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The Unique Branching Patterns of Deinococcus Glycogen Branching Enzymes Are Determined by Their N-Terminal Domains\textsuperscript{V}

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Glycogen branching enzymes (GBE) or 1,4-\(\alpha\)-glucan branching enzymes (EC 2.4.1.18) introduce \(\alpha\)-1,6 branching points in \(\alpha\)-glucans, e.g., glycogen. To identify structural features in GBEs that determine their branching pattern specificity, the \textit{Deinococcus}\textit{ geothermalis} and \textit{Deinococcus}\textit{ radiodurans} GBE (GBE\textsubscript{Dg} and GBE\textsubscript{Dr}, respectively) were characterized. Compared to other GBEs described to date, these \textit{Deinococcus} GBEs display unique branching patterns, both transferring relatively short side chains. In spite of their high amino acid sequence similarity (88\%) the \textit{D. geothermalis} enzyme had highest activity on amylose while the \textit{D. radiodurans} enzyme preferred amylopectin. The side chain distributions of the products were clearly different: GBE\textsubscript{Dg} transferred a larger number of smaller side chains; specifically, DP5 chains corresponded to 10\% of the total amount of transferred chains, versus 6.5\% for GBE\textsubscript{Dr}. GH13-type GBEs are composed of a central (\(\beta/\alpha\)) barrel catalytic domain and an N-terminal and a C-terminal domain. Characterization of hybrid \textit{Deinococcus} GBEs revealed that the N2 modules of the N domains largely determined substrate specificity and the product branching pattern. The N2 module has recently been annotated as a carbohydrate binding module (CBM48). It appears likely that the distance between the sugar binding subsites in the active site and the CBM48 subdomain determines the average lengths of side chains transferred.

Glycogen is an energy reserve polymer of many animals and microorganisms. It is composed of a backbone of glucose residues linked by \(\alpha\)-1,4 glucosidic bonds with \(\alpha\)-1,6-linked side chains (7, 31). In bacteria, the linear \(\alpha\)-1,4-glucan is synthesized from ADP-glucose by the enzyme glycogen synthase, which is thought to be involved in both initiation and elongation of the chain (40). Side chains are introduced by glycogen branching enzyme (GBE) or 1,4-\(\alpha\)-glucan branching enzyme (EC 2.4.1.18). This enzyme catalyzes formation of an \(\alpha\)-1,6 branch points by cleaving an \(\alpha\)-1,4 glucosidic linkage in the donor substrate and transferring the nonreducing end-terminal fragment of the chain to the C-6 hydroxyl position of an internal glucose residue that acts as the acceptor substrate (4). Depending on its source, GBEs have a preference for transferring different lengths of glucan chains (1, 23). Most GBEs are members of subfamily 8 (\textit{Eukaryota}) or 9 (\textit{Bacteria}) of glucoside hydrolase family 13 (GH13) (34). Recently, the first GBE from family GH57 was described (28) (http://www.cazy.org).

GH13-type GBEs are composed of three major domains of secondary structure, a central (\(\beta/\alpha\)) barrel catalytic domain or A domain, an N-terminal domain, and a C-terminal domain (1). Domain A is present in all members of family GH13 and consists of a highly symmetrical fold of eight parallel \(\beta\)-strands encircled by eight \(\alpha\)-helices. However, some variations occur in GBEs (a missing \(\alpha\)-helix 5 and insertion of extra \(\alpha\)-helices) (1). Domain A contains the four conserved amino acid regions (I to IV) typical for enzymes of family GH13 (35). In most GH13 enzymes, an extra domain is present, inserted between \(\beta\)-strand 3 and \(\alpha\)-helix 3 (domain B), which affects their catalysis and product specificity (16). In GBEs, the length of this loop is only 40 residues, not long enough to be considered a separate domain (1). Domain C is found in most GH13 enzymes and is believed to shield the hydrophobic residues of the catalytic domain from contacts with the solvent. Domain C has also been suggested to be involved in substrate binding (25).

Domain N is typical for GH13 enzymes cleaving or forming endo-\(\alpha\)-1,6 linkages (17), namely, isoamylase (EC 3.2.1.68; subfamily 11) (18), pullulanase (EC 3.2.1.41; subfamilies 12 to 14) (27), and both starch (subfamily 8) and glycogen branching enzymes (subfamilies 8 and 9). An exception is the 4-\(\alpha\)-d-\{(1\(\rightarrow\)4)-\(\alpha\)-d-glucano\}trehalose trehalohydrolase (EC 3.2.1.141; subfamily 10), which hydrolyzes linear maltooligosaccharide-like substrates (6) (39). The crystal structures of most of these enzymes with their N domains (all or part) have been published previously (1, 6, 18, 27, 39). The exact function of this N domain has remained unclear, and the similarity between the N domains in these different enzymes is low. They vary in length, and some of them consist of two or three modules. However, they all possess one common module that was recently classified as a family 48 carbohydrate-binding module (CBM48) (19) (http://www.cazy.org/).

In GBEs domain N comprises a module of 150 amino acids, termed the N2 module, that contains the putative CBM48. In some branching enzymes, it is preceded by a module of 100 to 150 amino acids, termed the N1 module. It has been proposed that the N1 module has originated from a DNA duplication of

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the N2 module (36). Based on the architecture and length of the N domain, GBEs can be divided into group 1, containing both the N1 and the N2 modules, and group 2, containing only the N2 module (12). A 112-amino-acid truncation of the N1 module in the N2 module (12). A 112-amino-acid truncation of the N1 module of E. coli GBE (group 1) resulted in a 40% reduction of enzyme activity (2) and an altered branching pattern (3). Further investigations of this N1 module, by sequential N-terminal deletions, showed that enzymes with the shorter N1 module transferred longer glucan chains (5). No studies have been reported thus far investigating the role of the N2 module (containing the putative CBM48 domain) in GBEs as well as in other GH13 members.

Here, we report a detailed biochemical characterization of two GH13 GBEs from the extremophilic bacteria Deinococcus geothermalis and Deinococcus radiodurans. These two GBEs (GBEDg and GBEDr, respectively) generate unique branching patterns by transferring glucosidic chains that are shorter than those of other GBEs reported to date (9, 36, 38, 41). To investigate the role of the different domains in these enzymes, chimeras of GBEDg and GBEDr were constructed. Their characterization revealed that substrate and chain length specificity achieved by overlap extension PCR (43). They were named according to the source of their N, A, and C domains (e.g., the GGR gene consists of the glgB A domain, catalytic A domain, and/or the C-terminal domain for each glgB gene). Appropriate templates and oligonucleotides were combined in subsequent PCRs (Table 2) to yield the respective hybrids. Templates, primers, and amplified fragments are listed in Table 2. The GGR, RRG, and GRR chimeric genes were cloned into Ndel and BglII restriction sites, resulting in plasmids pDg and pDr with N-terminal His tags.

Construction of truncated and chimeric genes. The 3′-207-nucleotide extension in domain C of glgB was truncated (resulting in CTTg) by PCR using plasmid pDr as a template and the primers Dr-FP and CTT-RP (Table 1). Similarly, the 5′ and 3′ truncated forms of glgB were amplified from genomic DNA by PCR using the oligonucleotides Dg-FP/Dg-RP and Dr-FP/Dr-RP, respectively (Table 1). Both PCR products were cloned separately from genomic DNA by PCR using the oligonucleotides Dg-FP/Dg-RP and Dr-FP/Dr-RP, respectively (Table 1). Both PCR products were cloned separately into the pET15b vector (Novagen) using Ndel and BglII restriction sites, resulting in plasmids pDg and pDr with N-terminal His tags.

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Expression and purification. Overexpression of all proteins, except for NTg, CTg, and GRR, was achieved by overnight growth of E. coli BL21(DE3) Star cells containing the corresponding plasmid at 37°C and 300 rpm in Luria-Bertani medium supplemented with 50 µg/ml ampicillin. NTg, CTg, and GRR were expressed successfully by induction with 1 mM isopropyl-ß-D-thiogalactopyranoside at an optical density of 600 nm of ~0.6, followed by 5 h of additional growth. For all proteins, the cells were harvested by centrifugation (10 min at 10,000 × g), washed with 50 mM sodium phosphate buffer, pH 8.0, and centrifuged again (10 min at 10,000 × g). The pellets were resuspended in 50 mM sodium phosphate buffer, pH 8.0, and the cells were disrupted by sonication (seven times for 15 s at 7 µm with 30-s intervals) and centrifuged (30 min at 15,000 × g). All proteins were found as soluble proteins in the supernatants except for NTg, CTg, and GRR, which were found in the pellets as inclusion bodies. Only GRR was successfully isolated from the inclusion bodies by resuspension of the pellet in 8 M urea, followed by centrifugation (30 min at 15,000 × g). The supernatant containing unfolded GRR was subjected to dialysis against sodium phosphate buffer (20 mM potassium phosphate, pH 7.0, and 20% glycerol).
buffer (25 mM; pH 8), leading to the refolding of GRR, as confirmed by circular dichroism.

All proteins were purified by His tag affinity chromatography using a HiTrap chelating column (Amersham Pharmacia, Uppsala, Sweden) charged with nickel sulfate. The eluates were pooled with a linear gradient of 0 to 500 mM imidazole on an Äkta prime purification system (Amersham Pharmacia). Fractions containing the protein of interest were pooled and dialyzed against sodium phosphate buffer (25 mM; pH 8). Protein concentrations were determined by measuring the absorbance of 1.0 per min at 280 nm. Circular dichroism. Multiple far-UV spectra (195 to 260 nm) were recorded on an Åkta prime purification system (Amersham Pharmacia). Fractions containing the protein of interest were pooled and dialyzed against sodium phosphate buffer (25 mM; pH 8).

Protein determination and sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). Protein concentrations were determined by measuring the absorbance at 280 nm on a Nanodrop ND-1000 spectrophotometer (Isogen Life Science, de Meern, The Netherlands) using the following extinction coefficients (in mg/ml−1 cm−1) estimated by the method of Gill and von Hippel (8): 2.38 for GBEDr, 2.12 for GBEg, 2.33 for CTDr, 2.11 for GGR, 2.39 for RRR, 2.41 for RGG, and 2.08 for GRR. Proteins were analyzed by SDS-PAGE on 10% polyacrylamide gels. The molecular mass was determined using a PageRuler Prestained Protein Ladder (Fermentas) as a standard, and proteins were stained with Bio-Safe Coomassie (Bio-Rad, Germany).

Circular dichroism. Multiple far-UV spectra (195 to 260 nm) were recorded in sodium phosphate buffer at pH 8.0 and 20°C using a concentration of protein of 0.1 mg/ml on a Jasco J-715 spectropolarimeter (Jasco, Tokyo, Japan) in quartz cuvettes. The following gradient of eluent A (1 ml/min) was used: 55% (10 min), 35% (4 min), 0% (7 min), and 95% (14 min). Enzyme activity assays. (i) Iodine assay. The total activity of the enzyme was measured using the iodine assay (10), which is based on formation of a blue complex between iodine-iodide and a linear α,1,4-glucan of a certain length. The sum of the transglycosylation and the hydrolytic activity of the enzyme can be measured by monitoring the decrease in absorbance. The reaction mixtures contained 150 μl of 0.125% (wt/vol) amylase V (Avebe, Foxthol, The Netherlands) or 0.25% potato amylopectin (type III; Sigma) and 50 μl of enzyme at the appropriate concentration (15 to 25 μg/ml). At each time point, aliquots of 15 μl were taken, and the reaction was stopped by addition of 1.5 μl of 1 M NaOH and 150 μl of iodine reagent (0.01% [wt/vol] I2, 0.1% [wt/vol] KI). One unit of enzyme activity is defined as the decrease in absorbance of 1.0 per min at 660 nm for amylase and at 530 nm for amylpectin.

To determine the optimal conditions for the activity of the enzyme, the assay was performed at temperatures ranging from 20°C to 70°C and pH 6.5 to 9.5 in Bis-Tris-propane-HCl buffer. For thermostability studies, the enzymes (0.5 mg/ml) were incubated in the absence of substrate for 1 h at different temperatures from 20°C to 70°C, and the residual activity in the supernatant (after centrifugation at 13,000 × g for 1 min) was measured at 34°C.

(ii) Branching assay. This method allowed determination of the amount of α-1,6 branch points introduced by the action of GBE by measuring the difference in amount of reducing ends before (hydrolytic activity) and after debranching (total activity) of the product by isoamylase (37). The reaction mixtures contained 50 μl of appropriately diluted GBE (1, 2, or 4 μg) in 1,400 μl of 0.125% amylase V (Avebe, Foxthol, The Netherlands) at pH 8.0. Samples (200 μl) were taken at different time points (0 to 20 min), and the reaction was stopped by boiling for 5 min. The numbers of reducing ends before and after debranching were measured at each time point by a 2,2’-binicchinone assay (42) using a maltotriose calibration curve. Debranching was performed as follows: 50 μl of reaction mixture was debranched for 20 h at 40°C in 129 μl of 25 mM sodium phosphate buffer (pH 8.0), 20 μl of 1 M acetate buffer (pH 3.8), and 1 μl (0.175 U) of Pseudomonas sp. isoamylase (Megazyme, Wicklow, Ireland). One unit of GBE branching activity is defined as 1 μmol of α-1,6 linkages synthesized per min.

Side chain distribution. To determine the side chain distribution of the final products, 10 ml of 0.125% (wt/vol) amylase V (Avebe) solution was incubated with 400 units (determined by iodine assay) of GBEg or GBEg for 72 h. The reaction was terminated by boiling the mixture for 10 min. The reaction mixture was divided in two equal parts; one part was treated with 10 units of isoamylase from Pseudomonas sp. (Megazyme) after the addition of 750 μl of 1 M citrate buffer, pH 4.0, for 20 h at 40°C to hydrolyze the α-1,6 glucosidic linkages. Both parts of the reaction mixture, before and after debranching, were freeze-dried, dissolved in 90% dimethyl sulfoxide (0.25 mg/ml) and analyzed by high-performance anion-exchange chromatography (HPAEC) analysis. Mixtures of oligosaccharides with degrees of polymerization ranging from 1 to 7 (DP1 to DP7) and a debranched waxy maize starch solution containing a broad mix of oligosaccharides of known composition were used as standards. Separation of oligosaccharides was achieved with a CarboPac PA1 anion exchange column (250 mm by 4 mm; Dionex) coupled to a CarboPac guard column (Dionex, Sunnyvale, CA). The following gradient of eluent A (0.1 ml/min) was used: 95% (10 min), 65% (10 min), 55% (30 min), 35% (4 min), 0% (7 min), and 95% (14 min). Eluent A was sodium hydroxide (0.1 M), and eluent B was sodium acetate (0.6 M) in sodium hydroxide (0.1 M). Detection was performed with an ED40 electrochemical detector (Dionex) equipped with an Au working electrode and an Ag/AgCl reference electrode with a sensitivity of 300 nC. The pulse program used was the following: +0.1 V (0 to 0.41 s), −2.0 V (0.41 to 0.43 s), +0.6 V (0.43 to 0.44 s), and −0.10 V (0.44 to 0.50 s). The integration time was 0.20 to 0.40 s. Data were integrated using a Totalchrom (PerkinElmer, Waltham, MA) data integration system.

RESULTS AND DISCUSSION

Amino acid sequence analysis of the glycon branching enzymes of Deinococcus. At present there is no proof for actual synthesis of glycon in the extremophilic bacteria D. geothermalis and D. radiodurans. However, the key enzymes involved in glycon metabolism, such as glycon branching enzyme (including a demonstration of its activity [this paper]), ADP-glucose pyrophosphorylase, and glycon synthase, have been annotated in both species (28).

D. geothermalis and D. radiodurans both contain a single gene in their genomes coding for a putative glycon branching enzyme. The D. geothermalis gene, Dgeo_0981, consists of 1,959 nucleotides and encodes an enzyme of 652 amino acids (GBEDr), which has a predicted molecular mass of 74.2 kDa. The DR1848 gene from D. radiodurans consists of 2,124 nucleotides and encodes an enzyme of 705 amino acids (GBEDr) that has a theoretical molecular mass of 80 kDa. Both enzymes belong to group 2 of GH13 GBEs. Furthermore, they contain the four conserved amino acid regions (I to IV) typical for enzymes of family GH13 (25) plus the four conserved amino acid residues specific for bacterial GBEs, namely W2898, Q101, S466, and H430 (E. coli GBE numbering) (Fig. 1) (1). Their N2 modules, containing the CBM48, possess the two consensual aromatic residues crucial for starch or glycon binding (26) (W77 and Y123 for GBEg and W61 and Y107 for GBEg).

GBEDg and GBEg show an overall identity in 622 amino acids of 81% (88% similarity). The similarity between both N

TABLE 2. Templates, primers, and amplified fragments for the construction of chimeric mutants by PCR

<table>
<thead>
<tr>
<th>Template(s)</th>
<th>Primers</th>
<th>Amplified fragment (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>pDr</td>
<td>Dr-FP, CT-T-RP</td>
<td>1,934</td>
</tr>
<tr>
<td>pDg</td>
<td>Dr-FP, H2</td>
<td>1,571</td>
</tr>
<tr>
<td>pDr</td>
<td>H1, Dr-RP</td>
<td>1,643</td>
</tr>
<tr>
<td>pDr</td>
<td>Dr-FP, Dr-RP</td>
<td>2,188</td>
</tr>
<tr>
<td>pDg</td>
<td>H2, Dr-RP</td>
<td>547</td>
</tr>
<tr>
<td>pDr</td>
<td>Dr-FP, H1</td>
<td>1,527</td>
</tr>
<tr>
<td>pDr</td>
<td>Dr-FP, H4</td>
<td>517</td>
</tr>
<tr>
<td>pDr</td>
<td>H3, Dr-RP</td>
<td>1,457</td>
</tr>
<tr>
<td>pDr</td>
<td>Dr-FP, Dr-RP</td>
<td>1,457</td>
</tr>
<tr>
<td>pDr</td>
<td>Dr-FP, H4</td>
<td>566</td>
</tr>
<tr>
<td>pDr</td>
<td>H3, Dr-RP</td>
<td>1,653</td>
</tr>
<tr>
<td>pDr</td>
<td>Dr-FP, Dr-RP</td>
<td>2,193</td>
</tr>
<tr>
<td>pDg</td>
<td>Dg-FP, Dg-C-T-RP</td>
<td>1,601</td>
</tr>
<tr>
<td>pDg</td>
<td>Dg-N-T-F, Dg-RP</td>
<td>1,521</td>
</tr>
</tbody>
</table>

*The N, A, and C domains and combinations of these domains (e.g., NA) are identified by the subscripted abbreviations used in the text for D. geothermalis (Dg) and D. radiodurans (Dr).
domains is in the same order (145 to 158 amino acids long, 81% identity, and 88% similarity in 136 amino acids). The identity in their catalytic A domains is relatively high (364 amino acids; 87% identity and 93% similarity). The two enzymes differ most in their C domains (130 amino acids in GBE\textsubscript{Dr} and 195 in GBE\textsubscript{Dg}, with only 70% identity and 77% similarity in 113 amino acids). Unique for the GBE\textsubscript{Dg} is a 66-amino-acid extension in the C domain, which is not present in any other GBE known to date. BLAST searches with the 66-residue-long extension did not give a significant result (data not shown).

Characterization of two Deinococcus branching enzymes. Both Deinococcus GBE genes were cloned, and the enzymes were expressed in \textit{E. coli} and purified to homogeneity by His tag purification (data not shown), yielding up to 30 mg of purified GBE per liter of \textit{E. coli} culture. The molecular mass of the proteins as determined by SDS-PAGE was 75 kDa for GBE\textsubscript{Dg} and 80 kDa for GBE\textsubscript{Dr}, in accordance with the calculated values. Both enzymes were active in a relatively broad range of pH (7 to 9) and temperature (30 to 40°C) values and showed maximum activity at pH 8.0 and 34°C, as measured by the iodine assay. Their specific activities on amylose V were 621.3 U/mg for GBE\textsubscript{Dg} and 404.2 U/mg for GBE\textsubscript{Dr} (Table 3). These are relatively high values compared to their specific activities on amylose as previously measured (see above). In contrast to the results with amylose, the specific activity on amylopectin was higher for GBE\textsubscript{Dg} (538.0 U/mg protein) than for GBE\textsubscript{Dr} (474.3 U/mg protein). The ratio of the specific activities of amylose to amylopectin was 1.31 for GBE\textsubscript{Dg} and 0.75 for GBE\textsubscript{Dr}. \textit{E. coli} GBE had an amylose/amylopectin ratio of 1.78, which is higher than observed for the two Deinococcus GBEs (2). Thus, in spite of their high overall sequence identity and similarity, GBE\textsubscript{Dg} prefers amylose over amylopectin whereas the opposite is true for GBE\textsubscript{Dr}.

The two Deinococcus GBEs clearly differ in substrate specificity. The specific activities of both GBEs were determined on amylopectin using the iodine assay (Table 3) and were compared to their specific activities on amylose as previously measured (see above). In contrast to the results with amylose, the specific activity on amylopectin was higher for GBE\textsubscript{Dg} (538.0 U/mg protein) than for GBE\textsubscript{Dr} (474.3 U/mg protein). The ratio of the specific activities of amylose to amylopectin was 1.31 for GBE\textsubscript{Dg} and 0.75 for GBE\textsubscript{Dr}. \textit{E. coli} GBE had an amylose/amylopectin ratio of 1.78, which is higher than observed for the two Deinococcus GBEs (2). Thus, in spite of their high overall sequence identity and similarity, GBE\textsubscript{Dg} prefers amylose over amylopectin whereas the opposite is true for GBE\textsubscript{Dr}.

The two Deinococcus GBEs have a preference for transferring short side chains. The products obtained after prolonged incubations of both enzymes with amylose showed a similar side chain distribution. Most side chains were between 4 and 17 glucose residues long, with side chains of 6 and 7 glucose residues (~35% of total) predominantly (Fig. 2). This branching pattern is significantly different from that of the other GH13 GBEs for which a quantitative analysis has been described to date, namely, \textit{E. coli} GBE (group 1 GBE) wild type

![Image](https://example.com/image.png)

FIG. 1. (A) Domain organization of group 1 and group 2 GH13 GBEs. N domain (gray), catalytic or A domain (black), and C domain (white) are shown. The N domain of group 1 GBEs consists of N1 and N2 modules, while only N2 is present in group 2 GBEs. The N2 module contains a putative CBM48. In domain A the four conserved regions (I to IV) for family GH13 are found. (B) Amino acid alignment of highly conserved regions in the catalytic domains of GBE\textsubscript{Dg}, GBE\textsubscript{Dr}, and \textit{E. coli} GBE. I to IV are conserved regions in GH13 enzymes. Amino acid positions are given. ■, putative catalytic nucleophile (25); ●, putative acid/base catalyst (25); ▼, putative transition state stabilizer (25); †, residue conserved in α-amylase family; ¥, residue conserved in bacterial GBEs (1).

![Image](https://example.com/image.png)

TABLE 3. Specific activity on amylose and amylopectin for the wild-type, the chimeric, and the truncated GBE\textsubscript{Dr} and GBE\textsubscript{Dg} enzymes

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Specific activity (U/mg) on:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Amylose</td>
</tr>
<tr>
<td>GBE\textsubscript{Dg}</td>
<td>621.3</td>
</tr>
<tr>
<td>GBE\textsubscript{Dr}</td>
<td>404.2</td>
</tr>
<tr>
<td>CTT\textsubscript{Dr}</td>
<td>442.3</td>
</tr>
<tr>
<td>GGR</td>
<td>468.8</td>
</tr>
<tr>
<td>RRG</td>
<td>411.7</td>
</tr>
<tr>
<td>RGG</td>
<td>624.1</td>
</tr>
</tbody>
</table>
| GRR | <0.5 | <0.5 | ND

*ND, not determined.*
and three N1 module-truncated variants (5) and *A. aeolicus* GBE (group 2 GBE) (41). In these GBEs, the preferred DP of chains transferred (~40 to 50%) lies between DP10 and DP14, with only 20 to 30% of chains shorter than 10 glucose residues, a value increasing to 70% for *Deinococcus* GBEs (Fig. 2). Side chain distributions of other GH13 GBEs have been reported, e.g., for *G. stearothermophilus* GBE (36) and *A. gottschalkii* GBE (38), both group 2 GBEs. Even though no quantitative data are available for these enzymes, their branching patterns are clearly different from those of the *Deinococcus* GBEs, with a preference for the transfer of longer chains, as in the case of *E. coli* and *A. aeolicus* GBEs. This unique side chain distribution of the *Deinococcus* GBEs may be a consequence of the fact that they are distantly related to other known GH13 GBEs. The two *Deinococcus* enzymes form a separate cluster, and although they both belong to group 2 of GH13-type GBEs, they appear equally related to group 1 and group 2 at the amino acid level (Fig. 3).

**Construction of chimeric *Deinococcus* enzymes showed the importance of the N domain in substrate specificity and branching pattern.** Comparison of the branching patterns of the two *Deinococcus* GBEs revealed that the branched product of GBE_Dg contained more short side chains overall, especially of DP5, which corresponded to about 10% of the total (only

**FIG. 2.** HPAEC-pulsed amperometric detection analysis of the end products obtained by incubation of GBE_Dg or GBE_Dr with amylose, followed by debranching with isoamylase. For comparison, the distribution of DPs of the debranched end products of the *E. coli* GBE (5) and *A. aeolicus* GBE (41) enzymes are also shown.

**FIG. 3.** Neighbor-joining tree of known GH13 GBEs (http://www.cazy.org) constructed using MEGA, version 3.1 (20). Bootstrap values are indicated on the nodes of each branch. The bar indicates 10% amino acid sequence difference. See Materials and Methods for accession numbers. *, GBE from group 1.
6.5% in the case of GBE$_{Dr}$) (Fig. 2). Thus, strikingly, even though both enzymes are highly similar (88% similarity and 81% identity), they exhibit distinct substrate specificities and clear differences in their branching patterns.

The relatively high overall amino acid sequence identity between GBE$_{Dg}$ and GBE$_{Dr}$ made them ideal candidates for investigating a possible role of the different domains in causing their differences in substrate preferences and branching patterns. In order to gain more insight into which domain (N, catalytic, or C domain) the differences in substrate specificity or branching pattern.

Interestingly, the side chain distribution of RGG closely resembled that of GBE$_{Dr}$ (Fig. 5A) and approximately 6.5% for RRG (Fig. 5B), in accordance with their respective wild types (Fig. 5A and B). This finding indicated that the C domain is not involved in determining the substrate specificity or branching pattern of the Deinococcus GBEs.

**Domain C does not influence substrate specificity or branching pattern.** The specific activity of CTT$_{Dr}$ was 442.3 U/mg on amylose and 468.8 U/mg on amylpectin. Both specific activities as well as their ratio of 0.79 were comparable to those of the wild-type GBE$_{Dr}$ (Table 3). Furthermore, the side chain distribution produced by CTT$_{Dr}$ was very similar to that made by GBE$_{Dr}$ (data not shown). The 66-amino-acid extension at the C terminus of GBE$_{Dr}$ thus does not affect substrate specificity or branching pattern.

**Domain N is involved in determining substrate specificity and branching pattern.** Of the N-domain exchange mutants, only RGG (but not GRR) had enough activity to enable further tests. Therefore, substrate specificity and side chain distribution were measured only for RGG. It exhibited a specific activity on amylose of 624.1 U/mg and on amylpectin of 343.2 U/mg. Its amylose/amylpectin activity ratio was 1.9. Interestingly, this is much higher than the value measured for either parent (Table 3). This result clearly shows that domain N (N2 module) influences the GBE substrate specificity.

The product synthesized by RGG had a branching pattern that was clearly different from the product of GBE$_{Dr}$ (Fig. 5C). Interestingly, the side chain distribution of RGG closely resembled that of GBE$_{Dr}$, which was the source of only the N domain of RGG. From this result, it is concluded that N domain plays a critical role in determining the length of the chains transferred by these GBEs.

It has previously been shown that the N1 module of domain N of GBEs of group 1 influences their branching patterns (2, 3, 5). However, no such information is available for GBEs belonging to group 2, which lack the N1 module. The N2 module has recently been annotated as a CBM48 and is most likely involved in binding of the substrate. The CBM48 found in AMP-activated protein kinase has been shown to bind glyco-gen as well as β-cyclodextrin and oligosaccharides such as maltoheptaose (19, 30). There are clear examples of the importance of CBMs for enzyme activity, e.g., in the case of CGTase, which has a carbohydrate binding site in domain C anchoring the enzyme to the starch granule (22), and the raw starch binding domain E (designated CBM20), which has two carbohydrate binding sites binding raw starch and guiding the linear starch chains toward the active site (29). In the crystal
structures of isoamylase and 4-α-D-[(1→4)-α-D-glucano]trehalose trehalohydrolase, the N domain (both with a putative CBM48) is in close proximity to the B domain [loop between the third β-strand and the third α-helix of the (β/α)₈ barrel] (25), which is known to be involved in catalysis and product specificity of GH13 enzymes (16). Moreover, it has been suggested that the N domain of *D. radiodurans* 4-α-D-[(1→4)-α-D-glucano]trehalose trehalohydrolase is involved in the initial steps of sugar binding by contributing to hydrophobic stacking interactions at the entrance of the channel leading to the active site (39). This channel in *D. radiodurans* 4-α-D-[(1→4)-α-D-glucano]trehalose trehalohydrolase can accommodate seven sugar units in subsites −1 to −7. Since GBE uses substrates longer than DP7, it is indeed possible that the N2 module accommodates the rest of the minus subsites (from subsite −8 on), thus determining the number of glucose units binding in the donor subsites (corresponding to the length of the chains transferred). It is also possible that by interacting with the −7 subsite, N2 influences substrate binding at the −6 subsite. A weaker binding of the donor substrate at the −6 and −7 subsites would result in an increase of transferred chains of DP5.

In the case of group 1 GBEs, the branching patterns are most likely determined by the combined action of both modules N1 and N2 of domain N. A dynamic mechanism in which a flexible N1 would move and restrict exposure of longer chains to the active site has been suggested (5). We propose that the N2 module helps in controlling the length of the chains transferred in these enzymes and plays a main role in determining them in group 2 GBEs. At present, we are studying this region of the protein in more detail to identify amino acids that are crucial for the fine-tuning of the activity of these enzymes.

**Conclusions.** Here, we report the first detailed characterization of the highly similar GH13 GBEs from *D. geothermalis* and *D. radiodurans*. The side chain distributions of their final products are unique and differ significantly from that of other GBEs described thus far in possessing a relatively large percentage of short chains. This exceptional branching pattern makes their products structurally unique. The physicochemical properties of such new, modified products remain to be determined, and they may have new food, cosmetics, and pharmaceutical applications.

Although both enzymes are highly similar (88% similarity and 81% identity), their specificities for amylose and amylopectin differ remarkably. Moreover, they display clear differences in their branching patterns. The variations observed apparently were not caused directly by differences in their catalytic domains (93% similar and 87% identical). Therefore, the influence of their noncatalytic domains was investigated. By constructing chimeric enzyme variants of the two *Deinococcus* GBEs, we demonstrated that the N domain (N2 module, recently annotated as a CBM48) is involved in substrate specificity and in determining the length of chains transferred by GBEs. Further research will focus on the influence of this putative carbohydrate binding domain on GBE enzyme activity.

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