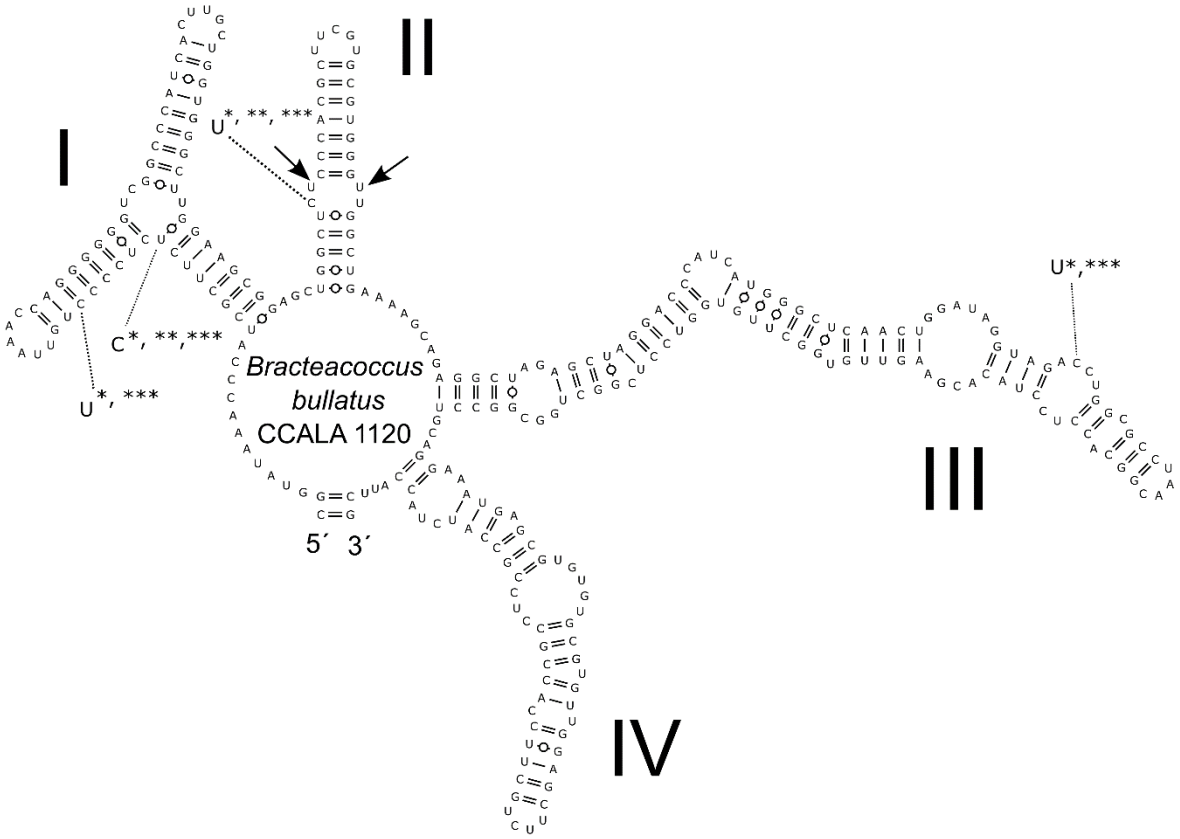
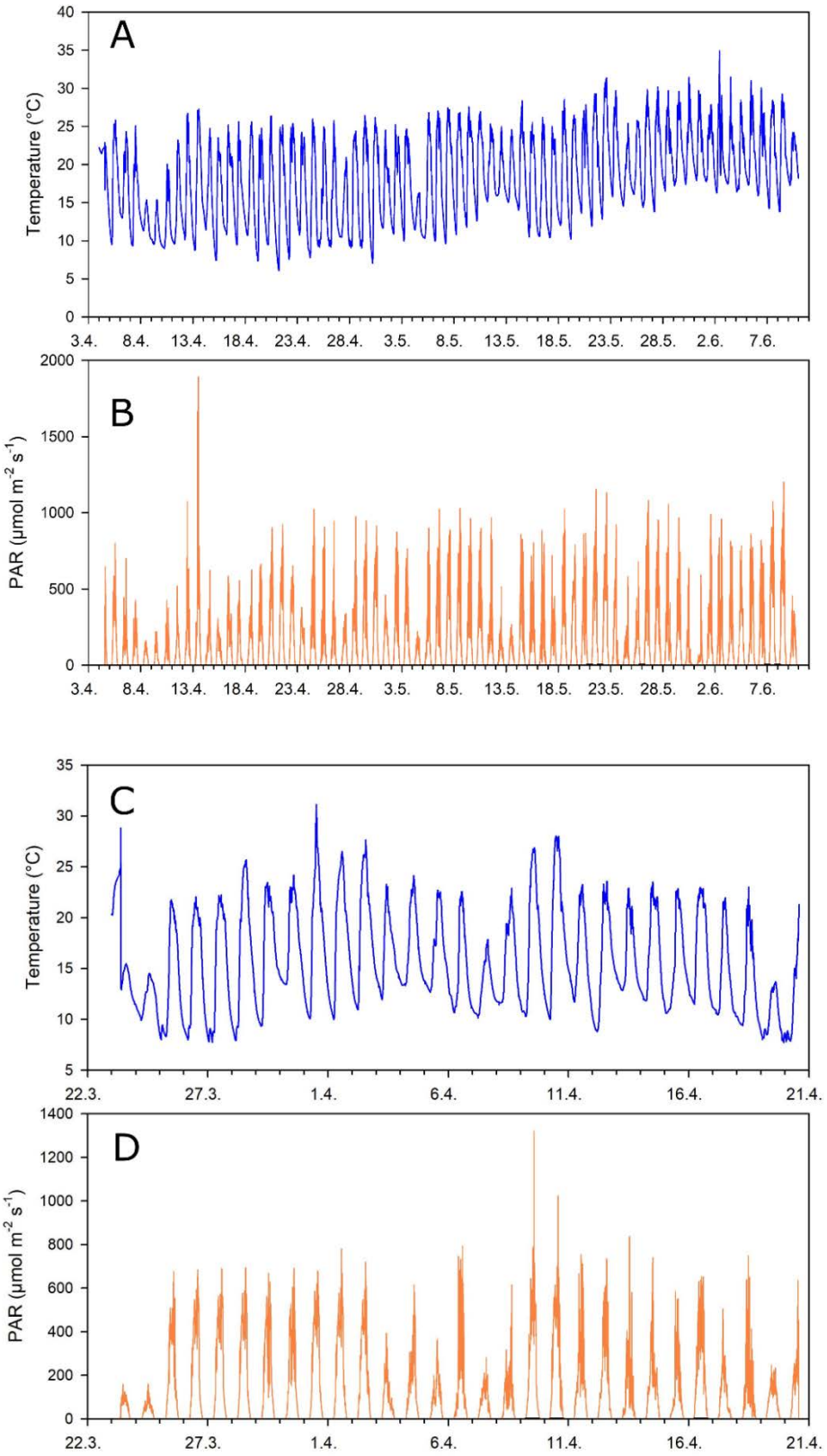
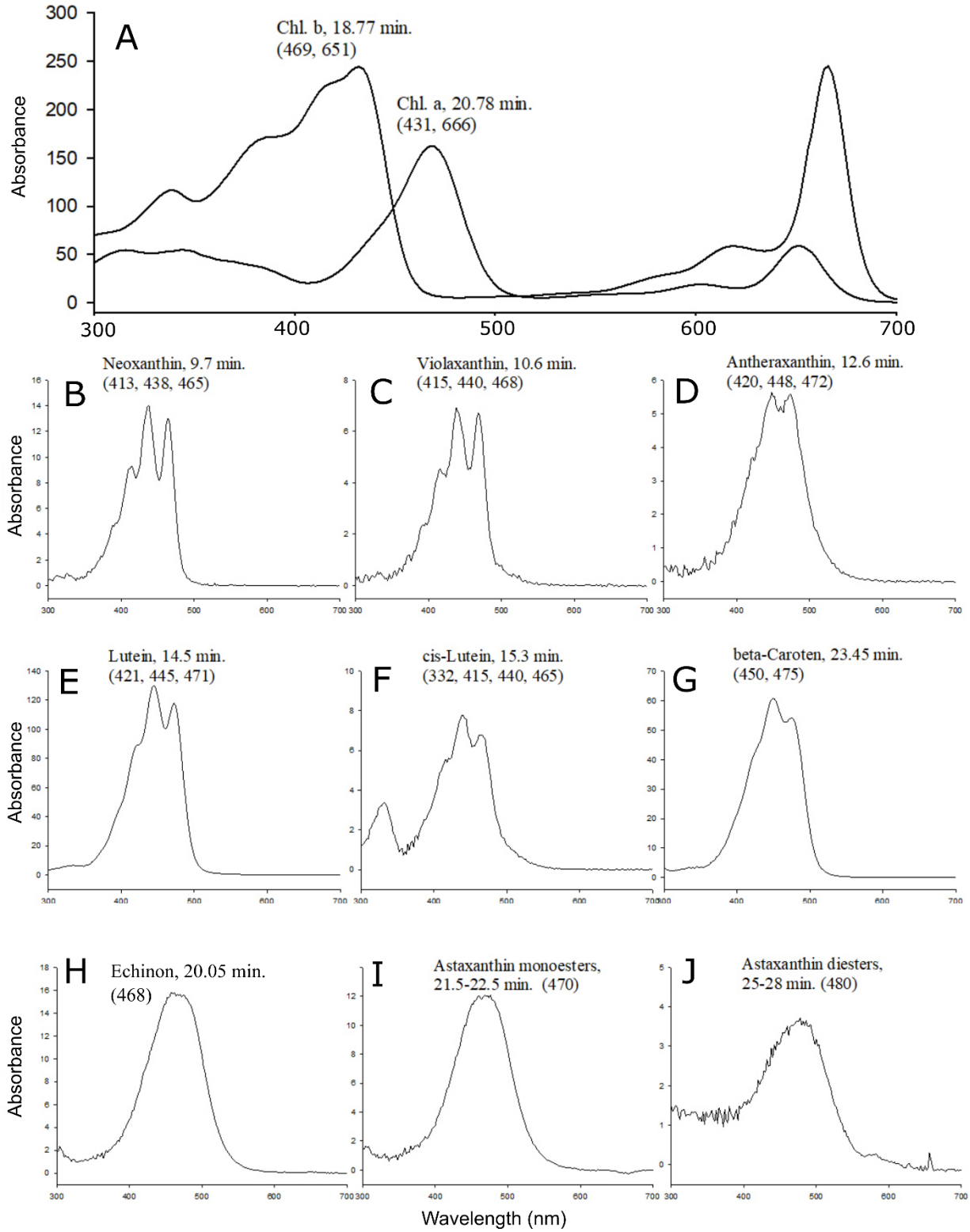
Supplementary Figure S1. Pilot-plant cultivation unit (a platform in a greenhouse) with *Bracteacoccus bullatus* CCALA 1120, area 12 m^2, volume 150 L, height of the suspension layer is about 10 mm.



Supplementary Figure S2. Comparison of the secondary structure of ITS2 rDNA transcripts between *Bracteococcus bullatus* CCALA 1120 (MT856650), *B. bullatus* type strain SAG 2032 (JQ281848), *B. bullatus* KF10 (JQ281851.1) and *B. bullatus* strain MZ-Ch11 (KY066480). Helices are labelled with Latin numbers. Nucleotide differences are outside the structure and linked by dotted lines. One asterisk means that the difference was detected in the type strain, two asterisks indicates a change in the KF10 strain, and three asterisks implies a change in the MZ-Ch11 strain. No compensatory base changes between the CCALA strain and all the other strains, including the type strain, were found. Note the U–U mismatch in helix II (arrows).



Supplementary Figure S3. Time course of **(A, C)** the temperature of the culture medium, **(B, D)** the PAR intensity in outdoor cultivation (greenhouse) on a platform. **(A, B)** The first cultivation April 4 – June 9 2016. **(C, D)** The second cultivation, March 23 – May 1 2017. A statistical summary of the data is included in Supplementary Table S2.



Supplementary Figure S4. Pigment spectra of *Bracteacoccus bullatus* CCALA 1120. **(A)** Chlorophyll a and b spectra. **(B-D)** Primary carotenoid pigments spectra. **(E-I)** Secondary carotenoid pigments spectra (astaxanthin monoester and diesters are marked as ATXme and ATXde, respectively, in the chromatogram shown in **Figure 7**).

Supplementary Table S1. List of primers used for amplification and sequencing of 18S rDNA (18S), ITS1 rDNA (ITS1), ITS2 rDNA (IT2S), and *rbc*L markers (F, forward; R, reverse). Coordinate numbers in relation to (1) *Chlorella vulgaris* 18S rDNA (accession number: X13688.1; Huss & Sogin (1990), (2) *Oryza sativa* 25S ribosomal RNA gene (accession number: M11585.1; Takaiwa et al. 1987) and (3) *Chlamydomonas reinhardtii rbc*L gene (accession number: J01399; Dron et al. 1982).

Primer	Marker	Direction	Sequence (5´-3´)	Position	Reference
NS1	18S	F	GTAGTCATATGCTTGTCT	20-37[1]	White et al. (1990)
18L	18S	R	CACCTACGGAAACCTTGTTACGACTT	1780-1750[1]	Hamby et al. (1988)
FA	18S	F	AACCTGGTTGATCCTGCCAGT	1-21[1]	Matsuzaki et al. (2015)
RD	18S	R	GCTGGCACCAGACTTGCCCTC	570-550[1]	Matsuzaki et al. (2015)
ITS1	ITS2	F	TCCGTAGGTGAACCTGCGG	1771-1787[1]	White et al. (1990)
ITS4	ITS2	R	TCCTCCGCTTATTGATATGC	60-41[2]	White et al. (1990)
AL1500af	ITS1, ITS2	F	GCGCGCTACACTGATGC	1464-1480[1]	Helms et al. (2001)
LR3	ITS1, ITS2	R	GGTCCGTGTTTCAAGACGG	658-640[2]	Vilgalys & Hester (1990)
rbcL1F	*rbc*L	F	GCTGGTGTTAAAGATTATCG	1233-1252[3]	Hoham et al. (2002)
rbcL4R	*rbc*L	R	GAAAATGAAACGGTCTCTCC	1850-1831[3]	Hoham et al. (2002)
rbcL8F	*rbc*L	F	GGTCTTTCAGCTAAAAACTACGG	1725-1747[3]	Hoham et al. (2002)
rbcL14R	*rbc*L	R	CGTTCWCCTTCAAGTTTACC	2206-2187[3]	Hoham et al. (2002)

Supplementary Table S2. Environmental conditions during pilot plant cultivations and biomass production. *n* – number of cases.

	Cultivation 1 Apr 4 – Jun 9, 2016	Cultivation 2 Mar 23 – May 1, 2017*	Cultivation 3 Dec 8, 2018 – Apr 25, 2019**
Cultivation duration (d)	66	39	139
Cultivation area (m^2)	12	12	12
Suspension volume (L)	150	150	150
Cultivation conditions			
n	9648	8234	20151/17219
Suspension temperature			
Mean (°C)	18.3	15.7	12.0
Median (°C)	18.3	14.5	9.5
Minimum (°C)	6.1	7.7	6.0
Maximum (°C)	34.8	31.1	30.8
Irradiance			
Mean (µmol m^{-2} s^{-1})	143	109	79
Median (µmol m^{-2} s^{-1})	37	15.1	0
Minimum (µmol m^{-2} s^{-1})	0	0	0
Maximum (µmol m^{-2} s^{-1})	1893	1320	942
Diel sum of radiation			
Mean (MJ m^{-2} d^{-1})	2.70	2.03	1.49
Median (MJ m^{-2} d^{-1})	2.71	1.99	1.26
Minimum (MJ m^{-2} d^{-1})	0.76	0.52	0.15
Maximum (MJ m^{-2} d^{-1})	5.28	3.42	4.31
Total sum of radiation during cultivation (MJ m^{-2})	181.0	58.7	179.3
Biomass production			
Total produced biomass (dry weight, g)	2115	1271	900
Mean daily biomass production per area (g DW m^{-2} d^{-1})	2.670	2.716	0.539
Mean daily biomass production per suspension volume (g DW L^{-1} d^{-1})	0.214	0.217	0.043

*microclimate data available till April 20, 2017

**loss of irradiance data between December 20, 2018 and January 8, 2019

Supplement REFERENCES

Dron M, Rahire M, and Rochaix JD (1982) Sequence of the chloroplast DNA region of *Chlamydomonas reinhardii* containing the gene of the large subunit of ribulose bisphosphate carboxylase and parts of its flanking genes. J. Mol. Biol. 162: 775–793.

Hamby RK, Sims L, Issel L, Zimmer E (1988) Direct Ribosomal RNA Sequencing : Optimization of Extraction and Sequencing Methods for Work with Higher Plants. Plant Mol. Biol. Rep. 6: 175–192, https://doi.org/10.1007/BF0266.

Helms G, Friedl T, Rambold G, Mayrhofer H (2001. Identification of photobionts from the lichen family Physiaceae using algal-specific ITS rDNA sequencing. Lichenologist 33: 73–86.

Hoham RW, Bonome TA, Martin ChW, Leebens-Mack JH (2002) A combined 18S rDNA and rbcL phylogenetic analysis of *Chloromonas* and *Chlamydomonas* (Chlorophyceae, Volvocales) emphasizing snow and other cold-temperature habitats. J. Phycology 38: 1051–1064.

Huss VAR, Sogin ML (1990) Phylogenetic position of some *Chlorella* species within the Chlorococcales based upon complete small-subunit ribosomal RNA sequences. J. Molecul. Evolution 31: 432–442.

Matsuzaki R, Kawai-Toyooka H, Hara Y, Nozaki H (2015) Revisiting the taxonomic significance of aplanozygote morphologies of two cosmopolitan snow species of the genus *Chloromonas* (Volvocales, Chlorophyceae). Phycologia 54: 491–502. doi:10.2216/15-33.1.

Takaiwa F, Oono K, Iida Y, Sugiura M (1987) The complete nucleotide sequence of a rice 25S rRNA gene. Gene 37: 255–259.

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptoccocus* species. J. Bacteriol. 172: 4238–4246.

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA Genes for phylogenetics. In PCR protocols: a guide to methods and applications, eds M. A. Innis, D. H. Gelfand, J. J. Sninsky, and T. J. White (London: Academic Press), 315-322.