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Regioselective synthesis of neo-erlose by the β-fructofuranosidase from *Xanthophyllomyces*

dendrorhous

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1 ABSTRACT

2 The β-fructofuranosidase from the yeast *Xanthophyllomyces dendrorhous* (Xd-INV) 3 catalyzes the synthesis of neo-fructooligosaccharides (neo-FOS of the 6G-series), which contain a $\beta(2\rightarrow 6)$ linkage between a fructose and the glucosyl moiety of 4 5 sucrose. In this work we demonstrate that the enzyme is also able to fructosylate 6 other carbohydrates that contain glucose, in particular disaccharides (maltose, 7 isomaltulose, isomaltose, trehalose) and higher oligosaccharides (maltotriose, 8 raffinose, maltotetraose), but not monosaccharides (glucose, fructose, galactose). 9 With maltose as acceptor, the reaction in the presence of Xd-INV proceeded with 10 high regioselectivity; the product was purified and chemically characterized, and 11 turned out to be 6'-O- β -fructosylmaltose (neo-erlose). Using 100 g/L sucrose as 12 fructosyl donor and 300 g/L maltose as acceptor, the maximum concentration of 13 neo-erlose was 38.3 g/L. Thus, novel hetero-fructooligosaccharides with potential 14 applications in the functional food and pharmaceutical industries can be obtained 15 with Xd-INV.

16

Keywords: fructooligosaccharides; food oligosaccharides; maltosylfructosides; neoerlose; *Xanthophyllomyces dendrorhous*.

1 1. INTRODUCTION

2	The Xanthophyllomyces dendrorhous yeast (formerly Phaffia rhodozyma)
3	produces an extracellular β -fructofuranosidase of 160-200 kDa (Xd-INV, formerly
4	described as an INVertase) with heterogeneous degree of glycosylation [1;2]. The
5	crystallization and preliminary X-ray diffraction analysis of this enzyme after a
6	deglycosylating treatment was performed [3]. The enzyme hydrolyzes efficiently
7	fructosyl- β -(2 \rightarrow 1) linked carbohydrates such as sucrose and 1-kestose. The level of
8	glycosylation affects the thermal behaviour of Xd-INV but not to its
9	transglycosylation/hydrolysis ratio [2]; the synthesis of fructooligosaccharides
10	(FOS) reaches its maximum at 60-70°C. Besides Xd-INV, an intracellular β -
11	fructofuranosidase of 33 kDa with an optimal temperature of 45°C and a similar
12	activity profile has been described in <i>X. dendrorhous</i> [4;5].
13	To our knowledge, Xd-INV is the most efficient enzyme for the synthesis of
14	FOS of the 6 G-series (neoFOS, e.g. neokestose and neonystose), which contain a β -
15	(2 \rightarrow 6) linkage between a fructose and the glucosyl moiety of sucrose. Several
16	studies indicate that such neoFOS possess enhanced properties and chemical
17	stability compared to ¹ F-FOS typically used as prebiotics (e.g. 1-kestose or nystose)
18	[6-9].
19	Undoubtedly, the distinctive property of Xd-INV is its ability to transfer a
20	fructosyl moiety to the glucose unit of sucrose. This contrasts with the behaviour

of other fructosylating enzymes, including levansucrases [10], inulosucrases [11]

and most β-fructofuranosidases [12-15], which commonly form β-(2→1) or β-(2→6)
 linkages between fructose units.

3	Some β -fructofuranosidases and fructosyltransferases also catalyze the
4	transfer of the fructose moiety from sucrose to other carbohydrates (acceptors),
5	thus forming hetero-fructooligosaccharides (hetero-FOS) with potential
6	applications in functional foods [16], pharmaceutical [17] and cosmeceutical [18]
7	industries. Examples of hetero-FOS include: lactosylfructoside (lactosucrose) that
8	is obtained with Zymomonas mobilis levansucrase [19] or dextransucrase B-512F
9	from Leuconostoc mesenteroides [20] and that selectively promotes the growth of
10	bifidobacteria [21]; cellobiofructose synthesized with Bacillus subtilis levansucrase,
11	which is employed as a low-calorie sweetener [22]; fructosylxyloside produced by
12	fructosyltransferase from <i>Bacillus macerans</i> [23]; maltosylfructosides synthesized by
13	inulosucrase from Lactobacillus gasseri [24].
14	In this work we have assessed the ability of Xd-INV to fructosylate a series
15	of carbohydrates that contain a glucose moiety in its structure. The aim of this
16	study was thus to obtain novel hetero-FOS that are difficult to produce by
17	all and inclusion

17 chemical synthesis.

1 2. MATERIALS AND METHODS

2 2.1. Materials

3	Sucrose, glucose and fructose were from Merck. 1-Kestose and nystose were
4	from TCI Europe. Maltose, palatinose, isomaltose, maltotriose, maltotetraose,
5	raffinose, trehalose, cellobiose, galactose, lactose, lactulose and turanose were from
6	Sigma-Aldrich. All other reagents were of the highest available purity.
7	
8	2.2. Organism, culture conditions and protein purification
9	The Xanthophyllomyces dendrorhous strain ATCC MYA-131 was grown at 24°C
10	on Maltose Minimal Medium (MMM) [0.7% yeast nitrogen base without
11	aminoacids (Difco), 2% (w/v) maltose] with shaking at 200 rpm. Growth was
12	monitored spectrophotometrically at 660 nm (A ₆₆₀). The extracellular β -
13	fructofuranosidase activity produced by one liter of <i>X. dendrorhous</i> culture (7.2
14	U/mL; A_{660} = 2.4) was purified as previously described [2]. Briefly, the
15	extracellular medium was concentrated through a 30,000 MWC PES membrane by
16	using a VivaFlow 50 system (Vivascience), dialyzed in 20 mM sodium phosphate
17	buffer pH 7.0, applied to a DEAE-Sephacel chromatography column and eluted at
18	0.1 M NaCl.
19	
20	2.3 Activity assay
21	The enzymatic activity towards sucrose was determined at 60° C in 0.1 M

22 sodium phosphate buffer (pH 5.0) by measuring the release of reducing sugars

23 from 20 g/L sucrose solution using the dinitrosalicylic acid (DNS) method [25].

The assay was adapted to 96-well microplates as described in our previous work
 [26]. A calibration curve was performed with a 5 g/L glucose solution. One unit
 (*U*) of activity was defined as that catalyzing the formation of 1 µmol of reducing
 sugars per minute under the above conditions.

5

6 2.4. Acceptor reaction with Xd-INV

The pure Xd-INV was added to a solution containing sucrose (100 g/L, 0.29 7 M) in the presence of the sugar acceptor (100 g/L), in 100 mM sodium acetate 8 buffer, pH 5.6. The final activity in the mixture was adjusted to 3 U/mL. Reaction 9 10 mixtures were incubated at 60°C and 100 rpm in a Vortemp 56 shaker. At different 11 reaction times (0-240 min), 50 µL aliquots were withdrawn, boiled for 10 min to 12 inactivate the enzyme and conveniently diluted with water (1:5 or 1:20). The 13 samples were filtered through 0.45 µm cellulose centrifuge filters (National 14 Scientific) for 5 min at 3500 rpm and analyzed by HPLC. In order to elucidate the 15 optimum donor/acceptor molar ratio in the production of fructosylmaltose, 16 different concentrations of sucrose and maltose were assayed to a final sugar 17 concentrations of 200 g/L (1:1) or 400 g/L (3:1; 1:3) under the above conditions. Each reaction was performed in duplicate. 18

19

20 2.5. HPLC analysis

The analysis and quantification of the different carbohydrates present in the
transfructosylation reactions was carried out by HPLC with a quaternary pump
(Delta 600, Waters) coupled to a 4.6 x 250 mm Luna-NH₂ column (5 μm, 100 Å)

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1	from Phenomenex. Detection was performed using a refractive index detector
2	(model 2410, Waters) equilibrated at 30°C. Acetonitrile/water 82:18 (v/v),
3	degassed with helium, was used as mobile phase at 1.0 mL/min for 25 min for the
4	reactions with disaccharides as acceptors, and 80:20 (v/v) for higher saccharides.
5	The column temperature was kept constant at 30°C. The data obtained were
6	analysed using the Varian Star 4.0 Software. Each analysis was performed in
7	duplicate. The transfer/hydrolysis ratio for each acceptor molecule was calculated
8	as the ratio between the chromatographic areas of all the fructosylated products
9	generated in the reaction (neokestose, 1-kestose and derivatives for the new
10	acceptors) and the free fructose.
11	
12	
12 13	2.6. Purification and characterization of the acceptor product with maltose
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13	
13 14	<i>Purification</i> . For the isolation of the acceptor product with maltose, the
13 14 15	<i>Purification.</i> For the isolation of the acceptor product with maltose, the biocatalytic reaction was scaled to 3 mL. At the point of maximum concentration of
13 14 15 16	<i>Purification.</i> For the isolation of the acceptor product with maltose, the biocatalytic reaction was scaled to 3 mL. At the point of maximum concentration of the unknown compound, the enzyme was inactivated at 100°C for 10 min. The
13 14 15 16 17	<i>Purification.</i> For the isolation of the acceptor product with maltose, the biocatalytic reaction was scaled to 3 mL. At the point of maximum concentration of the unknown compound, the enzyme was inactivated at 100°C for 10 min. The carbohydrates in the mixture were purified by semi-preparative HPLC using a
 13 14 15 16 17 18 	<i>Purification.</i> For the isolation of the acceptor product with maltose, the biocatalytic reaction was scaled to 3 mL. At the point of maximum concentration of the unknown compound, the enzyme was inactivated at 100°C for 10 min. The carbohydrates in the mixture were purified by semi-preparative HPLC using a system equipped with a Waters Delta 600 pump coupled to a 5 µm Kromasil-NH ₂
 13 14 15 16 17 18 19 	<i>Purification.</i> For the isolation of the acceptor product with maltose, the biocatalytic reaction was scaled to 3 mL. At the point of maximum concentration of the unknown compound, the enzyme was inactivated at 100°C for 10 min. The carbohydrates in the mixture were purified by semi-preparative HPLC using a system equipped with a Waters Delta 600 pump coupled to a 5 µm Kromasil-NH ₂ column (10 x 250 mm; Analisis Vinicos). A three-way flow splitter (model

23 The column temperature was kept constant at 30°C. After collection of the different

oligosaccharides, the mobile phase was eliminated by rotary evaporation in a R 210 rotavapor (Buchi).

Analysis of purity. The purity of the acceptor product with maltose was 3 4 analyzed by high-performance anion-exchange chromatography with pulsed 5 amperometric detection (HPAEC-PAD) on a ICS3000 Dionex system (Dionex 6 Corp., Sunnyvale, CA) consisting of a SP gradient pump, an AS-HV autosampler 7 and an electrochemical detector with a gold working electrode and Ag/AgCl as 8 reference electrode. All eluents were degassed by flushing with helium. A 9 pellicular anion-exchange 4 x 250 mm Carbo-Pack PA-1 column (Dionex) connected to a CarboPac PA-1 guard column at 30°C was used. For eluent 10 preparation, MilliQ water and 50% (w/v) NaOH (Sigma-Aldrich) were used. The 11 12 flow rate was 1.0 mL/min during the analysis. The initial mobile phase was 20 mM NaOH for 13 min. A mobile phase linear gradient from 20 mM to 100 mM 13 NaOH and from 0 to 40 mM sodium acetate was performed in 7 min, and the latter 14 composition was kept constant for 10 min. Then a linear gradient from 40 to 100 15 16 mM sodium acetate in 5 min maintaining 100 mM NaOH was programmed, and the mobile phase composition was kept constant for 2 min. The peaks were 17 18 analyzed using Chromeleon software. The identification of the different 19 carbohydrates was done based on commercial standards and purified FOS as 20 described elsewhere [1;12].

21 *Mass spectrometry.* The molecular weight of the unknown carbohydrate was
 22 analyzed by MALDI-TOF mass spectrometry (Bruker, model Ultraflex III

TOFTOF) using 2,5-dihidroxybenzoic acid doped with sodium iodide as matrix, in
 positive reflector mode.

Nuclear magnetic resonance (NMR). The structure of the purified carbohydrate 3 4 was elucidated using a combination of 1H, 13C- and 2D-NMR (COSY, TOCSY, 5 NOESY, HSQC) techniques. The spectra of the sample (ca. 10 mM), dissolved in 6 deuterated water, was recorded on a Bruker AVANCE DRX500 spectrometer 7 equipped with a tuneable broadband 1H/X probe with a gradient in the Z axis, at 8 a temperature of 298 K. Chemical shifts were expressed in ppm with respect to the 9 0 ppm point of DSS, used as internal standard. COSY, TOCSY, NOESY and HSQC 10 sequences were provided by Bruker. COSY, TOCSY (80 ms mixing time), and 11 NOESY (500 ms mixing time) experiments were performed with 16, 8, and 48 12 scans, respectively, with 256 increments in the indirect dimension and with 1024 13 points in the acquisition dimension. The spectral widths were 9 ppm in both dimensions. The HSQC experiment (16 scans) also used 256 increments in the 14 15 indirect dimension and with 1024 points in the acquisition dimension. The spectral 16 width was 120 ppm in the indirect dimension and 9 ppm in the acquisition one.

1 3. RESULTS AND DISCUSSION

2 **3.1.** Hetero-oligosaccharides synthesis with Xd-INV

3	Neokestose and 1-kestose are the main transglycosylation products from
4	sucrose obtained with Xd-INV, a yeast extracellular glycoprotein characterized by
5	its high thermostability [1]. The level of glycosylation of Xd-INV does not affect its
6	hydrolase and transferase activities, both optimal in the range of 60-70°C [2].
7	When other saccharides coexist with sucrose as acceptors, some glycosidases
8	and transglycosidases may synthesize novel heterooligosaccharides [27;28]. In
9	order to assess the transferase activity of Xd-INV towards different carbohydrates,
10	purified enzyme (a mixture of 160-200 kDa glycoforms) was incubated at 60° C in
11	presence of 100 g/L sucrose as the fructosyl donor and different sugar acceptors
12	(maltose, isomaltose, trehalose, isomaltulose, lactose, lactulose, turanose, cellulose,
13	maltotriose, raffinose or maltotetraose) at the same concentration (100 g/L).
14	Fig. 1 shows some representative HPLC profiles of the transfer reaction
15	using trehalose, isomaltulose and maltose. Using maltose as acceptor, a new peak
16	(10) appeared at the end of the chromatogram in addition to the neokestose and 1-
17	kestose (peaks 7 and 8) previously described [1;2]. New peaks were also obtained
18	in the acceptor reactions with isomaltulose (peak 9), trehalose (peak 11),
19	isomaltose, maltotriose, maltotetraose and raffinose (chromatograms not shown).
20	However, the fructosyl moiety of sucrose was not transferred to cellobiose,
21	lactulose, lactose or turanose and neither to the monosaccharides fructose, glucose
22	or galactose.

We followed the concentration of total biosynthetic products (neokestose, 1-1 2 kestose and acceptor derivatives) in the reaction mixture during 240 min with the different acceptor sugars (Fig. 2). In the case of maltose, isomaltose and 3 4 isomaltulose, acceptor products reached about 8% (w/w), referred to the total 5 amount of sugars in the reaction mixture. The lowest concentration of acceptor 6 product was obtained with trehalose, not surpassing 2% (w/w). In a control 7 reaction by using 200 g/L of sucrose as the sole substrate, only neokestose and 1kestose were obtained (15.6 g/L, 7.8% of total sugars). 8

9 Considering that the response factor of the refraction index detector is very 10 similar for most carbohydrates, we defined the acceptor efficiency of the different 11 sugars as the ratio between the area of the main acceptor product –at the point of 12 maximum concentration- and the area of FOS (neokestose plus 1-kestose) at the 13 same point of the reaction. As shown in Table 1, isomaltulose, maltotetraose, 14 maltotriose, maltose and isomaltose displayed efficiencies higher than 1.0, which indicated that they were better acceptors than sucrose itself. In addition, these 15 acceptors gave rise to transfer/hydrolase ratios (calculated as described in section 16 17 2.5) in the range 1.2-1.6, which were at least 4-fold higher than those obtained 18 using monosaccharides, cellobiose, lactulose or turanose (sugars unable to act as 19 fructose acceptors; ratio of 0.2-0.3) and even trehalose (poor fructose acceptor; 20 Table 1). The transfer/hydrolase ratio was 0.96 in the reaction based exclusively on 21 sucrose (200 g/L), which suggests that the monosaccharides and disaccharides not

acting as acceptors possibly displayed an inhibitory effect towards the transfer
 reaction.

3

4 **3.2.** Structural characterization of the acceptor product with maltose

5	The new fructosyl derivative obtained in the reaction with maltose as
6	acceptor was purified by semipreparative HPLC. The purity of the fructosyl-
7	maltose was evaluated by HPAEC-PAD due to its higher sensitivity compared
8	with conventional HPLC. Fig. 3A illustrates the typical HPAEC-PAD
9	chromatogram of the acceptor reaction with maltose, and Fig. 3B shows the
10	chromatogram of the purified oligosaccharide. The purity of the maltose
11	derivative was only 75% (the main contaminants were maltose and neokestose)
12	but allowed its chemical characterization.
13	The mass spectrum of compound 10 confirmed that it was a trisaccharide.
14	The 1D and 2D $^1\mathrm{H}$ NMR spectra displayed three anomeric signals. Two of them
15	were identified as arising from an α/β equilibrium. From the combination of the
16	signals from COSY, TOCSY, NOESY, HSQC and HMBC, the signal pattern for
17	fructose and three glucose units were readily identified. In fact, the sequential
18	assignment was completed from the individual the 1H and 13C resonance signals
19	(Fig. 4). Thus, it was possible to identify the compound as the trisaccharide 6'- O - β -
20	fructosylmaltose [Fru- $\beta(2\rightarrow 6)$ -Glc- $\alpha(1\rightarrow 4)$ -Glc] (Fig. 5), which was recently named
21	neo-erlose [24]. This trisaccharide was not a good acceptor for the Xd-INV because

22 no tetrasaccharides were observed by HPLC and HPAEC-PAD; in contrast, the

1	inulosucrose from Lactobacillus gasseri produces a mixture of maltosylfructosides
2	with different polymerization degree, including erlose and neo-erlose [24].
3	When the acceptor is a reducing sugar such as maltose, most fructosylating
4	enzymes, especially levansucrases, transfer the fructosyl moiety of sucrose to the
5	anomeric carbon of the acceptor. Thus, levansucrase from Microbacterium
6	laevaniformans transfers the fructosyl moiety of sucrose to the C1-OH position of
7	the glucose residue of melibiose, maltose and cellobiose [29]. Recently, Tian and
8	Karboune synthesized a variety of hetero-FOS using the levansucrase from <i>Bacillus</i>
9	amyloliquefaciens with sucrose-maltose mixtures [10]; the major transfructosylation
10	product was identified to be the non-reducing trisaccharide erlose [Glc- $\alpha(1\rightarrow 4)$ -
11	Glc- $\alpha(1\rightarrow 2)$ - β -Fru]. The same product (erlose) was obtained with the levansucrase
12	from <i>Bacillus subtilis</i> [30].
12 13	from <i>Bacillus subtilis</i> [30]. Most β -fructofuranosidases such as that from <i>Aspergillus niger</i> are only able
13	Most β -fructofuranosidases such as that from <i>Aspergillus niger</i> are only able
13 14	Most β -fructofuranosidases such as that from <i>Aspergillus niger</i> are only able to transfer the fructosyl moiety of sucrose to the 1-OH group of terminal
13 14 15	Most β-fructofuranosidases such as that from <i>Aspergillus niger</i> are only able to transfer the fructosyl moiety of sucrose to the 1-OH group of terminal fructofuranosides such as sucrose, 1-kestose, inulobiose and raffinose [31].
13 14 15 16	Most β-fructofuranosidases such as that from <i>Aspergillus niger</i> are only able to transfer the fructosyl moiety of sucrose to the 1-OH group of terminal fructofuranosides such as sucrose, 1-kestose, inulobiose and raffinose [31]. Muramatsu and Nakakuki reported that the good acceptors for β-
 13 14 15 16 17 	Most β-fructofuranosidases such as that from <i>Aspergillus niger</i> are only able to transfer the fructosyl moiety of sucrose to the 1-OH group of terminal fructofuranosides such as sucrose, 1-kestose, inulobiose and raffinose [31]. Muramatsu and Nakakuki reported that the good acceptors for β- fructofuranosidase from <i>Aspergillus sydowi</i> were the saccharides having a furanose
 13 14 15 16 17 18 	Most β-fructofuranosidases such as that from <i>Aspergillus niger</i> are only able to transfer the fructosyl moiety of sucrose to the 1-OH group of terminal fructofuranosides such as sucrose, 1-kestose, inulobiose and raffinose [31]. Muramatsu and Nakakuki reported that the good acceptors for β- fructofuranosidase from <i>Aspergillus sydowi</i> were the saccharides having a furanose ring in their chemical structure, such as D-xylose, L-arabinose and raffinose, except
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characterization (work in progress) will certainly provide light on the basis of its
regiospecificity. The reaction profile of Xd-INV in the absence or presence of
maltose is represented in Fig. 5. On the basis of the enzyme specificity, the
proposed structures obtained with the different acceptors are included in Table 1.

5

6 3.3. Kinetics of formation of 6'-O-β-fructosylmaltose (neo-erlose)

7 The transfructosylating activity of Xd-INV towards maltose was assayed in 8 detail during 240 min using the conditions described above. Fig. 6 shows the 9 evolution of different sugar content in the reaction mixture. The amount of 10 fructose detected was slightly lower than that of glucose, a finding clearly 11 indicative of the fructosyltransferase activity of the enzyme even at moderate 12 sucrose concentration (100 g/L). At the point of maximum neo-erlose production 13 (240 min), the reaction mixture contained 26.8 g/L of fructose, 43.7 g/L of glucose, 14 11.1 g/L of sucrose, 86.2 g/L of maltose, 3 g/L of neokestose, 1.3 g/L of 1-kestose 15 and 16.8 g/L of neo-erlose. The new linkage formed between the fructosyl unit 16 and maltose appears to be stable under the reaction conditions, because the 17 concentration of neo-erlose increased continuously until at least 80% sucrose 18 conversion. This contrasts with the typical behaviour of FOS formation, whose 19 maximum concentration is commonly achieved at lower sucrose conversions; after 20 that, product hydrolysis becomes the major process [33;34].

21

1 **3.4.** Effect of donor/acceptor ratio in the synthesis of neo-erlose

In order to increase the yield of synthesized neo-erlose, several concentrations 2 3 of sucrose and maltose were assayed. Lowering the molar ratio donor 4 (sucrose)/acceptor (maltose), a significant enhancement in the concentration of 5 neo-erlose was observed (Table 2). Thus, a 2.3-fold improvement in the synthesis 6 of neo-erlose was obtained using a molar ratio donor/acceptor 1:3 compared with 7 1:1. In this situation only 5.2 g/L of neokestose plus 1-kestose were obtained, 8 which indicates that maltose clearly competes with sucrose for the fructosyl 9 residue. Using a molar ratio of sucrose/maltose of 3:1 the yield of neokestose plus 10 1-kestose was twice that of neo-erlose.

11

12 4. CONCLUSIONS

Xd-INV is able to fructosylate maltose and other carbohydrates containing a
glucose moiety. Compared with other fructosyl-transferring enzymes such as
levansucrases, inulosucrases and most β-fructofuranosidases, the enzyme displays
high regiospecificity towards the 6-OH hydroxyl group of the glucose at the nonreducing end. No further fructosylation of the synthesized hetero-FOS was
observed with this enzyme. The Xd-INV may become an appropriate tool for the
single fructosylation of glucooligosaccharides, glucosides or glucoconjugates.

20

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- 6

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14		

1 Figure legends

3	Fig. 1. HPLC chromatograms of the reaction of sucrose with Xd-INV using
4	different acceptors. The chromatograms correspond to the reaction mixture after
5	240 min. Experimental conditions: 100 g/L sucrose, 100 g/L acceptor, 3 U/mL,
6	100 mM sodium acetate buffer (pH 5.6), 60°C. Peak assignation: (1) fructose; (2)
7	glucose; (3) sucrose; (4) isomaltulose plus sucrose; (5) maltose; (6) trehalose; (7)
8	neokestose; (8) 1-kestose; (9) fructosyl-isomaltulose plus 1-kestose; (10) fructosyl-
9	maltose; (11) fructosyl-trehalose.
10	
11	Fig. 2 . Formation of acceptor products <i>vs.</i> FOS. The percentage (w/w) of acceptor
12	products (black bars) and neokestose plus 1-kestose (grey bars) refers to the total
13	amount of sugars in the mixture. Experimental conditions: 100 g/L sucrose, 100 m
14	g/L acceptor, 3 U/mL, 100 mM sodium acetate buffer (pH 5.6), 60°C. Standard
15	deviations were lower than 5%.
16	
17	Fig. 3. HPAEC-PAD analysis of the reaction with maltose as acceptor. (A)
18	Chromatogram of the reaction mixture with Xd-INV; (B) Chromatogram of the
19	purified fructosyl-maltose. Peak assignation: (1) fructose; (2) glucose; (3) sucrose;
20	(5) maltose; (7) neokestose; (8) 1-kestose; (10) fructosyl-maltose; (*) unknown
21	compound.
22	

1	Fig. 4. 2D-NMR DEPT-HSQC spectrum of the trisaccharide Fru- $\beta(2\rightarrow 6)$ -Glc-
2	$\alpha(1 \rightarrow 4)$ -Glc (neo-erlose). The signals are assigned and labelled. The key points for
3	identifications are also shown.
4	
5	Fig. 5 . Scheme of the reactions catalyzed by Xd-INV. (1) fructose; (2) glucose; (3)
6	sucrose; (5) maltose; (7) neokestose; (8) 1-kestose; (10) neo-erlose; (12) neonystose.
7	
8	Fig. 6. Kinetics of neo-erlose and FOS synthesis . Conditions: 100 g/L sucrose,
9	100 g/L maltose, 3 U/mL of Xd-INV, 100 mM sodium acetate buffer (pH 5.6),

10 60°C. Standard deviations were lower than 5%.

Acceptor	Acceptor	Synthesized product
	efficiency ^a	
Isomaltulose	5.2	Fru- $\beta(2\rightarrow 6)$ -Glc- $\alpha(1\rightarrow 6)$ -Fru ^b
Maltotetraose	2.6	Fru- $\beta(2\rightarrow 6)$ -[Glc- $\alpha(1\rightarrow 4)$] ₃ -Glc ^b
Maltotriose	2.4	Fru- $\beta(2\rightarrow 6)$ -[Glc- $\alpha(1\rightarrow 4)$] ₂ -Glc ^b
Maltose	1.8	Fru- $\beta(2\rightarrow 6)$ -Glc- $\alpha(1\rightarrow 4)$ -Glc
Isomaltose	1.2	Fru- $\beta(2\rightarrow 6)$ -Glc- $\alpha(1\rightarrow 6)$ -Glc ^b
Raffinose	0.8	$Fru-\beta(2\rightarrow 6)$ -Gal- $\alpha(1\rightarrow 6)$ -Glc- $\alpha(1\rightarrow 2)$ - β - Fru^{b}
Trehalose	0.4	$Fru-\beta(2\rightarrow 6)$ -Glc- $\alpha(1\rightarrow 1)$ - α -Glc ^b

Table 1. Acceptor specificity of Xd-INV.

^a Defined as the ratio between the areas of the main acceptor product and the formed FOS (neokestose plus 1-kestose). Standard deviations were lower than 5%.

^b Proposed structure based on the specificity of this enzyme.

Table 2. Effect of the ratio sucrose/maltose in the synthesis of neo-erlose and FOS catalyzed by Xd-INV.^a

[Sucrose]	[Maltose]	[Neo-erlose] ^b	[Neokestose + 1-Kestose] ^b
(g/L)	(g/L)	(g/L)	(g/L)
100	100	16.8	9.1
100	300	38.3	5.2
300	100	8.9	17.5

^a Conditions: 3 U/mL, 100 mM sodium acetate buffer (pH 5.6), 60°C.

^b The concentration of the products corresponds to 240 min reaction. Standard deviations were lower than 5%.

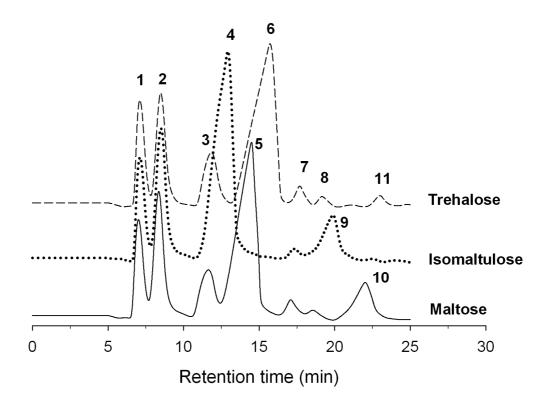


Fig. 2

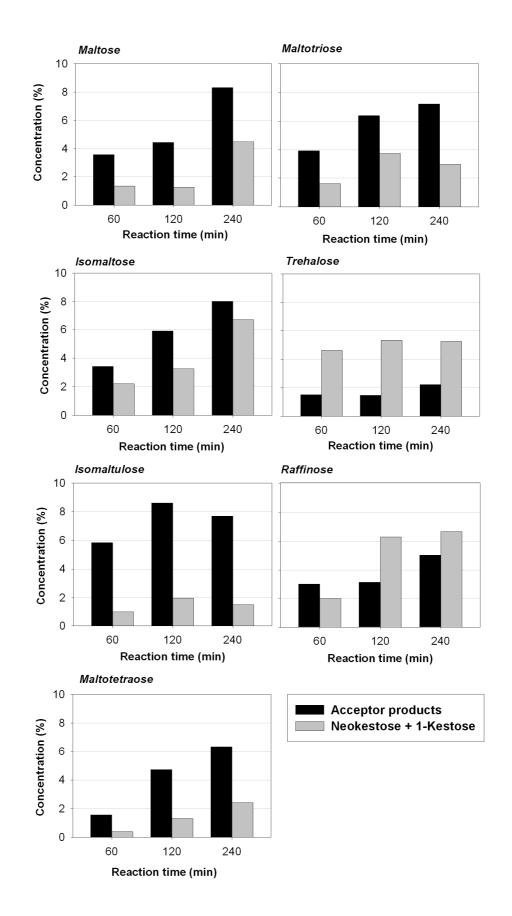
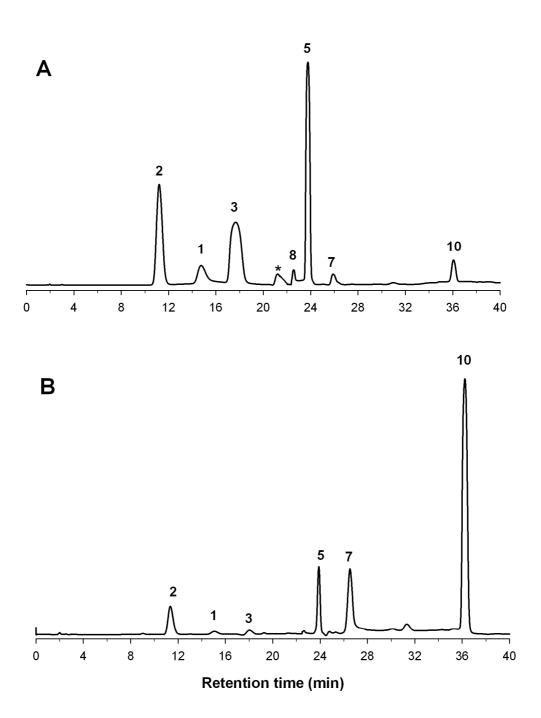
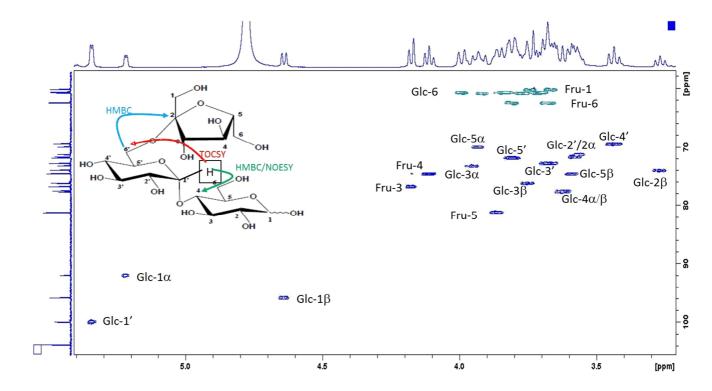


Fig. 3









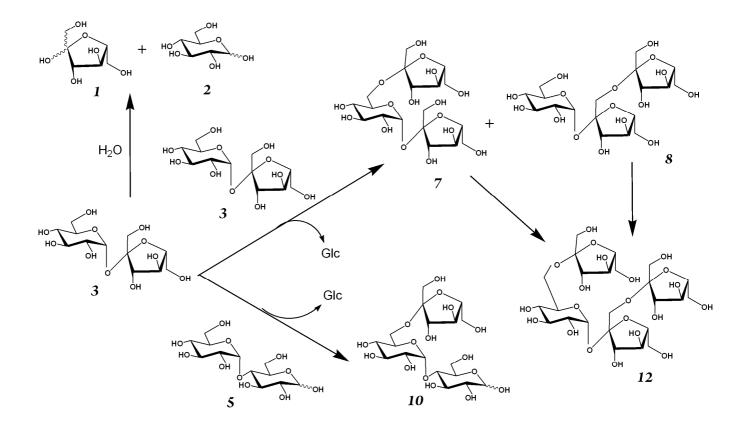


Fig. 6

