

**Table S1.** Effect of supplemented compounds used in different solutions on cryopreservation results of *Le. gibba* 7742 after rewarming.

	Tested substances	Pre-cultivation	Cryoprotection (PVS3)	Washing	Re-growth	Effect on bleaching delay after rewarming
1	1 mM ATP	-	-	-	+	No delay, getting brown during 1-2 days
2	0.1 g/l casein hydrolysate	+	+	+	+	No delay, getting brown during 2-3 days
3	0.5 g/l glutamine, 0.5 g/l cysteine, 0.5 g/l proline	-	-	-	+	No delay, getting brown during 2-3 days
4	0.5 g/l PVP10000	-	-	+	+	Up to 17-20 days (in combination with attenuated illumination regime and working on ice in protected against light condition)
5	1 mM dithiothreitol	-	+	+	+	Up to 30 days (in combination with attenuated illumination regime and working on ice in protected against light condition)
6	3 mM Na <sub>2</sub> S <sub>2</sub> O <sub>3</sub>	-	+	+	+	No delay
7	30 µM Ag <sub>2</sub> S <sub>2</sub> O <sub>3</sub>	-	-	+	+	No delay
8	10 mM glutathione	-	-	+	+	No delay, getting brown during 2-3 days
9	0.4 mg/l gibberellic acid	-	-	-	+	No delay
10	1 mg/l 6-benzylaminopurine + 0.3 mg/l indole-3-acetic acid + 0.4 mg/l gibberellic acid	-	-	-	+	No delay
11	1 mg/l 6-benzylaminopurine + 0.3 mg/l indole-3-acetic acid + 0.4 mg/l gibberellic acid + 30 µM Ag <sub>2</sub> S <sub>2</sub> O <sub>3</sub>	-	-	-	+	No delay

**Table S2.** Regrowth of *Le. gibba* 7742 depends on pre-culture condition.

	Medium	Condition	Number of regrowth events after cryo, per cryo-tube (25-50 fronds in cryo-tube)
1	SH, 5 g/l (15 mM) sucrose	Standard growth condition: in climate chamber (12/12h light/dark cycle, PPFD 60 µmol·m <sup>-2</sup> ·s <sup>-1</sup> , 25°C/22°C for the light/dark periods)	0 - 1
2	SH, 5 g/l (15 mM) sucrose	Cold: in fridge (4°C, darkness)	0
3	SH, 5 g/l (15 mM) sucrose	Imitation of night frost: in climate chamber (16/8h light/dark cycle, PPFD 60 µmol·m <sup>-2</sup> ·s <sup>-1</sup> , 25°C/-1°C for the light/dark periods)	0 - 1
4	SH, 0.4 M sucrose	Standard growth condition: in climate chamber (12/12h light/dark cycle, PPFD 60 µmol·m <sup>-2</sup> ·s <sup>-1</sup> , 25°C/22°C for the light/dark periods)	2 - 4
5	SH, 0.4 M sucrose	Cold: in fridge (4°C, darkness)	0 0
6	SH, 0.4 M sucrose	Imitation of night frost: in climate chamber (16/8h light/dark cycle, PPFD 60 µmol·m <sup>-2</sup> ·s <sup>-1</sup> , 25°C/-1°C for the light/dark periods)	0 - 1

SH – nutrient medium Schenk and Hildebrand, PPFD - the photosynthetic photon flux density.

**Table S3.** Parameters of chlorophyll fluorescence and photosynthesis performance for intact *Le. gibbba* 7742 culture.

Parameter	F <sub>0</sub>	F <sub>m</sub>	F <sub>v</sub>	F <sub>v</sub> /F <sub>m</sub>	Φ <sub>PSII</sub>
Value	92.7±15.8	441.5±86.2	348.9±71.4	0.8±0.05	0.7±0.05

**Table S4.** Distribution of potential regulatory DNA cis-elements in promoter region of *CBF* genes in *A. thaliana* and duckweed.

cis-element	<i>AtCBF1</i>	<i>AtCBF2</i>	<i>AtCBF3</i>	<i>LgCBF1</i>	<i>LgCBF2</i>	<i>LgCBF3</i>	<i>LpCBF1</i>	<i>LpCBF2</i>	<i>SpCBF1</i>	<i>SpCBF2</i>
G-box	2	1	2	3	1	2	1	5	2	2
E-box	6	5	10	6	9	18	8	11	10	11
EE, evening element*	2	3	3	0	0	0	0	0	0	0
CGCG-box, CAMTA binding site**	1	2	3	7	4	5	12	4	4	4
CBS, CCA1 binding site*	7	6	7	3	5	4	1	3	1	2
MYB*	6	5	7	1	2	0	3	4	2	9
BRRE, brassinosteroid response element	3	0	0	0	0	1	7	5	9	1
TIME, TOC1 morning element*	21	13	24	4	7	14	11	16	9	7
ABRE, abscisic acid responsiveness	4	2	7	4	4	6	6	5	15	6
MeJA-responsiveness**	3	0	2	5	3	4	11	3	10	4
ERE, Ethylene-responsive element**	1	0	1	4	1	3	1	0	0	0
MYC, Water stress and dehydration responsiveness	1	3	7	2	2	10	1	1	0	3
TCA-element, salicylic acid responsiveness*	1	2	1	0	1	0	2	2	1	0
TGA-element, auxin-responsive element	0	1	1	1	0	1	1	1	0	2

Reduced (\*) and increased (\*\*) number of *cis*-elements compared to *Arabidopsis* are marked in blue and red, respectively.

**Table S5.** List of RT-qPCR primers used for evaluating expression of the *CBF* genes in *Le. gibba*, *La. punctata* and *Sp. polyrhiza*.

Gene	Forward primer	Reverse primer	PCR product, length in bp
<i>LgCBF1</i>	CTCTCCGCCTCATCACGTC	GCAAGGATATGCCGCGTC	137
<i>LgCBF2</i>	TCCGTCTGAACTAAGAGGCG	ACACATAGTAGCTCCCAACGG	100
<i>LgCBF3</i>	CGATAGTGGAGAGGTGCCA	CAGCCATGCCGTTGTATTGA	102
<i>LgHistone3</i>	CCGCAAGTACCAGAAGAGCA	AGGTATGCTTCGGCTGCTTC	147
<i>LgActin</i>	TGAGCATGGAATCGTCAGCA	GCCTTCGGATTCAGAGGAGC	129
<i>LpCBF1</i>	TCCAAGGAACTCTCGGCCAT	GTGGCGTAAGTCTCCTCGTC	119
<i>LpCBF2</i>	TTGGGACTACTGGAGAGCGT	GGGACACGTCAGACTCTGTG	103
<i>LpHistone3</i>	CCCTCCGTGAAATTCGCAAG	GGCTCTGGAACCTCAGATCG	147
<i>SpCBF1</i>	ACCTGGCCAACATGAGGATG	CGCCACGTCAGATGGAGTAG	132
<i>SpCBF2</i>	GAGAGCTCGAGGATGCCTTC	CAGAGGGACACGTCGGATTC	107
<i>SpHistone3</i>	CGCAAGTACCAGAAGAGCAC	CGAAGAGACCCACGAGGTAG	160
<i>SpActin</i>	TGTTTTCCCAAGTATCGTC	TCCCAGTTGGTGACGATT	153