

Optimization of β -1,4-endoxylanase production by a new *Aspergillus niger* strain growing on wheat straw and application in xylooligosaccharides production

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Abstract

Plant biomass constitutes the main resource of renewable carbon in the planet and its valorization has traditionally been focused on the use of cellulose, although hemicellulose is the second most abundant group of polysaccharides on earth. Enzymes involved in its degradation are usually glycosyl hydrolases and filamentous fungi are good producers of these enzymes. In this study, a new strain of *Aspergillus niger* was utilized for hemicellulase production under solid state fermentation using wheat straw as a single carbon source. Physicochemical parameters for production of an endoxylanase were optimized by using one factor at a time approach and response surface methodology (RSM). Maximum xylanase yield after RSM optimization was increased 3-fold. The enzyme was purified by ultrafiltration and ion-exchange chromatography 1.41-fold, with 6.2 % yield. Highest xylanase activity was observed at 50 °C and pH 6. A high pH and thermal stability were found, greater than 90% residual activity between pH 3.0-9.0 and between 30-40°C, after 24 h of incubation, presenting half-lives of 30 min at 50 and 60°C. Enzyme was mostly active for wheat arabinoxylan, and displayed the following kinetic parameters K_m of 26.06 mg·ml⁻¹ and V_{max} of 5,647 U·mg⁻¹·min⁻¹. Wheat straw xylan hydrolysis with the purified β-1,4 endoxylanase showed that it was able to release xylooligosaccharides, making it suitable for different applications in food technology.

Keywords: Fungi, enzymes, hemicellulose, wastes, hydrolysis

1. INTRODUCTION

Each year, transformation of the animal and plant feedstock, and its intermediate and terminal products, yields 140 billion tons of agricultural and industrial residues. Just 3% of the 13 billion tons/year of plant-biomass residues are utilized in producing goods (Morganti, 2013). The current management system is highly depending on various fossil energy sources like oil, coal and natural gas (Sarkar, Ghosh, Bannerjee, & Aikat, 2012). The development of technologies for renewable energy production is one of the greatest challenges in the twenty-first century, due to the serious problems on energy production and use (Hussein, 2015). Much alternative energy can alter the fossil fuels needs in the future, like biomass, solar, wind and hydrothermal energy. Between these energy sources, the biomass is one of the carbon-based sustainable energy most consumed in the world (Faraco, 2013).

Underutilization of agriculture products yields residues, frequently rich in nutrients, can provide an excellent habitat for the development of microorganisms. Lignocellulose, the main renewable resource in nature and the most abundant carbohydrate in biosphere, is the central component of plant biomass. It consists of three principal constituents: i) cellulose, a homopolysaccharide composed of units of D-glucopyranose linked by β -1,4 O-glycosidic bonds, constituting long linear chains which interact giving rise to microfibrils (Klemm, Philipp, Heinze, & Wagenknecht, 1998), ii) hemicellulose, which groups a series of polysaccharides with heterogeneous structures, that differ from each other in their backbone and branches (Scheller & Ulvskov, 2010), and iii) lignin, an amorphous and complex heteropolymer, highly branched and composed by phenylpropane units, which reinforce plant cell wall structure (A. Pandey, Soccol, & Larroche, 2008).

Respect to hemicellulose, xylan is the most abundant non-cellulosic plant polysaccharide, being the main component in the secondary cell wall of dicotyledons and cereal grains (Ebringerová, 2005). It is composed of a backbone of β -1,4-linked D-xylopyranosyl units, frequently acetylated and highly branched by short side chains of arabinose or glucuronic acid. The abundance of each of these substituents depends largely on the nature of the plant biomass. Usually full catabolic processes are achieved in Nature by the synergistic action of different microorganisms found in biomass rich environments (Hu et al., 2007). However, during last years the studies about the enzymatic microbial system involved in the process have increase, by the economical relevance of exploiting this heteropolysaccharide on different biotechnological applications. Due to its complexity, xylan hydrolysis requires the action of different enzymes for its degradation but, among them, two types of glycosidases play a key role in the process: i) endo- β -1,4-xylanases, which hydrolyze the polysaccharide by attacking internal links in the main chain, releasing oligosaccharides with different polymerization degrees and ii) β -xylosidases, which complete the degradation process by converting the xylooligosaccharides into xylose (Biely, 1985).

Although xylanases can be produced by several organisms (including crustaceans, protozoans, snails, insects, bacterial or fungi), the filamentous fungi are usually chosen for these studies by the secretion of high enzyme levels to the culture (facilitating its purification and further characterization), and their robustness against environmental factors (Polizeli, 2005). Fungi from genus *Aspergillus*, *Trichoderma*, *Rhizopus* and *Penicillium* are very well known producers of xylanase activities. Specially, *Aspergillus* and *Trichoderma* species have been studied extensively for their ability to secrete high-levels of enzymes in solid-state fermentation (Chen, 2013). *Aspergillus* genus is usually employed to produce xylanolytic enzyme cocktail in industrial plants for applications like paper manufacturing, bread-making, animal feed, juice and wine industries (Loureiro, Romanini, & Tubio, 2016; Takahashi, Kawabata, & Murakami, 2013). However, since the enzymatic system secreted by fungi depends of the strain and the culture conditions, it is interesting to study new strains to produce efficient and robust enzymes.

Solid-state fermentation of lignocellulosic biomass has successfully been applied for biofuels, biotransformation, biological detoxification, and bioremediation, in solving an energy crisis and environmental pollution, and the application in environmental protection by biotransformation of crops and waste products to enhance their nutritional value. These biotransformation processes for crops and waste can be optimized to achieve a suitable high yield. The classical methods for optimization focus on changing one variable, while maintaining the others into fixed levels. This single-dimensional approach is an incomplete approach to produce optimized conditions since it does not consider interactions between factors. The response surface method (RSM), on the contrary, is a strong model for establishing optimal process conditions under complex interactions between independent variables (Montgomery, 2017).

The objective of this study was to optimize fermentation conditions, using one factor at a time (OFAT) and response surface methodology (RSM) approaches of a new *Aspergillus niger* BG strain growing on wheat straw to produce high levels of β -1,4-endoxylanase. In addition, this enzyme was purified, its physico-chemical and kinetics properties were studied, and a process to generate xylooligosaccharides by hydrolysis of wheat straw xylan was designed.

2. MATERIALS AND METHODS

2.1. Microbial strain and growth conditions

A. niger BG strain was isolated from olive tree decomposing soil from Akbou area, Bejaia, located in North-east of Algeria (Azzouz, et al., 2020). It was cultivated using solid-state fermentation (SSF) in a 500 mL flask containing 10 g wheat straw moistened at 70% with Mandels medium (Mandels & Weber, 1969) and pH adjusted to 5.0. A spore suspension (10^7 spores/g of substrate) of *A. niger* BG strain was prepared from 7 days grown PDA agar plates in 1% (v/v) Tween 80. The spore count was performed in a Malassez counting chamber (Marienfeld, Germany) (Ang et al., 2015). This spore suspension was seeded in a 500 mL flask and incubated at 28°C for 7 days. Thereafter, the enzymatic extracts were harvested by crushing the contents of the flasks in 100 mL of distilled water with a glass rod and then shaking on an orbital shaker at 100 rpm for 10 min at room temperature. The filtrate was centrifuged at $10,000 \times g$ for 10 min at 4 °C. The clear supernatant was used as crude enzyme with endoxylanase activity and stored at 4 °C until its use. For optimization studies, the composition of the culture medium was varied according to the experimental data, while the inoculum size and source of carbon (wheat straw) were constant.

2.2. Enzyme assay

Endoxylanase activity was measured by the method of Bailey et al., (1992) with slight modification. The liberation of reducing sugars from beechwood xylan was estimated by the dinitro-salicylic-acid method (Miller, 1959), using D-xylose as a standard. Reaction mixtures contained 100 µL of properly diluted enzyme with 900 µL of 2% (w/v) beechwood xylan (Sigma-Aldrich), dissolved in 50 mM citrate buffer (pH 5), and they were incubated for 5 min at 50 °C. Reactions were terminated by the addition of 1.5 mL 3,5-dinitrosalicylic acid reagent (DNS), placed in a boiling water bath for 5 min and cooled in ice water. The absorbance was read at 540 nm. One unit of activity has been defined as the quantity of enzyme needed to release 1.0 µmol of xylose per minute (min) at pH 5 and at 50 °C. For each assay in this study, triplicate measurements were conducted. The concentration of the protein was measured by the method of Bradford (Bradford, 1976), using bovine serum albumin (BSA) as a standard.

2.3. Determination of optimal physicochemical parameters using classical one-factor-at-a-time approach

The production of endoxylanase from wheat straw under SSF was optimized by classical OFAT approach. In this method, one parameter is changed while maintaining the others to predefined levels (Banu, Ali, Rahman, & Konneh, 2020). This was used to study the effects of physicochemical parameters as culture time (1 to 7 days), incubation temperature (20 to 40 °C), moistening agent level (30 to 95%) and initial pH value (2 to 9). All experiments were run in triplicates and data obtained were subjected to one-way analyses of variance (ANOVA) carried out using XLSTAT software (version 2009.1.02), determining the Fisher's least significant difference in the mean variable. A p -value < 0.05 between the variables was considered significant.

2.4. Determination of optimal physicochemical parameters with response surface model using Box–Behnken design

Box–Behnken design (BBD) is used for optimization purposes since it allows to estimate the main effects of some factors simultaneously (Wahid & Nadir, 2013). Parameters and levels used for this optimization were selected by classic OFAT (Table 1). A polynomial model based on 27 experiments with 3 replicates was built (Table 2) using Design-Expert 11® software (Version 11.0.5.0.USA). The number of experiments (N) required was defined according to equation Eq (1):

$$(1) \quad N = 2k \cdot (k - 1) + C_0$$

Where k and C_0 are the numbers of factors and central points respectively.

The trial data is then fitted through the response surface model (RSM) to discover the relationship between the controllable factors and the response factors (Xie et al., 2020). Regression analysis of the data to fit a second-order polynomial equation (quadratic model) was carried out according to the following general Eq 2, which was used to predict the optimum conditions of the extraction process.

$$R = \beta_0 + \sum_{i=1}^n \beta_i X_i + \sum_{i=1}^n \beta_{ii} X_i^2 + \sum_{i=1}^n \sum_{j=1}^n \beta_{ij} X_i X_j + \varepsilon \quad (2)$$

Where R represents the response surfaces, β_0 is the constant term (intercept), β_i , β_{ii} and β_{ij} are the coefficients of linear, quadratic, and interaction, respectively, while X_i , X_i^2 and $X_i X_j$ are linear variables, quadratic variables,

and term for interaction of the variables respectively, and ϵ is the residual associated to the experiments (the prediction error, represents the difference between measured R values and predicted R and quantifies the random variability in our design of the experiment. The surface plots were plotted by varying the values of two factors and keeping the values of other factors constant at zero level. The second-order polynomial model that RSM developed consists of linear, quadratic, and interaction models (Eq. 2) (Srivastava et al., 2018). The determination coefficient (R^2) is selected to calculate the goodness of fitting (Eq.3). The closer the value is to 1, the better the model fits.

$$R^2 = 1 - \left[\sum_{i=1}^n (R_i - \bar{R}_i)^2 + \sum_{i=1}^n (R_i - \bar{R})^2 \right] \quad (3)$$

Where n, R_i , \bar{R}_i , and \bar{R} are the number of measures, the i-th observation value, the i-th predict value, the number of trials, and the average of the response factors respectively.

The model prediction ability can be enhanced by omitting it, when the influence of the corresponding item is significant and vice versa. The prediction determination coefficient (R^2_{predict}) is used to calculate the prediction ability of the model as given in Eq. (4).

$$R^2_{\text{predict}} = 1 - \left(1 - R^2 \right) \left[\frac{n-1}{n-(k+1)} \right] \quad (4)$$

Where n is the number of observations and k is the number of independent variables in the regression equation. The closer R^2_{predict} is to 1, the better the prediction ability of the mode is. The model is simplified by rounding off the insignificant items in the model and the new RSM model is obtained, then, the new model will have better prediction ability (Xie et al., 2020).

2.5. Purification of β -1,4-endoxylanase

Five hundred mL of crude extract, recovered after 96 h culture of *A. niger* BG strain produced in the SSF culture using the optimal production conditions obtained after optimization, were centrifuged for 15 min at $10,000 \times g$ to remove mycelia and spore cells. The supernatant was sequentially filtered, using 0.8, 0.45 and 0.22 μm filter membranes (Merck-Millipore). Then, filtrated supernatant was concentrated and dialyzed against 10 mM sodium phosphate buffer pH 6.0 by ultrafiltration, using a 3-kDa cut-off membrane. All purification steps were performed using an AKTA purifier system (GE Healthcare). Initially, this crude extract was applied to a 5 mL-HiTrap QFF (GE-Healthcare) cartridge, pre-equilibrated with the protein dialysis buffer, at a flow rate of 3 mL/min. Elution was carried out by applying a linear gradient of 1 M NaCl, prepared in the same buffer, from 0 to 50% in 45min. Protein profile was followed by the absorbance at 280 nm. Fractions with endoxylanase activity were pooled, dialyzed in the previous mentioned buffer and concentrated by ultrafiltration using 3-kDa cut-off membrane Amicon Ultra-15 centrifugal devices (Merck-Millipore). Finally, the samples were applied into a Mono Q 5/50 GL (GE Healthcare), equilibrated in the same buffer, at a flow rate of 1 mL/min and elution was carried out by applying a linear gradient of 1 M NaCl (0 to 10% for 35 min). The fractions with the purified protein were pooled, concentrated by ultrafiltration, as previously mentioned, and stored at 4 °C.

2.6. Characterization of β -1,4-endoxylanase

2.6.1. Polyacrylamide gel electrophoresis, mass spectrometry and NH_2 -terminal amino-acid sequencing

The homogeneity and molecular mass of the purified enzyme were determined by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE), following the method of Laemmli (1970), using 12% polyacrylamide gel and Precision Plus protein dual-color standards (Bio-Rad). Proteins were stained with Coomassie brilliant blue R-250 (Sigma-Aldrich).

The Native-PAGE (non-reducing conditions) of the purified xylanase was performed using 12% resolving gel. Xylanase activity was detected according to the protocol described by Yan et al., (2008) with slight modifications. Once the electrophoresis was finished, the gel was washed two times (each for 10 min) with 20 mL of 10 mM phosphate buffer, pH 6.0. The treated gel was then pre-incubated in 20 mL of the buffer containing 10 mM xylanase substrate (EnzChek™ Ultra Xylanase Assay Kit, Invitrogen™), followed by incubation at 10 min at room temperature. Finally, the detection of xylanase activity was visualized by fluorescence under ultraviolet light by use of the Gel Doc XR +system (Bio-Rad). The protein identification was determined by matrix-assisted laser desorption ionization-time of the flight mass spectrometry (MALDI-TOF), with an Autoflex III instrument (Bruker Daltonics), and the peptide fingerprinting was compared with those available in the NCBI database, with the MASCOT search engine (Matrix Science).

2.6.2. Effect of pH and temperature on enzyme activity and stability

The effect of pH on endoxylanase activity was investigated at pH values ranging from 2.0 to 9.0 at 50 °C for 5 min using beechwood xylan as substrate. The optimum temperature was measured by starting the reaction at different temperatures (30–90 °C) and the relative activity was calculated considering the maximum activity as 100%. The pH stability test was carried out by incubating the enzyme in different pH buffers (2.0 to 9.0) for 30 min, 2, 4, and 24 h at 25 °C followed by the activity assay. The thermostability of the enzyme was assessed by incubating the enzyme at temperatures of 30–80°C for 30 min, 1, 2, 3, 4, 5, 6, and 24 h, before measuring residual activities. Initial activity was determined as 100%.

2.6.3. Substrate specificity and kinetic parameters determination

Substrate specificity was investigated by incubating the purified enzyme with beechwood xylan, wheat arabinoxylan (WARX), avicel, and starch, detecting release of reducing sugars by DNS method. The relative activity was calculated using beechwood xylan as a reference.

Kinetic parameters (K_m and V_{max}) of xylanase towards WARX were determined using substrate concentrations from 2 to 50mg/ml. The data were fitted to a Michaelis–Menten equation using Graph-pad PRISM 7 software (version 7.00).

2.7. Wheat straw xylan hydrolysis using β -1,4-endoxylanase

The hydrolysis products released by enzymatic hydrolysis of wheat straw xylan kindly provided by Andromaco Laboratories (Spain) were analyzed by thin-layer chromatography (TLC). In a 1.5-mL tube, 500 μ L of substrate (20mg/ mL) was mixed with 0.03U of pure enzyme. The mixtures were incubated at 40 °C for 5 min, 15 min, 30 min, 1 h, 2 h, 4 h, 6 h, and 24 h. The samples were centrifuged at $14,000 \times g$ for 5 min, and the supernatant was used to analyze the hydrolysis products by TLC analysis. For every sample, 5 μ L of hydrolysis product were spotted onto TLC plates (POLYGRAM® SIL G/UV₂₅₄, Germany) and the plates were developed with the solvent system butanol/acetic acid/water (3:1:1, v/v/v). The TLC plates were air dried for 15-30 min and visualized by spraying with a solution methanol/sulfuric acid (95:5, v/v), followed by heating at 110 °C for 10 min. A xylooligosaccharides solution (xylose, xylobiose, xylotriose, xylotetraose, and xypentaose) was used as standard.

3. Results and discussion

3.1. Endoxylanase optimization using the classical OFAT method

In the last years, interest on endoxylanases have increased since they are essential enzymes to convert xylan in sugars that could be used in different biotechnological applications, as prebiotics, animal food or fuels (Ebringerová, Hromádková, & Heinze, 2005). As previously mentioned, *Aspergillus* species are one of the most studied organisms because they are a promising source of robust cellulases and xylanases. After a previous screening, using 62 fungal strains isolated from lignocellulose wastes, a new *A. niger* BG strain was selected by its ability to secrete high levels of enzymes involved in the degradation of plant cell polysaccharides (Azzouz, Bettache, Djinni, et al., 2020). In this work, the capabilities of this strain to produce an interesting endoxylanase, using SSF conditions and wheat straw as a single carbon source, was analyzed. Initially, the maximal activity was obtained after 7 days of incubation at 28 °C (314.47 ± 0.6 U/mL), when wheat straw was moistened with Mandels solution (70%) at pH 5 and inoculated with 10^7 spores/g suspension. To increase yield, operating conditions, such as pH, temperature, moisture agent level, and incubation time were varied. Figure 1 shows the variations over time of endoxylanase activity in the different tests carried out by using classical OFAT approach, as explained below.

3.1.1. Effect of the incubation period

The incubation period is an important parameter when considering enzymatic production. Fig.1a shows the impact of the incubation period on the xylanase production when wheat straw was used by *A. niger* BG strain as a substrate of fermentation. The endoxylanase production increased during the first days of incubation, reaching its maximal levels at 3 days-old cultures (330.49 ± 0.6 U/mL) and remaining practically stable during the rest of the studied period. The stabilization on enzymatic production could be related to the reduction of the nutrients in the fermentation medium along time, which impacts in the fungal physiology (Nochur, Roberts, & Demain, 1993). This is an adequate result, since shorter incubation time for enzyme production reduces the possibility of contamination and benefits its economic development for industrial xylanase production (Fadel, et al., 2014). It is necessary to remark that maximal production of this activity has been reported for *Geobacillus thermodenitrificans* X1, *Rhizopus oryzae* UC2 and *Aspergillus fumigatus* MS16 at 4,5 and 6 old-days cultures, by using raw oil palm frond leaves, wheat straw, and banana peels as carbon sources respectively (Verma et al., 2020; Ezeilo et al., 2019 and Zehra et al. 2020). However, maximum xylanase production was observed after 2 days of incubation with strains *A. fumigatus* F-993 and *Aspergillus flavus*, using white corn flour, wheat bran, and pearl millet stover under SSF, respectively (Fadel et al., 2014; Gautam, Kumar, & Dutt, 2015).

3.1.2. Effect of incubation temperature

The maximum endoxylanase activity (355.16 ± 0.3 U/mL) was found at 36 °C. At lower temperature, the production of xylanase decreased owing to lower transfer of substrates in the cell membrane, while higher temperature could reduce growth due to the denaturation of enzymes, which results in the higher preservation energy for cellular growth and lower metabolites generation (Pal & Khanum, 2010). Irfan et al. (2014), and Gautam et al., (2015), registered the maximum xylanase activity at 30 °C by *Aspergillus foetidus*, and *A. flavus* ARC-12 respectively. The maximum xylanase production was also reported at 35 °C and 25°C by *A. fumigatus* MS16 (Zehra et al., 2020). These variations could be related to the diversity of the microorganisms and their environmental conditions. Temperature is one of the vital factors, which heavily influences the SSF process, affecting different parameters as cell growth, and production of enzymes and metabolites (Mandal & Ghosh, 2017).

3.1.3. Effect of moisture agent level

The importance of moisture agent level in the SSF medium and its influence on enzyme production and microbial growth can also be attributed to the effect of moisture on the physical properties of solid substrate used for fermentation (Bakri et al., 2008). The increased moisture agent level from SSF had a significant effect on endoxylanase secretion. Fig 1c shows that xylanase production reaches maximum activity at 95% moisture agent level (462.49 ± 0.2 U/mL).

The moisture level was very different in other fungal growth in SSF conditions. Behnam et al., (2016), found that a moisture level of 71.8% was optimum for maximum xylanase production by strain *R. oryzae*. Also, Mandal and Ghosh (2017), found that cellulase production by strain *A. niger* using banana peel as substrate was maximum with a moisture ratio 3:1(w/v). More porous substrates can enhance the gaseous transfer, and still retain the right amount of moisture agent level supporting the stability of the extracellular enzyme and nutrient solubility (Bharti et al., 2018). Conversely, Ezeilo et al., (2019), Zehra et al., (2020), and Pandey et al., (2016), achieved maximum xylanase production at 40%, 45%, and 50% moisture agent level respectively, using strains of *R. oryzae* UC2, *A. fumigatus* MS16 and *R. oryzae* SN5, and were obtained with raw oil palm frond leaves, banana peels, and wheat bran as carbon sources under SSF respectively.

3.1.4. Effect of pH

The pH in a SSF medium is a key variable that directly influences the stability of inter-membrane transportation, microbial growth, and ultimately the production enzyme. In particular, this is very important for extracellular enzymes, since its release into the medium depends on the mechanism of membrane transport, which is regulated by the concentration of the hydrogen in the medium (Bibi et al., 2014). To examine the optimum initial medium pH for xylanase production, experiments were implemented at different pH values ranging from 2 to 10. Fig 1d shows that xylanase production was quite affected by the initial pH value in the *A. niger* BG strain cultures growing in wheat straw under SSF conditions. The maximum endoxylanase activity was achieved at pH 9.5 (494.56 ± 0.54 U/ml).

Most of the fungus exhibit the highest xylanase activity level in acidic environment, in medium at pH 4.5 (Irfan et al., 2014) or 6.5 (Carmona et al., 2005). However, the optimization of xylanase production was also reported by Verma et al., (2020) at pH 7–8 in *G. thermodenitrificans* X1 and in more alkaline conditions (pH 8–9) for *R. oryzae* UC2 (Ezeilo et al., 2019), *Aspergillus fischeri* (Senthilkumar et al., 2005), and *Trichoderma* SG2 (Nanjundaswamy & Okeke, 2020). In summary, a classical approach to optimize xylanase production by *A. niger* BG strain on wheat straw indicates that the production was enhanced by the short incubation time (three days), alkaline pH (9.5), high humidification level (95%), and mesophilic temperature (36°C). Under these conditions, *A. niger* BG strain produced high amounts of xylanase with a maximum activity of 494.56 ± 0.54 U/ml.

3.2. Box-Behnken analysis of xylanase production-based RSM design

After classical optimization of xylanase production, a statistical procedure was achieved by RSM using Box-Behnken Design (BBD). Four factors, incubation temperature (X_1), moisture agent level (X_2), pH (X_3) and, incubation time (X_4), were found to have a greater influence on xylanase production by *A. niger* BG strain. All factors were kept constant individually at the optimum level that they obtained in the OFAT trial. Afterward, the BBD design was used to optimize the level of these factors to study their interaction. Experimental conditions and results for xylanase production are presented in Table 2.

3.2.1. Model performance and fitting using RSM

The significance of the model was estimated by analysis of variance (ANOVA). Table 3 shows the ANOVA results for the quadratic model. The model *F*-value of 12.83 implies that the model is significant (*p*-value <0.001), with only a 0.01% chance that an *F*-value this large could occur due to noise. Within the model, X_1

(incubation temperature), X_2 (moisture agent level), X_2X_4 (moisture agent level vs. incubation time), X_3^2

(moisture agent level²), and X_4^2 (incubation time²) are significant model terms (table 3) with a p -values less than 0.05. As for factors X_3 (pH), X_4 (incubation time), X_1X_2 (incubation temperature vs. moisture agent level), X_1X_3 (incubation temperature vs. pH), X_1X_4 (incubation temperature vs. incubation time), X_2X_3 (moisture agent level vs. pH), X_3X_4 (pH vs. incubation time), X_1^2 (incubation temperature²), and X_2^2 (moisture agent level²), indicates that the factors and interaction between influencing factors are insignificant since the p -values are more than 5%. Lack-of-Fit with F -value of 3.36 implies this is not significant relative to the pure error. There is a 25.11% chance that a Lack-of-Fit F -value this large could occur due to noise and non-significant lack of fit is good.

The calculation of the determination coefficient value (R^2) is 0.9374, indicating the acceptability of the model in estimating the predicted values from the experimental values. The model is adequate in explaining most of the variability in the trial results since the R^2 value is greater than 0.75 (Wan et al., 2009). The Adjusted R^2 value (0.8643) validates the proposed model. By measuring the signal to noise ratio (Adeq Precision), the precision of the model can be indicated, which should be greater than 4 (Shojaei & Shojaei, 2017). In this report the value was 12.433, which shows a high level of precision and an appropriate response ratio. The Adequate Precision and the coefficient of variation (CV%; 19.92%) (Table 3), suggested that the model was reliable and reproducible by previous reports comparing the average prediction error at design points with the range of predicted values (Cao et al., 2008; Pathania et al., 2017).

Fig. 2 shows the results of the predicted values of xylanase production vs. the actual values of the response surface method. It demonstrates a good correlation with the actual and predicted values of xylanase production and linear distribution is indicative of a good-fitted model. This figure shows the model is fairly realistic although it shows that the discrepancy is very small between the actual and predicted values (He et al., 2018), and the R^2 value is 93.74%, which indicated the correct precision between the model and the data. So this model can be utilized to sail the design space. Hence, based on the statistical properties, it may be concluded that the model is adequate to establish the principal impacts of the factors (Banu et al., 2020).

The final model of the second-order polynomial quadratic regression equation was developed for xylanase production and is presented by the final equation in terms of coded factors (Eq.5)

$$R = +379.67 - 197.83X_1 - 293.67X_2 - 9.50X_3 + 58.83X_4 + 59.50X_1X_2 + 31.75X_1X_3 - 18.75X_1X_4 - 6.00X_2X_3 + 145.00X_2X_4 + 79.75X_3X_4 + 70.79X_1^2 - 79.71X_2^2 + 135.54X_3^2 + 299.79X_4^2 \quad (5)$$

Where R ; Xylanase production (U/ml), X_1 ; incubation temperature, X_2 ; moisture agent level X_3 ; pH and, X_4 ; incubation time. The negative sign in front of the design terms indicates an antagonistic effect, and the positive sign indicates a synergistic effect. The development-based model with coded factors is a desirable one since it can help to determine the more significant factors that will have an impact on the response (Montgomery, 2017).

3.2.2. Analysis of the interactions between influencing factors

The interaction of significant parameters and the effects on response were investigated by interaction plots and three-dimensional response surfaces plots (Fig. 3a-b) based on the regression analysis of BBD. The variation in response of xylanase production and the interaction between X_2X_4 (moisture agent level and incubation time) having significant p -value (0.0251) proved the presence of interactions between moisture agent level and incubation time (Fig.3a), and was found to be more favorable for enhanced xylanase production compared to the results of the other interactions. Fig. 3b depicts the effect of X_2X_4 on the xylanase activity when the incubation temperature and the initial pH were fixed at level 0. The xylanase activity increase significantly ($p < 0.05$) by increasing the incubation time and the moisture agent level. The xylanase production mainly depends on the moisture agent level, as its quadratic and linear effects were highly significant ($p < 0.0001$), confirming the single-factor experiment results (Table 3), and the influence in the metabolic rate of the interaction between these two parameters.

Similarly, Behnam et al., (2019), reported that the interaction term of moisture agent level and incubation time, was significant for xylanase production from *Mucor indicus* and were insignificant for *Mucor hiemalis* and *R. Oryzae* xylanase and cellulose production through SSF on wheat bran. According to studies conducted by de Almeida Antunes Ferraz et al., (2020), and Azzouz et al. (2020a;2020b) an interaction between the moisture agent level and an incubation time has proved to be insignificant on the biomass and xylanase production by strains *Penicillium roqueforti* ATCC 10110, *Trichoderma afroharzianum*, and *A. niger* BG strain using yellow mombin residue and wheat bran under solid-state fermentation respectively. As a result, the moisture agent level and cultivation time affect xylanase production by *A. niger*. The optimum moisture agent level will depend on the microorganism requirement, type of substrates and end products, and short incubation times provide conditions for the economical production of enzymes.

3.2.3. Validation of the model

According to the database generated with software Design Expert 11.6.0, the optimum values variables were determined. Validation of the statistical model and the regression equation was performed from the optimum conditions proposed by the model. The model validation was tried by running the 02 trial run created with the numerical optimization team in the model (Table 4). According to the 02 trial run the actual and predicted xylanase production was not significantly different and therefore it is concluded that the actual model was good predicted the xylanase production. Hence the values of the four variables were found as 35°C (incubation temperature, X1), 96% (moisture agent level, X2), 11 (medium pH, X3), and 96 h (incubation time, X4), yielding a maximum predicted xylanase activity of 1344 U/ml which was found to have been closed at the actual activity of 1413.88 ± 0.2 U/mL. Many researchers are using RSM modeling strategy for improving the xylanase production of several fungi with wheat straw as the substrate. These fungi include *Aspergillus candidus* (Garai & Kumar, 2013), *A. fumigatus* ABK9 (Das et al., 2013). Therefore, it may be concluded that BBD based RSM can significantly enhance the xylanase production and demonstrated a xylanase activity of 1413.88 ± 0.2 U/mL. The specific activity of the xylanase enzyme on RSM optimized condition was registered as 516.01 U/mg of protein. The effect of the optimization method is shown by the increased enzyme production and also by the decrease in enzyme production cost, which is mostly based on the use of inexpensive and easily accessed complex substrates like wheat straw and bran (Allala et al., 2020).

3.3. Purification and physicochemical properties of *A. niger* BG endoxylanase

Crude proteins with maximum activity (1413.88 U/ml) were collected for xylanase purification under the procedure described in materials and methods. After two anionic-exchange chromatographic steps, a fraction with xylanase activity was purified with a yield of 6.2%. During the process, the specific activity was increased from 516.06 to 728.25 U/mg (1.41-fold purification) (Table 5).

The homogeneity of the protein was analyzed by SDS-PAGE, showing a unique protein band with a molecular mass of approximately 20 kDa (Fig. 4a). This was also corroborated by the zymogram of native xylanase on PAGE, showing a unique activity band (Fig. 4b). MALDI-TOF analysis of the purified xylanase revealed several peptides that were sequenced and compared with NCBI protein database. Xylanase protein showed 94 % amino acid identity to an endoxylanase from *A. niger* (BAO02695.1) with a theoretical molecular mass of 22.671 kDa. The higher molecular mass of protein obtained by SDS-PAGE may be caused by glycosylation of the fungal protein, a conserved posttranslational modification that is found in all eukaryotes, very important for protein stability and secretion (Deshpande et al., 2008). This experimental molecular mass is close to those reported in other *A. niger* xylanases, as those from *A. niger* strain DSM 195, *A. niger* strain BCC14405, IBT-90, CGMCC1067, and *A. niger* strain IBT-90, which are also glycoprotein with higher experimental molecular mass (35.5; 21 and 20 kDa) than those corresponding to their sequences (Deng et al., 2006; Do et al., 2013; Korona et al., 2006).

The optimum temperature for purified xylanase was 50 °C, as shown in Fig 5a. It is the same optimum temperature reported for endoxylanase from *A. fumigatus* R1 (Deshmukh et al., 2016) and *Aspergillus nidulans* (Maitan-Alfenas et al., 2016). However, it was higher than those reported from *A. oryzae* LC1 and *A. niger* XZ-3S, which had an optimal temperature around 30 and 40 °C, respectively (Bhardwaj et al., 2020; Fu et al., 2012). In addition, the endoxylanase for the new *A. niger* BG strain, was very stable at 30 and 40 °C, since it maintained more than 90% of its activity after 24h of incubation, and more than 60% of activity remained at 50 and 60 °C after 30 min of incubation (Fig. 5a). In this sense, endoxylanases stable at 40 °C are necessities for xylooligosaccharides production, as well as in baking industry (Numan & Bhosle, 2006). Furthermore, the stability of the endoxylanase from *A. niger* BG strain at 30, 40, and 50 °C, as well as its stability at acidic conditions, suggest that this enzyme presents suitable properties to be utilized for lignocellulosic biomass treatments (Brienzo et al., 2015). At higher temperatures, such as 50 and 60 °C, 60% enzyme activity was conserved in the first 30 min, but after 1 h the xylanase activity was partially lost, probably due to protein denaturation. Previous studies reported xylanase thermostability from *Aspergillus* strains, indicates that they are generally stable at temperatures 35–45 °C (Fu et al., 2012), and 40–60 °C (Deshmukh et al., 2016).

The effect of pH value (2–9) on the activity and stability of purified endoxylanase is shown in Fig. 5b. The results indicated that the highest xylanase activity is observed at pH 6, being very active between 3–7. It showed a broad range of pH stability, from 3 to 9 after 24 h incubation at 25 °C, suggesting its ability to acts at both acidic and basic pH (Fig. 5b). Some studies indicate that xylanase produced by *Aspergillus* have optimum pH at the acid region, usually at pH 4.8, 5.0, 5.5, and 6.0, as i.e. *Aspergillus terreus*, *A. oryzae* LC1, *A. fumigates* FC2-2 or *A. nidulans*, respectively (Narra et al., 2014; Yang et al., 2015; Maitan-Alfenas et al., 2016; Bhardwaj et al., 2020). The optimum pH in the acid range permits the application of xylanase in the wine industry, mostly in reactors where maceration and fermentation occur concurrently, but pH stability is more important for industrial applications. In the current study, the purified endoxylanase showed stability in a pH range 3–9, similar to that

reported in the main xylanase of *A. oryzae* LC1, expressed in prokaryotic system *E. coli* (Bhardwaj et al., 2020), and higher than those described for other *A. niger* strain (pH 3.0-7.0) (Karaoglan et al., 2014).

3.4. Substrate specificity and kinetic parameters of *A. niger* BG endoxylanase

The action of purified endoxylanase towards various substrates is shown in Figure 5c. The results show that the enzyme was specific to xylan-containing substrates, being the highest activity obtained on wheat arabinoxylan (165.70%), and taking as 100% the activity on beechwood xylan, the standard substrate used in this work. Both xylns have high xylose content, but outstanding differences can be noticed. Beechwood xylan has few ramifications, containing approximately 94% xylose whereas wheat arabinoxylan is highly branched with arabinose residues (Nieto-Domínguez et al., 2019). In addition, this enzyme acts, although with minor efficiency, on Avicel (43.9%), which is microcrystalline cellulose. The results suggest that the new *A. niger* endoxylanase is a versatile enzyme able to act efficiently on linear and ramified xylan but also on polysaccharides with β -1,4-glucose bonds. However, *A. niger* endoxylanase is not active on starch, a homogenous polysaccharide consisting of numerous glucose units joined by α -1,4-glycosidic bonds, which indicates the enzyme selectively acts on β -linkage.

Kinetic parameters of purified xylanase were determined according to the Michaelis–Menten plots using various concentrations of wheat arabinoxylan substrate. K_m and V_{max} values of the enzyme were found to be 26.06mg/mL and 5647U/mg x min, respectively. The small K_m value shows that the purified xylanase has a high affinity for the substrate, which is a significant characteristic for industrial processes. The V_{max} value (5647 U/mg) in the present study is relatively high compared to the V_{max} of xylanases reported for other fungal strains (Table 6).

3.5. Xylooligosaccharides production

Wheat straw xylan was hydrolysed by purified β -1,4-endoxylanase, and the xylooligosaccharides products were determined by TLC. The relative migration of hydrolyzed product indicated that β -1,4-endoxylanase released xylopentaose, xylootetraose and xylootriose after 5 min (Fig 6), whereas xylobiose appears after 4 h of incubation time. According to the results, the reducing sugars are as a function of hydrolysis time, when increasing the incubation time, the concentrations of xylooligosaccharides are enhanced. Previous studies have indicated that endoxylanase is a key step in the conversion of xylns into shorter oligosaccharides (xylopentaose, xylootetraose, xylootriose, and xylobiose) (Long et al., 2020; Verma et al., 2020). Furthermore, enzymatic production of xylooligosaccharides is favored over chemical methods (Tan et al., 2008). The ability to produce oligosaccharides is a reasonable and reliable alternative for large amounts production on an industrial scale such as those needed in aquaculture and poultry industry (Aachary & Prapulla, 2011), because they have been qualified as anti-diabetic, anti-hypercholesterolemic, or anti-apoptotic molecules (Kim et al., 2006). The application of enzymatic produced xylooligosaccharides present a promoting green alternative, and have been studied as a promoting prebiotic constituent (Nieto-Domínguez et al., 2017), because they are not degraded by the human digestive enzymes, and fermented into the gastrointestinal tract (Amorim, Silvério, Prather, & Rodrigues, 2019). Accordingly, the β -1,4-endoxylanase has a high yield of xylooligosaccharides production and is a potentially suitable candidate for the enzymatic treatment of biomass.

4. CONCLUSION

The production of xylanase by *A. niger* BG strain using wheat straw was statistically optimized using classical optimization OFAT approach and RSM. The purified enzyme showed high stability at a large range of pH (3-9) and temperature (30-60°C), also showed maximum specificity towards wheat arabinoxylan. It was successfully used to produce xylooligosaccharides from wheat straw xylan. These results suggest that it could be of interest for biotechnological processes.

ACKNOWLEDGEMENTS

The authors thank technical service of CIB-CSIC and CNB-CSIC for MALDI analysis.

FUNDING

This work has been funded by Projects GLYSUS RTI2018-093683-B-I00 (MCIU/AEI/FEDER) and RETOPROSOST2 S2018/EMT-4459 (Comunidad de Madrid).

AUTHORS' CONTRIBUTIONS

Zahra Azzouz: Conceptualization, Methodology, Validation, Writing - original draft. Azzeddine Bettache and Nawel Boucherba: Methodology, Writing - review & editing, Investigation. Laura I. de Eugenio: Methodology, Validation, Writing - review & editing, Formal analysis, Investigation. Maria Jesus Martinez: Resources, Writing - review & editing, Supervision. Said Benallaoua: Writing-review & editing, Supervision, Project administration.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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Table 1 Independent variables and levels of variation in Box-Behnken design (BBD).

Study Type	Response Surface					
Design Type	Box-Behnken		Runs	27		
Design Mode	Quadratic		No Blocks			
Factor	Name	Units	Type	Level (-1)	Level (+1)	Level (0)
X ₁	Temperature	°C	Numeric	32	40	36
X ₂	Moisture	%	Numeric	90	100	95
X ₃	pH		Numeric	8	11	9.5
X ₄	Time	hour	Numeric	48	96	72
Response	Name	Units				
R	Xylanase	U/ml	Analysis	Polynomial		

Table 2 BBD for 27 runs of experiments

Ru n	Factor 1 X ₁ : Temperature °C	Factor 2 X ₂ : Moisture %	Factor 3 X ₃ : pH	Factor 4 X ₄ : Time hour	Response Xylanase Activity U/mL
1	40	95	11	72	334 ± 0.18
2	32	95	8	72	874 ± 0.03
3	40	90	9.5	72	608 ± 0.03
4	36	95	8	48	860 ± 0.01
5	40	95	9.5	48	465 ± 0.01
6	36	95	9.5	72	304 ± 0.1
7	36	95	11	96	1041 ± 0.05
8	40	95	8	72	411 ± 0.21
9	36	90	9.5	96	759 ± 0.03
10	32	95	9.5	48	923 ± 0.06
11	36	90	9.5	48	894 ± 0.46
12	36	95	9.5	72	424 ± 0.05
13	36	95	9.5	72	411 ± 0.05
14	32	100	9.5	72	126 ± 0.25
15	36	100	9.5	48	123 ± 0.05
16	36	95	8	96	870 ± 0.01
17	32	95	11	72	670 ± 0.28
18	36	95	11	48	712 ± 0.33
19	40	95	9.5	96	456 ± 0.05
20	36	90	11	72	743 ± 0.38
21	36	100	11	72	116 ± 0.01
22	40	100	9.5	72	61 ± 0.30
23	36	100	9.5	96	568 ± 0.01
24	32	90	9.5	72	911 ± 0.36
25	36	100	8	72	56 ± 0.02
26	36	90	8	72	659 ± 0.30
27	32	95	9.5	96	989 ± 0.42

Table 3 ANOVA for quadratic model

Source	Sum of squares	DF ^a	Mean of squares	F-value	Prob> F	
Model	2,309E+06	14	1,650E+05	12.83	< 0.0001	Significant
Linear						
X₁-Temperature	3,881E+05	1	3,881E+05	30.18	0.0001	
X₂-Moisture	1,035E+06	1	1,035E+06	80.47	< 0.0001	
X₃-pH	1083.00	1	1083.00	0.0842	0.7766	
X₄-Time	41536.33	1	41536.33	3.23	0.0975	
Interaction						
X₁X₂	14161.00	1	14161.00	1.10	0.3147	
X₁X₃	4032.25	1	4032.25	0.3135	0.5858	
X₁X₄	1406.25	1	1406.25	0.1093	0.7466	
X₂X₃	144.00	1	144.00	0.0112	0.9175	
X₂X₄	84100.00	1	84100.00	6.54	0.0251	
X₃X₄	25440.25	1	25440.25	1.98	0.1849	
Quadratic						
X₁²	26727.79	1	26727.79	2.08	0.1750	
X₂²	33884.90	1	33884.90	2.63	0.1305	
X₃²	97981.56	1	97981.56	7.62	0.0173	
X₄²	4,793E+05	1	4,793E+05	37.27	< 0.0001	
Residual	1,543E+05	12	12860.26			
Lack of Fit	1,457E+05	10	14565.05	3.36	0.2511	Not significant
Pure Error	8672.67	2	4336.33			
Cor Total	2,4604E+06	26				
Model Summary Statistics						
Std. Dev.	113.40	R ²		0.9374		
Mean	569.19	Adjusted R ²		0.8643		
C.V. %	19.92	Adeq Precision		12.4331		

^aDFa Degree of Freedom**Table 4** Validation of quadratic model for xylanase production with *A. niger* BG strain optimized by RSM

Solutions number	Temperature (°C)	Moisture level (%)	agentpH	Incubation time (h)	Xylanase Predicted (U/ml)	Xylanase Actual (U/ml)	Desirability
1	35	96	11	96	1344	1413.88±0.2	1.000
2	33	90	9.0	48	911	824.54 ±0.6	1.000

Table 5 Purification steps of xylanase from *A. niger* BG strain

Purification step	Protein(mg/mL)	Activity (U/ml)	Specific activity (U/mg)	Purification (fold)	Yield (%)
Supernatant	2.74	1413.88	516.01	1.00	100.00
Ultrafiltration	1.95	1065.74	546.53	1.06	75.38
Hitrap QFF	0.52	506.93	974.88	1.89	36.83
Mono Q	0.12	87.39	728.25	1.41	6.20

Table 6 Comparative production data of native xylanase from different fungal strains

Xylanase	Source species	Activities U/mg	pH Optimal	Optimal Temperature (°C)	Substrate	pH Stability	Thermo- Stability (°C)	Molecular Weight (kDa)	Km mg/ml	Vmax U/mg	References
Native	<i>A. niger</i> BG strain	728.25	6.0	50	Wheat straw	3.0-9.0	30-60	20	26.06	5647	This study
xyn11B	<i>A. niger</i> BCC14405	317	5	55	Birchwood xylan	5.0-10	50	21	8.9	11.10	(Krisana et al., 2005)
xyn11A	<i>A. pullulans</i> Y-2311-1	2.240	4.8	54	Birchwood xylan	3.8-5.4	50	25	7.	2.650	(X. L. Li, Zhang, Dean, Eriksson, & Ljungdahl, 1993)
xyn11A	<i>F. oxysporum</i> f. sp. Lycopersici F3	331	6	60	Oat spelt xylan	4.0-10	//	21	0.41	//	(Christakopoulos , Nerinckx, Kekos, Macris, & Claeysens, 1996)
xyn11A	<i>P. sp.</i> thermophila J18	1180	7	75-80	Birchwood xylan	6.0-11	75	25.8	1.6	1424	(L. Li, Tian, Cheng, Jiang, & Yang, 2006)
xyn11C	<i>P. occitanis</i> P016	358	3	45	Oat-spelt xylan	2.0-10	45	22	14.13	806.3	(Driss et al., 2011)
xyn11A	<i>P. sp.</i> 40 strain 40	1250	2	50	Oat-spelt xylan	2.0-5.0	30	25	8.3	6100	(Kimura et al., 2000)
xyn11A	<i>S. Commune</i> Delar/ATCC 38548	15	5	45-50	Soluble larch xylan	6.0-8.0	//	33	8.37	0.443	(Paice, Jurasek, Carpenter, & Smillie, 1978)
xyn11B	<i>T. funiculosus</i> IMI134756	196	3.7-4.7	//	Birchwood xylan	//	//	27.84	22	506	(Furniss, Williamson, & Kroon, 2005)
xyn11A	<i>T. sp.</i> SC9	426	6	42.5	Birchwood xylan	3.5-9.0	35	20.5	2.1	//	(Zhou, Zhu, Yan, Katrolia, &

