased to 75.7, 80, 83.5 and 85% in presence of 5 mM of Ca²⁺, Mg²⁺, Cu²⁺ and Zn²⁺, respectively. Inkyung and Jaiesoon [52] adduce a report about stimulation of *Paenibacillus* sp. strain K1J1 xylanase by Ca²⁺, Zn²⁺, Co²⁺, Cu²⁺, and Mn²⁺. In a comparable study of Lee *et al.* [53], presence of Ca²⁺, Co²⁺, Zn²⁺, Cu²⁺, and Mn²⁺ revealed a stimulation to *B. licheniformis* xylanase. While, Collins *et al.* [10] showed inhibition of *Pseudoalteromonas haloplanktis* xylanase in the presence of Cu²⁺ and Zn²⁺. In the present study, *R. oligosporus* xylanase activity was completely inhibited in the presence of Hg²⁺ ions. The destruction of the xylanolytic ability by Hg²⁺ ions may be because of its interaction with sulphhydryl groups, proposing that there is an essential cysteine residue in or near to the substrate binding site of the enzyme. Hg²⁺ has formerly been reported to completely inhibit the enzymatic activity of xylanase from many different sources *B. circulans*, *Paenibacillus macquariensis* and *T. inhamatum* [6,33,54].

Table 3: Effect of different metal ions on activity of *R. oligosporus* xylanase

	% Remaining activity	
	5 mM	10 mM
Non	100	100
Al ³⁺	54.0	81.9
Ba ²⁺	61.7	88.1
Ca ²⁺	75.7	94.3
Co ²⁺	57.2	80.7
Cu ²⁺	83.5	99.6
K ⁺	69.6	98.5
Mg ²⁺	80	101.8
Zn ²⁺	85	107.1
Ni ²⁺	90	103.5
Na ⁺	101	103.5
Hg ²⁺	0	0

CONCLUSION

Xylanase is a standout amongst the most critical enzymes used in agriculture and industry. It is produced by various microorganisms, such as yeast, bacteria and fungi. The present study focused on production of xylanase by *Rhizobus oligosporus* under solid state fermentation. The produced xylanase was purified and characterized. Additionally, activity of the purified xylanase enzyme toward different metals has been also determined. This manuscript presents the first report about the purification and properties of xylanase from *R. oligosporus* by a simple and inexpensive procedure. Furthermore, a comparison of the results indicates possible employment of such enzymes in some industrial processes. Since thermostability, acid conditions and wide-ranging pH stability are required properties for many industrial applications of xylanases, such as for animal feed, juice, wine, paper and textile industries in order to meet various industrial needs under the harsh environmental conditions.

REFERENCES

[1] Sakthiselvan P, Naveena B and Partha, N. Brazilian Journal of Microbiology 2014; 45(4):1293-1302.
 [2] Dobrev GT, Pishtiyski IG, Stanchev VS and Mircheva R. Bioresource Technology 2007; 98:2671-2678.
 [3] Luo L, Cai, J, Wang C, Lin J, Du X, Zhou A and Xiang, M. Journal Chemical Technology and Biotechnology 2016; 91:1093-1098.

- [4] Nair SG, Sindhu R and Shashidhar S. African Journal of Microbiology Research 2008; 2(4):82-86.
- [5] Poorna CA and Prema. Bioresource Technology 2007; 98:485-490.
- [6] Silva LAO, Terrasan CRF and Carmona EC. Electronic Journal of Biotechnology 2015; 18:307-313.
- [7] Wipusaree N, Sihanonth P, Piapukiew J, Sangvanich P and Karnchanatat A. African Journal of Microbiology Research 2011; 5(31):5697-5712.
- [8] Lombard V, Golaconda RH, Drula E, Coutinho PM and Henrissat B. Nucleic Acids Research 2014; 42:D490-D495.
- [9] Motta FL, Andrade CCP, Santana MHA. INTECH, Chennai 2013, pp. 251-275.
- [10] Collins T, Gerday C and Feller G. FEMS Microbiology Reviews 2005; 29:3-23.
- [11] Goulart AJ, Carmona EC and Monti R. Brazilian Archives of Biology and Technology 2005; 48(3):327-333.
- [12] Kumar V, Pandey P, Gupta S and Shukla P. International Journal of Current Microbiology and Applied Sciences 2014; 3(4):501-506.
- [13] Haltrich D, Nidetzky B, Kulbe KD, Steiner W and Zupancic S. Bioresource Technology 1996; 58:137-161.
- [14] Gupta U and Kar R. Brazilian Archives of Biology and Technology 2009; 52(6):1363-1371.
- [15] Pithadiya D, Nandha D and Thakkar A. Archives of Applied Science Research 2016; 8(2):1-10.
- [16] Kamble RD and Jadhav AR. International Journal of Microbiology 2012; Article ID 683193: 1-8.
- [17] Ninawe S, Kapoor M and Kuhad RC. Bioresource Technology 2008; 99:1252-1258.
- [18] Pal A and Khanum F. Process Biochemistry 2011; 46:879-887.
- [19] Galbe M and Zacchi GA. Applied Microbiology and Biotechnology 2005; 59(6):618-628.
- [20] Dhiman SS, Sharma J Battan B. Bioresource 2008; 3:1377-1402.
- [21] Kumar V, Marín-Navarro J and Shukla P. World Journal of Microbiology and Biotechnology 2016; 32:34. DOI 10.1007/s11274-015-2005-0
- [22] Biswas SR, Jana SC, Mishra AK and Nanda G. Biotechnology and Bioenergetic 1990; 35:244-51.
- [23] Chen WP and Anderson AW. Biotechnology and Bioengineering 1980; 22(3):519-531.
- [24] Saha BC. Process Biochemistry 2002; 37:1279-1284.
- [25] Miller GL. Analytical Chemistry 1959; 31:426-429.
- [26] Warburg O and Christian W. Biochemistry Zoology 1942; 310:386-421.
- [27] Bradford MM. Analytical Biochemistry 1976; 72:248-54.
- [28] Laemmli UK. Nature 1970; 227:680-685.
- [29] Paloheimo M, Mantyla A, Kallio J, Puranen T and Suominen P. Applied and Environmental Microbiology 2007; 3215-3224
- [30] Li S, Yao J and Yu Z. Plasma Science and Technology 2007; 9:248-251.
- [31] Gessesse A. Applied and Environmental Microbiology 1998; 64(9):3533-3535.
- [32] Mahatman KK, Garg N, Chauhan R and Kumar A. Iranica Journal of Energy and Environment 2010; 1(4):265-274.
- [33] Sharma M, Mehta S and Kumar A. Advances in Microbiology 2013; 3:32-41.
- [34] Ahmad Z, Butt MS, Riaz M. Pakistan Journal of Agriculture and Science 2013; 50(3):433-437.
- [35] Dheeran P, Nandhagopal N, Kumar S, Jaiswal YK and Adhikari DK. Journal of Industrial Microbiology and Biotechnology 2012; 39(6):851-860.
- [36] Ryan SE, Nolan K, Thompson R, Gubitz GM, Savage AV, Tuohy MG. Enzyme Microbiology and Technology 2003; 33:775-785.
- [37] Lin J, Nudlovu LM, Singh S and Pillay B. Biotechnology and Applied Biochemistry 1999; 30(1):73-79.
- [38] Blanco A, Vidal T, Colom FJ and Pastor JIF. Applied and Environmental Microbiology 1995; 61(12):4468-4470.
- [39] Irfan M, Umar A, Muhammed N, Rubiana N and Quartulain S. Journal of Radiation Research and Applied Sciences 2016; 139-147.
- [40] Nakamura S, Wakabayashi K, Nakai R, Aono R and Horikoshi K. Applied and Environmental Microbiology 1993; 59(7):2311-2316.
- [41] Gowdhaman D, Jeyalakshmi G, Sugumaran K, Subramanian NS, Santhosh RS and Ponnusami V. Turkish Journal of Biochemistry 2014; 39(1):70-77.
- [42] Goswami GK and Rawat S. International Journal of Pure Applied Bioscience 2015; 3(2): 534-541.
- [43] Sunny D, Bajaj BK, karri S, Bhasin A, Razdan K, Gupta N and Sethi N. International Journal of Current Microbiology and Applied Science 2014; 3(3):365-377.
- [44] Araki T, Enoue N and Morisita T. The Journal of General and Applied Microbiology 1998; 44(4):269-274.
- [45] Tenkanen H, Puls J and Poutanen K. Enzyme Microbiology and Technology 1992; 14:566-574.
- [46] Fengxia L, Mei L, Zhaoxin L, Xiaomei B, Haizhen Z and Yi W. Bioresource Technology. 2008; 99:5938-5941.



- [47] Khandeparker R, Verma P and Deobagkar D. *New Biotechnology* 2011; 28(6):814-821.
- [48] Kumar SS, Panday DD and Naik GR. *World Journal of Science and Technology* 2011; 1:09-16.
- [49] Monisha R, Uma MV and Murthy VK. *Kathmandu University Journal of Science Engineering and Technology* 2009; 5(II):137-148.
- [50] Simphiwe P, Ademola B, Olaniran O and Pillay B. *African Journal of Microbiology Research* 2011; 5(7):742-752.
- [51] Kavita T, Gupta S and Kuhad RC. *Bioresource Technology* 2002; 85:39-42.
- [52] Inkyung P and Jaiesoon C. *African Journal of Microbiology Research* 2010; 4(12):1257-1264.
- [53] Lee CC, Kibblewhite-Accinelli RE, Smith MR, Wagschal K, Orts WJ and Wong DWS. *Current Microbiology* 2008; 57(4):301-305.
- [54] Qureshy AF, Khan LA and Khanna S. *Indian Journal of Microbiology* 2002; 42:35-41.