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# Article The architecture of monospecific microalgae biofilms

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10 Abstract: Microalgae biofilms have been proposed as an alternative to suspended cultures in 11 commercial and biotechnological fields. However, little is known about their architecture which 12 may strongly impact biofilm behavior, bioprocess stability and productivity. In order to unravel the 13 architecture of microalgae biofilms, four species of commercial interest were cultivated in 14 microplates and characterized using a combination of confocal laser scanning microscopy and FTIR-15 spectroscopy. In all the species, the biofilm biovolume and thickness increased over time and 16 reached a plateau after 7 days, the final biomass reached was very different though. The roughness 17 decreased during maturation, reflecting cell division and voids filling. The extracellular polymeric 18 substances content of the matrix remained constant in some species and increased over time in some 19 others. Vertical profiles showed that young biofilms presented a maximum cell density at 20 µm 20 above the substratum co-localized with matrix components. In mature biofilms, the maximum 21 density of cells moved at a greater distance from the substratum (30-40 µm) whereas the maximum 22 coverage of matrix components remained in deeper layer. Carbohydrates and lipids were the main 23 macromolecules changing during biofilm maturation. Our results revealed that the architecture of 24 microalgae biofilms is species-specific. However, time is similarly affecting the structural and 25 biochemical parameters.

Keywords: biofilm; microalgae; architecture, confocal laser scanning microscopy, FTIR spectroscopy

#### 28 1. Introduction

29 In the last decades microalgae have been recognized as a valuable source of bio-products such 30 as pigments, anti-oxidants and food supplements and they have gained popularity in a wide range 31 of commercial activities. In conventional photobioreactors (PBRs), microalgae present low biomass 32 concentrations (1-3  $g \cdot L^{-1}$ ; [1,2]) and 12 to 2000 L of liquid medium are required for the production of 33 1 Kg of microalgae dry mass [3]. This high water fraction requires energetic expenses for culture 34 agitation (up to 385.71 MJ · Kg<sup>-1</sup>; [2]) and for biomass harvesting, dewatering and drying (up to 82 MJ 35 · Kg<sup>-1</sup>; [2]). Biomass production in typical PBRs is therefore constrained by high energy and operating 36 costs [4].

Biofilm-based cultivation systems are promising technologies overcoming the drawbacks of conventional PBRs. Such systems can reach high productivities (up to 35 g DW  $\cdot$  m<sup>-2</sup>  $\cdot$  day<sup>-1</sup>) and biomass concentration (up to 96 g  $\cdot$  L<sup>-1</sup>; [2]). Furthermore, harvesting is simply carried out by scraping the attached biomass with minimal energy demand [3]. Finally, there is an increasing interest from the industrial sector about the great variety of molecules excreted by microalgae when developing biofilms [5]. Biofilm-based systems seem therefore to address most of the challenges of suspended cultures.

In a biofilm, microbial cells are associated with a surface and enclosed in a matrix, which is
 mainly composed of water, polysaccharides, proteins and nucleic acids [6]. The spatial arrangement
 of microorganisms and matrix components define the size and quantity of voids and channels,

- 47 altering in turn the transport of nutrients and gases [7]. The biofilm architecture induces therefore
- 48 marked gradients of nutrients, gases and light along depth, inducing the cells to acclimate or displace 49 in order to maintain an optimal growth [8.9]. Therefore, structural data are of major importance to
- in order to maintain an optimal growth [8,9]. Therefore, structural data are of major importance tobetter understand the complex behavior of biofilms (i.e. development and activity) and to improve
- 51 productivity of biofilm-based technologies.

52 Structural changes in bacteria biofilms have been well characterized experimentally under 53 several growth conditions, and it has been shown that the architecture is strongly species and strain 54 dependent [10-13]. From a compositional point of view, it has been shown that changes of structural 55 parameters in bacterial biofilms are strongly correlated to the biochemical composition of 56 exopolymers [14-17]. Phototrophic biofilms, especially microalgae biofilms, have been far less 57 studied [8,18–22]. In particular, little is known about the link between architecture and extracellular 58 polymeric substances production for different species. In addition, the role played by the matrix in 59 biofilm development has been only addressed in studies regarding mixed communities (i.e. bacteria, 60 microalgae etc.) [8,23,24], even though microalgae are known to excrete exopolymers with specific 61 carbohydrates:proteins:lipids:nucleic acids ratios [25,26].

In this work, we aimed therefore at better understanding how various microalgae monospecific biofilms differ in their architecture and composition depending on the species. Four biofilm-forming microalgae species of actual or potential biotechnological interest were selected, including two green algae, a red algae and a diatom. Biofilm structural dynamics and macromolecular composition were characterized by a combination of non-destructive techniques including confocal laser scanning microscopy (CLSM, which allows to characterize several structural parameters such as biovolume,

68 thickness, roughness and diffusion distance) and vibrational spectroscopy (ATR-FTIR spectroscopy).

#### 69 2. Materials and Methods

70 2.1. Microalgae strains and planktonic culture maintenance

71 Chlorella vulgaris SAG 211-11b (Göttingen, Germany) was grown in 3N-Bristol [27], the marine 72 strain Chlorella autothrophica CCMP 243 (Bigelow, Maine, USA) was grown in Artificial Sea Water 73 [28], whereas the diatom Cylidrotheca closterium AC170 (Caen, France) and Porphyridium purpureum 74 SAG 1380-1e (Göttingen, Germany) were cultivated in filtered natural seawater. The marine media 75 were supplemented with Walne's medium [29]; 1mL · L-1). All biofilms were inoculated from 76 suspended stock cultures grown in a PSI MC1000 multicultivator (Photon systems instruments, 77 Czech Republic) in borosilicate tubes filled with 70 mL of growth medium. The cultures were bubbled 78 and maintained semi-continuously at 25°C under a continuous photon flux density of 80 µmol 79 photons  $\cdot$  m<sup>-2</sup>  $\cdot$  s<sup>-1</sup>. Cells from the stock cultures were harvested during the exponential phase (cell 80 density of  $2-3 \cdot 10^6$  cell  $\cdot$  mL<sup>-1</sup>).

#### 81 2.2. Biofilms cultivation: inoculum, initial adhesion and growth

82 Biofilms were grown in polystyrene µClear ® 96-well microplates (Grenier Bio-one, France). The 83 inoculum was prepared by diluting a volume of suspended cells (see above) to a final concentration 84 of  $1 \cdot 10^6$  cell  $\cdot$  mL<sup>-1</sup> ( $1 \cdot 10^5$  cell  $\cdot$  mL<sup>-1</sup> for *C. closterium*) and by transferring 250 µL of such suspension 85 in the wells. This cell concentration corresponded to similar starting biovolume for all the species (~5 86  $\mu$ m<sup>3</sup> ·  $\mu$ m<sup>-2</sup>). The cells were then left for 24 hours adhering to the surface of the wells and subsequently 87  $200 \ \mu L$  of the medium were removed in order to eliminate any unattached cell. After the first 24 88 hours, 80 µL of medium were removed and replaced with new medium every two days to 89 compensate for evaporation and to buffer nutrient and CO<sub>2</sub> limitations. A continuous photon flux 90 density of 100 µmol photons · m<sup>-2</sup> · s<sup>-1</sup> was used. Light (PAR 400-700 nm) was homogeneously 91 provided by two sets of light emitting diode (Alpheus LED, Montgeron, France). Biofilms growth 92 was monitored for 11 days and each day the biofilms were scanned using CLSM to detect cells signal. 93 At day 2, 7 and 11 the biofilms were also stained to characterize the matrix and samples were 94 harvested for ATR-FTIR spectroscopy.

#### 95 2.3. Confocal laser scanning microscopy (CLSM): cells and matrix characterization

96 Images (512 · 512 pixels) were acquired using an inverted Zeiss LSM700 confocal microscope 97 (Carl Zeiss microscopy GmbH, Germany) controlled using the Zen 10.0 software black edition (Carl 98 Zeiss microscopy GmbH, Germany). All biofilms were scanned with a LD Plan-Neofluar 20x/0.4 Korr 99 M27 objective with a 0.4 N.A. (numerical aperture). Each image was 638 · 638 µm in size with a z-step 100 of 3.94 µm. The settings of the confocal microscope are reported in Table S1. After preliminary trials, 101 a low magnification lens was preferred to a higher one (e.g. 63x), because allowing to scan wider 102 biofilm areas (essential to properly capture microalgae cell patterns) and to acquire z-stacks over the 103 whole biofilm depth. However, we have to point out that this choice comes with side effects, such as 104 a greater point spread function and a lower resolution of the images.

- 105 Two laser lines were used to respectively detect microalgae and the matrix surrounding them. 106 Microalgae cells were observed by detecting chlorophyll *a* auto-fluorescence. Lectins and dextran 107 (3kDa), both labelled with fluorescein (FITC), were added at day 2, 7 and 11 to detect glycoconjugates 108 and to visualize non-specifically the matrix, respectively [30-33]. The pool of extracellular 109 glycoconjugates (i.e. exopolysaccharides, glycoproteins etc.) specifically detected by the lectins will 110 be identified here as EPS (extracellular polymeric substances). Dextran on the other hand is supposed 111 to diffuse into the channels, voids and to get finally non-specifically trapped into the matrix [30–33]. 112 A fresh cocktail of 20 lectins (Kit I, II and III, Vector Laboratories, Peterborough, UK) or dextran were 113 supplied at a final concentration of 13  $\mu g \cdot mL^{-1}$ . The microplates were then incubated in the dark for 114 30 minutes. Afterwards, the excess of dyes present in the wells was removed by carefully removing 115 140 µL of the medium and by adding other 140 µL of fresh medium (specific for each species) in each 116 well. This process was repeated one time for the dextran and two times for the lectins. We have to 117 point out that since a mixture of lectins was used to detect the matrix, it is possible that the interaction 118 among the single lectins and the competition for similar targets may have occurred.
- 119 Chlorophyll *a* was excited with the 639 nm line of a 5 mW solid state diode laser and the emission 120 of chlorophyll *a* auto-fluorescence was observed using the long pass (LP) filter 615 nm. Lectins and 121 dextran were excited with the 488 nm laser line of a 10 mW solid state diode laser and their 122 fluorescence detected using the band pass (BP) filter 490-530 nm. Unlabeled organisms and wells 123 filled with growth media but not inoculated with microalgae were used as a staining control. Each 124 well was scanned on at least three random positions (three z-stacks) resulting in a total surface area 125 of at least 1.2 mm<sup>2</sup>.
- 126 2.4. Image analysis

127 The plug-in COMSTAT 2.1 (Technical University of Denmark; [11]) running in ImageJ 1.48v [34] 128 was used to extract from the images the quantitative parameters typically used to characterize biofilm 129 structures. The complete list of parameters is reported in Table S2. Images binarization was 130 automatically computed in the plug-in by selecting a threshold value using the Otsu algorithm [35] 131 and the function "connected volume filtering" was unchecked.

Since the auto-fluorescence of the cells comes from the chlorophyll within the chloroplasts, we have to point out that the structural parameter calculated from the images reflect such organelle rather than the whole cell, even though the overlapping of fluorescence and transmission images revealed good matching of the two acquisition mode (data not shown). However, to be consistent with the terminology present in most of the literature, we considered that the auto-fluorescence of the chlorophyll quantifies the cells.

138

#### 139 2.5. ATR-FTIR spectroscopy

140 At day 2, 7 and 11, the biofilms were scrapped from four wells for each species. The samples 141 were centrifuged at  $8000 \cdot g$  for 5 minutes and the supernatant removed. After that, 1 mL of distilled 142 water in the case of *C. vulgaris* and 1 mL of a solution of NaCl (35 g · L <sup>-1</sup>) for the marine species were

143 used to wash the biofilm suspensions from salts that would otherwise interfere with the cell and

- 144 matrix spectral signature. Afterward, the pellet was re-suspended in 5-10  $\mu$ L of distilled water or
- 145 NaCl and 1.5 μL were transferred on a 45° ZeSe flat crystal of an ATR-FTIR PerkinElmer Spectrum-
- 146 two spectrometer (PerkinElmer, Waltham, USA) and the sample was dried at room temperature for
- 147 20 minutes. Spectra were acquired in the range 4000 and 400 cm<sup>-1</sup> using 32 accumulations at a spectral
- resolution of 4 cm<sup>-1</sup>. Before each measurement, the empty crystal was measured using the same instrumental setting and used as a blank.
- 150 Institution setting and used us a blank.
  150 Spectra were baselined using the rubberband algorithm and the ratios between the main macromolecular pool (proteins, lipids and carbohydrates) were calculated as the ratios between the

152 maximum absorption values for the spectral ranges corresponding to each macromolecular pool:

- 153 proteins (Amide I; 1700-1630 cm<sup>-1</sup>), lipids (C=O; 1750-1700 cm<sup>-1</sup>) and carbohydrates (C-O-C, C-C and
- Si-O-Si in diatoms; 1200-950 cm<sup>-1</sup>). Since no separation between cells and matrix components was performed, the spectra reflected both the physiological changes occurring in the cells and those
- 155 performed, the spectra reflected both t156 related to EPS.
- 157 2.6. Statistics
- 158 Statistics was performed using GraphPad prism 5.0 (San Diego, CA, USA) and R [36]. One-way 159 and two-way ANOVA were used to test the statistical significance of mean differences among 160 different species and over time. The level of significance was always set at 5%. The logistic function 161 [37,38] was fit to the biovolume vs. time curves and the maximal cell biovolume (i.e. the biovolume 162 at the *plateau*) and the specific growth rate ( $\mu$ ) were obtained in order to make quantitative 163 comparisons between the species.
- 164 Correlation matrices, using the Pearson's coefficient, were computed using the package 165 "corrplot" [39] present in R to investigate the relationship among structural parameters (obtained 166 from CLSM) and biofilms macromolecular composition (FTIR ratios).
- All results are reported as mean and standard deviations of several independent biological replicates. Biofilm dynamics were repeated on at least four independent microplates. In each microplate, for each species and for each time point, at least three separate wells were analyzed by CLSM. In each well, at least three randomly chosen biofilm areas were scanned.
- 171 **3. Results**
- 172 3.1. Biofilm development over time: structural characteristics

Examples of 3D biofilm reconstructions are reported in Figure 1a. The biovolume of the cells within the biofilm increased over time and after seven days the *plateau* was reached for all the species (Figure 2a). *C. autotrophica* and *P. purpureum* exhibited the highest biovolume, whereas *C. vulgaris* and *C. closterium* presented almost 50% lower biovolume. *C. autotrophica* also exhibited the highest growth

177 rate whereas no significant difference was found among the other microalgae (Table 1 and Figure 2a;

178 *p*>0.05).



Figure 1. Representative three-dimensional reconstructions of the microalgae biofilms (a) and maximum intensity projection (b) of cells (red signal), lectins (green signal) and dextran (green signal) signals of the biofilms at day 11. In panel (a), day 0 represents the inoculum, day 2, 7 and 11 are the days at which the biofilms were stained and analyzed by ATR-FTIR spectroscopy. The brightness of the images was adjusted for better visualization. Images size in (a) and (b) is 638 · 638 µm. The XY ticks interval in (a) is 100 µm and the scale bar in (b) is 100 µm.

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197	Table 1. Growth parameters (growth rate and maximal biovolume) obtained by fitting the logistic
198	regression to the biovolume vs. time curves. Data are reported as the mean and standard deviation of at least
199	nine independent biological replicates. Different letters represent statistically different means (p<0.05) as
200	determined by pair-wise comparisons after one-way ANOVA

Microalgae species	μ (d <sup>-1</sup> )	Maximal biovolume (μm³ · μm²)
C. autotrophica	0.72ª (0.24)	$50.47^{a}$ (4.09)
C. vulgaris	0.45 <sup>b</sup> (0.14)	31.22° (8.49)
P. purpureum	0.65 <sup>ab</sup> (0.20)	43.02 <sup>b</sup> (4.92)
C. closterium	0.43 <sup>b</sup> (0.13)	22.42 <sup>d</sup> (2.59)

<sup>201</sup> 

201

Roughness presented an opposite trend to biovolume and decreased (from 1.2 to 0.2 a.u.) over
 time in *C. autotrophica, C. vulgaris* and *P. purpureum*. The roughness coefficient of *C. closterium* instead,
 remained stable at values around one (Figure 2b).

205 Over time, the increase in biomass resulted in a thickening of the biofilms (Figure 2c,d). C. 206 autotrophica developed the thickest biofilms (~100 µm) and its maximum thickness remained stable 207 over time. P. purpureum and C. closterium presented a similar increase of the maximum thickness 208 reaching values like those of C. autotrophica. C. vulgaris presented thinner biofilms with a maximum 209 thickness around 30-40 µm. The average thickness of C. autotrophica increased rapidly during the first 210 four days and then levelled off around 80 µm at day 7. P. purpureum, C. closterium and C. vulgaris 211 exhibited a more linear increase of the average thickness. P. purpureum reached a similar thickness to 212 that of C. autotrophica whereas C. closterium and C. vulgaris at the end presented 40-50% lower 213 thicknesses with respect to C. autotrophica.

The maximum diffusion distance increased over time in all the species but *C. vulgaris* (Figure 215 2e). At the end of the assay *C. autotrophica* and *C. closterium* presented similar values and reached the

216 highest values among all species, followed by *P. purpureum* and *C. vulgaris*. The average diffusion

distance followed a similar pattern to biovolume: it increased rapidly the first four days and then

218 leveled off from day 7 (Figure 2f). *C. autotrophica, C. vulgaris* and *P. purpureum* presented comparable

average diffusion distance (0.6-0.9  $\mu$ m) whereas *C. closterium* exhibited the lowest (0.1-0.3  $\mu$ m; *p*<0.05).



Figure 2. Dynamics of the structural parameters obtained from the z-stacks acquired at the CLSM: biovolume (a), roughness (b), maximum thickness (c), average thickness (d), maximum diffusion distance (e) and average diffusion distance (f). The results are reported as the mean and standard deviation of 12 independent biological replicates. The fitting of the logistic model is also presented for the biovolume.

#### 226 3.2. Matrix characterization: lectins and dextran volumes

In order to characterize the matrix of the biofilms, the volume of binding lectins and of dextran was quantified. The volume of lectins reflected the fraction of glycoconjugates (EPS) in the matrix and dextran was used to quantify voids, water channels and non-specifically the whole matrix (Figure 1b).

*C. vulgaris* presented the lowest amount of EPS (Figure 3a), whereas it increased over time in *P. purpureum* and *C. closterium* biofilms, which volume of EPS doubled from day 2 to day 7. No temporal change was observed for *C. autotrophica* and *C. vulgaris* (*p*>0.05). *C. closterium* presented the highest lectins to cells ratio (Figure 3b). Over time, *C. autotrophica* exhibited a decrease over time in the lectins

to cells ratio (p < 0.05) whereas in the other species the ratio remained stable.



#### 236

Figure 3. Structural parameters characterizing the biofilm matrix at day 2, 7 and 11. Volume of binding lectins ((a); specifically binding to glycoconjugates), lectins to cells ratio (b), volume of dextran ((c); used to stain non-specifically the matrix), and dextran to cell ratio (d). The results are reported as the mean and standard deviation of at least four independent biological replicates. Bars with different letters represent statistically different means (p<0.05) as determined by pair-wise comparisons after two-way ANOVA.

243 At day 2, the volume of dextran was the highest in C. autotrophica biofilms (~65  $\mu$ m<sup>3</sup> ·  $\mu$ m<sup>2</sup>). P. 244 purpureum and C. closterium presented 50% and 30% lower volume of dextran in their matrix, but at 245 day 7 and 11, they approached the values of *C. autotrophica* (Figure 3c). *C. vulgaris* always presented 246 the lowest volume of dextran in the matrix (~30  $\mu$ m<sup>3</sup> ·  $\mu$ m<sup>-2</sup>). In *C. autotrophica* and *C. vulgaris,* no 247 significant change was observed over time (Figure 3c). Similarly to lectins, the dextran to cells ratio 248 was always the highest in C. closterium and it decreased from day 2 to 7 and then levelled off. A 249 similar ratio was found for C. autotrophica C. vulgaris and P. purpureum. C. autotrophica presented a 250 decreasing trend from day 2 to day 7 similar to C. closterium. C. vulgaris and P. purpureum biofilms 251 did not show any significant change over time of the dextran to cells ratio (Figure 3d).

#### 252 3.3. Areal coverage over depth: cells vs. matrix vertical profiles

Regardless of the species, the maximum of cell density was reached at day 2, at a distance from the substratum of 10  $\mu$ m, where the cells were already covering almost 50% of the area, except for *C. closterium* that only covered 30% of the area (Figure 4g). On the other hand, during maturation, the maximal percentage of cell coverage moved at a greater distance (30-40  $\mu$ m) above the substratum and the depth at which it was reached and the percentage of coverage were species-specific (ranging from 40 to 90% of covered area; Figure 4).



259

Figure 4. Vertical profiles of cells (a, c, e, g) and EPS (b, d, f, h) coverage of four different monospecific microalgae biofilms after 2, 7 and 11 days of maturation. The vertical profiles are reported as the percentage of coverage of cells or of EPS obtained from the z-stacks acquired at the CLSM. The vertical profiles are reported as the mean and standard deviation of at least four independent biological replicates.

Dextran and lectins presented comparable distributions over depth (Figure 4b,d,f,h and Figure
 S1). Interestingly, although the cells profile over depth changed as a function of time, the highest
 density of EPS and voids seemed to be positioned close to the substratum (20-30 μm) at all time points
 and for all the species.

In addition, the depth of maximum cells density presented a positive correlation with the average biofilm thickness ( $R^2 = 0.78$ , *p*=0.0001). On the other hand, for the EPS the regression slope was not significantly different from zero (Figure S2;  $R^2 = 0.005$ , *p*=0.81).

3.4. Biofilm biochemical characterization by ATR-FTIR spectroscopy and correlation analysis with structural
 data

The average FTIR spectra of the biofilms at the different sampling times (day 2, 7 and 11) are reported in Figure S3. *C. autotrophica* and *P. purpureum* were the species that presented the greatest macromolecular changes along time.

Similar carbohydrates to proteins ratios were observed for all the samples and the ratio did not
change in *C. vulgaris, C. closterium* and *C. autotrophica* (Figure 5a; *p*>0.05). In contrast for *P. purpureum*,
the carbohydrates to proteins ratio was 50% higher at day 11 than that at day 2 (Figure 5a; *p*<0.05). *P. purpureum* and *C. vulgaris* biofilms did not exhibit any change in the lipids to proteins ratio (Figure

- 281 5b; p>0.05). For C. autotrophica biofilms, the lipids to proteins ratio increased by 50% at day 11
- compared to day 2 (Figure 5b; *p*<0.05) and for *C. closterium* it increased by 30% at day 7 compared to
- 283 day 2.

![](_page_10_Figure_5.jpeg)

284

285Figure 5. Macromolecular composition of the biofilms after 2, 7 and 11 days of maturation. The panel286(a) depicts the carbohydrates to proteins ratio, the panel (b) depicts the lipids to proteins to ratio and287the panel (c) represents the carbohydrates to lipids ratio. The results are reported as the mean and288standard deviation of at least four independent biological replicates. Bars with different letters289represent statistically different means (p<0.05) as determined by pair-wise comparisons after the two-290way ANOVA.

In *C. autotrophica* and *C. vulgaris* biofilms, the carbohydrates to lipids ratio did not change over time (*p*>0.05). For *P. purpureum* it tripled between day 2 and day 11. In *C. closterium*, the ratio was lower at day 7 compared to day 2 (almost 50%), but no difference was found between day 11 and day 2 (Figure 5c).

A correlation analysis was carried out to identify the possible correlations among the macromolecular ratios and the matrix of structural data (Figure S4). In *P. purpureum*, the EPS and dextran volumes were positively correlated to the carbohydrates to proteins and to the carbohydrates to lipids ratios whereas they were negatively correlated to the lipids to proteins ratio. In all the other species, only minor correlations were found between matrix components and the macromolecular pools (Figure S4). In contrast, for these species the macromolecular ratios were correlated to the structural parameters obtained from cells autofluorescence such as thickness, biovolume, diffusion

302 distance and roughness (Figure S4).

#### 303 4. Discussion

304 Our results show that the architecture of microalgae biofilms is species dependent. But the 305 structure evolution over time seemed to follow some general common rules that resemble those 306 described for bacteria and fungi [11,40–42].

307 During the first stages of substrate colonization the biofilms were irregular in their surfaces (i.e. 308 high roughness), thin and for some of the species the volume of EPS was higher than that of the cells 309 (Figure 2 and 3). As the biofilms matured, the biovolume increased reflecting active cell division, 310 similarly to what was reported for phototrophic biofilms by Mueller et al. [8] and Kernan et al. [20]. 311 Mueller et al. [8] reported a linear increase whereas our growth curves and those from Kernan et al. 312 [20] reached a *plateau* (Figure 2a). Mueller et al. [8] focused on a natural mixed community including 313 bacteria and different species of microalgae. Therefore, the species succession over time with different 314 physiological requirements may have led to a continuous growth. In our case and for Kernan et al. 315 [20], the biofilms were composed by a single species that may have experienced over time energy or 316 nutrients limitation leading to a slowdown of the growth. Since nutrients were replenished every two 317 days, light was probably the limiting factor. Barranguet et al. [23] reported for instance that light was 318 attenuated up to 90% in mature phototrophic biofilms [23], whereas Schnurr et al. [43] reported that 319 the transmitted light for a biofilm with a thickness of  $100 \ \mu m$  (similar to the ones reported in this 320 study) was only 12% of the incident light. This means that for a photon flux density of 100  $\mu$ mol  $\cdot$  m<sup>-</sup> 321  $^{2} \cdot s^{-1}$  the cells in the deeper layers of the biofilm would receive only 12  $\mu$ mol  $\cdot$  m<sup>-2</sup>  $\cdot$  s<sup>-1</sup>, an intensity far 322 below the light compensation point measured for example in C. vulgaris biofilm (30-60 µmol photons 323  $\cdot m^{-2} \cdot s^{-1}; [44]).$ 

324 The roughness of the biofilms decreased over time along with the progressive filling of the initial 325 voids by new daughter cells (Figure 2b). A similar behavior has been described for natural multi-326 specific river biofilms [45] and for bacteria biofilms [10,41]. Mueller et al. [8] on the other hand, 327 reported a positive correlation between biovolume and roughness and a parallel increase of diatoms 328 over time. This is in agreement with the biofilm of the diatom *C. closterium* that exhibited only minor 329 changes of roughness over time (Figure 2b). The progression from rough to smoother surfaces as a 330 biofilm mature has been proposed to be dependent either on cells metabolic rate or on the maximum 331 internal transport rate of nutrients [46,47]. In the case of cells with low metabolic activity (and 332 therefore high nutrient availability) the valley between the biofilm peaks grow and merge with 333 adjacent peaks decreasing the roughness of a biofilm. Cells with high metabolic rate might become 334 nutrient limited and division will proceeds only at the biofilm peaks (i.e. along the vertical nutrient 335 gradients; [46,47]), inducing the formation of finger-like structures. Based on these observations, the 336 development of smoother biofilms along time, in P. purpureum, C. vulgaris and C. autotrophica, as 337 compared to the rougher structured biofilms in C. closterium, may reflect different cell metabolic rates. 338 Further metabolic investigations, such as intracellular measurements or O<sub>2</sub> evolution, will be 339 necessary to validate these conclusions.

340 As the majority of studies on photosynthetic biofilms focused on natural mixed communities 341 (i.e. formed by bacteria and microalgae), little is known about EPS dynamics in microalgae biofilms. 342 Here, we report the ability of microalgae to set up a supporting matrix and the dynamics of EPS 343 during biofilm development. Interestingly, whereas the dynamics of cells were similar among all the 344 species (Figure 2), those of EPS were more species-specific (Figure 3a): the two green algae did not 345 show any quantitative change of the EPS whereas *P. purpureum* and *C. closterium* presented a greater 346 volume of EPS over time. These different trends are in agreement with the great variety of dynamics 347 reported elsewhere as a function of the community composition. Trends of EPS production in 348 photosynthetic biofilms present in the literature are indeed very disparate [8,23,24]. Ratios of matrix 349 components (either considering lectins or dextran) to cells were not significantly different over time

for all species, which may indicate a stable physiological state of the cells within the biofilm. Interestingly, they were positively correlated to the biofilm roughness coefficient, indicating that irregular surfaces were associated with high EPS content and low cell biovolume. Similar ratios of EPS to cells have been reported for stream mixed biofilms by Battin et al. [45], which proposed that high EPS content may be advantageous for the attachment of the cells and first colonization of the substratum.

356 During biofilm development, several processes such as cell growth, EPS excretion or 357 consumption [48], as well as the establishment of chemical and physical gradients may be responsible 358 for the vertical distribution of cells and matrix components [9]. The few literature data about z-359 profiles in photosynthetic biofilms indicate that the distribution of cells and EPS is very much 360 dependent on the culture conditions and on the biofilm nature (bacteria, algae or mixed 361 communities), nevertheless some patterns can be drawn [8,18,20,23]. The maximal coverage for 362 photosynthetic organisms seems to occur within the first 40 µm from the substratum, whereas EPS 363 seem to match the cells position in young biofilms and to be mostly placed in layers above the cells 364 in older biofilms. In our work, at day 2 the cell z-profile was consistent with the patterns described 365 in the literature: maximal areal coverage of the cells positioned at 20 µm from the substratum (Figure 366 4) and greatest coverage of EPS typically co-localized with the cells in proximity of the substratum 367 (~20 µm). This means that the matrix components were mostly interspersed between the cells [49]. 368 Along time, the maximal areal coverage of the cells moved at greater distances from the substratum 369 as described in Cole et al. [18] but the location of the maximum EPS density remained stable over 370 time (Figure 4). It is therefore likely that the production of EPS in deep layers may have been 371 responsible for the upward growth of the biofilm by global advection [48,50] This is also supported 372 by the fact that the maximum cell coverage moved upward as a function of the biofilm thickness 373 whereas the EPS maximal coverage remained stable (Figure S2).

374 In bacteria, changes in biofilms structures have been reported to be strongly related to qualitative 375 shift in the macromolecular composition of the EPS, which in turn may alter biofilms functions and 376 properties [14,15,17,51]. In order to evaluate the relationships among macromolecules and structures 377 in microalgae biofilms, a correlation analysis using the CLSM and FTIR results was performed. Lipids 378 and/or carbohydrates changed in concentration as the biofilms matured and their architecture 379 became more complex (Figure 5 and S3). The lack of correlation between the macromolecular changes 380 and the EPS and dextran volumes (except for *P. purpureum*) might indicate a reallocation of carbon in 381 the cells rather than changes in matrix components. P. purpureum behaved differently, and such 382 changes were positively correlated to the EPS and dextran volumes (Figure S4), suggesting an 383 increase in glycoconjugates in the matrix as the biofilm matured [52].

384 Concluding, the development, architecture and macromolecular composition of monospecific 385 microalgae biofilms seem to be strongly species-dependent. The selection of a microalgae strain for 386 further cultivation in biofilm-based systems is therefore a crucial step for the whole process as specific 387 structural features maybe more or less advantageous under a certain set of culture conditions. Future 388 studies will be required to address how hydrodynamics and the fluctuating light conditions, 389 characteristic of outdoor cultivation systems, influence the structures and composition of algal 390 biofilms. The data recorded in this study may be used to feed and calibrate photosynthetic growth 391 models to better understand the mechanisms behind biofilm development under different conditions 392 [53]. Extension of these models for large-scale production can be used for optimal process design or 393 to guide the process operations. Furthermore, microfluidic tools or larger flow-cells are promising 394 tools for completing the picture and eventually providing an overview of the advantages and pitfalls 395 of using microalgae biofilm-based system [22]

Supplementary Materials: The following are available online at www.mdpi.com/xxx/s1, Figure S1: Vertical profiles of cells and dextran, Figure S2: Dependency of the depth of maximal coverage of cells and glycoconjugates (EPS) as a function of the average biofilm thickness, Figure S3: ATR-FTIR spectra of microalgae biofilms, Figure S4: Correlation plot, Table S1: Instrumental settings of the confocal microscope, Table S2: Biofilm 400 structural parameters calculated using COMSTAT 2.1.

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