

Purification, crystallization and preliminary diffraction study of β -galactosidase from *Penicillium* sp.

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Crystals of an extracellular β -galactosidase from *Penicillium* sp. (MW = 120 \pm 5 kDa) have been obtained from a sodium phosphate buffer using PEG as precipitant. The crystals belong to the tetragonal space group $P4_1$ or $P4_3$, with unit-cell parameters $a = b = 110.82$, $c = 161.28$ Å, and diffract to 1.85 Å resolution at a synchrotron source.

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1. Introduction

β -Galactosidase (E.C. 3.2.1.23) is an enzyme that hydrolyzes $\beta(1-3)$ - $\beta(1-4)$ galactosyl bonds in poly- and oligosaccharides. Many carbohydrases have been found to catalyse not only the hydrolysis reaction but also the reverse reaction of condensation or transglycosylation. This property, found in β -galactosidases from various sources, has been used for the enzymatic synthesis of galactose-containing oligosaccharides. The high degree of stereospecificity enables β -galactosidases to be used for chemo-enzymatic synthesis of galactooligosaccharides with $\beta(1-3)$ and $\beta(1-4)$ bond configurations (Usui *et al.*, 1993; Mori *et al.*, 1997). Thus, the enzymes from *Bacillus circulans* and from bovine testes have been successfully applied to the synthesis of Gal- β -1,3-Glc-NAc, a key oligosaccharide of sialyl-Lewis antigen (sLe^a; Fujimoto *et al.*, 1998; Hedbys *et al.*, 1989). The same transglycosylation activity has been applied to the synthesis of Gal- β -1,3-Gal-NAC, which is an important constituent of the mucin-type glycoproteins, and for the synthesis of *N*-acetylallolactosamine (D-Gal- β -1,6-Glc-NAC; Vetere & Paoletti, 1996). To synthesize sialyl *N*-acetylactosamine, β -galactosidase from *Diplococcus pneumoniae* has been used together with sialidases (Ajisaka *et al.*, 1994). The transglycosylation ability of β -galactosidase has been used to obtain β -galactosylserine derivatives (Cantacuzene & Attal, 1991). The extracellular β -galactosidase from *Penicillium* sp. is found to have a high transglycosylation activity toward *p*-nitrophenyl β -D-galactopyranoside, lactose and methyl β -D-galactopyranoside, and appears to be a promising tool for many enzymatic syntheses. The structure and the mode of action of β -galactosidases are not well known as yet. The current work represents a first step toward the crystallographic structure elucidation of this enzyme.

2. Materials and methods

2.1. Protein preparation

Penicillium was incubated for 48 h as described previously for *Trichoderma* sp. (Savel'ev *et al.*, 1997) and the extracellular β -galactosidase was purified from 5 l of culture liquid. The mycelium was removed by centrifugation (3000g, 40 min) and the resulting supernatant was concentrated tenfold and transferred in 20 mM sodium acetate buffer pH 4.2 (buffer A) using hollow fibres. This crude solution was loaded on an SP-Sephadex column equilibrated with buffer A and eluted with 1 M NaCl in the same buffer. The resulting protein solution was concentrated to 20 ml using an Amicon PM-30 membrane, dialysed against 20 mM Tris-HCl buffer pH 7.2 (buffer B) and loaded onto a DEAE 5PW column (21.5 \times 150 mm) equilibrated with the same buffer. The β -galactosidase was eluted with a linear gradient (0–0.5 M) of sodium chloride in buffer B. The fractions containing β -galactosidase were pooled, concentrated to 5 ml on an Amicon PM30 membrane and dialysed against buffer B. The resulting protein solution was passed through a MonoQ HR5/5 chromatography column equilibrated with buffer B in the same gradient of sodium chloride. Finally, the β -galactosidase fraction obtained was saturated with solid ammonium sulfate to a concentration of 1.7 M and applied to a phenyl Superose HR5/5 column equilibrated with 1.7 M ammonium sulfate in buffer A and eluted with a decreasing concentration (1.7–0 M) of ammonium sulfate. The single peak corresponding to the β -galactosidase activity was collected and the purified enzyme was dialysed against water and then lyophilized.

2.2. Biochemical analysis

The activity of the enzyme was monitored during purification steps using *p*-nitrophenyl-

Table 1
Data-collection statistics.

Values in parentheses are for the highest resolution shell.

Number of frames	107
Space group	$P4_1$ ($P4_3$)
Unit-cell parameters (Å)	$a = b = 110.82$, $c = 161.28$
Resolution range (Å)	30.0–1.85 (1.93–1.85)
Total No. of reflections	695824 (44634)
No. of unique reflections	163512 (12364)
Redundancy	4.3 (3.6)
R_{sym}^\dagger (%)	11.0 (44.0)
Completeness (%)	99.8 (99.6)
$(I/\sigma(I))$	14.2 (2.1)

$$^\dagger R_{\text{sym}} = \sum(I - \langle I \rangle) / \sum I.$$

β -D-galactopyranoside as a substrate (Bahl & Agrawal, 1969). The unit of enzyme activity was defined as the amount of enzyme that hydrolyses 1 μmol of *p*-nitrophenyl- β -D-galactopyranoside per min at 310 K and pH 6.

All measurements of transglycosylation activity were carried out in 20 mM sodium acetate buffer pH 4.2 at 310 K. The reactions were terminated by boiling for 5 min. The transglycosylation activity was measured by analysing the reaction products using reversed-phase HPLC when *p*-nitrophenyl- β -D-galactopyranoside was used as the substrate (Eneyskaya *et al.*, 1998) or by HPLC on a Lichrosorb-NH₂ column when methyl- β -galactopyranoside and lactose were used as substrates (Savel'ev *et al.*, 1996).

2.3. X-ray diffraction

X-ray data were collected on a MAR Research 345 image-plate detector at the Laboratório Nacional de Luz Síncrotron (LNLS) protein crystallography beamline (Polikarpov, Oliva *et al.*, 1998; Polikarpov, Perles *et al.*, 1998) using the oscillation method. The X-ray wavelength was set to 1.38 Å to maximize the signal-to-noise ratio and to optimize the rate of data collection (Polikarpov *et al.*, 1997; Teplyakov *et al.*, 1998). The crystal-to-detector distance was set to 200 mm and the oscillation range was 1°. The crystals were quickly frozen in a gaseous nitrogen stream at 100 K (Oxford Cryosystems). The X-ray diffraction data (Table 1) were processed using the programs

DENZO and *SCALEPACK* (Otwinowski & Minor, 1997).

3. Results and discussion

3.1. β -Galactosidase properties and transglycosylation activity

The isolated β -galactosidase had a specific activity of 58 U per milligram of protein. The purified enzyme contained less than 0.1% admixture of carbohydrase activities. The estimation of molecular mass by SDS-PAGE yielded a value of 120 ± 5 kDa. This value coincided with the mass calculated from the elution profile on a Sephacryl S-300 column assuming that the enzyme exists as a monomer in solution.

β -Galactosidase revealed a high transglycosylation activity in the hydrolysis of *p*-nitrophenyl- β -D-galactopyranoside, methyl- β -D-galactopyranoside and lactose (donors) and galactose as the acceptor. HPLC analysis showed a high yield of products, up to 40–45%, in all reactions.

3.2. Crystallization and data collection

The lyophilized protein was dissolved in water to a final concentration of 5–10 mg ml⁻¹ and 5–10 μl drops of the protein solution were mixed with equal volumes of 15% PEG 8000 in 50 mM sodium phosphate buffer at pH \approx 4.0 in crystallization trials. Hanging drops were equilibrated against 1 ml of the same PEG solution at room temperature. An amorphous precipitant was formed after 1–2 d and bipyramidal crystals started to grow after 4–5 d, reaching a maximal size of about 0.2 mm in each dimension.

The crystals belonged to the tetragonal space group $P4_1$ or $P4_3$, with unit-cell parameters $a = b = 110.82$, $c = 161.28$ Å, and diffracted to around 1.8 Å resolution. Calculation of the Matthews coefficient (Matthews, 1968) suggests the presence of one dimer per asymmetric unit ($V_M = 2.06 \text{ \AA}^3 \text{ Da}^{-1}$) with a solvent content of 40.3%.

The freezing of the crystals significantly improved their stability in the X-ray beam, allowing data to be collected to higher resolution. The cryoprotection proved to be

important in the process of data acquisition. A high-resolution native data set was collected (see Table 1). Screening for heavy-metal derivatives is under way.

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