Supporting Information

Characterization of the first α-(1→3) branching sucrases of GH70 family

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Table S1: Ratios and amounts of sucrose and dextran used to synthesize α-(1→3) branched dextrans

Ratio	5.6	3	1	0.5	0.25	0.1	0.05
Sucrose (g L^{-1})	170	150	100	50	25	10	5
Dextran (g L^{-1})	30	50	100	100	100	100	100

Table S2: Main sequence features of the putative branching sucrases

				BRS-A query			BRS-B query		
Enzyme	Organism	Size[a]	SP[b]	% id[c]	% si[d]	% QC[e]	% id	% si	% QC
BRS-C	*Ln. fallax* KCTC3537	1774 aa 197.1 kDa	Yes	49%	64%	99%	54%	69%	99%
BRS-D	*Lb. kunkei* EFB6	1463 aa 163.6 kDa	No	56%	70%	69%	50%	63%	69%

[a] The size is given in amino acids (aa) and in kDa
[b] SP : Signal peptide

[c] %id : percentage of identity
[d] %si : percentage of similarity
[e] QC : Query coverage

Table S3. Expression system (vector and expression host) used to produce recombinant branching sucrase (BRS-C and BRS-D) and their production level in *E. coli* cells

	Expression system		
	Vector	Host	Production level (U L^{-1} of culture)
BRS-C	pET-55-DEST	*E. coli* BL21 star DE3	2000
BRS-D	pET28b	*E. coli* BL21 star DE3	150

Table S4. Reaction on sucrose (292 mM) using BRS-C and BRS-D branching enzymes. Comparison of the production yields.

	Leucrose yield	Glucose yield	Small oligosaccharide yield
BRS-C	49%	44%	7%
BRS-D	6%	76%	18%

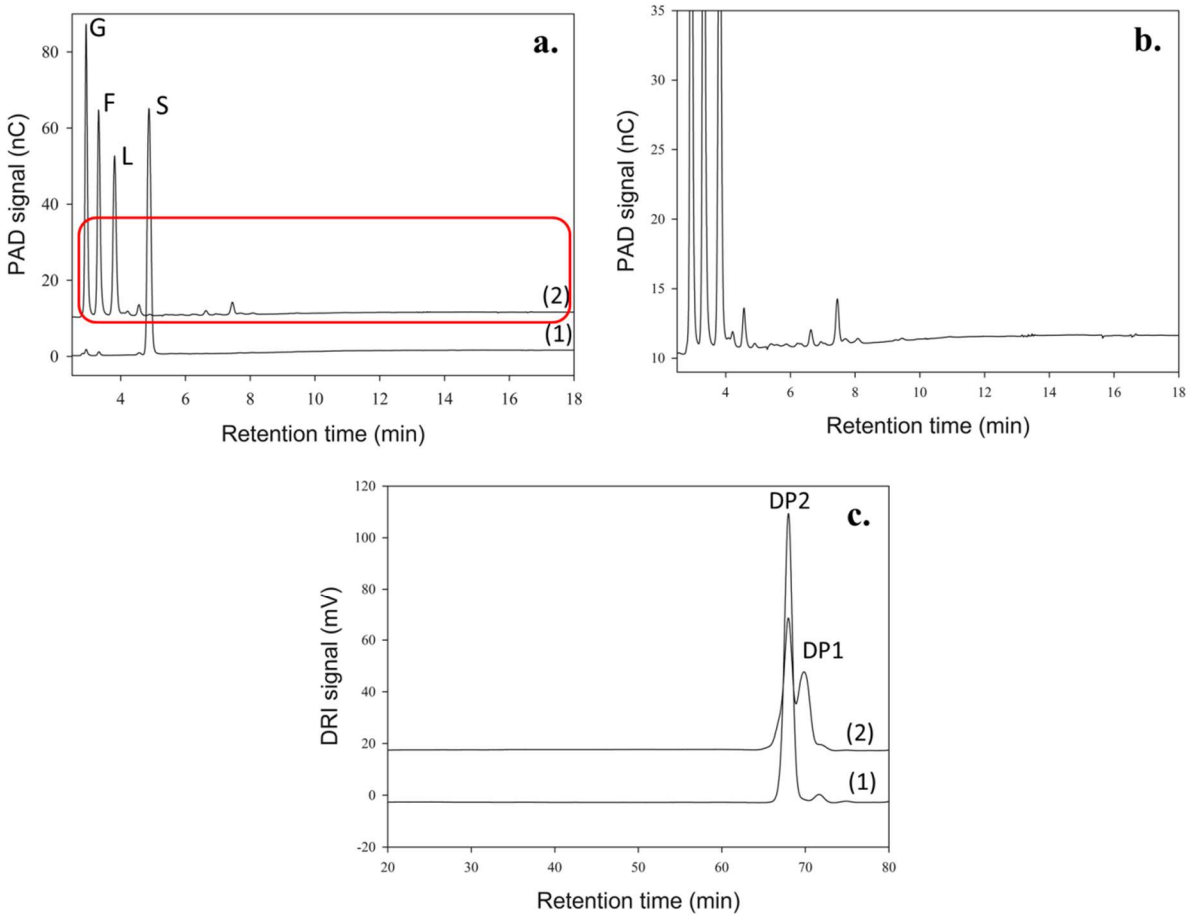

FIGURE S1. Analysis of the products synthesized using BRS-B enzyme from sucrose (292 mM). **(a)** HPAEC-PAD chromatograms of (1) Enzymatic reaction stopped after 1 minute and (2) Enzymatic reaction stopped after 8 hours. G indicates peak corresponding to glucose, F, fructose, L, leucrose and S, sucrose. **(b)** Enlargment of HPAEC-PAD chromatograms, corresponding to the red fram in the chromatogram (a). (c) HPSEC-RI profile of (1) Enzymatic reaction stopped after 1 minute and (2) Enzymatic reaction stopped after 8 hours. DP1 indicates peak corresponding to monosaccharides (glucose and fructose) and DP2 indicates peak corresponding to disaccharides (sucrose and leucrose).

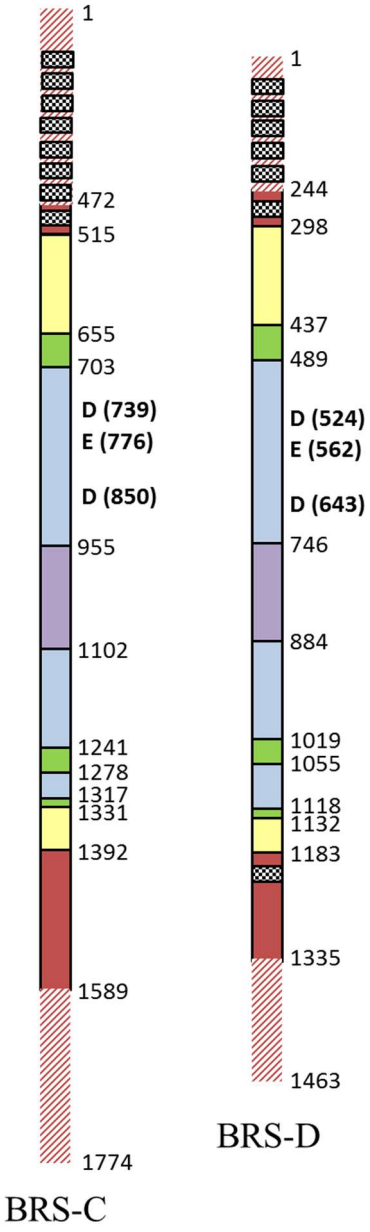

FIGURE S2. Schematic organization of the three putative branching sucrases (BRS-C and BRS-D) based on protein sequence alignment with GTF-180-ΔN. Domain V is represented in red, domain IV in yellow, domain B in green, domain A in blue and domain C in purple. Catalytic residues are highlighted in bold and YG repeats are indicated with chequered motifs. Hatched red lines represent zones where no 3D structure information is available for GTF-180-ΔN

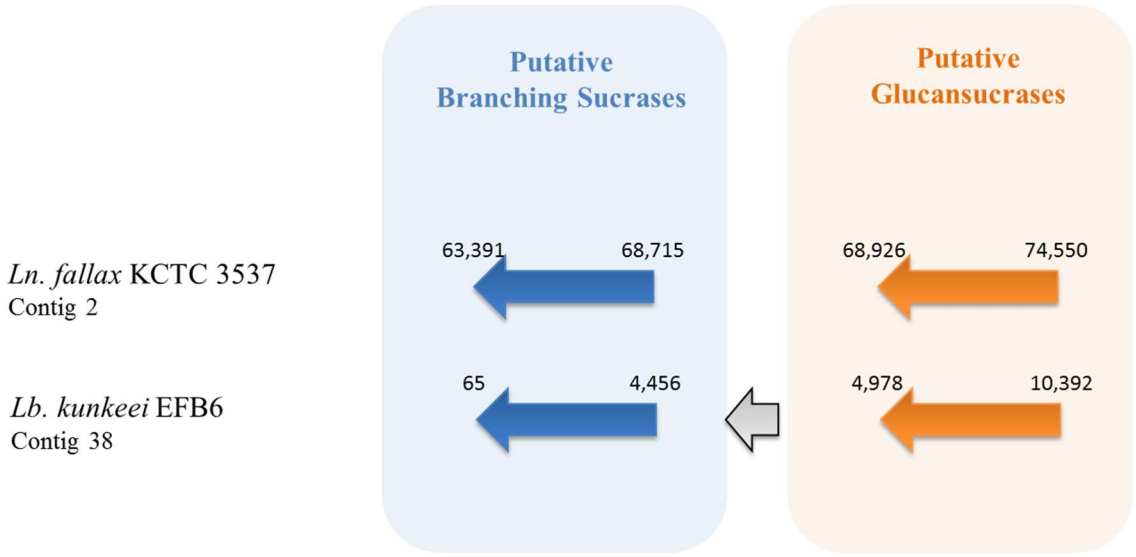

FIGURE S3. Representative tandem organization of the three putative branching sucrases (BRS-C and BRS-D) with other putative glucansucrases.