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The diversity of glycogen branching enzymes in microbes

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Chapter 4

Synthesis of highly branched α -glucans with different structures using GH13 and GH57 glycogen branching enzymes

Xuewen Zhang, Hans Leemhuis, and Marc J.E.C. van der Maarel

Abstract

Glycogen branching enzymes (GBEs) convert starch into branched α -glucan polymers. To explore if the amylose content of substrates effects the structure of the branched α -glucans, mixtures of amylose and amylopectin were converted by four thermophilic GBEs. The degree of branching and molecular weight of the products increased with an increasing percentage of amylose with the GH57 GBEs of *Thermus thermophilus* and *Thermococcus kodakarensis*, and the GH13 GBEs of *Rhodothermus marinus* and *Petrotoga mobilis*. The only exception is that the degree of branching of the *Petrotoga mobilis* GBE products is not influenced by the amylose content. A second difference is the relatively high hydrolytic activity of two GH57 GBEs, while the two GH13 GBEs have almost no hydrolytic activity. Moreover, the two GH13 GBEs synthesize branched α -glucans with a narrow molecular weight distribution, while the two GH57 GBEs products consist of two or three molecular weight fractions.

Introduction

Glycogen is produced by many microorganisms as a carbon and energy reserve (1). It is a branched polymer of anhydroglucose residues linked via α -1,4-glycosidic linkages and α -1 \rightarrow 4,6-glycosidic bond branches. The branches are synthesized by glycogen branching enzymes (GBEs, EC 2.4.1.18), which cleave an α -1,4-glycosidic linkages in a linear chain and attach the cleaved off fragment onto the 6-hydroxyl group of an anhydroglucose moiety located in a chain segment of α -1,4-linked anhydroglucose residues (2-4). GBEs are classified in two glycoside hydrolase (GH) families, 13 and 57 (5-8). Although the GH13 and GH57 GBEs have a different three-dimensional structural fold (9-14), they use the same catalytic steps, involving a double displacement mechanism and a covalent glucosyl-enzyme intermediate (15,16).

While *in-vivo* GBEs act on growing α -glucan chains, *in-vitro* GBEs can be utilized to modify starch, amylose, and amylopectin. GBE modified starch, or (highly) branched maltodextrin, is characterized by the absence of long linear α -1,4-glucan chains and an increased percentage of α -1 \rightarrow 4,6 branches. The resulting product is highly soluble in water, and has no tendency to retrograde because of the absence of amylose and long linear α -1,4-linked chains. Various applications for highly branched maltodextrins have been reported, among which paper coating, slowly digestible starch, sport drinks ingredient, spray drying aid, and bio-friendly adhesive (17-20).

Currently, only the *Rhodothermus obamensis* GBEs is commercially available, under the tradename Branchzyme® from Novozymes. However, many more bacterial GH13 GBEs have been characterized, among which the GBEs of *Aquifex aeolicus* (21,22), *Butyrivibrio fibrisolvans* (23), *Deinococcus geothermalis* and *Deinococcus radiodurans* (24), *Geobacillus stearothermophilus* (25), *Geobacillus thermoglucosidans* (26,27), *Mycobacterium tuberculosis* (28), *Thermomonospora curvata* (29), and *Vibrio vulnificus* (30). Today only four GH57 GBEs have been characterized: *Pyrococcus horikoshii* (12), *Thermococcus kodakarensis* (31), *Thermus thermophilus* (14) and AmyC from *Thermotoga maritima* (chapter 2). The biochemical studies have reported variations in substrate specificity, with the GH57 GBEs having a higher catalytic activity with amylose than amylopec-

tin, a substrate preference not seen with the GH13 GBEs. The GH57 GBEs have, in addition, a significant hydrolytic side activity, whereas the GH13 GBEs show hardly any hydrolytic activity (14,24,30). The differences in reaction specificity are potentially advantageous in the starch processing industry, as it may lead to different types of highly branched α -glucan products.

Here the syntheses of branched α -glucan by four thermophilic GBEs is explored, revealing that the structure of the branched α -glucans is depended on the amylose content of the substrate and the GBE used.

Materials and Methods

Materials

Amylose V and waxy potato starch (Eliane 100) were provided by Avebe (Veendam, Netherlands). Isoamylase (EC 3.2.1.68, specific activity 260 U/mg), pullulanase M1 (EC 3.2.1.41, specific activity 34 U/mg) and β -amylase (EC 3.2.1.2, specific activity 10,000 U/mL) were obtained from Megazyme (Wicklow, Ireland). General chemicals were obtained from Sigma Aldrich (Darmstadt, Germany) and VWR (Amsterdam, Netherlands).

Production and purification of glycogen branching enzymes

Codon optimized genes encoding the GBEs from *T. thermophilus* HB8 (*Ttgbe*) and *T. kodakarensis* KOD1 (*Tkgbe*) were synthesized by Baseclear (Leiden, The Netherlands), cloned into the pRSET A (Thermo Fisher Scientific, Waltham, US) expression vector and overexpressed in *E. coli* BL21 (DE3). The codon optimized genes encoding the GBEs from *R. marinus* (*Rmgbe*) and *P. mobilis* (*Pmgbe13*) were synthesized by GeneScript (Hong Kong, China), and cloned into the pE-T28a expression vector and overexpressed in *E. coli* BL21 (DE3). The four encoded proteins carry a 6 \times His-tag at their N-terminus. *E. coli* was cultivated in Luria-Bertani (LB) medium (10 g/L of tryptone, 5 g/L yeast extract, and 10 g/L NaCl). 100 μ g/mL ampicillin was supplemented for *Ttgbe* and *Tkgbe* expression and 50 μ g/mL kanamycin was applied for *Rmgbe* and *Pmgbe13* expression. Gene expression was induced by 0.1 mM IPTG at 18 °C, and cultivation was continued

for 20 h with shaking at 150 rpm. The cells were harvested by centrifugation (5,000×g, 10 min, 4 °C), washed twice with 5 mM phosphate buffer pH 7.0, and resuspended in binding buffer (20 mM sodium phosphate, 500 mM NaCl, and 20 mM imidazole, pH 7.4). Cells were lysed using a high-pressure homogenizer (Emulsiflex-B15; Avestin, Ottawa, Canada). The soluble fraction of the cell lysates was collected by centrifugation (20,000×g, 20 min, 4 °C). The proteins were purified in two steps. The soluble fraction was incubated at 65 °C for 10 min, followed by removal of denatured proteins by centrifugation (20,000×g, 20 min, 4 °C); the heat treatment was repeated once. Subsequently, the His-tagged proteins were purified using the HisPur™ Ni-NTA Resin according to the manufacturer's protocol. Protein concentrations were quantified using the Quick Start™ Bradford Protein Assay kit (Bio-Rad Laboratories, Veenendaal, Netherlands). The purity and molecular mass of the proteins were checked by SDS-PAGE.

Enzyme activity assays

Amylose V, dissolved in 1 M NaOH, and then neutralized to pH 7.0 with 1 M HCl, was used as a model substrate. Branched α -glucan products were prepared at the optimal reaction conditions: 0.125% (w/v) substrate, 35 μ g/mL TtGBE57, 65 °C, pH 6.5; 30 μ g/mL TkGBE57, 70 °C, pH 7.0; 3.0 μ g/mL RmGBE13, 65 °C, pH 7.0 and 3.0 μ g/mL PmGBE13, 50 °C, pH 7.0.

Branching activity, representing the newly synthesized α -1,6-glycosidic linkages, was quantified by measuring the increase in reducing ends upon debranching of the product. The amount of reducing ends was measured by bicinchoninic acid (BCA) method (32). Briefly, 0.125% amylose V was incubated, with different GBEs, in 50 mM sodium phosphate buffer, as described above. Samples of 200 μ L were taken at regular time intervals and the reaction was stopped by boiling for 10 min. Of the samples taken, 50 μ L was debranched by adding 1 μ L of 0.1 M HCl (which lowers the pH to 5.0), 0.7 U isoamylase, 0.5 U pullulanase and 5 mM CaCl₂, and incubated at 40 °C for 16 h. The hydrolytic activity was also quantified, by following the increase in reducing ends within the reaction mixture in time. Branching activity is simply the difference in the amount of reducing ends

after debranching minus the amount of reducing ends before debranching. One unit of branching activity is defined as 1 μmol of branches formed per minute (14). The branching activity of TtGBE57, TkGBE57 and PmGBE13 was calculated from the increase in branches formed within the first 30 min (10 min for RmGBE13), while the hydrolytic activity is calculated from the increase in reducing ends over 24 h. The branching activity on amylopectin was calculated from the increase in branches formed within the first 15 min, while the hydrolytic activity is calculated from the increase in reducing ends over 24 h.

Oligosaccharide analysis

Oligosaccharide analyses was carried out by High Performance Anion Exchange Chromatography (HPAEC) on a Dionex ICS-3000 system (Thermo Fisher Scientific) equipped with a 4 \times 250 mm CarboPac PA-1 column. A pulsed amperometric detector with a gold electrode and an Ag/AgCl pH reference electrode was used. The system was run with a gradient of 30-600 mM NaAc in 100 mM NaOH 1 mL/min. Chromatograms were analyzed using Chromeleon 6.8 chromatography data system software (Thermo Fisher Scientific, Waltham, US). A mixture of glucose, maltose, maltotriose, maltotetraose, maltopentaose, maltohexaose, and maltoheptaose was used as reference for qualitative determination of elution time of each component.

The chain length distribution was determined by debranching the branched α -glucans (2 mg/mL in 5 mM sodium acetate buffer pH 5.0) with 0.7 U/mL isoamylase and 0.5 U/mL pullulanase at 40 °C for 16 h. The debranching reactions were stopped by boiling for 5 min, and denatured proteins were removed by centrifugation, and analyzed by HPAEC.

¹H-NMR spectroscopy

¹H-NMR spectra were recorded at a probe temperature of 323 K on a Varian Inova 500 spectrometer (NMR Center, University of Groningen). Before analysis, samples were exchanged twice in D₂O (99.9 atom% D, Sigma-Aldrich Chemical) with intermediate lyophilization, and then dissolved in 0.6 mL D₂O. Spectra were processed using MestReNova 5.3 software (Mestrelabs Research SL, San-

tiago de Compostella, Spain), using Whittaker Smoother baseline correction and zero filling to 32 k complex points. Carbohydrate structures were determined using the previously developed $^1\text{H-NMR}$ structural-reporter-group concept of $\alpha\text{-D-glucans}$ (33). The $\alpha\text{-1,6}$ -signal is presented at δ 4.98, originating from H1 in 1,4- $\alpha\text{-glucose-1,6}$, and $\alpha\text{-1,4}$ -signal is at δ 5.36 from the H1 in 1,4- $\alpha\text{-glucose-1,4}$ and 1 \rightarrow 4,6- $\alpha\text{-glucose-1,4}$ residues. The degree of branching ($\alpha\text{-1,6}$ -linkage ratio) was calculated by dividing the area of $\alpha\text{-1,6}$ -linkage peak by the total area of $\alpha\text{-1,4}$ -linkage and $\alpha\text{-1,6}$ -linkage peaks in the NMR spectra.

Molecular weight distribution

Molecular weight distributions were measured by GPC-SEC run with DMSO-Li-Br. DMSO-LiBr (0.05 M) was prepared by stirring for 3 h at room temperature. Samples were dissolved at a concentration of 2 mg/mL in DMSO-LiBr at 80 °C for 3 h with shaking and then filtered through a 0.45 μm Millex PTFE membrane (Millipore Corporation, Billerica, USA). The Size Exclusion Chromatography (SEC) system setup (Agilent Technologies 1260 Infinity) from PSS (Mainz, Germany) consisted of an isocratic pump, auto sampler without temperature regulation, an online degasser, an inline 0.2 μm filter, a refractive index detector (G1362A 1260 RID Agilent Technologies, Santa Clara, US), viscometer (ETA-2010 PSS, Mainz, Germany), and MALLS (SLD 7000 PSS, Mainz, Germany). WinGPC Unity software (PSS) was used for data processing. The samples were injected with a flow rate of 0.5 mL/min into a PFG guard-column and three PFG SEC columns 100, 300 and 4000 connected in series. The columns were held at 80 °C, and the detectors were held at 60 °C (Visco) and 45 °C (RI). A standard pullulan kit (PSS) with molecular weights from 342 to 805,000 Da was used to generate a universal calibration curve, in order to determine the hydrodynamic volume from the elution volume. The specific RI increment value dn/dc was measured by PSS and is 0.072.

Fractionation of branched $\alpha\text{-glucans}$

The branched $\alpha\text{-glucans}$ obtained from amylose by TtGBE57 modification were separated into a high and low molecular weight fractions using size-exclusion

chromatography (Hiprep 26/60 Sephacryl S-500 HR column). Briefly, 25 mg branched α -glucan in 5 mL was injected, and the column was run at 2.5 mL/min water with 0.02% NaN_3 . The collected fractions were freeze dried, and subsequently analyzed by NMR and GPC-SEC, as described above.

Modification of different amylose content substrates

The mixtures of amylose and amylopectin were prepared by combining solutions of amylose V and waxy potato starch at different ratios. Firstly, 5 mg/mL amylose V was dissolved into 1 M NaOH, and then neutralized to pH 7.0. Waxy potato starch (7.5 mg/mL) was dissolved in 50 mM phosphate buffer with pH 7 by boiling. The enzymatic reaction conditions were as above. The reactions were stopped by boiling for 10 min, the denatured proteins removed by centrifugation, and the supernatant dialyzed using a dialysis tube with a cutoff size of 100 – 500 Da. The samples were freeze dried and analyzed, as described above.

Results and Discussion

Branching and hydrolytic activity of glycogen branching enzymes

Two GH57 *gbe* genes, from *T. thermophilus* and *T. kodakarensis*, and two GH13 *gbe* genes, from *R. marinus* and *P. mobilis*, were overexpressed in *E. coli* and the corresponding GBEs were purified by a combination of heat treatment and His-tag affinity chromatography (Fig. 1). The two GH13 GBEs, RmGBE and PmGBE13, have a considerable higher branching activity than the two GH57 GBEs, TtGBE and TkGBE, using amylose V and amylopectin as substrates (Table 1). The two GH57 GBEs have a slightly higher branching activity on amylose, the RmGBE13 shows 40% more branching activity with amylopectin, and PmGBE13 has two times more branching activity on amylose.

In addition to the branching activity, GBEs also possess a low hydrolytic activity, which results in the formation of oligo and polysaccharides smaller than the substrate. Acting on amylose V, both GH57 GBEs have a considerably lower ratio of branching over hydrolytic activity than the two GH13 GBEs (Table 1), which is in agreement with previous publications (14,24). Indeed, upon prolonged

incubation of amylose with the two GH57 GBEs, about 15% of the catalytic actions had resulted in the formation of a new reducing end (hydrolysis activity), and 85% in the formation of a new branch (branching activity) (Fig. 2). The two GH57 GBEs are even more hydrolytic with amylopectin as substrate, with 40% hydrolysis and 60% branching (Supplementary Fig. S1). The two GH13 GBEs, in contrast, formed almost only branches, with both amylose and amylopectin (Fig. 2 and Supplementary Fig. S1). Indeed, HPAEC analysis shows substantial amounts of short oligosaccharides in the products made by the two GH57 GBEs (Fig. 3), which are basically absent in the products made by the two GH13 GBEs. Thus, the two GH57 GBEs are far more hydrolytic than two GH13 GBEs, when acting *in-vitro* on pre-existing α -glucan polymers. Although out of scope for this publication, it remains an intriguing question whether GH57 GBEs are also relative hydrolytic *in-vivo*.

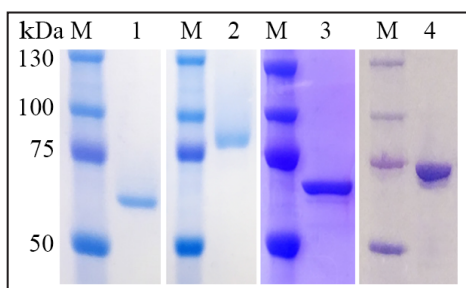


Figure 1. SDS-PAGE of TtGBE57 (Lane 1), TkGBE57 (Lane 2), RmGBE13 (Lane 3), and PmGBE13 (Lane 4).

Table 1. The branching and hydrolytic activities of GBEs.

GBEs	Amylose as substrate			Amylopectin as substrate		
	Branching activity (mU/mg)	Hydrolytic activity (mU/mg)	Branching/Hydrolytic	Branching activity (mU/mg)	Hydrolytic activity (mU/mg)	Branching/Hydrolytic
TtGBE57	490	1.7	288	380	2.9	131
TkGBE57	560	2.6	215	450	4.3	105
PmGBE13	6,100	7.5	813	8,800	4.2	2095
RmGBE13	18,700	7.1	2,634	7,500	3.3	2272

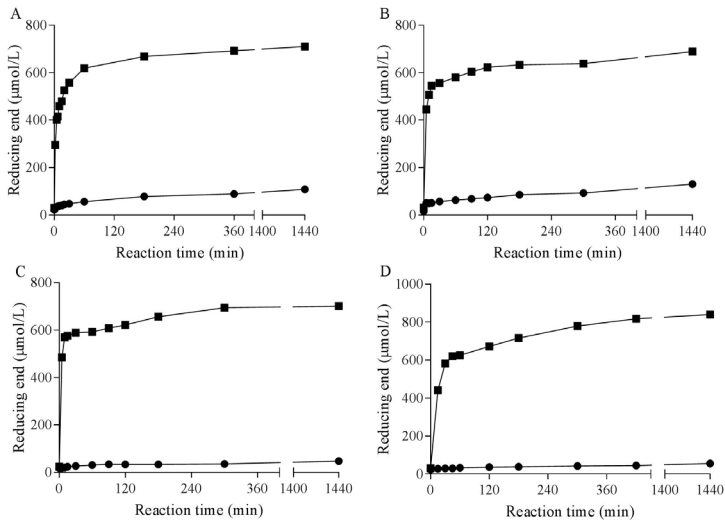


Figure 2. Branching and hydrolysis reaction progress. Reaction progress is followed by quantifying the increase in reducing end over time. A: TtGBE57 products; B: TkGBE57 products; C: RmGBE13 products and D: PmGBE13 products. Black dot: the reducing end concentration of the reaction contents; Black square: the reducing end concentration increase upon debranching.

The structure of branched α -glucan made by GBEs is influenced by the amylose to amylopectin ratio

As native starches are composed of amylopectin and amylose, with the amylose content ranging from as low as 0 up to 70% in commercially available starches (34), it was explored if the amylopectin to amylose ratio affects the structure of the branched α -glucan synthesized. Therefore various ratios of amylose and amylopectin were incubated with the four GBEs and the obtained products were analyzed in detail. Firstly, the chain length distribution of the branched α -glucans derived from 100% amylose and 100% amylopectin were compared. This revealed that the two GH57 GBEs form products with a wider chain length distribution. While the products of the two GH13 GBEs are particularly rich in chains up to \sim DP 10, the two GH57 GBE products contain clearly more relative long chains of DP 10 to 15 (Fig. 3 & 4). The two GH57 GBE products derived from amylopectin even show a bimodal pattern, with maxima at DP7 and DP11 (Fig. 4). Although

the products of the two thermophilic GH13 GBEs explored here have very similar chain length distribution, not all GH13 GBEs synthesized similar products. For examples, the potato SBEI and SBEII GH13 branching enzymes form branched α -glucans with distinct chain length distributions (35).

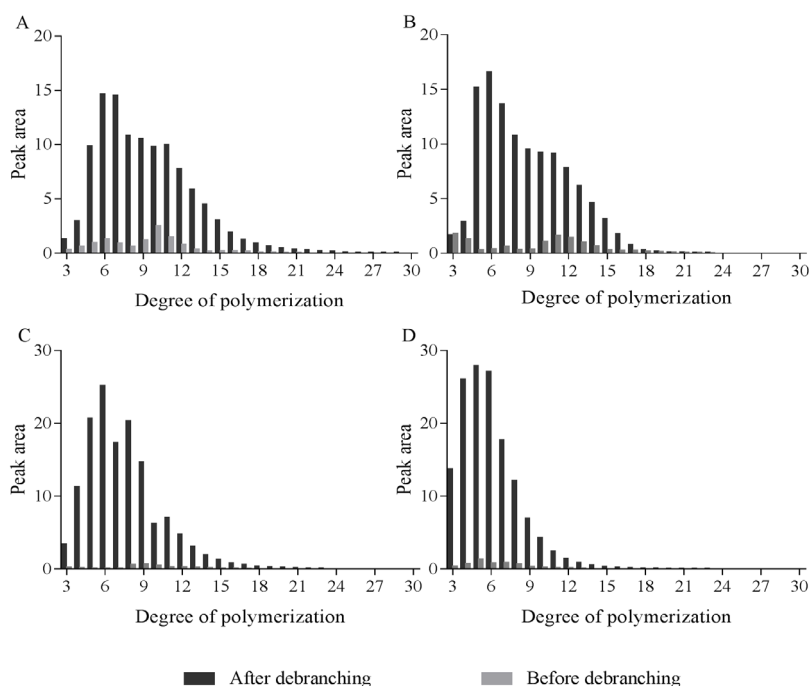


Figure 3. Chain length distribution of the branched glucans derived from amylose V. TtGBE57 (A), TkGBE57 (B), RmGBE13 (C) and PmGBE13 (D). The branched glucans were debranched by isoamylase/pullulanase and analyzed by HPAEC-PAD.

Subsequently the degree of branching of all samples was determined, demonstrating that the two GH13 GBEs form products with a higher degree of branching. Surprisingly, it was also observed that the degree of branching is positively correlated with the percentage of amylose in the substrate with the two GH57 GBEs (Fig. 5). The same correlation is seen with the GH13 RmGBE13, although the effect is somewhat milder, while the effect is absent with the GH13 PmGBE13 (Fig. 5). Since the initial branching activity of the two GH57 GBEs with amylose and amylopectin are quite similar (Table 1), the much higher degree of branching reached with amylose indicates that the branches are distributed more

efficiently starting with amylose, compared to amylopectin. However, a previous study reported that GBE formed slightly less branched α -glucans with increasing amylose content of the substrate (Sorndech et al., 2016). Sorndech et al. used high Mw (5,500 kDa) barley amylose and waxy maize amylopectin, while in the current study potato amylose with a much lower Mw (100 kDa) was used. Possibly branching enzymes are more effective with shorter substrates.

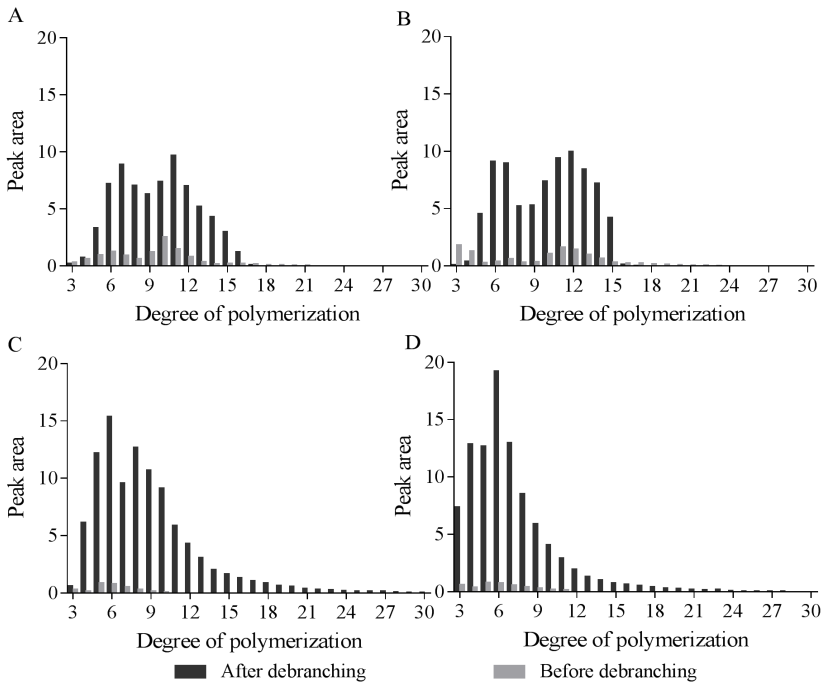


Figure 4. Chain length distribution of the branched glucans derived from amylopectin. TtGBE57 (A), TkGBE57 (B), RmGBE13 (C) and PmGBE13 (D). The branched glucans were debranched by isoamylase/pullulanase and analyzed by HPAEC-PAD.

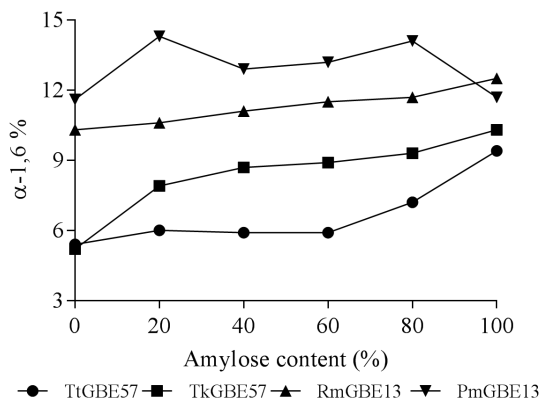


Figure 5. The correlation between amylose content of the substrates and degree of branching. The amylose fractions were made by mixing amylose V and amylopectin, both from potato.

Branched α -glucans derived from amylose and amylopectin have different molecular weight profiles

Besides the degree of branching and the chain length distributions also the molecular weight (Mw) is a key structural parameter of branched α -glucans. To determine if the Mw is influenced by the amylose content of the substrate the branched α -glucans derived from amylose and amylopectin were analyzed by GPC. The first observation is that the four GBEs synthesize branched α -glucans with distinct Mw distributions. Acting on amylose the two GH13 GBEs generate products with a relative mono disperse Mw distribution (Fig. 6); $\sim 1 \times 10^5$ Da for RmGBE13 and $\sim 2 \times 10^5$ Da for PmGBE13. The two GH57 GBEs surprisingly generated products consisting of a low and a high Mw fraction (Fig. 6A). Separation of the high and low Mw fractions of the TtGBE57 product, using size-exclusion column chromatography, revealed that the low Mw fraction ($< 4 \times 10^4$ Da) contains only 5% branches and the high Mw fraction ($> 7 \times 10^4$ Da) contains 10% branches. This indicates that the low Mw fraction consist mainly of the products resulting from hydrolysis with mild branching, whereas the high Mw fraction is the result of the branching reaction.

The picture is distinctively different with amylopectin as substrate. The most remarkable difference being the lower Mw of the branched α -glucans derived from amylopectin compared to the products derived from amylose. Subsequently the mixtures of amylose and amylopectin were converted by the four GBEs revealing that the average Mw increase with Mw increases with increasing amylose. The same phenomena has also been observed for the GH13 GBE from *Rhodothermus obamensis* (36), and now also in this study. From these observations it is concluded that GBEs convert the high Mw amylopectin into branched α -glucans with lower Mw, whereas amylose is converted into branched α -glucans with a Mw corresponding to that of amylose. The Mw distributions of the branched α -glucans derived from amylose and amylopectin show, however, also similarities. The GH13 RmGBE13 product is again rather mono disperse, whereas the GH57 products consist of two or three Mw fractions (Fig. 6B). The GH13 PmGBE13 derived from amylopectin product is special in the sense that it consists of two Mw fractions, while the enzyme converts amylose in a mono disperse branched α -glucan (Fig. 6). Thus, the different GBEs create highly branched α -glucan with various Mw distributions, and the GH13 RmGBE13 is the best choice for the production of product with a uniform Mw distribution.

Synthesis of branched α -glucans from a waxy starch and a high amylose starch.

The question arises if the trends seen with the artificial mixtures of amylose and amylopectin also hold in the conversion of natural starches, which vary widely in their amylose content (35,36). To test this, waxy corn and a high amylose pea starch (with 35% amylose) (37,38) were treated with the GBEs. NMR analysis of the branched α -glucans obtained demonstrated that the degree of branching of these products (Table 2) is in good agreement with the values obtained with the artificial mixtures of amylose or amylopectin (Fig. 5). Thus, the two GH13 GBEs synthesized branched α -glucans with a higher degree of branching than the GH57 GBEs (Table 2). Secondly, the GH57 GBEs create products with a higher degree of branching from the amylose rich pea starch than from the waxy maize starch, as predicted by the model system employing a mixture of amylose and amylopectin.

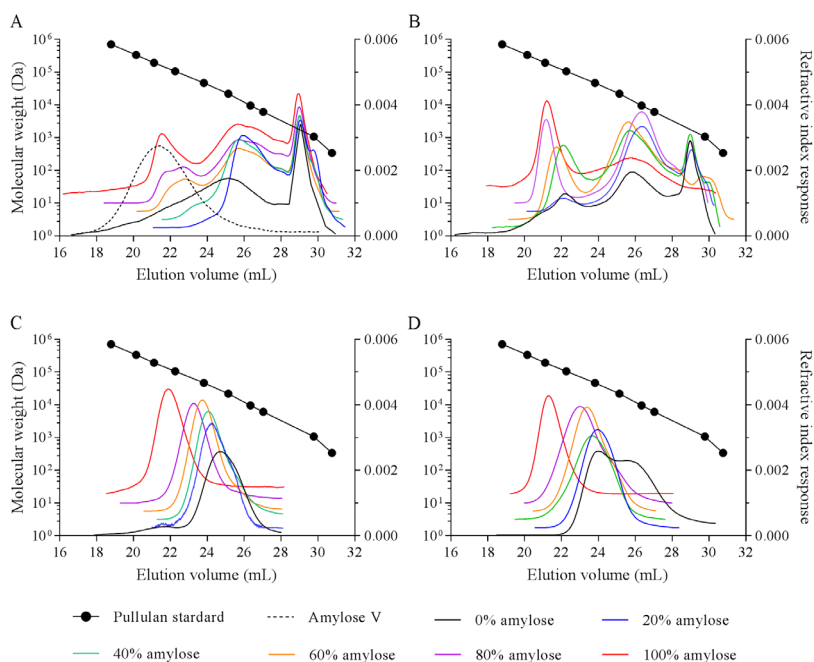


Figure 6. The molecular weight distribution of the branched α -glucans derived from amylose V (A) and amylopectin (B). The analysis was performed by GPC-MALLS-RI run with DMSO containing 50 mM LiBr.

Table 2. The DB of pea and waxy corn starches modified with *T. thermophilus*, *T. kodakarensis*, *R. marinus*, and *P. mobilis* GBE. Based on the results of triplicate analyses.

GH Family	GBE	Pea starch	Waxy corn starch
57	<i>T. thermophilus</i>	6.2 \pm 0.44	5.3 \pm 0.65
	<i>T. kodakarensis</i>	6.2 \pm 0.64	5.0 \pm 0.21
13	<i>R. marinus</i>	10.9 \pm 0.20	10.2 \pm 0.12
	<i>P. mobilis</i>	13.1 \pm 0.30	12.7 \pm 0.49

Conclusions

Here we report the synthesis of branched α -glucans by four thermophilic GBEs. Whereas amylose is converted in highly branched α -glucans by all four GBEs, conversion of amylopectin yields highly branched and modest branched products with the GH13 and GH57 GBEs, respectively. The two GH13 GBEs products

have a narrow molecular weight distribution, while the two GH57 GBEs products have a wide molecular weight distribution. We speculate that the production of branched α -glucans with a narrow molecular weight distribution requires GBEs with very low hydrolytic activity. Indeed, the commercially available RmGBE13 (Branchzyme, Novozymes) has the highest branching over hydrolysis specificity and synthesizes the branched α -glucan with the most mono disperse molecular weight distribution of the GBEs evaluated.

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Supplementary

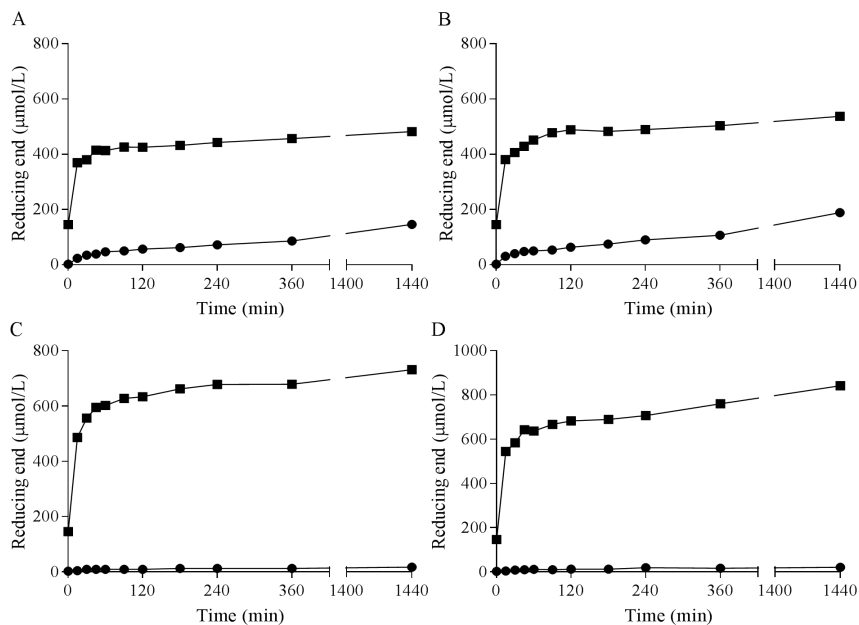


Figure S1. Branching and hydrolysis reaction progress. Reaction progress is followed by quantifying the increase in reducing ends over time in the conversion of amylopectin. TtGBE57 (A); TkGBE57 (B); RmGBE13 (C) and PmGBE13 (D). Black dot: the reducing end concentration of the reaction contents; Black square: the reducing end concentration increase upon debranching.v