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Journal Pression

Graphical abstract



- 1 Method development for PPB culture screening, pigment analysis with UPLC-UV-HRMS
- 2 vs. spectrophotometric methods, and spectral decomposition-based analysis

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5

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12 Abstract

13 PPB carotenoids are usually measured through spectrophotometric analysis, measuring total 14 carotenoids (TCs) which has low accuracy and cannot identify individual carotenoids or 15 isomers. Here, we developed an ultra-performance liquid chromatography method with 16 ultraviolet and high-resolution mass spectrometry detection (UPLC-UV-HRMS) to quantify 17 neurosporene, lycopene, and bacteriochlorophyll a contents in PPB cultures. The method 18 exhibited satisfactory recoveries for individual pigments (between 82.1% and 99.5%) and was 19 applied to a range of mixed PPB cultures. The use of a C_{30} column also enabled the detection 20 of three different isomers of lycopene. In addition, a method for anaerobic photoheterotrophic 21 PPB cultivation to acquire live-cell spectrophotometric information was developed and tested 22 by modifying a standard microbial culture microplate system. A rapid, and relatively low effort 23 principal component analysis (PCA) based decomposition of the whole-cell spectra for 24 pigment analysis in the microplates was also developed. Analysing whole-cell spectra via PCA 25 allowed more accurate prediction of individual pigments compared to absorption methods, and

- 26 can be done non-destructively, during live-cell growth, but requires calibration for new media
- and microbial matrices.

28 Graphical abstract



29

30 Keywords

31 Purple phototrophic bacteria; Pigments; Carotenoid; Lycopene; Bacteriochlorophyll

32

33 Highlights

- A UPLC-UV-HRMS method to detect and quantify PPB pigments was developed
- A C₃₀ column enabled detection and quantification of two lycopene isomers
- A microplate method for photoheterotrophic PPB cultivation was developed
- Pigment contents can be determined by PCA on the whole-cell spectra

39 Acronyms and Symbols

- 40 APCI Atmospheric pressure chemical ionization
- 41 ASV Amplicon sequencing variants
- 42 BChl Bacteriochlorophyll
- 43 BHT Butylated hydroxytoluene
- 44 COD Chemical oxygen demand
- 45 DNA Deoxyribonucleic acid
- 46 $E_{\overline{X}}$ Estimated error at 95% confidence level
- 47 HPLC High-performance liquid chromatography
- 48 HPLC-MS High-performance liquid chromatography-mass spectrometry
- 49 HRMS High-resolution mass spectrometry
- 50 IR Infrared
- 51 LC Liquid chromatography
- 52 LED Light-emitting diode
- 53 LHC Light harvesting complexes
- 54 MeOH Methanol
- 55 MP Mobile phase
- 56 MTBE Methyl-tert-butyl ether
- 57 OD Optical density
- 58 PCA Principal component analysis
- 59 PC Principal component
- 60 pCOD Particulate COD

61	PCG	Photosynthetic gene cluster
62	PPB	Purple phototrophic bacteria
63	R ²	Coefficient of determination
64	RNA	Ribonucleic acid
65	rRNA	Ribosomal ribonucleic acid
66	RSD	Relative standard deviation
67	SCOD	Soluble chemical oxygen demand
68	SCP	Single-cell protein
69	S_{Xi}	Standard deviation
69 70	S _{xi} TC	Standard deviation Total carotenoids
69 70 71	S _{Xi} TC TCOD	Standard deviation Total carotenoids Total chemical oxygen demand
69 70 71 72	S _{Xi} TC TCOD UPLC	Standard deviation Total carotenoids Total chemical oxygen demand Ultra-high performance liquid chromatography
69 70 71 72 73	S _{Xi} TC TCOD UPLC UV	Standard deviation Total carotenoids Total chemical oxygen demand Ultra-high performance liquid chromatography Ultraviolet
69 70 71 72 73 74	S _{xi} TC TCOD UPLC UV VIS	Standard deviation Total carotenoids Total chemical oxygen demand Ultra-high performance liquid chromatography Ultraviolet Visible
69 70 71 72 73 74 75	S_{Xi} TC TCOD UPLC UV VIS \overline{X}	Standard deviation Total carotenoids Total chemical oxygen demand Ultra-high performance liquid chromatography Ultraviolet Visible Average value

77 1 Introduction

The production and extraction of natural carotenoids from microbial cultures is an area of research receiving increasing attention. To date, around 600 naturally occurring carotenoids with various functional properties have been identified [1, 2]. Natural carotenoids are significantly superior to synthetic compounds in terms of beneficial properties [3] but also incur significantly higher production costs compared with synthetic products. This is mainly due to harvesting and extraction, which account for up to 90% of the production costs [4, 5]. For

84 example, the β -carotene extraction costs from Dunaliella salina are 10.38 ± 0.99 USD kg^{-1} when using organic solvents and 7.7 ± 0.83 USD kg^{-1} with supercritical carbon dioxide 85 86 extraction [6]. As an alternative, carotenoids contained in pure or mixed microbial cultures can 87 be used as whole-cell products (e.g. as carotenoid-rich single-cell protein (SCP)) [7]. In this 88 context, purple phototrophic bacteria (PPB) are a group of anoxygenic phototrophic 89 microorganisms that generate bacteriochlorophyll (BChl) and carotenoids during 90 photoheterotrophic growth under anaerobic-illuminated conditions. Without dedicated content 91 manipulation, carotenoid contents of PPB biomass were reported in the range of 1.0 to >12 mg·VS⁻¹[8], but can reach >1.7 $g_{carotenoids}$ ·L⁻¹ in concentrated biofilms [9]. 92

The most commonly used method to quantify the carotenoid content in PPB biomass has been solvent (acetone/methanol) extraction combined with ultraviolet-visible (UV–VIS) absorption detection, measuring the TC content. However, the accuracy of this quantification method for PPB with an unknown carotenoid composition is questionable because the extinction coefficients are unknown, especially for carotenoid mixtures. However, PPB samples normally consist of an unknown, complex matrix of more than one carotenoid, which differs depending on the species, growth stage, and growth conditions [10].

100 Separation through liquid chromatography on pigment extract is required to determine the 101 carotenoid profile. The use of analytical standards in High Performance Liquid 102 Chromatography (HPLC) studies on PBB carotenoids is rare and the identification is usually 103 based on the retention time and UV spectra [11-13]. The main reason for this is that carotenoid 104 standards are expensive and notoriously unstable due to UV light, temperature, and oxygen 105 enhanced degradation [14, 15]. A further limitation of PPB studies using HPLC is the 106 widespread use of C_{18} columns, which are not able to resolve geometrical isomers and 107 inefficiently resolve positional isomers [11-13]. Yet, in nature carotenoids exist in different 108 isomer forms (the main difference with synthetic products), which results in different 109 bioavailability and effects when ingested with the diet [16, 17]. A non-endcapped reverse 110 phase (RP)-HPLC column with triacontyl (C₃₀) can be used to maximise chromatographic

resolution and selectivity of carotenoids and their isomers [18, 19]. High-performance and ultra-performance liquid chromatography coupled with mass spectrometry (HPLC-MS, UPLC-MS) and using suitable analytical standards are the most effective tools for the detection and quantification of PPB carotenoids [20, 21]. However, methods based on these techniques are expensive, somewhat slow, and cannot be used *in* or *ex-situ* during growth experiments (*e.g.*, to determine maximum carotenoid extent), since an extraction and analysis process is required.

This study aims to address pigment identification and quantification in PPB by using ultra-118 119 performance liquid chromatography with UV and high-resolution mass spectrometry detection 120 (UPLC-UV-HRMS), to analyse and quantify neurosporene, lycopene, and BChl a. We also 121 developed a modified high-throughput microplate culture protocol to enable anaerobic 122 photoheterotrophic PPB cultivation with live-cell absorption spectrum collection (in a plate 123 reader). Whole (live) cell, as well as extract spectra are decomposed by principal component 124 analysis, and the principal components analysed for the ability to predict UPLC extract 125 analysis of lycopene and BChl. This provides a non-destructive, rapid pigment analysis 126 method for PPB cultures, also assessing the relevance of spectrophotometric methods for 127 pigment quantification.

128

129 2 Material and methods

130 **2.1** Inoculum, media composition, and enrichment procedure

Six enrichments cultures were started using inoculum sources from sediments harvested from the Brisbane River (Tuckean Broadwater, -28.987226, 153.407759) and Ballina Mangrove Habitat (28.84159418, 153.5703618) in New South Wales (Australia), as well as samples of poultry and domestic wastewaters (Brisbane, Australia). NaCl was added to the enrichments in different concentrations to increase the salinity to 30 and 70 mS·cm⁻¹, aiming to select for halotolerant and halophilic PPB genera [22] and thus increase the overall microbial diversity,

which would allow to test and validate the proposed pigment quantification method (see
Section 2.4) under different scenarios. The resulting enrichments were designated as E1-E6,
corresponding to sediments from Tuckean Broadwater and sea salt addition of 30 mS·cm⁻¹
(E1), Ballina Mangrove Habitat, and salt addition of 30 mS·cm⁻¹ (E2) and 70 mS·cm⁻¹ (E3),
Brisbane River (E4), poultry processing wastewater (E5) and domestic wastewater (E6).

142 For these enrichments, six reactors (Schott bottles with a working volume of 500 mL) were 143 filled with 400mL of the different environmental sources and inoculated with 500 mg COD·L⁻¹ 144 of acetic acid, and the different NaCl concentrations for 10 days, until a visible colour shift developed. Subsequently, the enrichments were maintained and fed every 5 days with fresh, 145 146 modified Ormerod medium [23], containing 500 mg COD·L⁻¹ of acetic acid and 405 mg·L⁻¹ of 147 NH₄Cl. The headspace of the bottles was flushed with N_2 to remove oxygen traces. Afterwards, the pH was adjusted to 6.8 (2M NaOH) and the bottles were closed and covered 148 149 with UV-VIS light absorbing foil (ND 1.2 299, Lee Filter, Transformation Tubes) to exclude 150 wavelengths lower than 790 nm. The bottles were incubated at ambient temperature (23-25 151 °C) mixed with magnetic stirrers at 150 rpm, and they were illuminated from the side with a 152 150 W fluorescence lamp (Nelson Clamp Flood Light), resulting in an incident intensity of ~90 153 W·m⁻².

154 **2.2** Microplate set-up and tests for in vivo and extracted spectral data acquisition

A series of custom-made stackable, non-transparent acrylic boxes (139 x 92 x 80 mm) were used to fit 12-well, transparent polystyrene microplates in an integrated, removable plate holder. This system allowed to minimise external light effects, avoid light attenuation issues and enable easy access for sampling (Figure 1).



159

Figure 1. (A) Schematic of the acrylic box, (B) LED stripes attached on the bottom of the boxes, (C) an example of PPB cultures grown in the set-up, and (D) picture of the set up showing a microplate.

Microplates were clear flat-bottom polystyrene plates with 12 wells, each with a volume of 6.9 163 mL (Costar®, Bio-Strategy Pty Limited, Tullamarine, Australia). The plate material did not 164 165 attenuate the light based on measurements (data not shown). Each box encased 4 rigid strips containing 12 infrared (IR; 850 nm/940 nm) light-emitting diodes (LEDs, LEDLightsWorld LTD) 166 167 placed at the bottom, at a distance of 50 mm from the microplate holder, to ensure optimal 168 light distribution (Figure 1B) (Note, NIR LED could be exchanged with other light sources to 169 study the effects). A dimmer enabled light intensity changes between 0 and 40 $W \cdot m^{-2}$ for each 170 set-up. The light intensity was measured with a StellarNet BLUE-Wave Spectrometer 171 (StellarNet Inc, Florida, USA). Specifically, the emitted irradiances were measured at 12 172 coordinates, corresponding to each of the microplate's wells. Irradiation levels were recorded 173 via SpectraWiz spectrometer software (OS v5.33, 2014, StellarNet Inc, Florida, USA). The 174 obtained grid point values were interpolated cubically over the irradiated area to calculate the 175 incident irradiance.

176 To start the test, a glass bead (3 mm) was placed inside each microplate well to ensure proper 177 mixing within the shaker before the wells were filled to maximum capacity with liquid (and 178 inoculum) to minimise the presence of oxygen. The microplate was carefully sealed with a 179 transparent, non-O₂ permeable, adhesive film (MicroAmp[™] Optical Adhesive Film, In Vitro 180 Technologies, Australia), avoiding the formation of bubbles between the liquid and the film to 181 ensure correct optical readings. The boxes containing the microplates were placed in a 182 temperature-controlled Shaker (ThermoFisher-MAXQ4000-Incubator-110, Thermo Fisher 183 Scientific, Massachusetts, and the USA), and experiments were conducted at ~28 °C and 150 184 rpm.

185 Microplate tests were performed to acquire in-vivo UV spectra data and to extract samples for 186 carotenoid extraction followed by spectrophotometric and UPLC-UV-HRMS analyses. Five 187 microplates were inoculated with a 10 vol% of PPB inoculum, fed with Ormerod media containing 500 mg COD·L⁻¹ of acetic acid. The microplates were illuminated with different IR 188 light intensities (dimmable LEDs) (*i.e.*, at 1.7, 5.7, 14.2, and 33.1 W·m⁻² (later referred to as 5 189 190 batch tests in microplates). A non-illuminated dark control microplate was executed in 191 equivalent non-illuminated setups. Full wavelength scans (1-1000 nm) were performed every 192 5 h approximately, in a plate reader (CLARIOstar Plus, BMG Labtech) of the whole-cell (WC), 193 in-vivo and previous to any pigment extraction. To follow biomass growth, the optical density 194 at 660 nm was used as a PPB biomass proxy (OD₆₆₀) (Figure S2). Wells were sacrificially 195 sampled from random locations at t₁₀, t₂₀, t₃₀ h after incubation, and at t_{final} (~55 h). The sample 196 at to was taken from the bulk initial mixture. Samples were extracted from the wells with a 197 syringe with a needle, to avoid removing the film covering the microplate. Approximately 2 mL 198 of sample was immediately filtered with a 0.45 mm membrane filter (Millipore, Millex[®]-HP) for 199 SCOD analysis. The remaining unfiltered sample was stored at -20 °C and later used to 200 measure TCOD, TC (via spectrophotometry), and BChl a, neurosporene, and lycopene contents, through UPLC-MS. TCOD and SCOD were determined by COD cell test (Merck, 201 202 1.14541.0001). TS/VS were determined according to

203 Standard Methods [24].

204 2.3 Pigment analysis

205 2.3.1 Analytical standards preparation

206 BChl a and lycopene were acquired from Sigma-Aldrich Pty Ltd (Castle Hill, NSW, Australia). 207 Neurosporene was purchased from Novachem (Heidelberg West, VIC, Australia). To prepare 208 stock solutions, lycopene and neurosporene analytical standards were dissolved in 209 hexane/2% CH₂Cl₂ and BChI was dissolved in methanol. To ensure preservation, 1% 210 butylated hydroxytoluene (BHT) was added to the standards, and the stock solutions were 211 flushed with argon and stored in amber vials at -20 °C. The exact concentration of each stock 212 solution was determined by UV photometry, using the absorption coefficients (mM⁻¹·cm⁻¹) 185, 213 159.4, and 54.8 for lycopene, neurosporene, and BChl a respectively, and by measuring the 214 absorbance of each compound at 470 nm, 438 nm and 771 nm using a UV-VIS spectrophotometer (Cary 50 conc, Varian) [25-27]. 215

216 2.3.2 Pigment extraction

Pigment extraction was carried out following Ruivo et al. (2012) [12], using a mixture of 217 218 acetone/methanol (7:2 v/v), and with the following modifications: i) the first supernatant 219 obtained by a first liquid-liquid extraction was discarded, as it resulted in no pigment recovery. 220 However, the addition of this step decreased variability between replicates in the following 221 extractions, indicating that this first extraction may serve as a wash-up step to remove other 222 polar components in the mixture that may interfere with the detection of carotenoids; (Figures 223 S1A and S1B); ii) wet biomass extract was used, as higher pigment recovery was obtained in 224 comparison to freeze-dried biomass extracts. Both wet and freeze-dried biomass samples 225 were kept at -20 °C until extraction. There was also less variability between replicates when 226 using wet biomass compared to freeze-dried biomass (data not shown); iii) samples were 227 centrifuged at a centrifugal force of 3270 x g using an Allegra X-12 centrifuge (Beckman 228 Coulter, Australia) and ultasonicated with a 10 L bath sonicator (100 W ultrasonic power, 229 FXP14, Unisonics, Australia) at a frequency of 40 kHz. Ultrasonication and centrifugation

times were fixed to 10 and 20 minutes, respectively, as longer times did not result in a significant increase in extracted pigments (data not shown); iv) the number of full extraction cycles from one sample was fixed to three, as it was found to be sufficient to recover most of the contained pigments (Figure S1C).

234 2.3.3 Pigment analysis by UPLC-UV-HRMS of BChl a (BChl-Ex-UPLC) and lycopene
235 (Lyc-Ex-UPLC)

236 A UPLC-UV-HRMS method for separating, detecting and quantifying pigments was 237 developed, including BChl a of the extract by UPLC (BChl-Ex-UPLC) and lycopene of extract 238 by UPLC (Lyc-Ex-UPLC). The UPLC separation was carried out on an UltiMate 3000 Rapid 239 Separation (RS) UPLC system (Thermo Fisher Scientific, Bremen, Germany), equipped with 240 an RS pump, a temperature control column compartment, an autosampler, and a variable 241 wavelength detector. A Thermo Fisher Scientific AcclaimTM C30 (2.1 mm x 250 mm; 3.0 µm) 242 column was used for the liquid chromatography (LC) separation. The LC parameters consisted 243 of 0.1% formic acid and 10 mmol ammonium formate (NH₄COO⁻) in methanol (MeOH) as 244 mobile phase A (MP A), and 100 % methyl-tert-butyl ether (MTBE) as mobile phase B (MP B), 245 running at 0.2 mL·min⁻¹, column oven temperature at 20.0 °C, and an injection volume of 15.0 246 µL. The starting mobile phase condition was 95%:5% (MP A:MP B) at 0.0 min and hold for 2.0 247 min before gradually increase to 90%:10% (MP A:MP B) at 4.0 min, followed by 60%:40% at 248 6.0 min, 50%:50% at 13.0 min, 40%:60% at 18.0 min and eventually to 1%:99% (MP A:MP B) 249 at 22.0 min and hold for 1.0 min until 23.0 min. Then, the solvent composition was adjusted 250 back to the starting condition by increasing the MP A composition from 1% at 23.0 min to 50% at 24 min and 95.0% at 26.0 min. Finally, MP A: MP B was maintained at 95%:5% for the last 251 252 4 min before completing the chromatography at 30.0 min. A Q-Exactive mass spectrometer (Thermo Fisher Scientific, Bremen, Germany) with an Atmospheric Pressure Chemical 253 254 Ionization (APCI) probe. The MS data were collected in the full scan positive mode at 70,000 255 FWHM mass resolution, scanning from 150 to 2000 m/z. The automatic gain control target 256 was set at 3.0.10⁶ and the maximum injection time at 200 ms. The source settings were as

257 follow: spray voltage at 3,500 (+), the capillary temperature at 256 °C, sheath gas at 48 258 arbitrary units (arb), auxiliary (aux) gas flow rate at 11 arb, aux gas heater temperature at 413 259 °C, S-lens radio frequency level at 50, and sweep gas flow rate at 2 arb. A 5 µg·mL⁻¹ mass 260 accuracy window was set for the mass extraction and detection setting. The UPLC-UV-HRMS 261 system was controlled by XcaliburTM 4.1, and the MS data were processed using 262 TraceFinderTM 4.1 software. Peaks were identified by comparing the retention times, MS, and 263 UV–VIS spectral data with those of the corresponding standards. For lycopene, the 537.4455 264 m/z was used as the quantification peak and 538.4489 m/z (the ¹³C isotope peak) as the 265 confirmation peak. UV was quantified at 470 nm. The developed method was validated in 266 terms of recovery. For the validation, and to test recovery, samples of pigment-free PPB 267 biomass, which pigments had been previously extracted, were spiked with low, medium, and 268 large concentrations of a mixed solution of known concentrations of analytical standards. The 269 spiked sample with low concentration contained 0.3 µg·mL⁻¹ lycopene and 3.6 µg·mL⁻¹ BChl, the medium concentrations sample had 1 µg·mL⁻¹ lycopene and 10 µg·mL⁻¹ BChl, and the 270 high concentration samples had 3 µg·mL⁻¹ lycopene and 25 µg·mL⁻¹ BChl. Lower 271 concentrations of neurosporene (1 ng·mL⁻¹, 2 ng·mL⁻¹, and 20 ng·mL⁻¹) were spiked based on 272 273 the amount detected in PPB samples. The spiked samples were then extracted as described 274 before. After performing UPLC-UV-HRMS analysis, the recovery of each carotenoid was 275 calculated. The UPLC-DAD analysis was carried out on an Agilent 1290 Infinity UPLC system 276 equipped with a 1290 binary pump, an auto-sampler, a column oven, and a diode array 277 detector (DAD). The chromatography conditions and column used for the UPLC-DAD analysis 278 were identical to the UPLC-UV-HRMS analysis mentioned earlier. The DAD data were collected from 190-640 nm range. 279

2.3.4 Pigment analysis by spectrophotometry of TC (TC-Ex-Abs) and BChl (BChl-ExAbs)

TC and BChl extracts were determined by absorbance (TC-Ex-Abs and BChl-Ex-Abs) using previously published methods [28] and a Quartz cuvette for measurements. The TC content

was calculated using the absorbance of the extracted pigments at 475 nm and using the spirilloxanthin extinction coefficient (94 mM⁻¹·cm⁻¹). The molecular weight of spirilloxanthin (596.94 g·mol⁻¹) was used to obtain the concentration of TC in mg·g⁻¹. BChl content was calculated by measuring absorbance at 771 nm, assuming a molar extinction coefficient of 65.3 mM⁻¹·cm⁻¹ [29]. The cuvette path length of 1 cm was used for all calculations.

289 2.4 Microbial analysis

290 The microbial composition of samples collected at the end of each batch test was analysed 291 via genomic sequencing by the Australian Centre for Ecogenomics (ACE). DNA extraction as 292 per Qiagen DNeasy Powersoil Kit and amplification were conducted by ACE. The universal 293 primer pair Univ_SSU_926F-1392wR was used, targeting regions of the 16S and 18S rRNA 294 genes [30]. Sequencing was conducted using the Illumina® platform. Reads identified as a 295 single read, with a relative abundance of less than 0.05% or sequence identity less than 60% 296 were discarded. Raw Illumina amplicon sequencing reads across samples were processed 297 using the DADA2 package (version 1.16) in R (version 4.0.2) to infer amplicon sequencing 298 variants (ASV) and their relative abundance. The taxonomic affiliation of the ASVs was 299 assigned in DADA2 with the SILVA rRNA gene database (version 138).

300 **2.5 Data processing and statistical analysis**

The measured results are presented as averages, and their variability is expressed as standard deviation, given as $\overline{X}(S_{Xi})$ where \overline{X} , is the average value for the data X_i , and S_{Xi} is the corresponding standard deviation. The calculated parameters are presented as average values, with uncertainty expressed as uncertainty in the mean value based on a two-tailed ttest at the 95% confidence level and with an appropriate number of degrees of freedom. Thus, values are given below as $\overline{X} \pm E_{\overline{X}}$, where $E_{\overline{X}}$ is the estimated error at a 95% confidence level.

307 2.5.1 Analysis of whole-cell spectra (Lyc-WC-PCA, BChl-WC-PCA)

The spectrum ranges of 450-550 nm (1 nm spacing), obtained across the 25 observations, corresponding to the 5 light conditions (0, 1.7, 5.7, 14.2, and 33.1 $W \cdot m^{-2}$) at 5 time-points each, were decomposed across the 25 observations by PCA on the 100 evenly spaced

311 spectral amplitudes. The top 20 principal components (of 100) were regressed (see below). 312 Both the whole-cell and extract spectra were analysed, but only the whole-cell results are 313 presented here. Spectrum PCs were assessed for their ability to predict UPLC results on all 314 samples analysed for extracted BChI (BChI-Ex-UPLC) and extracted lycopene (Lyc-Ex-315 UPLC). Similarly, the capability of spectrophotometric-absorbance measures of extracted TC 316 (TC-Ex-Abs) and BChI (BChI-Ex-Abs) to predict UPLC-UV-HRMS results was assessed. TC-317 Ex-Abs and BChl-Ex-Abs were centred on the lycopene and BChl means (*i.e.*, TC and BChl 318 means and slopes were normalised) to best estimate their ability to predict BChl and Lyc 319 contents, and allow a consistent comparison to PCA based predictions (see below). This was 320 done on all 25 whole-cell samples, and on the 20 extracted samples.

321 PCAs (with centred covariance) were performed using Matlab 2020b (function pca()). 322 Correlation analysis (function Correl()) in Excel 16 was used to determine which combination 323 of PCs could be used as a predictor for measured values, and the general linear model in 324 Excel 16 (function list()) was used to build models for UPLC (BChI-Ex-UPLC) and Lycopene 325 (Lyc-Ex-UPLC) concentrations from PCs without considering interaction or parabolic effects.

326

3 Results and discussion

327 3.1 Neurosporene, lycopene and BChl detection and guantification through UPLC-328 UV-HRMS: method development and recovery efficiency

329 The mean lycopene recovery from 6 spiked samples at the three different spike levels (0.30, 1.02, and 3.00 ug (g⁻¹) were 97.5%, 85.0%, and 83.8% analysed under full scan HRMS and 330 331 98.7%, 82.2 %, and 87.0% at UV 470 nm (Table 1). Both HRMS and UV detection gave very 332 similar average recoveries across the three different spiked levels at 88.8% and 89.3%. The 333 average relative standard deviations (RSD) calculated from the mean recoveries for the 334 HRMS, and UV detections were 8.6% and 9.6%, suggesting that both methods have good 335 precision and reproducibility (average RSDs <10%). The mean neurosporene recoveries were 336 88.5%, 96.3%, and 113.7% at the three different spiked levels (0.002, 0.005, and 0.020 ug·g⁻ 337 1), respectively for HRMS detection (UV detection was not sensitive enough at the spiked

- 338 levels). BChl showed a lower mean recovery (73.6% and 82.1% for HRMS and UV,
- respectively), which may be linked to its rapid degradation or an insufficient extraction.
- 340

341 **Table 1.** Recovery of neurosporene, lycopene, and BChl as measured by UPLC-UV_HRMS

342 (n = 6 at each spiked level).

Analyte	Spiking	Detected	Recovery	Avg Recovery	RSD,
	Level, µg∙g⁻¹	($\overline{X}(S_{Xi})$), µg·g ⁻¹	$(\overline{X}(S_{Xi})),$	$(\overline{X}(S_{Xi})), \%$	%
		Lyo	copene		
HRMS	0.30	0.29 (0.04)	97.5 (13.3)		
	1.02	0.87 (0.12)	85.0 (11.6)	88.8 (7.6)	8.6
	3.00	2.52 (0.49)	83.8 (16.3)		
UV	0.30	0.30 (0.04)	98.7 (12.8)		
	1.02	0.84 (0.13)	82.2 (12.3)	89.3 (8.5)	9.6
	3.00	2.61 (0.48)	87.0 (16.0)		
		Neur	osporene		
HRMS	0.002	1.77 (0.24)	88.5 (11.8)		
	0.005	4.82 (0.23)	96.3 (4.5)	99.5 (12.5)	12.6
	0.020	22.7 (0.32)	113.7 (1.6)		
		В	Chl a		
HRMS	5.15	4.52 (0.55)	87.7 (10.6)		
	20.13	14.03 (2.21)	69.7 (11)	73.6 (12.6)	17.1
	50.14	31.78 (3.83)	63.4 (7.6)		
UV	5.15	5.52 (1.66)	107 (32.2)		
	20.13	14.52 (2.95)	72.1 (14.7)	82.1 (21.7)	26.4
	50.14	33.69 (4.48)	67.2 (8.9)		

343

344 **3.2** UPLC-UV-HRMS detection and quantification of pigments in PPB enrichments

345 Several PPB cultures enriched from domestic wastewater, poultry processing wastewater, Brisbane River, and sediments (E1-E6; described in 2.1) were analysed for their pigment 346 347 contents. Representative isotropic profiles of lycopene (M+H) (C₄₀H₅₆), and a comparison of 348 the chromatograms from the lycopene standard (retention time of 20.7 min), from the lycopene present in a PPB sample monitoring the lycopene molecular ion (537.4455 m/z, black peak), 349 350 and the isotope ion (538.4489 m/z, red peak), are presented in Figure S3. All the enrichments 351 except for E1 contained lycopene, eluting at 20.8 min as in the analytical standard (all-352 trans lycopene). However, the method also enabled the detection of two other lycopene-like compounds, eluting at 16.38 and 17.6 min and designated as isomer 1 and isomer 2 (Figure 353

354 2A). Although different lycopene isomers have been widely studied in dietary sources such as 355 tomato, and human serum and tissues, this is the first time that the detection and quantification 356 of different lycopene isomers in PPB are described in the literature. The isomers content varied 357 between samples, most likely because of the different PPB communities resulting from the 358 different inoculum sources and growth conditions (Figure 2B). While Rhodopseudomonas sp. 359 and *Rhodobacter sp.* (dominant in piggery wastewater (E5) and domestic wastewater (E6)) 360 showed a similar isomer distribution (mainly the all-trans lycopene), samples with dominant 361 Rhodobacteraceae also showed the presence of an isomer 2 peak, in higher concentrations 362 than all-trans lycopene. Although neurosporene was detected in negligible amounts in PPB 363 enrichments, the method may be relevant in the future to enable the analysis of this compound 364 under different growth conditions. While other illumination sources including UV-VIS might 365 impact individual carotenoids, NIR generally produces both, BChl and carotenoids as relevant 366 genes for their synthesis are grouped in photosynthetic gene cluster (PGC) [31-34]. In fact, carotenoids are essential for the formation of the light harvesting complexes (LHC) [11] 367



Figure 2. (A) Distribution of the three major lycopene isomers detected at RT: 16.38 (isomer
1), 17.6 (isomer 2), and 20.8 min (lycopene) among 6 PPB mixed cultures enriched from

371 sediments from Tuckean Broadwater and sea salt addition of 30 mS (E1), Ballina Mangrove
372 Habitat and salt addition of 30 mS (E2) and 70 mS (E3), Brisbane River (E4), poultry
373 processing wastewater (E5) and domestic wastewater (E6). (B) Relative abundance of
374 different microbial communities corresponding to each of the enriched PPB cultures.

375 The UV spectra for lycopene, isomer 1, and isomer 2 were obtained by running the samples 376 (E1-E6) through UPLC coupled with a DAD detector. The UPLC-DAD chromatogram at 470 377 nm, the UPLC-UV chromatogram, and the UPLC-HRMS chromatogram of each PPB 378 enrichment sample were compared to identify the peaks with m/z corresponding to lycopene 379 and thus be able to access the individual UV spectra, as shown in Figure 3 for sample E3. 380 Three different UV spectra profiles were observed for each compound (lycopene, isomer 1, 381 and isomer 2) when matching the UV chromatogram from the two different instruments (MS and DAD) in all the PPB enrichment samples (see Table 2 and Figure S4). Isomer 2 and 382 383 lycopene showed a very similar UV spectrum; however, their distinct elution times (16.3 and 384 20.8 min) make isomer 2 a lycopene isomer candidate (see Figure S5 for an example with 385 isomer 2). Isomer 1 had a more distinct UV spectrum, with maximum absorbance peaks 386 shifted to shorter wavelengths when compared to isomer 2 and lycopene. Although this 387 method enabled the detection of different lycopene isomers, there are no available analytical 388 standards for accurate identification of the isomers and further isolation and structural 389 elucidation (e.g. by using NMR) should be performed to fully elucidate these compounds.

390

391	Table 2.	Identification	data for	lyco	pene	isomers.
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Lycopene Isomer	RT (min)	λ max (nm)			
Isomer 1	16.3	280	430	454	487
Isomer 2	17.6	294	446	472	504
Lycopene	20.8	294	446	470	502



Figure 3. Composition analyses of lycopene in E3. (A) UPLC-MS chromatogram at 537 m/z,
(B) UPLC-UV chromatogram at 470 nm, and (C) UPLC-DAD chromatogram at 470 nm.

396 The combined lycopene contents did not exceed 0.3 mg lycopene g VS⁻¹ (combined isomers), which is on the lower end of literature values where up to 2 mg g^{-1} (dry weight) was reported 397 398 for the purple phototrophic bacterium *Rhodospirillum rubrum* after genetic manipulation [35], 399 and up to 18 mg g⁻¹ (dry weight) were reported in other genetically engineered microorganisms 400 [36]. At this stage, we cannot state standard lycopene contents of mixed PPB cultures under 401 non-engineered conditions. The data show that the UPLC-UV-HRMS method can be used to 402 analyse the lycopene content in environmental samples, with greater accuracy compared with 403 spectrophotometric methods. Due to the use of a polymeric C_{30} column, the developed method 404 also enables lycopene isomers separation, which cannot be resolved by the commonly used 405 C₁₈ columns [37]. Different isomers have varying functions and potencies [38, 39], which 406 makes the isomer identification relevant to assess the potential absorption and health benefits 407 of the lycopene produced in PPB cultures, e.g. when used as SCP in feed. For example, the 408 antioxidative properties of cis-lycopene have been reported inferior to all-trans-lycopene [38]. 409 On the other side, cis-isomers have repeatedly been shown to be substantially more 410 bioavailable than all-trans lycopene [16].

411 **3.3** Plate reader tests and spectral decomposition-based analysis

412 The microplate set-up enabled the recording of PPB photoheterotrophic growth in 12 well 413 microplates. Growth curves were recorded by measuring OD₆₆₀ in a plate reader (with an 414 acceptable CI95%). OD₆₆₀ measurements for the four light intensities over time are shown in Figure 4. This is an effective predictor for particulate COD ($R^2 = 0.9908$), shown in Figure S2, 415 416 which can be used as biomass proxy, especially in clean substrate tests (without native 417 particulate COD due to serial dilutions). Additionally, each well's absorbance spectrum was 418 scanned to monitor characteristic peaks of carotenoids (400-500 nm) and BChl a (800-900 419 nm).



Figure 4. PPB growth curves measured as OD₆₆₀ in microplates using different light intensities
(0, 1.7, 5.7, 14.2, and 33.1 W·m⁻²).

Time series whole-cell spectra collected during experiments in the microplates were decomposed via covariance PCA as noted in the methods (2.5.1). The vast majority of covariance was held in PC1 (99.97%), which was related to change in overall spectrum amplitude. This effectively removes the background of general cellular material. Of the remaining covariance, 99.999% was contained in PCs 2-10.

428 A full correlation table of Lycopene and BChl via UPLC-UV-HRMS (Lyc-Ex-UPLC and BChl-429 Ex-UPLC), to the individual spectral PCs for whole-cell and extract is given in Table S1. Lyc-430 Ex-UPLC was correlated with PC2, PC3, and PC12, while BChI-Ex-UPLC was correlated with 431 PC2, PC8, and PC13 (and to a lesser extent, PC1 and PC10). PC2 therefore likely contains 432 common features to both BChl and Lyc, but it is important to note that the other PCs are 433 different, and BChl and Lyc can be fitted separately using different features. To develop a 434 predictive model for Lyc-Ex-UPLC and BChl-Ex-UPLC from the spectral PCs, data were 435 randomly split into fitting (20 points) and validation (5 points). Increasing the number of predictors (PCs) as inputs to the model improved the R² to the fit points (up to 0.99) but caused 436

validation to become excessively poor, likely because PCs were used to improve fits on 437 438 individual points with excessive empirical inputs. To address this, the number of predictors was limited to achieve similar R² values between fitting and validation data sets, and in each 439 440 case, this resulted in 3 predictors. The optimised models and individual parameter p-values 441 are shown in Table 3. The low p-value for PC8 indicates it could be eliminated in the model for BChI-Ex-UPLC, but this resulted in the fit R² value dropping to 0.73 (from 0.77) without an 442 improvement in validation R². Analysis of the extract PC spectroscopy resulted in similar model 443 444 qualities (with an increased contribution from PC1 and decreased variance in PC1). Because 445 it was not superior to the whole-cell PCA and is considerably more effort (requiring solvent extraction), it is not presented here (but included as Table S1). 446

447 Table 3. Whole-cell PCA models for Lycopene and BChl by UPLC (Lyc-Ex-UPLC and BChl-448 Ex-UPLC).

PCA-Lycopene Model					
Predictor	PC2	PC3	PC12	Intercept	
Parameter	-6.06±0.67	-15.20±4.9	199±137	0.70	
p-value	1x10 ⁻¹⁴	3x10⁻ ⁶	8x10 ⁻³		
PCA-BChl Model					
Predictor	PC2	PC8	PC13	Intercept	
Parameter	-25.2±5.0	-520.9±419	-1627.2±690	6.87	
p-value	8x10 ⁻¹⁰	2x10 ⁻²	1x10 ⁻⁴		

449 Uncertainty in parameters (±) are 95% confidence intervals

450 The correlation table for the three methods (Ex-UPLC, Ex-Abs, WC-PCA) and two target 451 compounds are shown in Table 4. The Ex-Abs values required significant correction by 452 regression to be effective predictors for the Ex-UPLC measures (particularly TC to Lyc) and even then, had significant issues. Correlation between extractive absorption (TC-Ex-Abs, 453 BChl-Ex-Abs) and the UPLC methods are reasonable at r=0.84 and r=0.85 for target 454 455 compounds. However, TC-Ex-Abs is also a good predictor for BChI-UPLC (*i.e.*, non-specific), 456 which means that BChl is potentially a strong interference for the TCA method. In addition, the 457 correlation between the two extraction-absorption (TC-Ex-Abs, BChl-Ex-Abs) was 0.91, which 458 means that these methods interact strongly. That is, both are largely measuring the same

459 compound (total pigments) rather than separate pigments. In contrast, the correlation 460 coefficient for WC-PCA methods was higher than for the Ex-Abs methods in both cases (to 461 UPLC), and PCA was more specific to the target compound. UPLC (Ex-UPLC) results vs 462 predictions from the whole-cell spectral PCA (WC-PCA) are shown in Figure S6A for TC, and 463 S5B for BChl.

464 As noted in the methods, due to loss of some extracted individual replicates (due to limited sample volumes), averages of technical triplicates for spectra, UPLC measurements, etc. 465 466 were used. To validate this for individual samples, the same procedure was also done on individual replicates excluding zero lycopene reads (total n=63). The results were consistent, 467 with PC2 and PC3 dominating correlation, and with an overall R² of 0.79. As seen in 468 469 supplementary Figure S7 (r=0.89), most of the errors are at very low lycopene levels (where the relative uncertainty in replicate analysis was highest). Due to the increased observations, 470 p-values were far lower $(x10^{-3})$ than shown in Table 3. 471

472

Table 4. Comparison of different methods to assess Lycopene and BChl (Pearson correlation

474	coefficient	t of	parity	model).
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	Lyc-Ex-UPLC	BChl-Ex-UPLC
Lyc-Ex-UPLC	<u> </u>	0.66
BChI-Ex-UPLC	0.66	<u>1.00</u>
TC-Ex-Abs	<u>0.84</u>	0.87
BChl-Ex-Abs	0.69	<u>0.82</u>
Lyc-WC-PCA	<u>0.88</u>	0.60
BChl-WC-PCA	0.68	<u>0.86</u>

475 *Target of analytical method is underlined and bold. Correlation between TC-Ex-Abs and BChl-Ex-Abs

476 is 0.92. Colours indicate correlation.

477 The absorbance of extract, while effective for plant samples, where the carotenoid profile is

478 known, is non-selective in microbial cultures. Limited improvement in the method is unlikely,

479 while whole-cell PCA has been analysed with only 25 (averaged triplicate) samples from 5

480 microplates batch tests (described in section 2.2 at different wavelengths) and will improve

481 substantially as more samples can be analysed. Both are subject to matrix issues, which may 482 include the flanking community, background coloured compounds (e.g., humics, cellular 483 polymers, etc), but this can be corrected in PCA. PCA on whole-cell spectrum can be done on 484 live cells, during the experiment, or for a pigment production platform, at an industrial scale, 485 and does not require pigment extraction. When the matrix changes, a large number of whole-486 cell spectra can be fit using a relatively small number of UPLC measurements, and this can 487 be continuously updated, with error analysis continuously applied. As far as we are aware, 488 this is the first instance of full spectra decomposition by PCA and comparison against chemical 489 analysis. Other methods, such as the Gauss-peak spectra method, have been applied to 490 qualify and quantify individual pigments from total absorbance spectra from higher plants, 491 brown algae, Euglena, Trichodesmium, and Anabaena. However, standards are necessary to 492 calibrate the methods (a spectrum fitting library is available) [40], which limits the application 493 for specific PPB pigments.

While UPLC remains the "best" technique, it is limited in terms of analytes. This is because 494 495 other carotenoids produced by PPB such as spirilloxanthin or okenone do not have readily 496 available commercial standards, which is a prerequisite for their reliable detection and 497 quantification e.g. with UV-HRMS detectors [21]. Increased interest in the PPB platform will 498 likely drive the availability of standards that can be used to calibrate the PCA method for 499 various individual carotenoids. This would enable high throughput methods e.g. to screen the 500 best conditions to accumulate specific carotenoids or control industrial production in mixed or 501 pure cultures. We note the PCA calibration will be required to include matrix effects of different 502 wastewaters and different communities and variability need to be further assessed.

503 4 Conclusions

504 Studies to optimise the biosynthesis of carotenoids in purple phototrophic bacteria require a 505 reliable analytical method that enables the detection and quantification of individual 506 carotenoids and their isomers. The UPLC-UV-HRMS method presented here was reliable for 507 the quantitative determination of neurosporene, lycopene, and BChl a. These compounds

508 were separated on a reverse-phase C_{30} carotenoid column, enabling the detection of three 509 different lycopene isomers. Compared to traditional spectrophotometric methods, this method 510 has the advantages of detecting individual carotenoids and of providing accurate identification 511 due to the use of analytical standards. Full identification of other carotenoids present in the 512 sample requires suitable standards, but the m/z and UV Spectra data could be used for 513 tentative identification of the other carotenoids. The classic extraction-absorption method was 514 not particularly effective in separating different pigments and had matrix effects. However, 515 analysing whole-cell spectra via PCA allowed more accurate prediction of individual pigments, 516 and can be done non-destructively, during live-cell growth. It does require calibration for media 517 and microbial matrices, but once calibrated, is a rapid, and relatively low effort method.

518

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- 638

Highlights

- A UPLC-UV-HRMS method to detect and quantify PPB pigments was developed •
- A C₃₀ column enabled detection and quantification of two lycopene isomers
- A microplate method for photoheterotrophic PPB cultivation was developed •
- Pigment contents can be determined by PCA on the whole-cell spectra •

Declaration of interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

□The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:

Julia Contra