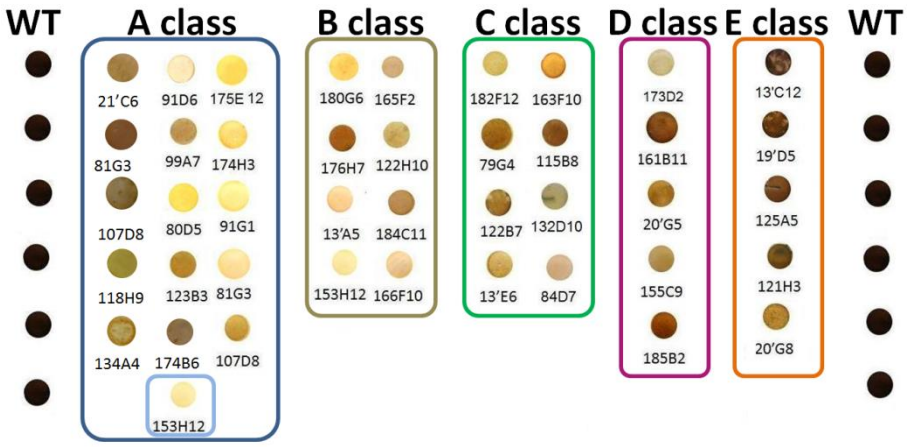
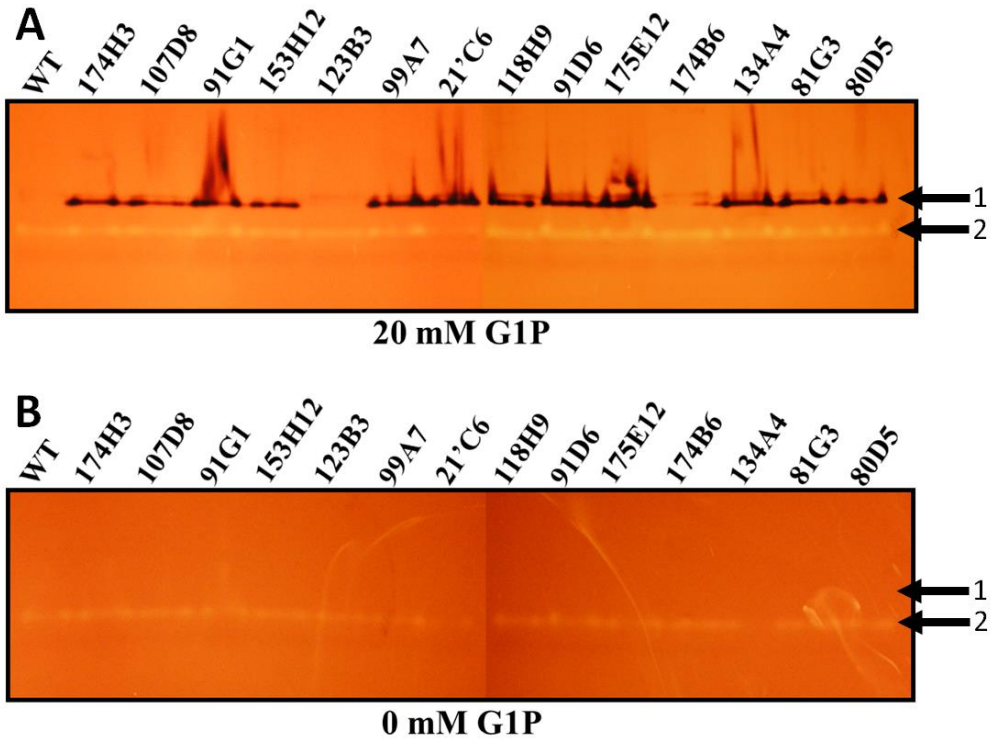
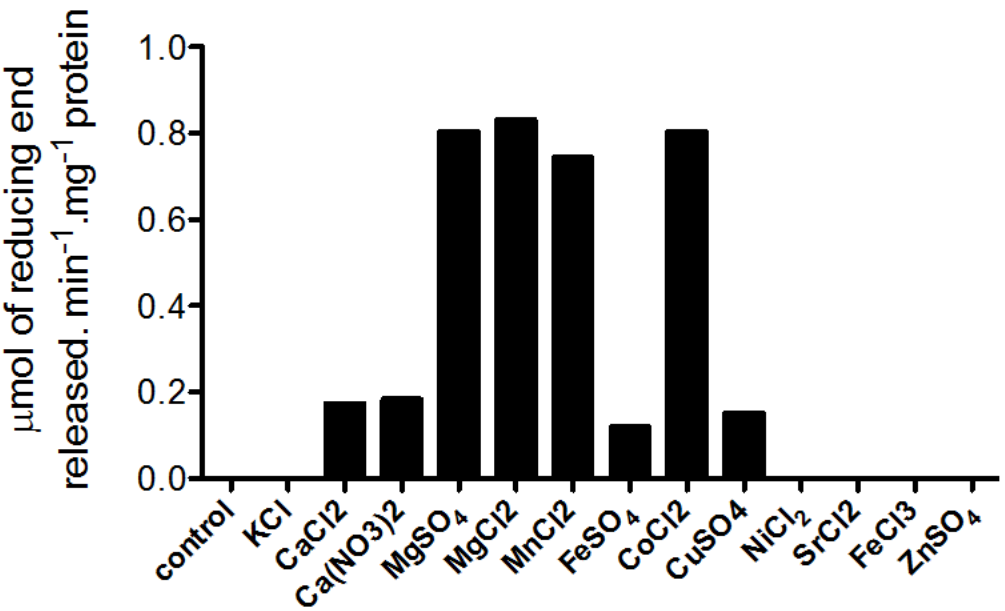


Supplemental figure 1: Cells patches of the five classes of mutant of *Cyanobacterium* sp. CLg1 stained with iodine vapors.

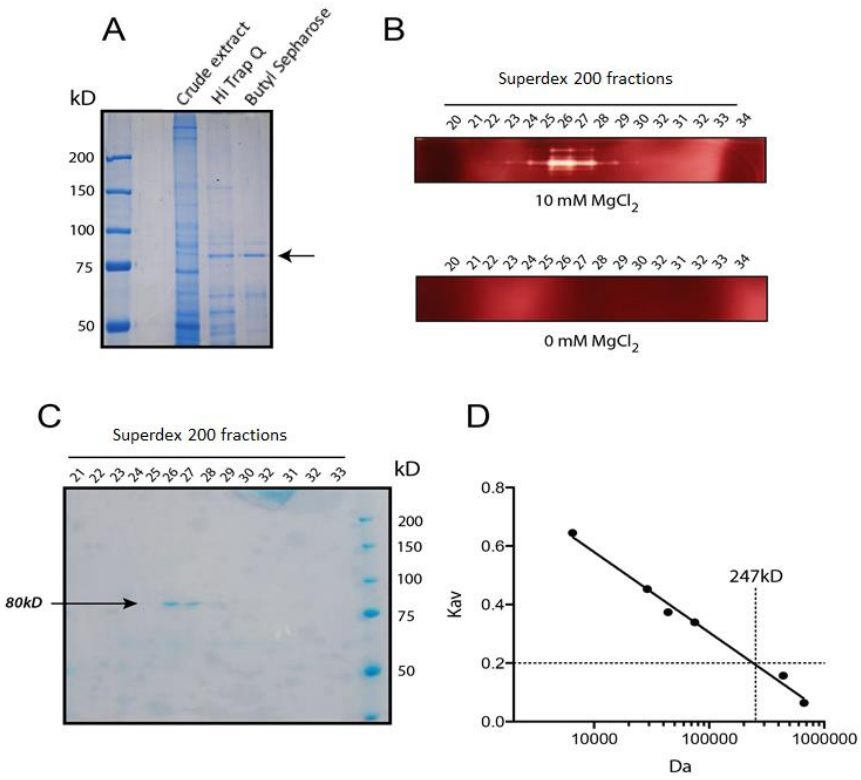
Mutants are grouped according to the percentage of residual water-soluble polysaccharides and starch-like granules measured in the mutant strains in comparison to the wild type strain (WT). Class A mutants (starch-like granule < 100% ; WSP >100 %). The mutant strain 153H12 harbors a yellow phenotype despite the presence of 10 % of starch-like granules (blue square). The intermediate phenotype class B mutants (starch-like granule < 100% ; WSP <100 %); class C (starch-like granule < 100% ; WSP = 100 %); class D mutants (starch-like granule = 100% ; WSP <100 %); Class E mutants (starch-like granule >100% ; WSP <100 %).



Supplemental figure 2: Zymogram of phosphorylase activity.
Zymogram analysis of phosphorylase activity from wild type and class A mutants. Total protein of WT and class A mutant strains were equilibrated and separated by native PAGE, followed by transfer of proteins to a native PAGE containing 0.6% (w/v) of glycogen. The native gels were then incubated with (A) or without (B) 20 mM Glucose-1-Phosphate (G-1-P). After overnight of incubation, gels are stained with iodine solution. Phosphorylase activity (arrow #1) is induced in all class A mutants, except for 174B6, 123B3 mutants and WT strain. A hydrolytic activity (arrow#2) is present in all crude extracts.



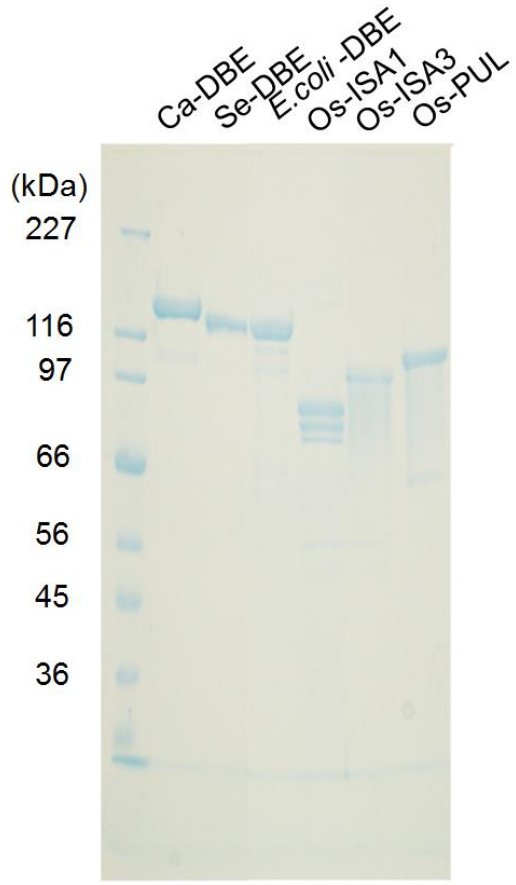
Supplemental figure 3: Effect of cations on the debranching enzyme activity.
Cation free debranching enzyme was incubated in absence (control) or in the presence of 5 mM of K^{+}, Ca^{2+}, Mg^{2+}, Mn^{2+}, Fe^{2+}, Co^{2+}, Cu^{2+}, Ni^{2+}, Sr^{2+}, Fe^{3+}, Zn^{2+} and 0,2% of amylopectin at 30°C during 30 minutes. Reactions were stopped by adding a volume of sodium 3,5-dinitrosalicylate (DNS) and boiled 10 minutes at 99°C. After cooling down, the absorbance is measured at 540 nm. The specific activity (µmol of reducing end.min^{-1}.mg^{-1} protein) was determined in presence of each cation.



Supplemental figure 4: Purification of cation dependent debranching enzyme activity. **A.** Cation dependent activity was purified at homogeneity using an anion exchange chromatography (HitrapQ), hydrophobic column (butyl sepharose) and gel permeation chromatography (superdex 200). The enrichment in GlgX2 protein is followed on SDS-PAGE after each purification step (black arrow). **B**. Debranching enzyme activity was monitored by using zymogram analysis performed in presence or in absence of 10 mM of $MgCl_2$ during the purification steps. **C.** SDS-PAGE analysis performed on superdex 200 fractions. A polypeptide of weight of 80 kD is visualized in fractions # 26 and #27 after Coomassie blue staining. **D.** Superdex 200 column (GE-Healthcare) pre-equilibrated with 150mM NaCl, tris/acetate buffer pH 7.5, 10 mM DTT was calibrated with standard proteins (669; 440; 75; 29 and 6.5 kD) and dextran blue. The determination of a partition coefficient (Kav) of 0.2 suggests an apparent molecular weight of the cation dependent activity estimated at 247 kD.

M L M G D E S M N P Q V W P G N P Y H L G A K W D G Q Q G T N F A L Y S E N A T T V E L C F F D R Q N Q E T R I P
L T E V Q N Y V W H A Y L P G I M P G Q R Y G Y R V D G V Y D P E E G H R F N V N K L L I D P Y A K A L D G E I G F
G E P I F G Y V W E D E D E D I S F S E L D S A H L V P K A V V V D E S F D W E G D K P L D I P E H E T I I Y E L H V K
G F T **K L H P D I P E D L R G** T F A G L A H P S T I V Y L K S L G I T A I E L M P I H H F L S Q P G H L V E K D L T N Y
W G Y D S I S Y L A P F S G Y C A T K T P Q D Q V K E F K A M V K A L H Q E G I E V I M D V V Y N H T G E G N H F G
P T L S L R G I D N A T Y Y R V V E E D P R **Y Y M D F T G C G N S L N** L K H P Q V M K L I M D S L R Y W V L E M H
V D G F R F D L A A A L A R E L L E V D C L A T F F D I I H Q D P V L S N I K L I A E P W D I G E D G Y H V G K F P V L
W S E W N G R Y R D T V R N F W R G E K **S I L A E F A Y R V T G** S S D L Y Q D N G R T P S A S I N F I T A H D G F T
L N D L V S Y N H K H N D A N G E E N K D G E Q F N H S W N C G E E G D S K D P E V L S L R N Q Q R R N F L V T L
M L S Q G V P M L T A G D E I G R T Q K G N N N A F C Q D N E I S W V D W S L E H K N A E L L K F V R D L I D L R
H Q H P V F R R R K W F Q G Q D I H G S G V S D I G W F N P D G F V T A E T Q W N L G F A K A I A L F L N G Q E I
P L K D Q Q G Q R V V D N S F L L F F N A H Y E A I E F V I P E S L G K Q D W I M V I D T T Q S R L L E S G K R Y R H
D V S I K V E A R S L V V L K T T N Stop

Supplemental figure 5: Identification of debranching enzyme activity.
Identification of a cation dependent activity by Nano-LC-MS-MS. NCBI blast search identifies seven trypsic peptides common in GlgX proteins (underlined peptides). In addition, three trypsic peptides match specifically with CLg1-GlgX2 (bold underlined peptides) and not with CLg1-GlgX1. These data suggest that the cation dependent activity is probably an homotrimeric or homodimeric complex of GlgX2 (see text).



Supplemental figure 6: SDS-PAGE of purified DBE preparations from rice, cyanobacteria and *E.coli.*

The Ca-DBE (DBE from *Cyanothece* ATCC51142), Se-DBE (DBE from *Synechococcus elongatus* PCC7942) and *E.coli* GlgX were expressed in the form of the trigger factor fusion protein, while OsISA3 (ISA3 from rice) was fused with the thioredoxin tag. The Os-ISA1 (ISA1 from rice) and Os-PUL (PUL from rice) were connected with the His tag. The actual molecular sizes of Os-ISA1, Os-ISA3, Os-PUL, Ca-DBE, Se-DBE and *E.coli* GlgX were calculated to be 84,136, 80,517, 99,166, 80,332, 78,956 and 66,953 Da, respectively. Since all the 3 OsISA1 protein bands were reacted with antibody raised against completely purified Os-ISA1 protein, these bands were considered to be derived from the Os-ISA1 protein, possibly by production from the multiple translation-starting positions. Each purified DBE preparation including about 1.0 μg of protein was loaded onto the SDS-PAGE gel. Molecular mass was indicated in the figure as kDa.

activity	gene	Strains				
		80D5	99A7	118H9	153H12	175 E12
Debranching enzymes	*glgX2*	-	-	-	-	-
	iDBE	-	-	-	-	-
	apu GH13	-	N.D.	-	-	-
	apu GH57	-	-	-	N.D.	-
Branching Enzymes	*glgB1*	-	N.D.	-	-	-
	glgB2	N.D.	-	-	-	-
	glgB3	-	-	-	-	-
	glgB GH57	N.D.	-	-	-	-
Starch synthases	*glgA1*	-	-	-	-	-
	glgA2	-	-	-	N.D.	-
	gbss	-	-	-	-	-
Phosphorylase	*pho*	N.D.	N.D.	-	N.D.	-
a-1,4 glucano transferase	*malQ*	-	-	-	-	-

Supplemental table 1: Summary table of starch metabolizing genes checked for mutations.

Molecular cloning and sequencing of genes involved in starch metabolism pathway in five class A mutants. Primers used sequenced the others gene coding branching enzyme, of the GH13 family (*glgB1*, and *glgB2*) and of the GH 57 family (*glgB57*), and the others gene coding debranching enzyme: the indirect debranching enzyme (*iDBE*) and the both amylopullanase of the GH 13 family (*apu13*) and the GH57 family (*apu57*). This table shows no others mutation in the different gene of the class A mutant.

Gene	Primer	5'-Sequence-3'	Temperature of hybridation
Amylopullulanase	apu13 Cloning For	GCATCCATATTAAAATGATCGCTAAGG	56.6°C
	apu13 Cloning Rev	TTCGTCCTTCGTCCCTCGTCCTT	
	apu13 Sequencing 1	GGTAATCGAGCTTTACCGAAAT	
	apu13 Sequencing 2	TCAAGATCTTCTCCTGCTACCGTTA	
	apu13 Sequencing 3	CAGCTAACCCAGTTAAATTTACTTGC	
	apu13 Sequencing 4	GATTGAATTTCGGTAAAGCTCGAT	
	Apu57 Cloning For	GGAGATCTTCTGCCCCTCTTTCA	58.6°C
	Apu57 Cloning Rev	AAAATAGCCAATAAACAGAAGCGA	
	Apu57 Sequencing 1	ACGAACTGCGAACCCAGAACTCC	
	Apu57 Sequencing 2	ACCCAATCCCCTGCCTTCGCAT	
	Apu57 Sequencing 3	GGCATATCAAAGGTACTCGTCATGG	
	Apu57 Sequencing 4	AGGTAAAGACAGGGGCTGTCAA	
Indirect debranching enzyme	idbe Cloning For	TCAATTATAAGTAGGGGTAGGAGA	55.9°C
	idbe Cloning Rev	ATGCTGAAAAAATCGTCCAAA	
	idbe Sequencing 1	CACAACTCTGATAACAGCCTCAA	
	idbe Sequencing 2	GTACACCTGACTCACCACCGTAA	
	idbe Sequencing 3	GATTGGCATATCAAAGGTACTCG	
	idbe Sequencing 4	ACCGCCTAGATAATGAGATTGGAT	
Branching enzyme	glgB3 Cloning Rev	TGACCATCCCATTTGGCTCCTA	61°C
	glgB3 Cloning For	AGTGAATAGCCAAAAATCAACGAT	
	glgB3 Sequencing 1	GTGGTTTAGGCAACTACGACGGTACA	
	glgB3 Sequencing 2	CGTTACGTATCATGGAACTAATTT	
	glgB3 Sequencing 3	CCAGGTGCGCCGATGATTTT	
	glgB3 Sequencing 4	TCGCCCCTGAATGATGATATAAAT	
	glgB2 Cloning For	TGCGAAAAGATGTCTTGCTATGCT	60°C
	glgB2 Cloning Rev	TCCACTCAGTCAAGTGTGAATCAA	
	glgB2 Sequencing 1	TTTTGACGGCTCATGGGGTTA	
	glgB2 Sequencing 2	ATTGTGATAGTTCGGGCGCTCAT	
	glgB2 Sequencing 3	AGCGCCCGAACTATCACAAT	
	glgB2 Sequencing 4	ACCATAGCGGGAAGTTGGTG	
	glgB1 Cloning For	TGAAACAGTCAGACAAGTTTTCCGT	60.4°C
	glgB1 Cloning Rev	TCCCGAACTGAGGTTAAGTATTGA	
	glgB1 Sequencing 1	CACCTCGGTTCTTGGCTACA	
	glgB1 Sequencing 2	TGCATCCAGCCCATATTCCA	
	glgB1 Sequencing 3	TCGCAGAAGAATCAACCGCTTGGT	
	glgB1 Sequencing 4	TGTAGCCAAGAACCGAGGTGT	
	glgB57 Cloning For	CGCCATTAGACTCTGCTAGG	59°C
	glgB57 Cloning Rev	TGGAGTTGTGGTTTCTTCTGTCA	
	glgB57 Sequencing 1	TGCGGTTATTACGGTGGCTT	
	glgB57 Sequencing 2	TAGCTAAACCCGCAGCATCG	
	glgB57 Sequencing 3	AACCAAATCCCTCTGGGAGCAA	
	glgB57 Sequencing 4	GAGCTTGCTTGTCGGCTAGT	
Debranching enzyme	glgX2 Cloning For	ATGTTAATGGGAGATGAATCTATGA	59.6°C
	glgX2 Cloning Rev	TAATTAGTGGTTTTTAGTACTACTAACG	
	glgX2 Sequencing 1	AGCAGTGGTAGTCGACGAATCT	
	glgX2 Sequencing 2	ACGTCGTTGCTGATTGCGTA	
	glgX2 Sequencing 3	GTAACTTCTGGCGTGGCGAAA	
	glgX2 Sequencing 4	AAGCCGGCAAATGTTCCTCGTA	

	glgX1 Cloning For	ATGAACCATAAAACGTTACCTG	59.1°C
	glgX1 Cloning Rev	CTATTTTGCCATTAATAAAATGCAAC	
	glgX1 Sequencing 1	TCGGATTCCTCTTGCTTCAACCGT	
	glgX1 Sequencing 2	TCATCGGTGTAGCTTGAGCGAGT	
	glgX1 Sequencing 3	CCACGATGGGGTGCAAAGAAACT	
	glgX1 Sequencing 4	ATGAAGCTAATGGTGAAGAGAACCGA	
Starch synthase	GBSS Cloning For	TCCTCATGAATTGGTGACATAGTATGTT	59.6°C
	GBSS Cloning Rev	CAGATACAGGTGAAAATCGTAACGC	
	GBSS Sequencing 1	AAAACGCCCCTGGAAAGCAATA	
	GBSS Sequencing 2	GCAATAGTCAGCACCAGCCGTGATA	
	GBSS Sequencing 3	TTTATCACGGCTGGTGCTGACT	
	GBSS Sequencing 4	ATGTTAAACATTTGCTTTGTCTCTACGGAA	
	glgA1 Cloning For	AATTGTTAACAAAGTGGGGAGAGAAA	60°C
	glgA1 Cloning Rev	GATAACGATCGTGATAACTTTTAAGGTA	
	glgA1 Sequencing 1	GCTCTGCAACATATGACTTGGTGTCCTGA	
	glgA1 Sequencing 2	CCATAATAACGAGCCGCAAATTCTGCTA	
	glgA2 Cloning For	AAGTGAATCAACTGAATGAAAACGA	59.8°C
	glgA2 Cloning Rev	CGGGTATCTGTAATCTAGAACTCCTCA	
	glgA2 Sequencing 1	ATGATTGGCAAACTGGATTGATCCCTGTA	
	glgA2 Sequencing 2	ACCACCAACACGAACTACAGGTACT	
	glgA2 Sequencing 3	TTAAACGGAATTGATTACAATACTTGGGA	
	glgA2 Sequencing 4	GATTGGAATAGACAATACCACCTTTCA	
Phosphorylase	Phosphorylase Cloning For	GCTTACTAAGACGAAATTGATTATGAGCGAT	62°C
	Phosphorylase Cloning Rev	TTCACCGTAACGCTATCAGCCGTAAT	
	Phosphorylase Sequencing 1	TTAGGTAACGGTGGTTTGGGAA	
	Phosphorylase Sequencing 2	CCAAAGATAAAGGTGCGGGGATA	
	Phosphorylase Sequencing 3	CTTCTTCTTAGAAGATATTCGTTCATGGTA	
	Phosphorylase Sequencing 4	GAGTTTGTTGTGTAATCGACCACGCTT	
	Phosphorylase Sequencing 5	AACTCTTGACGGTGCCAATATTGA	
	Phosphorylase Sequencing 6	CTAAACCTGGATCTGGCTCTTCTT	
MalQ	MalQ Cloning For	CGCAGGTCCTGTGATTGTCT	62°C
	MalQ Cloning Rev	CCATCTACCGGTAACGCTGTAA	
	MalQ Sequencing 1	CTTCAGCGACAATCGGCAACT	
	MalQ Sequencing 2	CCACGATCGGTTGGTTTGATA	
	MalQ Sequencing 3	TGGTTGGATGACTACGCTCTGT	
	MalQ Sequencing 4	TGCAAATACCCCTTTGATGCT	

Supplemental table 2: List of primers used for genes cloning and sequencing of genes involved in the storage polysaccharide metabolism of *Cyanobacterium* sp. CLg1.

Supplemental methods 1: Parameter values for phylogenetic analysis

Determination of Best fit model according to ProtTest 3.2 for the alignment, of GlgX of bacteria and Archaeplastida isoamylase.

This determination was performed with:

- "-all-distribution" parameters including models with rate variation among sites, number of categories and both.
- "-F" parameters including models with empirical frequency estimation.
- "-AIC" parameters displaying model sorted by the Akaike Information Criterion.
- "-S 2" parameters using the optimizing strategy developed for Maximum Likelihood analysis.

Results:

```
*******************************************************
        AKAIKE INFORMATION CRITERION
*******************************************************

*************************************************************************
Best model according to AIC: LG+G
Confidence Interval: 100.0
*************************************************************************
Model         deltaAIC      AIC          AICw         -lnL
-------------------------------------------------------------------------
LG+G          0.00          170602.28    0.70         85051.14
LG+I+G        1.68          170603.96    0.30         85050.98
LG+G+F        173.72        170776.00    0.00         85119.00
LG+I+G+F      174.89        170777.18    0.00         85118.59
WAG+G         663.83        171266.12    0.00         85383.06
WAG+I+G       665.67        171267.96    0.00         85382.98
RtREV+I+G+F   848.35        171450.63    0.00         85455.32
RtREV+G+F     850.47        171452.76    0.00         85457.38
WAG+G+F       890.11        171492.39    0.00         85477.20
WAG+I+G+F     891.55        171493.84    0.00         85476.92
VT+G          988.07        171590.36    0.00         85545.18
VT+I+G        988.83        171591.11    0.00         85544.56
VT+G+F        1251.84       171854.12    0.00         85658.06
VT+I+G+F      1252.15       171854.43    0.00         85657.22
Blosum62+G    1582.98       172185.27    0.00         85842.63
Blosum62+I+G  1583.76       172186.05    0.00         85842.02
RtREV+I+G     1707.47       172309.75    0.00         85903.87
RtREV+G       1709.75       172312.03    0.00         85906.02
Blosum62+I+G+F 1846.25      172448.53    0.00         85954.27
Blosum62+G+F  1846.52       172448.80    0.00         85955.40
CpREV+G+F     1940.10       172542.38    0.00         86002.19
CpREV+I+G+F   1942.06       172544.34    0.00         86002.17
CpREV+G       2034.40       172636.69    0.00         86068.34
CpREV+I+G     2036.41       172638.70    0.00         86068.35
JTT+G         2129.92       172732.20    0.00         86116.10
JTT+I+G       2131.09       172733.37    0.00         86115.69
JTT+G+F       2571.15       173173.43    0.00         86317.71
JTT+I+G+F     2572.57       173174.85    0.00         86317.43
```

DCMut+G	3449.82	174052.10	0.00	86776.05
Dayhoff+G	3451.65	174053.93	0.00	86776.97
DCMut+I+G	3451.76	174054.04	0.00	86776.02
Dayhoff+I+G	3453.60	174055.89	0.00	86776.94
DCMut+G+F	3638.15	174240.43	0.00	86851.22
Dayhoff+G+F	3638.78	174241.06	0.00	86851.53
DCMut+I+G+F	3640.09	174242.37	0.00	86851.19
Dayhoff+I+G+F	3640.74	174243.02	0.00	86851.51
MtREV+G+F	4338.60	174940.89	0.00	87201.44
MtREV+I+G+F	4340.54	174942.82	0.00	87201.41
FLU+I+G+F	5672.13	176274.42	0.00	87867.21
FLU+G+F	5672.83	176275.11	0.00	87868.55
MtArt+I+G+F	6601.29	177203.57	0.00	88331.78
MtArt+G+F	6605.84	177208.13	0.00	88335.06
FLU+G	6723.16	177325.45	0.00	88412.72
FLU+I+G	6724.20	177326.48	0.00	88412.24
HIVb+I+G	7423.14	178025.43	0.00	88761.71
HIVb+G	7428.28	178030.56	0.00	88765.28
HIVb+I+G+F	7671.82	178274.10	0.00	88867.05
HIVb+G+F	7675.66	178277.94	0.00	88869.97
MtMam+G+F	9375.19	179977.47	0.00	89719.74
MtMam+I+G+F	9377.24	179979.53	0.00	89719.76
VT+I	9499.48	180101.77	0.00	89800.88
WAG+I	9505.33	180107.61	0.00	89803.80
WAG	9619.70	180221.99	0.00	89861.99
VT	9637.06	180239.35	0.00	89870.67
MtREV+G	9651.66	180253.95	0.00	89876.97
MtREV+I+G	9652.93	180255.22	0.00	89876.61
LG+I	9707.67	180309.95	0.00	89904.97
VT+I+F	9732.05	180334.33	0.00	89898.16
WAG+I+F	9774.08	180376.37	0.00	89919.18
LG	9840.27	180442.55	0.00	89972.28
VT+F	9873.45	180475.73	0.00	89969.87
WAG+F	9892.92	180495.20	0.00	89979.60
LG+I+F	9987.22	180589.51	0.00	90025.75
Blosum62+I	10021.91	180624.20	0.00	90062.10
LG+F	10127.76	180730.04	0.00	90097.02
Blosum62	10152.81	180755.10	0.00	90128.55
Blosum62+I+F	10218.61	180820.90	0.00	90141.45
Blosum62+F	10356.99	180959.28	0.00	90211.64
RtREV+I+F	10470.84	181073.12	0.00	90267.56
RtREV+F	10606.43	181208.71	0.00	90336.36
RtREV+I	11092.73	181695.01	0.00	90597.50
RtREV	11208.58	181810.87	0.00	90656.43
CpREV+I+F	11320.79	181923.08	0.00	90692.54
CpREV+I	11340.27	181942.56	0.00	90721.28
CpREV+F	11426.95	182029.24	0.00	90746.62
CpREV	11437.57	182039.85	0.00	90770.93
JTT+I	11559.32	182161.61	0.00	90830.80
JTT	11706.03	182308.32	0.00	90905.16

JTT+I+F	12008.62	182610.91	0.00	91036.45
MtArt+I+G	12126.46	182728.74	0.00	91113.37
MtArt+G	12129.83	182732.12	0.00	91116.06
JTT+F	12159.34	182761.63	0.00	91112.81
DCMut+I	13201.66	183803.94	0.00	91651.97
Dayhoff+I	13224.06	183826.34	0.00	91663.17
DCMut	13337.48	183939.77	0.00	91720.88
Dayhoff	13359.50	183961.78	0.00	91731.89
DCMut+I+F	13560.91	184163.20	0.00	91812.60
Dayhoff+I+F	13583.06	184185.34	0.00	91823.67
DCMut+F	13700.54	184302.82	0.00	91883.41
Dayhoff+F	13722.27	184324.56	0.00	91894.28
HIVw+I+G+F	13850.90	184453.19	0.00	91956.59
HIVw+G+F	13857.70	184459.99	0.00	91960.99
MtMam+G	14665.21	185267.49	0.00	92383.75
MtMam+I+G	14666.65	185268.93	0.00	92383.46
MtREV+I+F	15727.32	186329.60	0.00	92895.80
MtREV+F	15807.24	186409.52	0.00	92936.76
FLU+I+F	16465.01	187067.30	0.00	93264.65
HIVw+I+G	16496.88	187099.16	0.00	93298.58
HIVw+G	16498.39	187100.67	0.00	93300.34
FLU+F	16619.53	187221.81	0.00	93342.91
FLU+I	17571.87	188174.16	0.00	93837.08
FLU	17712.25	188314.53	0.00	93908.27
HIVb+I	19181.53	189783.81	0.00	94641.91
HIVb	19375.83	189978.12	0.00	94740.06
HIVb+I+F	19810.57	190412.86	0.00	94937.43
HIVb+F	20004.11	190606.39	0.00	95035.20
MtArt+I+F	21099.55	191701.83	0.00	95581.91
MtArt+F	21245.59	191847.87	0.00	95655.94
MtREV+I	22657.05	193259.33	0.00	96379.67
MtREV	22738.64	193340.93	0.00	96421.46
MtMam+I+F	24440.36	195042.65	0.00	97252.32
MtMam+F	24528.71	195131.00	0.00	97297.50
HIVw+I+F	25476.13	196078.41	0.00	97770.21
HIVw+F	25690.42	196292.71	0.00	97878.35
HIVw+I	27881.13	198483.42	0.00	98991.71
HIVw	28055.00	198657.29	0.00	99079.64
MtArt+I	30144.63	200746.91	0.00	100123.46
MtArt	30307.92	200910.21	0.00	100206.10
MtMam+I	33032.04	203634.32	0.00	101567.16
MtMam	33117.07	203719.35	0.00	101610.68

****

Relative importance of parameters

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alpha (+G): 0.698

p-inv (+I): 0.000

alpha+p-inv (+I+G): 0.302

freqs (+F): 0.000

****
Model-averaged estimate of parameters
****
alpha (+G): 0.974
p-inv (+I): NaN
alpha (+I+G): 0.980
p-inv (+I+G): 0.001

Determination of the Maximum Likelihood (ML) tree
In order to determine the ML tree, RAxML was performed as follow:

- "-N 1000" parameter indicating 1000 bootstrap repeat
- "-m PROTGAMMALG" : the substitution model performed was LG+G
- "-p 123456" indicating 6 parsimony Random Seed
- "-x 123456" indicating 6 rapid Bootstrap Random Seed
- "-f a" indicating that RAxML was instructed to conduct a rapid Bootstrap analysis and look for the best-scoring ML tree in one single program run.

The tree obtained was rooted on the branch uniting the Archaeplastida sequences. This was done to reflect our current understanding that supports Archaeplastida monophyly.