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Screening of marine microalgae: Investigation of new exopolysaccharide producers

C. Gaignard[a], C. Laroche[a], G. Pierre[a], P. Dubessay[a], C. Delattre[a,d], C. Gardarin[a], P. Gourvil[b], I. Probert[b], A. Dubuffet[c], P. Michaud[a,*]

[a] Université Clermont Auvergne, CNRS, SIGMA Clermont, Institut Pascal, F-63000 CLERMONT-FERRAND, France
[b] Station Biologique de Roscoff (SBR), FR2424, Sorbonne Université, CNRS, Place Georges Teissier, 29680, Roscoff, France
[c] Université Clermont Auvergne, CNRS, Laboratoire Microorganismes: Génome et Environnement, F-63000 CLERMONT-FERRAND, France
[d] Institut Universitaire de France (IUF), 1 rue Descartes 75005 Paris, France

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ABSTRACT

Biopolymers, such as exopolysaccharides are widely exploited by industry as hydrocolloids (gelling, thickening agents) and biological agents (anti-inflammatory, anti-parasitic, antioxidant, *etc.*). In this study, 166 marine microalgae and cyanobacteria species have been screened in order to identify strains producing original exopolysaccharides. This screening allowed the highlighting of 45 positive strains. In a second time, the monosaccharide compositions from 20 EPS of them were determined by GC/MS and HPAEC-PAD. The results led to a discovery of 8 new genera of microalgae producing EPS, including polymers with a very original composition like richness in GlcA. Finally, a phylogenic tree has been contructed in order to assess the link between the phylogeny of microalgae and the global composition of their exopolymers, based on data obtained in this study and from the literature.

1. Introduction

Microalgae and cyanobacteria are single-cell photoautotrophic microorganisms which can produce biomass with a great efficiency using solar energy, water and CO_2. These organisms represent a huge diversified group including theoretically between 200 000 and 800 000 different species, 35 000 of them being really identified in marine and fresh water environments but also acidic lakes, hypersaline waters, or desert areas [1]. These photosynthetic microorganisms can be divided into blue-green algae or cyanobacteria and major eukaryotic groups including green microalgae (Chlorophyta and Charophyta), red microalgae (Rhodophyta) and brown-golden microalgae (Ochrophyta, Haptophyta and Miozoa). This large taxonomic diversity makes microalgae very attractive to produce valuable and diverse biomolecules such as pigments, proteins including some enzymes, polyunsaturated fatty acids (PUFAs), lipids, and exopolysaccharides (EPS). These compounds present some interests for many diverse industrial areas, like pharmaceutical, nutraceutical, cosmetic and food/feed production [2,3]. However, the development and commercialization of these metabolites is still early and only niche markets are currently available for microalgae products. Their low usage is very surprising but may be easily explained by the costs involved in microalgae production, limiting their applications to the field of high value products. These costs are linked to the photoproduction, the harvest of microalgae in diluted media, the recycling of culture media and the difficulty to refine this biomass [4,5].

Among the high value compounds from microalgae, EPS are very promising. Even if polysaccharides from animals, fungi and higher plants (including macroalgae) have been studied for many years, interest of the scientific community for EPS produced by microalgae and cyanobacteria is much more recent as described by Rossi and De Philippis [6] and Delattre et al. [7]. Based on their function, polysaccharides from photosynthetic microorganisms can be divided into three families: i) structural polysaccharides from cell walls, ii) storage polysaccharides which are intracellular and iii) matricial polysaccharides released into the environment. Some of them are not completely released into the medium and remain linked to the cell. So, matricial polysaccharides were split into two categories by authors: i) those which are retained to the cell and called cell-bound polysaccharides or capsular polysaccharides and ii) those completely released into the environment and described as extracellular polysaccharides, extracellular polymeric substance or exopolysaccharides (EPS). Today, there is always a thin line between these categories and the term “EPS” is often clumsily used to qualify cell bound

* Corresponding author.
E-mail address: philippe.michaud@uca.fr (P. Michaud).

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polysaccharides. The first publication focusing on EPS from microalgae was published in 1964 by Tischer and Moore and revealed the composition of a polymer produced by *Palmella mucosa* [8]. Since the number of species of microalgae/cyanobacteria producing EPS described in literature has increased at a moderate level. Even if the effects of environment (culture conditions) on the EPS production by microalgae and cyanobacteria appear as species dependent, nutrient limitation and notably nitrogen starvation is the most described environmental constraint leading to EPS synthesis [7]. The main families characterized for the EPS production are Desmidiaceae, Chlamydomonadaceae, Chlorellaceae, Porphyridiaceae and Glaucosphaeraceae in microalgae, and Nostocaceae, Oscillatoriaceae and Microcoleaceae in cyanobacteria. Note also that some microalgae belonging to the Chromista kingdom and more especially those from the Bacilariophyceae class have also been described for the production of EPS. This rise is not really correlated with the large taxonomic diversity of microalgae despite the detection of *in vivo* and *in vitro* biological activities associated to the presence of these biopolymers such as immunomodulatory [9], anti-oxidative [10], anti-inflammatory [11], anticoagulant [12], antibacterial [13], anticancer [14], or anti-parasitic [15] ones. Some interesting rheological properties revealed also the potential of these EPS as gelling and thickening agents [7]. Based on these observations but also on the large diversity of unstudied microalgae, these microorganisms are very attractive regarding the production of new EPS.

The aim of this study was to increase the knowledge about the diversity of microalgae/cyanobacteria producing original EPS and to screen them for this phenotype. It has been done as part of the French Polysalgue project funded by the French National Research Agency (ANR) and aims to identify new strains of microalgae and cyanobacteria for the production of high value EPS. Previous screening studies had been done by De Philippis et al. [16,17] but they were restricted to 15 and 25 strains of the *Cyanothece* and *Nostoc* genera (cyanobacteria), respectively. In this work 166 original strains including 150 microalgae and 16 cyanobacteria from diverse phylogenetic groups collected and distributed by the Roscoff Culture Collection (RCC), France (http://roscoff-culture-collection.org/) were screened for the production of EPS. Strains were selected based on their phylogenic diversity, their promising phenotype and their belonging to species not previously described as EPS producers. Positive strains were able to growth under chosing conditions of culture and to produce a minimum of 0.05 $g.L^{-1}$ of extracellular carbohydrates after 30 days of culture. The results obtained were discussed and compared to the literature in order to highlight a possible relationship between phylogenetic microalgae groups and EPS production/composition.

2. Material and methods

2.1. Screening procedure

The screening was performed on 166 marine microalgae and cyanobacteria species from the RCC (Table 1 and Supplementary data 1 Fig. S1). The f/2 medium was used for microalgae cultivation [18]. It was composed of $NaNO_3$ 0.075 g, $NaH_2PO_4.2H_2O$ 0.0055 g, Na_2EDTA 0.00416 g, $FeCl_3.6H_2O$ 0.00315 g, $CuSO_4.5H_2O$ 0.00001 g, $ZnSO_4.7H_2O$ 0.000022 g, $CoCl_2.6H_2O$ 0.00001 g, $MnCl_2.4H_2O$ 0.00018 g, $Na_2MoO_4.2H_2O$ 0.000006 g, cyanocobalamin (B12) 0.0000005 g, thiamin (B1) 0.0001 g and biotin 0.0000005 g dissolved in 1 L of artificial sea water (ASW). ASW was composed of NaCl 28.13 g, KCl 0.77 g, $CaCl_2.2H_2O$ 1.60 g, $MgCl_2.6H_2O$ 4.80 g, $NaHCO_3$ 0.11 g, $MgSO_4.7H_2O$ 3.50 g dissolved in 1 L of milliQ water. The pH was adjusted to 8–8.2 and the medium was sterilized by filtration (0.22 µm). The medium used for cyanobacteria was the PCR-S11 described by the RCC (http://roscoff-culture-collection.org/medium-id/pcr-s11-red-sea) and adapted from [19]. It was composed of one liter of Red Sea salt solution at 33.3 $g.L^{-1}$ supplemented by 1 mL of HEPES-NaOH 1 M (pH 7.5) buffer, 1 mL of Na_2-EDTA/$FeCl_3$ solution, 1 mL of Na-PO_4 50 mM (pH 7.5) buffer, 1 mL of $(NH_4)_2SO_4$ solution (400 mM), 100 µL of trace metals « Gaffron + Se » and 100 µL of vitamin B12 (10 $mg.mL^{-1}$). The red Sea salt solution was sterilised at 121 °C during 20 min whereas the other solutions were filet-sterilized (0.22 µm). The HEPES-NaOH 1 M (pH 7.5) buffer was composed of 119.5 g of HEPES dissolved in 250 mL of milliQ water. The pH of the solution was adjusted to 7.5 before diluting with milliQ water to a final volume of 500 mL. The Na_2-EDTA/$FeCl_3$ complex solution was prepared dissolving $FeCl_3.6H_2O$ (1.08 g) and Na_2-EDTA (1.488 g) in 40 mL of HCl (0.1 M) and 40 mL of NaOH (0.1 M), respectively, before mixing and diluting with milliQ water to a final volume of 2 L. The « Gaffron + Se » trace metal solution used contained for one litre of milliQ water H_3BO_3 (0.186 g), $MnSO_4.H_2O$ (0.101 g), $(NH_4)_6MO_7O_{24}.4H_2O$ (0.00198 g), KBr (0.00516), KI (0.00714 g), $ZnSO_4.7H_2O$ (0.00498 g), $(Cd(NO_3)_2.4H_2O$ (0.01725 g), $Co(NO_3)_2.6H_2O$ (0.00925 g), $CuSO_4.5H_2O$ (0.00876 g), $NiCl_2.6H_2O$ (0.0071 g), $Cr(NO_3)_3.9H_2O$ (0.0024 g), $VOSO_4.5H_2O$ (00,015 g), $KAl(SO_4)2.12H_2O$ (0.0284 g) and SeO_2 (0.0033 g). Finally, the Na-PO_4 50 mM (pH 7.5) buffer was composed of 6 g of NaH_2PO_4 dissolved in 1 L of milliQ water mixed with 3.55 g of Na_2HPO_4 dissolved in 500 mL of milliQ water. The pH of the buffer was then adjusted to 7.5.

Strains were cultivated photoautotrophically during 30 days in 50 mL flasks containing 20 mL of medium inoculated with 4 mL of microorganism culture. Cultures were performed at 20 °C under stirring (120 rpm). The values of irradiance were 150 and 300 µmoL m^{-2} s^{-1} in parallel with a light:dark regime (16h: 8 h). These irradiance values were chosen in order to be suitable for strains growing at low (150 µmoL m^{-2} s^{-1}) and high (300 µmoL m^{-2} s^{-1}) light intensities in accordance with literature [3,7]. This also allowed studying the impact of the light intensity on the production of EPS for further experiments. Samples of 1 mL were collected throughout the process to follow cell growth, nitrate consumption and extracellular sugars production.

2.2. Growth, nitrate consumption and EPS production measurements

Growth of microalgae/cyanobacteria was followed by spectrophotometry (A_{750}). This wavelength was chosen to avoid interferences with the pigments. Nitrate and ammonium concentrations were measured on supernatant of culture samples treated by centrifugation (10 000 *g* for 10 min at 20 °C) according to the method of Caswe et al. [20] modified by A.P.H.A [21], and Patton and Crouch [22]. Total sugars contents in the same supernatants desalted using a 10 kDa membrane were determined according to the phenol sulphuric assay [23] and expressed as D-glucose equivalent ($g.L^{-1}$).

2.3. Exopolysaccharide production

Strains identified as potential EPS producers were transferred to a modified f/2 medium supplemented in nitrogen and phosphorous sources (1 g of $NaNO_3$ and 0.2 g of $NaH_2PO_4.2H_2O$) and called enriched f/2 medium. These concentrations were determined based on a stoichiometric approach [24,25]. Strains were maintained photoautotrophically in 500 mL flasks containing 200 mL of enriched f/2 medium inoculated with 20 mL of microalgae culture in exponential phase of growth. Culture conditions were similar to those of screening. Strains were let growing in these conditions during 60 days in order to maximize the biomass production, including EPS.

2.4. Exopolysaccharide extraction

Cultures were centrifuged at 10 000 *g* for 15 min at 20 °C. EPS in supernatants were desalted by cycles of concentrations-dilutions (milliQ water) using an Amicon centrifugal filter equipped with a 10 kDa NMWCO membrane. EPS were considered as purified when the conductivity of the filtrates was near to that of milliQ water (around 2 µS.cm^{-1}). Finally, EPS solutions were freeze-dried during 48 h and

Table 1
Growth (A_{750}), production of extracellular carbohydrates and phenotype of 166 microalgae and cyanobacteria from the RCC.

part 1

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Bacteria	Cyanobacteria	Cyanophyceae	Chroococcales	Microcystaceae	*Microcystis*	sp.	26	+	0.00	EPS-
			Nostocales	Aphanizomenonaceae	*Nodularia*	*spumigena*	4299	+	0.00	EPS-
			Pleurocapsales	Xenococcaceae	*Xenococcus*	sp.	2703	+	0.00	EPS-
			Spirulinales	Spirulinaceae	*Spirulina*	sp.	1786	+	0.00	EPS-
			Synechococcales	Acaryochloridaceae	*Acaryochloris*	*marina*	1983	+	0.00	EPS-
						tomasi	1774	+	0.00	EPS-
				Leptolyngbyaceae	*Leptolyngbya*	sp.	232	+	0.00	EPS-
				Prochloraceae	*Prochlorococcus*	sp.	269	+	0.00	EPS-
				Synechococcaceae	*Cyanobium*	sp.	2436	+	0.00	EPS-
					Synechococcus	sp.	2380	+	0.12*	EPS+
							1084	+	0.00	EPS-
							2035	+	0.00	EPS-
							2368	+	0.00	EPS-
							2381	+	0.00	EPS-
							2383	+	0.00	EPS-
							4555	+	0.00	EPS-

part 2

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Chromista	Ochrophyta	Bacillariophyceae	Bacillariales	Bacillariaceae	*Cylindrotheca*	sp.	2608	–	–	NGS
					Nitzschia	sp.	2638	–	–	NGS
			Fragilariales				2598	+	0.00	EPS-
			Naviculales	Naviculaceae	*Navicula*	sp.	3092	–	–	NGS
		Chlorarachniophyceae	Chlorarachniales	Chlorarachniaceae	*Bigelowiella*	*natans*	2352	+	0.05*	EPS+
		Coscinodiscophyceae	Rhizosoleniales	Rhizosoleniaceae	*Guinardia*	*flaccida*	3093	–	–	NGS
		Cryptophyceae	Chromulinales	Chromulinaceae	*Ochromonas*	sp.	2350	–	–	NGS
				Chrysamoebaceae	*Chrysamoeba*	sp.	377	–	–	NGS
			Cryptomonadales	Hemiselmidaceae	*Chroomonas*	sp.	1504	–	–	NGS
						sp.	3436	+	0.02	EPS-
					Hemiselmis	sp.	2614	–	–	NGS
			Pyrenomonadales	Geminigeraceae	*Proteomonas*	sp.	3072	+	0.02	EPS-
						sulcata	3649	–	–	NGS
				Pyrenomonadaceae	*Rhinomonas*	sp.	821	+	0.00	EPS-
						sp.	1978	+	0.02	EPS-
		Dictyochophyceae	Florenciellales		*Pseudochattonella*	*verruculosa*	1082	–	–	NGS
			Rhizochromulinales	Rhizochromulinaceae	*Rhizochromulina*	sp.	4438	–	–	NGS

part 3

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Chromista	Ochrophyta	Mediophyceae	Chaetocerotales	Chaetocerotaceae	*Chaetoceros*	sp.	2564	–	–	NGS
		Mediophyceae	Cymatosirales	Cymatosiraceae	*Papiliocellulus*	sp.	2624	+	0.00	EPS-
					Minutocellulus	sp.	1863	–	–	NGS
			Eupodiscales	Eupodiscaceae	*Odontella*	sp.	2558	–	–	NGS
			Lithodesmiales	Lithodesmiaceae	*Ditylum*	*brightwellii*	775	–	–	NGS
			Thalassiosirales	Skeletonemataceae	*Skeletonema*	sp.	2932	–	–	NGS
				Thalassiosiraceae	*Minidiscus*	*trioculatus*	4657	–	–	NGS
					Thalassiosira	sp.	1714	–	–	NGS
						weissflogii	76	–	–	NGS
		Pelagophyceae	Pelagomonadales	Pelagomonadaceae	*Aureococcus*	*anophagefferens*	96	–	–	NGS
							4094	–	–	NGS
					Pelagococcus	sp.	3069	+	0.10**	EPS+
			Sarcinochrysidales	Sarcinochrysidaceae	*Andersenia*	*nodulosa*	4631	+	0.01	EPS-
					Aureoumbra	*lagunensis*	97	–	–	NGS
							2696	+	0.01	EPS-
		Phaeothamniophyceae	Aurearenales	Aurearenaceae	*Aurearena*	*cruciata*	4621	+	0.01	EPS-
		Pinguiophyceae	Pinguiochrysidales	Pinguiochrysidaceae	*Glossomastix*	sp.	1196	+	0.01	EPS-

(*continued on next page*)

Table 1 (*continued*)

part 4

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Chromista	Ochrophyta	Pinguiophyceae	Pinguiochrysidales	Pinguiochrysidaceae	*Glossomastix*	sp.	3685	+	0.06*	EPS+
						sp.	3688	+	0.10**	EPS+
						sp.	3707	+	0.11*	EPS+
					Phaeomonas	sp.	4470	+	0.07**	EPS+
		Raphidophyceae	Chattonellales	Fibrocapsaceae	*Fibrocapsa*	*japonica*	1501	–	–	NGS
					Heterosigma	*akashino*	1502	+	0.01	EPS-
		Synchromophyceae	Synchromales	Synchromaceae	*Guanchochroma*	*wildpretii*	3390	–	–	NGS
							CC 19	+	0.13*	EPS+
	Haptophyta	Coccolithophyceae	Coccolithales	Calcidiscaceae	*Calcidiscus*	*leptoporus*	1170	–	–	NGS
					Oolithotus	*fragilis*	2321	–	–	NGS
				Calyptrosphaeraceae	*Calyptrosphaera*	sp.	1180	+	0.77**	EPS+
						sphaeroidea	1178	–	–	NGS
				Coccolithaceae	*Coccolithus*	*braarudii*	3777	–	–	NGS
				Hymenomonadaceae	*Hymenomonas*	*coronata*	1337	+	0.05*	EPS+
					Ochrosphaera	*verrucosa*	3650	+	0.05*	EPS+
						sp.	3635	+	0.05*	EPS+
							2976	–	–	NGS

part 5

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Chromista	Haptophyta	Coccolithophyceae	Isochrysidales	Isochrysidaceae	*Chrysotila*	sp.	4633	+	0.22*	EPS+
						sp.	CCAP 904/1	+	0.16*	EPS+
						roscoffensis	1395	+	0.03	EPS-
			Isochrysidales	Isochrysidaceae	*Isochrysis*	*braarudii*	3686	+	0.06*	EPS+
					Ruttnera	*lamellosa*	4061	+	0.05*	EPS+
					Tisochrysis	*lutea*	3699	+	0.02	EPS-
				Noelaerhabdaceae	*Emiliania*	*huxleyi*	1216	+	0.07**	EPS+
							1217	+	0.02	EPS-
					Gephyrocapsa	*oceanica*	1314	–	–	NGS
			Phaeocystales	Phaeocystaceae	*Phaeocystis*	*globosa*	739	–	–	NGS
							1719	–	–	NGS
					Phaeocystis	sp.	851	–	–	NGS
							908	–	–	NGS
							925	–	–	NGS
							940	–	–	NGS
							2055	–	–	NGS
							3539	–	–	NGS
			Prymnesiales	Prymnesiaceae	*Prymnesium*	*parvum*	3426	+	0.12*	EPS+

part 6

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Chromista	Haptophyta	Coccolithophyceae	Prymnesiales	Prymnesiaceae	*Imantonia*	*rotunda*	1342	+	0.04	EPS-
					Haptolina	*hirta*	3421	–	–	NGS
				Chrysochromulinaceae	*Chrysochromulina*	*camella*	1186	–	–	NGS
			Zygodiscales	Pontosphaeraceae	*Scyphosphaera*	*apsteinii*	1456	–	–	NGS
							3704	+	0.05*	EPS+
		Pavlovophyceae	Pavlovales	Pavlovaceae	*Diacronema*	sp.	3514	+	0.29**	EPS+
						lutheri	1537	+	0.01	EPS-
						viridis	3459	+	0.02	EPS-
					Exanthemachrysis	sp.	1536	+	0.06*	EPS+
							1544	+	0.10*	EPS+
					Pavlova	*enorae*	1525	+	0.05*	EPS+
						gyrans	1545	+	0.05*	EPS+
						sp.	4037	+	0.09*	EPS+
							4120	+	0.08*	EPS+
							4070	+	0.07*	EPS+
							3438	+	0.39*	EPS+
					Rebecca	sp.	1528	+	0.05**	EPS+

(*continued on next page*)

Table 1 (*continued*)

part 7

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Chromista	Haptophyta						6688	+	0.10*	EPS+
	Miozoa	Dinophyceae	Gonyaulacales	Ostreopsidaceae	*Alexandrium*	*minutum*	1490	+	0.01	EPS-
			Gymnodiniales	Brachidiniaceae	*Karenia*	*brevis*	4635	–	–	NGS
						mikimotoi	1513	–	–	NGS
				Gymnodiniaceae	*Amphidinium*	*carterae*	1522	+	0.05**	EPS+
					Cochlodinium	*polykrikoides*	4634	–	–	NGS
					Lepidodinium	*chlorophorum*	1489	–	–	NGS
			Peridiniales	Heterocapsaceae	*Heterocapsa*	sp.	3466	+	0.01	EPS-
							2616	–	–	NGS
			Prorocentrales	Prorocentraceae	*Prorocentrum*	*micans*	1517	–	–	NGS
			Suessiales	Suessiaceae	*Biecheleriopsis*	sp.	3656	–	–	NGS
					Pelagodinium	sp.	3003	–	–	NGS
					Symbiodinium	*kawagutii*	4019	+	0.02	EPS-
						voratum	1521	+	0.03	EPS-
			Thoracosphaerales	Thoracosphaeraceae	*Thoracosphaera*	*heimii*	1512	+	0.01	EPS-
					Scrippsiella	*trochoidea*	1515	+	0.01	EPS-

part 8

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Plantae	Chlorophyta	Chlorodendrophyceae	Chlorodendrales	Chlorodendraceae	*Tetraselmis*	*chui*	128	+	0.05*	EPS+
						globosa	1564	+	0.05*	EPS+
						rubens	133	+	0.05*	EPS+
						striata	130	+	0.02	EPS-
						sp.	4435	+	0.21**	EPS+
							119	+	0.03	EPS-
		Chlorophyceae	Chlamydomonadales	Chlamydomonadaceae	*Chlamydomonas*	sp.	3443	+	0.01	EPS-
				Dunaliellaceae	*Dunaliella*	sp.	5	+	0.06**	EPS+
						tertiolecta	6	+	0.02	EPS-
		Mamiellophyceae	Mamiellales	Bathycoccaceae	*Bathycoccus*	*prasinos*	4222	–	–	NGS
				Mamiellaceae	*Micromonas*	*commoda*	827	+	0.01	EPS-
					Ostreococcus	*tauri*	1108	+	0.01	EPS-
		Nephrophyceae	Nephroselmidales	Nephroselmidaceae	*Nephroselmis*	sp.	1805	+	0.03	EPS-

part 9

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) ±	Dubois assay [22]	Groups
Plantae	Chlorophyta	Palmophyllophyceae	Prasinococcales	Prasinococcaceae	*Prasinococcus*	sp.	2684	+	0.07*	EPS+
					Prasinoderma	sp.	2686	+	0.02	EPS-
		Picocystophyceae	Picocystales	Picocystaceae	*Picocystis*	*salinarum*	3402	+	0.02	EPS-
		Pyramimonadophyceae	Pseudoscourfieldiales	Pycnococcaceae	*Pycnococcus*	*provasolii*	2336	+	0.01	EPS-
							3439	+	0.01	EPS-
			Pyramimonadales	Pyramimonadaceae	*Pyramimonas*	sp.	4212	–	–	NGS
		Trebouxiophyceae	Chlorellales	Chlorellaceae	*Chlorella*	sp.	2340	+	0.05*	EPS+
					Nannochloris	sp.	3644	+	0.00	EPS-
					Picochlorum	sp.	3065	+	0.00	EPS-
				Coccomyxaceae	*Coccomyxa*	sp.	903	+	0.05*	EPS+
							3440	–	–	NGS
	Rhodophyta	Porphyridiophyceae	Porphyridiales	Porphyridiaceae	*Porphyridium*	sp.	4628	+	0.23*	EPS+
		Rhodellophyceae	Glaucosphaerales	Glaucosphaeraceae	*Rhodella*	*maculata*	655	+	0.06*	EPS+
		Stylonematophyceae	Stylonematales	Stylonemataceae	*Chroodactylon*	*ramnosum*	654	+	0.01	EPS-
					Stylonema	sp.	2964	+	0.00	EPS-

(*continued on next page*)

Table 1 (*continued*)

part 10

Kingdoms	Phyla	Classes	Orders	Families	Genera	Species	RCC numbers	Growth (A_{750}) $^{\pm}$	Dubois assay [22]	Groups
							3452	+	0.06*	EPS+
							A13 880	+	0.08*	EPS+
							CC 21	+	0.05*	EPS+
							CC 76	+	0.05*	EPS+
							3641	+	0.01	EPS-
							4078	+	0.01	EPS-
							18/1	+	0.00	EPS-
							AST 713	+	0.01	EPS-
							CC 14	+	0.01	EPS-
							CC 20	+	0.02	EPS-
							3448	–	–	NGS
							3473	–	–	NGS
							AST 714	–	–	NGS
							JAP PR7	–	–	NGS
							JAP PR8	–	–	NGS
							KO 334	–	–	NGS
							OSH 51	–	–	NGS

The classification was done according to the AlgaeBase database [29]: no classification available. +: positive result, -: negative result, EPS+: positive strain, EPS producer, EPS-: negative strain, no EPS producer, NGS: Not Growing-Strain, * value obtained at 150 and µmol $m^{-2}.s^{-1}$ and** value obtained at 300 µmoL $m^{-2}.s^{-1}$, $^{\pm}$ growth expressed as significant increase of A_{750} in time.

samples were stored at room temperature until further analyses.

2.5. Monosaccharide compositions

Monosaccharides compositions of EPS were both determined by High-Pressure Anion Exchange Chromatography equipped with Pulsed Amperometric Detection (HPAEC-PAD) and Gas Chromatography coupled to Mass Spectrophotometer with Electron Ionization (GC/MS-EI) to ensure data complementary. For both methods results were expressed in molar ratio percentages.

For HPAEC-PAD analyses, 10 mg of EPS were dissolved in 1 mL of 2 M trifluoroacetic acid (TFA) solution in a glass tube and heated at 120 °C for 90 min. The samples were stirred 3 times during the hydrolysis. After hydrolysis, pH was adjusted to 7 by addition of ammonium hydroxide (35 % w/v) and the solutions were centrifuged at 14 000 *g* for 15 min at room temperature. Supernatants were filtered through 0.2 µm membrane filter and analyzed by HPAEC with an ICS 3000 system (Dionex Corporation, Sunnyvale (CA), USA) equipped with pulsed amperometric detection (PAD) and AS 50 autosampler. Twenty-five µL of samples were injected in the system and eluted into a pre-column CarboPac PA1-column (4 × 50 mm) and an analytical CarboPac PA1-column (4 × 250 mm) equilibrated 15 min with 18 mM NaOH. Samples were eluted isocratically with 18 mM NaOH for 25 min, followed by a linear gradient between 0 to 0.5 M sodium acetate in 200 mM NaOH for 20 min to elute acidic monosaccharides. Run was followed by 15 min washing with 200 mM NaOH. The eluent flow rate was kept constant at 1 $mL.min^{-1}$. Columns were thermostated at 25 °C. Data were collected and analyzed with Dionex Chromeleon 6.80 software (Sunnyvale, USA). L-Rha, D-Rib, L-Fuc, L-Ara, D-Xyl, D-Man, D-Gal, D-Glc, D- GlcA, and D-GalA were used as standards.

For GC/MS analyses, 15 mg of EPS were dissolved in 1.5 mL of TFA in a glass tube followed by heating at 120 °C for 90 min. The samples were mixed each 30 min. The preparations were then evaporated under nitrogen stream. The dried residues were dissolved in BSTFA: TMCS (99: 1) following the procedure described by Pierre et al. [26,27], then evaporated again under nitrogen stream. Dichloromethane was finally added to the derivatized products prior to injection onto GC/MS-EI apparatus. Standards (L-Rha, D-Rib, L-Fuc, L-Ara, D-Xyl, D-Man, D-Gal, D-Glc, D-GlcA, D-GalA, D-GlcN, D-GalN) were prepared following the same procedure. Analyses were carried out by GC/MS-EI using an Agilent 6890 Series GC System coupled to an Agilent 5973 Network Mass Selective detector. Derivatives were analyzed using an OPTIMA-1MS (30 m, 0.32 mm, 0.25 mm) column, under helium flow of 2.3 $mL.min^{-1}$. The helium pressure was set to 8.8 psi and the split ratio to 50:1. The temperature was programmed to 100 °C for 3 min then raised to 200 °C at 8 $°C.min^{-1}$ keeping for 1 min then continuing with a final temperature increment to 215 °C at 5 $°C.min^{-1}$. The ionization was carried out by Electronic Impact (EI, 70 eV). The trap temperature was fixed to 150 °C and the target ion was from 40 to 800 *m/z*. Data processing was done with LC/MSD Trap Version 5.3 and MestreNova Version 7.1 Softwares (Agilent).

2.6. Relationship between phylogeny and exopolysaccharide composition

2.6.1. Statistics analysis

Differences in levels of each monosaccharide were tested between 5 of the 6 microalguae phyla. Miozoa were not included in the analysis, since only two monosaccharide compositions were available. For each monosaccharide, Kruskal-Wallis tests were performed. When a significant difference was found ($p < 0.05$), this test was followed by multiple pairwise comparisons between phyla (Mann-Whitney tests), with significance levels adjusted according to the Benjamini and Hochberg method [28].

2.6.2. Phylogenetic tree

Monosaccharide compositions of 81 EPS from microalgae (including those from the strains CCAP 904/1, RCC4633, RCC3686, RCC6688, RCC3514, RCC1544, RCC1545, RCC4037, RCC4120, RCC3438, RCC3688, RCC3685, RCC3707, RCC2380, RCC1564, RCC133, RCC4435, RCC5, RCC2684 and RCC4628), belonging to 6 major phyla and 15 different classes, were compiled in a phylogenetic tree. The classification used was that of Algaebase database (http://www.algaebase.org). Algaebase is an on-line database providing free access to authoritative taxonomic, distributional and nomenclatural information [29]. The nucleotide sequences coding for 18S ribosomal RNA (18S rRNA) were searched on the National Center for Biotechnology Information (NCBI) database for all these strains. For 41 species, 1–3 sequences were found on this database. For the others, sequences obtained from species belonging to the same genus were used. Other sequences have also been added to construct a phylogenetic tree consistent with recently published phylogenetic trees [30–32]. 214 sequences were obtained and aligned using the MUSCLE algorithm [33] available in the MEGA 7 software [34]. Then the tree was constructed using the Neighbor-Joining method with the MEGA 7 software over a

total of 1248 positions, based on the p-distance method with 2000 bootsraps. All positions containing gaps and missing data were eliminated. The monosaccharide compositions (in % of the total composition or presence/absence) of 81 strains were added to this phylogenetic tree using the iTOL tool [35]. All classes were supported by bootstrap values higher than 0.92, except for Zygnematophyceae (0.55), Chlorophyceae (0.54) and Trebouxiophyceae (0.35).

3. Results and discussion

3.1. Screening of strains with EPS + phenotype

Hundred and sixty-six (150 microalgae and 16 cyanobacteria) strains were selected from the 5852 strains of the RCC based on the following criteria: i) cover a maximum of phylogenetic diversity, ii) target classes and orders not described for the production of EPS, iii) select different species to study the diversity of compositions within the same genus and iv) choose strains with a "promising phenotype" as both biofilm and gel formations or slimy appearance during the cultures. Short morphologic descriptions of strains for which genus and species names are not known are available on the Roscoff Culture Collection (http://roscoff-culture-collection.org/). To identify positive strains two conditions were required: growing under the chosen conditions and producing a minimum of 0.05 $g.L^{-1}$ of true EPS at D30 (30 days). These criteria were evaluated thanks to the results of A_{750}, nitrate (or ammonium) and total carbohydrates assays (Table 1; Supplementary data Fig. S1). In support of these results, the 166 strains were classified into three groups.

The first group (EPS+) was composed of strains (45/166) for which the total carbohydrates assays [23] gave a positive result for at least one of the two light intensities. The Table 1 gives the higher value of EPS production (obtained with an irradiance of 150 or 300 µmoL $m^{-2}.s^{-1}$) for each strain. Some strains EPS + produced EPS at the two irradiances (strains A13 880, CC19, CCAP904/1, RCC1180, RCC1544, RCC1545, RCC2684, RCC3426, RCC3438, RCC3514, RCC3685, RCC3688, RCC3707, RCC4037, RCC4120, RCC4435, RCC4470, RCC4628, RCC4633 and RCC6688) whereas some other strains were detected as EPS producers at only 150 µmoL $m^{-2}.s^{-1}$ (CC21, CC76, RCC128, RCC133, RCC655, RCC903, RCC1337, RCC1525, RCC1536, RCC1564, RCC2340, RCC2352, RCC2380, RCC3452, RCC3635, RCC3650, RCC3686, RCC3704 and RCC4070) or 300 µmoL $m^{-2}.s^{-1}$ (RCC5, RCC1216, RCC1522, RCC1528 and RCC3069) irradiances. For the major part of these strains, the production of exocellular carbohydrates was correlated with a nitrogen starvation into the culture medium, as described in the literature [7]. This group included microalgae and cyanobacteria, together representing 7 phyla, 13 classes, 15 orders, 18 families and 24 genera. It was essentially composed of eukaryotes belonging to Chromista (30 species) or Plantae (10 species) kingdoms. Surprisingly, the *Synechococcus* sp., previously known for EPS production, was the sole member of prokaryotic domain whereas a large number of cyanobacteria has been described in previous studies for the production of EPS [36,37]. This observation could be explained by the very low number of screened cyanobacteria (only 16) but also by their ability to produce cell bound polysaccharides which are not measured in the extracellular medium. Four microalgae could not be phylogenetically classified due to a lack of information available in the RCC. The strains EPS + from the kingdom Chromista belong mainly to the Haptophyta and Ochrophyta phyla. Haptophyta are essentially represented by the Coccolithophyceae and Pavlovophyceae classes. The family Isochrysidaceae was the most represented in Coccolithophyceae with 45 % of EPS + strains. The family Pavlovaceae was the only representative of Pavlovophyceae. Among the Ochrophyta, the Pinguiochrysidaceae family included four strains belonging to the genera *Phaemonas* and *Glossomastix* among the five EPS+. The strains found EPS + in the kingdom Plantae belong to the Chlorophyta and Rhodophyta phyla. In Chlorophyta, the family Chlorodendraceae was detached from others as it accounted for 40 % of EPS + strains. All these strains belong to the sole *Tetraselmis* genus. Regarding the Rhodophyta, two EPS + strains belonging to the genera *Rhodella* and *Porphyridium*, which are well known in literature as EPS producers were detected [7].

The second group included strains not detected as EPS producers (EPS-) in the tested culture conditions. It was composed of 46 strains of microalgae and 15 strains of cyanobacteria. These strains are spread among 7 phyla, 20 classes, 29 orders, 34 families and 42 genera. Cell growth has been observed for all of them but not EPS production. For many microalgae strains, the release of EPS in the environment has been described to occur in response to a "stress", relating to a nutrient deficiency (nitrogen or phosphorous sources for instance), or the quality and the intensity of light or the salinity of the medium [38–44]. Nevertheless, the low amounts of nitrogen and phosphorous in the f/2 nutrient associated with growth cells observed by A_{750} measurements and the depletion of nitrogen (due to nitrate consumption) showed a nutrient deficiency, without production of EPS. Some strains of the group EPS- were able to grow to 300 µmoL $m^{-2}.s^{-1}$, suggesting that a high light intensity was not sufficient to induce an EPS production. Finally, other screening conditions may have prevented the EPS production, like inadequate pH, temperature or agitation for example. Indeed, in nature benthic microalgae are less tolerant to shear stress than pelagic ones [45]. Stirring at 120 rpm during the screening could affect the production of EPS for some strains. Another possible explanation would be the production of BPS, not measured by the methodology used during this work. Note also that despite their "promising phenotype" leading to their selection for this screening, these strains or a part of these strains could simply not be EPS producers.

The third group corresponded to the strains for which no growth was observed during the screening, called "Not Growth-Strain" (NGS). It was composed of 60 strains distributed into 5 phyla, 13 classes, 28 orders, 35 families and 42 genera. The lack of growth could come from the composition of the culture medium due to the possible lack of some essential elements. For example, the silica is mandatory for the development of the Bacillariophyta (diatoms belonging to the Ochrophyta) [46]. This hypothesis was supported by the fact that most of diatoms fall into this group (except two, which were found EPS-). The salinity of the medium (28 $g.L^{-1}$) can also be questioned.

Some strains belonging to families present in EPS- and NGS groups, including microalgae and cyanobacteria were also present in the EPS + group such as Synechococcaceae (Cyanobacteria), Chlorodendraceae (Chlorophyta), Isochrysidaceae and Pavlovaceae (Haptophyta). However most of the microalgae and cyanobacteria present in these two groups belong to classes, and more specifically to genera that do not appear in the group of EPS + strains. Table 2 presents an exhaustive list of strains identified in literature as EPS producers. Comparing the two data sets, most of them (20/25 total) belong to genera which were unknown for the production of soluble EPS. Additional analyzes should be needed to confirm the nature of extracellular sugars produced by EPS+ strains as EPS.

3.2. Exopolysaccharide production and analysis

Cultures of EPS + strains were carried out for 60 days in order to produce EPS which were subsequently extracted. Then analyses by HPAEC-PAD and GC/MS-EI were performed to validate the positive results from the colorimetric assays. Analyses concerned 5 of the 7 phyla and 7 of the 15 orders of the EPS + strains (45 % of the total strains). Some analyses were also performed on several EPS + strains from the same family, and sometimes on different species belonging to the same genus in order to study the variability of the compositions. Table 3 shows the results obtained using each method. Despite few differences the results of the compositions were similar, with the same main monosaccharides (Pearson: $R^2 = 0.963$; $p < 0.001$). Among the 11 genera whose EPS compositions were analysed, 3 have been already

Table 2
Monosaccharide and non sugars groups compositions of EPS from microalgae/cyanobacteria described in current literature.

part 1:

Genera (phyla)	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Achnanthes (Oc)	*longipes*	+	+ + +	+	+	+	–	+	+ +	+	–	nd	Nd		[58]
Amphora (Oc)	*coffeaeformis*	+	+ +	+	+	nd	nd	+	+ + +	+	nd	nd	Nd		
	holsatica	+	nd	+	+	nd	nd	nd	+	+	nd	nd	Nd		[64]
	rostrata	+	+ +	+	+	nd	nd	+	+ + +	+	nd	+	+	pyruvate	[57]
Ankistrodesmus (Chl)	*densus*	+	+ +	+	+	nd	nd	+	+ + +	+	–	–	Nd	linkages	[66]
Aulacoseira (Oc)	*granulata*	+ + +	+	nd	+	+	–	+	+	+ +	nd	nd	Nd	GlcNAc	[67]
Botryococcus (Chl)	*braunii*	+	+ + +	+	tr	tr	–	tr	+ +	+	–	nd	+		[68]
Bracteacoccus (Chl)	sp.	+ +	+ +	+	+ + +	nd	nd	+	+	+	–	+	Nd		[56]
Chaetoceros (Oc)	*affinis*	+	+	+	–	nd	nd	–	+	–	nd	+	Nd		[69]
	curvisetus	+	+ +	–	–	nd	nd	–	+ + +	–	–	+	Nd	linkages	[70]
	decipiens	+ + +	+ +	–	+	nd	nd	+	+ + +	+	–	nd	Nd	linkages	[71]
Chlamydomonas (Chl)	*agustae*	–	+	+	+ + +	+ +	–	+	–	+	–	nd	+	linkages	[72]
	corrosa	–	+ + +	+ +	+	–	+	–	–	–	–	nd	+	linkages	
	humicola	+	+	+ +	+ +	+	–	–	–	+ + +	–	nd	+		[73]

part 2

Genera (phyla)	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Chlamydomonas (Chl)	*peterfii*	–	+ + +	+	+	–	+ +	–	–	–	–	nd	+		[73]
Chlamydomonas (Chl)	*reinhardtii*	+	+	+	+	–	+	–	–	+	+	nd	–	pyruvate	[74]
	mexicana	+	+	+	+ + +	nd	nd	+	+ +	+	+	nd	Nd		[75]
	sajao	+	+ + +	+ +	+	nd	nd	+	–	+	–	nd	Nd		
	sajao	–	+ + +	+	+	–	+ +	–	–	–	–	nd	+		[73]
	stigmatophora	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	Nd		[76]
	sp.	–	–	–	+	–	–	–	+	+	–	nd	Nd		[77]
Chlorella (Chl)	*autotrophica*	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	Nd		[48]
	mirabilis (678 F)	+	+ + +	+ +	+	nd	nd	+	+	+	–	+	Nd		[56]
	mirabilis (7410 G)	+	+ + +	+	+	nd	nd	+	+ +	+	–	tr	Nd		
	ellipsoidea	+	+ + +	+	+	nd	nd	+ +	+	+	+	+	Nd		
	pyrenoidosa	+	+	+	+	–	–	+	+	+	–	nd	Nd		[78]
	vulgaris	+	–	–	+	+	–	–	–	+	–	nd	Nd		[77]
	ellipsoidea	–	–	+	+	+	–	–	+	–	–	nd	Nd		
	sp.	+	–	+	+	+	–	–	–	–	–	nd	Nd		
Closterium (Cha)	sp.	+	+	+	+	+ + +	–	+	+ +	+	–	nd	Nd	linkages	[54]
Cochlodinium (Mi)	*polykrikoides*	–	+	–	+	+	+	+	–	–	–	+	–		[79]

part 3

Genera (phyla)	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Coscinodiscus (Oc)	*nobilis*	+	tr	–	+	+	–	+ +	+ + +	+	nd	+	Nd		[80]
Cosmarium (Cha)	sp.	+	+ +	+	+	nd	nd	+	+ + +	+	+	+	+		[52]
Crypthecodinium (Mi)	*cohnii*	nd	+ +	nd	+ + +	nd	nd	+	+	nd	+	nd	Nd		[81]
Cylindrotheca (Oc)	*closterium*	+	+	–	+ +	nd	nd	+	nd	+ + +	nd	–	+		[82]
	fusiformis	+	+ + +	–	+ +	nd	nd	+	+	+	–	+	Nd		[83]
Cymbella (Oc)	*cistula*	+	+ + +	tr	+	–	–	+	–	+ +	–	nd	Nd		[58]
	mexicana	+	+ + +	tr	+	tr	–	+	+	+ +	–	nd	Nd		
Desmococcus (Chl)	*olivaceus*	+	+ + +	+	+ +	tr	tr	+	+	+	–	nd	+	linkages	[84]
Dixoniella (Rh)	*grisea*	+ +	+	+	+	+	–	tr	tr	+ + +	–	nd	+	methyl groups	[91]
Dunaliella (Chl)	*bardawil*	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	Nd		[48]
	tertiolecta	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	Nd		
	salina	–	+	–	+	–	–	–	–	+	–	nd	Nd		[43]
Flintiella (Rh)	*sanguinaria*	+	+ +	+	+	+	–	–	–	+ + +	–	tr	+	methyl and acetyl groups	[85]
Geminella (Chl)	*terricola*	+ +	+	+	+	nd	nd	+ + +	+	+	–	+	Nd		[56]
Gyrodinium (Mi)	*impudicum*	–	+ + +	–	–	+	+	–	–	–	–	+	+		[61]
Haematococcus (Chl)	*lacustris*	nd	+ +	nd	+	nd	nd	+ + +	nd	nd	nd	tr	Tr		[86]
Heterosigma (Chl)	*akashiwo*	+ +	+	+	+	+	–	+ + +	+	+	nd	+	Tr	ManA, linkages	[60]
Hyalotheca (Cha)	*dissiliens*	+	+ +	+	–	+ + +	–	–	+	+	–	nd	Nd	linkages	[55]
Klebsormidium (Cha)	*flaccidum* (749B)	+ +	+	+	+	nd	nd	+ + +	+	+	–	–	Nd		[56]

(*continued on next page*)

Table 2 (*continued*)

part 4

Genera (phyla)	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Klebsormidium (Cha)	*flaccidum* (446C)	+ + +	+	+	+	nd	nd	+ +	+	+	–	tr	nd		[56]
Klebsormidium (Cha)	*flaccidum* (748A)	+	+	+	tr	nd	nd	+ + +	+ +	+	–	+	nd		
Melosira (Oc)	*nummuloides*	+	tr	+	+	nd	nd	nd	+	+	nd	nd	nd		[65]
Micrasterias (Cha)	*denticulata*	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd		[87]
Navicula (Oc)	*directa*	+	+	+	+ +	nd	nd	nd	+ + +	+	nd	nd	nd		[65]
	salinarum	+	+	–	+ + +	nd	nd	+	nd	+ +	nd	+	+		[82]
	subinflata	+	+ +	+	+ + +	nd	nd	+	+	+	+	+	+	pyruvate	[88]
Netrium (Cha)	*digitus*	+	+	+	+	nd	nd	+	+ + +	+ +	tr	+	+		[52]
	interruptum	+	+	+	+	nd	nd	+	+ +	+ + +	+	+	+		
	oblongum	+	+ + +	+	+	nd	nd	+	+	+ +	tr	+	+		
Oocystis (Chl)	sp.	–	+	+	–	+	–	–	+	–	–	nd	nd		[77]
Palmella (Chl)	*mucosa*	–	–	+	+	+	–	–	+	–	–	nd	nd		
Penium (Cha)	*cylindrus*	+	+	+	+	nd	nd	+	+ + +	+ +	tr	+	nd		[52]
	spirostriolatum	+	+ +	+ + +	+	nd	nd	+	+	+	tr	+	+		
	margaritaceum	–	+	+	+	+	–	+	+ +	+ + +	–	nd	nd	methyl groups	[89]
Pleurotaenium (Cha)	*trabecula*	+	+	+	+	+	+	+	+ +	+ + +	+	+	+		[52]
Porphyridium (Rh)	*aerugineum*	–	+ +	–	+	+	–	–	–	+ + +	–	+	+	methyl groups	[50]

part 5

Genera (phyla)	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Porphyridium (Rh)	*cruentum*	+	+ +	+	+	nd	nd	+	+	+ + +	–	+	+		[47]
	cruentum	–	+	–	+ +	+	–	–	–	+ + +	–	+	+	methyl groups	[50]
	marinum	–	+ +	–	+	+	–	–	tr	+ + +	–	+	nd		[49]
	purpureum	–	+ + +	–	+	–	–	–	tr	+ +	–	+	–		[15]
	sp.	–	+ +	–	+	nd	nd	–	–	+ + +	–	+	nd	linkages	[90]
Rhodella (Rh)	*reticulata*	+	+	–	+ +	+	–	+	–	+ + +	+	nd	+		[92]
	maculata	+	+ + +	+	+	+	–	–	–	+ +	–	+	+		[15]
	violacea	+ +	+	+	+	+	–	–	–	+ + +	–	+	+		[25]
Scenedesmus (Chl)	*quadricauda*	nd	nd	nd	nd	nd	nd	nd	nd	nd	Nd	nd	nd		[93]
Spondylosium (Cha)	*panduriforme*	tr	+ +	+	+	+	–	–	+ +	+	–	–	+	linkages	[53]
Staurastrum (Cha)	*iversenii*	+	+ +	–	–	–	–	–	+ + +	+	–	–	+		[94]
Stichococcus (Chl)	*bacillaris* (772B ; 747C)	+ + +	+	+	+	nd	nd	+	tr	+ +	–	tr	nd		[56]
	bacillaris (774E ; 677A)	+ + +	+ +	+	+	nd	nd	+	+	+	–	tr	nd		
Tetmemorus (Cha)	*brebissonii*	+	+ +	+	+	nd	nd	+	+ + +	+	Tr	+	+	linkages	[52]
Thalassiosira (Oc)	sp.	+ +	+	–	+	+	–	+ + +	+	+	Nd	nd	+	GlcNAc, GalNAc, linkages	[95]

part 6

Genera	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Anabaena	*augstmalis*	tr	+	–	+ + +	–	+ +	+	+	–	–	nd	nd	GalN	[63]
	cylindrica	tr	+	–	+ + +	+	–	+	+	+ +	–	nd	nd	other uronic acid	[96]
	flos-aquae	–	–	–	+	+	–	–	–	+	+	nd	nd		[77]
	sp.	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd		[97]
	spiroides	+ +	+	nd	+	+ + +	–	+	+	+	nd	nd	nd	GlcNAc, GalNAc	[67]
	sphaerica	–	+ + +	tr	+	+	+	+	–	–	–	nd	nd		[98]
	torulosa	+ +	+	+	+	+	+	–	+	+ + +	–	nd	nd	GlcN	
Anacystis	*nidulans*	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd		[99]
Aphanocapsa	*halophytia*	+	+	–	+ +	–	–	+	+ + +	+	–	+	+		[100]
Aphanothece	*halophytica*	–	+	+	+ + +	+	–	+	+ +	–	–	nd	nd	linkages	[101]
Arthrospira	*maxima*	+ +	+	–	+ +	+	+	+	+	+ + +	–	nd	nd		[102]
	platensis	+	+ + +	tr	+	tr	+	tr	+	+ +	nd	tr	+		[103]
	platensis	+ + +	+	nd	+	+ +	+ +	tr	nd	+	nd	+	nd		[12]
Calothrix	*pulvinata*	+	+	+	+ + +	nd	nd	+	+	+	–	tr	nd		[56]
	sp.	–	+ +	+	+ + +	tr	+	+	+	+	–	nd	nd	GlcN	[63]
Chlorogloeopsis	sp.	+	+	+	+ +	+	+ + +	+	+	–	–	nd	nd		[98]

(*continued on next page*)

Table 2 (*continued*)

part 7

Genera	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Chroococcus	*minutus*	+	+	+	+ + +	+	tr	+ +	+	+	–	nd	+	GlcN, methyl groups	[104]
	submarinus	+	+	+	+ +	+	+	+	+ +	+ + +	+	+	+	GlcN	[64]
Cyanospira	*capsulata*	–	–	+	+	–	+ + +	+	+	–	–	–	+		[105]
Cyanothece	sp.	–	+	–	+ + +	+	+	+ +	+	+	–	–	tr		[106]
	sp.	–	–	–	+ + +	–	–	–	–	+ +	+	+	+		[62]
Fischerella	muscicola	–	+	–	+ + +	+	+	+	+	+	–	nd	nd		[98]
Gloeocapsa	*kuetzingigiana*	+ +	+	+ + +	+ + +	+	+ +	nd	+	+ + +	+	nd	nd	GalN, trace GlcN	[107]
	sp.	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd		[13]
Gloeocapsosis	*crepidinum*	+	+	+	+ +	+	+	nd	+ + +	+	+	nd	nd	GlcN, GalN	[107]
Gloeothece	sp.	+	+ +	–	+ + +	nd	nd	+	–	+	–	+	+	methyl groups	[108]
Johannesbaptistia	*pellucida*	+	+	+	+	+	+	+	+	+	–	+	+		[64]
Leptolyngbya	*foveolarum*	+ +	+	–	+ + +	nd	nd	+	–	+	–	nd	nd		[56]
	tenuis	+ +	+	–	+ + +	nd	nd	+	+	+	–	tr	nd		
	sp.	+	tr	tr	+ + +	+	+ +	nd	+	+	+	nd	nd	GalN, traces GlcN	[107]
Lyngbya	*conferviodes*	tr	+ +	tr	+ + +	+	nd	+	tr	tr	–	nd	nd		[109]
Microcoleus	*vaginatus*	+	+ +	+	+ + +	+	+	+	+	+	–	nd	+		[41]

part 8

Genera	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Microcoleus	*vaginatus*	+	+	+	+ +	+	+	+ + +	+	+	–	nd	+	GlcNAc, linkages	[84]
Microcystis	*aeruginosa*	+ +	+	nd	+	–	+	+	+	+ + +	nd	nd	nd	GlcNAc, GalNAc	[67]
	aeruginosa	+ + +	–	–	+	nd	nd	+ +	–	–	–	–	–		[110]
	aeruginosa flos-aquae	–	–	–	+ + +	nd	nd	+ +	–	–	–	–	–		
	viridis	+ +	–	–	+ + +	nd	nd	+	+	–	–	nd	nd		
Nostoc	*calcicola*	+	+	+	+ + +	+	+	+	+	+ +	–	nd	+		[73]
	carneum	–	–	–	–	–	–	+ + +	–	+ +	–	–	+		[62]
	commune	–	+ +	–	+ + +	–	nd	+	–	–	nd	nd	nd		[111]
	flagelliforme	–	+ +	+	+	+	nd	tr	+	+ + +	nd	nd	nd		
	sp.	–	+	+	+	–	–	+	–	–	–	nd	nd		[77]
	sp.	+	+ +	–	+ + +	+	+	+	–	+	–	nd	+		[40]
	insulare	–	–	+ +	+ + +	+	–	–	–	–	–	–	tr	trace acetate, linkages	[112]
	insulare	tr	tr	+	+ + +	+ +	+	+	+	tr	–	nd	+		[104]
	muscoru	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd		[13]
	entophytum	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd		
	sp.	+	+	+	+ + +	+	+	+	+	+ +	–	nd	nd		[63]
Oscillatoria	*amphibia*	+	+	tr	+ + +	nd	nd	+ +	tr	+	–	nd	nd		[109]

part 9

Genera	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Oscillatoria	*corallinae*	+	+	+	+ + +	+	nd	+ +	+	+	–	nd	nd		[109]
	sp.	tr	–	–	+ + +	–	–	–	tr	tr	–	–	+	other uronic acid	[64]
	sp.	–	+	+	+ +	+	+ + +	–	+	+	–	nd	nd		[98]
	sp.	–	–	–	+ + +	–	–	–	–	+ +	+	–	+		[62]
Phormidium	*autumnale*	+ + +	tr	–	+	–	+	+	tr	tr	+	nd	nd		[63]
	battersii	–	+ +	+	+ + +	+	+	+ +	+	+	–	+	+		[64]
	ambiguum	+ + +	+ +	+	+ +	+	+	+	+	+	–	tr	nd		[56]
	corium (442D & 746B)	+ +	+	+	+ + +	nd	nd	+	+	+	–	tr	nd		
	corium (444A)	+	+ + +	+	+ +	nd	nd	+	+	+	–	tr	nd		
	corium (674A)	+ +	+	–	+	nd	nd	+	–	+ + +	–	nd	nd		
	corium (743D)	+	+	–	+ + +	nd	nd	+ +	–	+	–	nd	nd		
	ectocarpi (K5)	+	+ +	tr	+ + +	+	nd	+	tr	+	–	nd	nd		[109]
	ectocarpi (ME3)	+	+	tr	+ + +	+	nd	+ +	tr	+	–	nd	nd		
	ectocarpi (N182 ; C86)	–	+	–	+ + +	+	nd	+ +	–	+	–	nd	nd		
	foveolarum (C52)	+	+	tr	+ + +	+	nd	+ +	tr	+	–	nd	nd		
	foveolarum (MEU)	+	+ +	+	+ + +	–	–	+	+	+	–	nd	nd		
	minutum (D5)	tr	+ + +	–	+ +	nd	nd	+	+	+	–	nd	nd		

(*continued on next page*)

Table 2 (*continued*)

part 10

Genera	Species	Rha	Gal	Ara	Glc	GlcA	GalA	Man	Fuc	Xyl	Rib	SO_4^{2-}	Proteins	Other informations	References
Phormidium	*minutum* (NB5)	tr	+	+	+ + +	nd	nd	+ +	–	+	–	nd	nd		[109]
	minutum (RT6)	+	+	+ +	+ + +	+	nd	+	+	+	–	nd	nd		
	sp. (CCAP1464/3 ; CCAP1463/4)	+	+ +	+	+ + +	+	nd	+	tr	+	–	nd	nd		
	sp. (PNG91 ; 90-14/1)	+	+	+	+ + +	nd	nd	+ +	+	+	–	nd	nd		
	sp.	+	+	+	+ + +	+	+	–	+	+ +	–	nd	nd		[98]
	tenue	+	+	+ + +	+ +	nd	tr	+	+	+	–	nd	+	GlcNAc, linkages	[84]
Plectonema	*usteri*	+	+ + +	+	+ +	nd	nd	+	+	+	–	tr	nd		[56]
	golenkinianum	–	–	–	+ + +	–	–	–	tr	tr	–	–	+		[64]
	sp.	+	+ +	nd	+ + +	tr	+	nd	tr	+	+	nd	nd	GlcN, trace GalN	[107]
Rhabdoderma	*rubrum*	–	+	–	+	tr	tr	+	+	+ +	–	+	+	GlcN + + +	[64]
Scytonema	*hofmanni*	–	+	–	+	+	+	+ + +	–	–	–	nd	nd		[98]
	javanicum	+	+ +	+	+ + +	tr	tr	+	tr	+	–	nd	+	linkages	[84]
Synechococcus	sp.	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd		[36]
Synechocystis	*aquatilis*	+	+	–	+ + +	+	+	+	+	+	–	nd	nd	GlcN + +	[63]
	sp.	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd		[13]
	sp. (PCC6803)	+	+	–	+ + +	+	+	+	+ +	+	–	+	+	GlcN, GalN	[113]
	sp. (PCC6714)	+	+ +	+	+ + +	+	+	+ +	+	+	–	+	+	GlcN, GalN	
Tolypothrix	*tenuis*	+	+	+	+ + +	+	+	+ +	+	–	–	nd	nd	GlcN	[98]
Trichormus	*variabilis* (VRUC162)	tr	+	tr	+ + +	–	–	+	+	+ +	+	nd	nd	GalN	[63]
	variabilis (VRUC168)	+	+	+	+ + +	+	+	+	+	+ +	–	nd	nd	GlcN	

+ + +: first major monosaccharide, + +: 2nd major monosaccharide, +: presence, -: absence, tr: trace, nd: non determined. Rha: rhamnose, Gal: galactose, Ara: arabinose, Glc: glucose, Man: mannose, Fuc: fucose, Xyl: xylose, Rib: ribose, GlcA: glucuronic acid, GalA: galacturonic acid, GlcN: glucosamine, GalN: galactosamine, ManA: mannuronic acid, GlcNAc: *N*-acetyl-glucosamine, GalNAc: *N*-acetyl-galactosamine.

described in literature, *i.e. Synechococcus* (RCC2380) [36], *Dunaliella* (RCC5) [43] and *Porphyridium* (RCC4628) [15,47–49]. In this study the EPS from *Dunaliella* sp. (RCC5) was mainly composed of Gal, Rha, Xyl, Man and GalA (28, 21, 17, 13 and 11 %, respectively) with some traces of other monosaccharides (Glc, Ara and GlcA). It presents some similarity with that previously described by Mishra and Jha [43] from *D. salina* which was composed of Xyl, Gal and Glc.

EPS from *Porphyridium* sp. (RCC4628) had also a composition very similar to those already determined in the literature on different species of *Porphyridium* including *aeruginum*, *marinum*, *cruentum* and *purpureum* [15, 47, 49–50]. It was a heteroxylan composed of Xyl, Gal and Glc (49, 27 and 20 %, respectively) and other minor monosaccharides. Phlips et al. [36] studied the physico-chemical properties of solutions of an EPS from a *Synechococcus* strain for which no monosaccharides composition was determined. Results obtained in this study revealed that the EPS from *Synechococcus* sp. (RCC2380) was composed of Glc, Gal and Fuc (49, 27 and 20 %, respectively).

This study also described for the first time the composition of EPS i) in species belonging to the Haptophyta phylum (*Chrysotila* (CCAP904/1, RCC4633), *Diacronema* (RCC3514), *Exanthemachrysis* (RCC1544), *Isochrysis* (RCC3686), *Pavlova* (RCC1545, RCC3438, RCC4120, RCC4037), ii) in two classes belonging to the Chlorophyta (Chlorodendrophyceae represented by the genus *Tetraselmis* (RCC133, RCC1564 and RCC4435) and Palmophyllophyceae with *Prasinococcus*

Table 3
Monosaccharides compositions (molar ratios) of EPS from strains EPS + obtained by GC/MS and HPAEC-PAD.

Genera	Species	RCC numbers	Rha		Gal		Ara		Glc		Man		Fuc		Xyl		Rib		GlcA		GalA	
			(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)	(1)	(2)
Chrysotila	*dentata*	CCAP 904/1	–	–	33	36	36	33	tr	tr	10	8	–	tr	17	16	–	–	4	4	–	tr
	sp.	4633	tr	tr	31	33	13	11	42	45	–	–	–	–	10	8	–	–	4	2	–	tr
Isochrysis	*braarudii*	3686	9	4	27	23	39	47	3	3	–	–	–	–	18	19	+	+	4	2	–	–
		6688	15	19	36	46	4	tr	–	–	34	32	–	–	–	–	–	–	11	tr	–	tr
Diacronema	sp.	3514	33	37	26	23	17	8	15	16	–	–	–	–	5	10	–	–	4	4	–	tr
Exanthemachrysis	sp.	1544	2	3	16	14	8	14	8	7	15	13	–	–	14	12	–	–	37	32	–	5
Pavlova	*gyrans*	1545	3	4	32	21	13	18	14	7	–	–	tr	6	21	25	–	–	9	11	8	7
	sp.	4037	46	36	10	11	26	23	6	10	–	–	–	2	12	14	–	–	–	2	–	2
	sp.	4120	7	7	34	40	13	4	23	35	4	–	–	7	19	2	–	–	tr	3	–	2
	sp.	3438	47	30	27	29	5	14	11	17	tr	–	–	–	3	6	–	–	5	4	–	–
Glossomastix	sp.	3688	28	20	4	2	–	–	–	–	–	–	54	57	–	–	–	–	9	10	5	11
	sp.	3685	20	19	–	–	–	–	–	–	–	–	56	57	–	–	–	–	10	8	14	13
	sp.	3707	31	27	2	3	–	–	–	tr	–	–	40	47	–	tr	–	–	6	7	21	15
Synechococcus	sp.	2380	–	tr	38	27	–	tr	38	49	–	–	24	20	–	–	–	–	–	tr	–	tr
Tetraselmis	*globosa*	1564	63	61	19	20	tr	tr	5	5	–	–	–	–	5	4	–	–	–	2	5	–
	rubens	133	nd	6	nd	89	nd	–	nd	tr	nd	–	nd	2	nd	tr	nd	–	nd	–	nd	2
	sp.	4435	5	3	33	35	24	19	5	7	8	7	–	9	23	14	–	–	2	4	–	2
Dunaliella	sp.	5	18	21	19	28	4	5	2	tr	11	13	–	–	13	17	–	–	19	4	14	11
Prasinococcus	sp.	2684	7	4	67	74	7	3	9	7	–	–	–	2	7	9	–	–	3	tr	–	–
Porphyridium	sp.	4628	–	–	29	27	2	2	22	20	–	–	–	–	44	49	–	–	3	2	–	–

(1): GC/MS analyses, (2): HPAEC-PAD analyses, +: presence, -: absence, tr: trace, nd: non determined : no classification available. The SD was < to 5 % for all experiments.

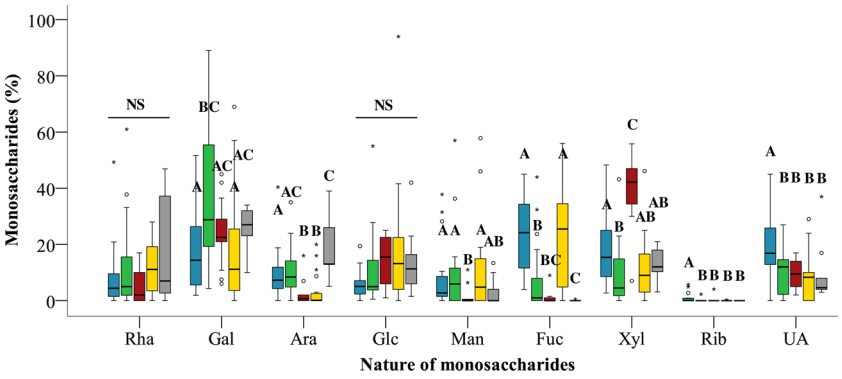

Fig. 1. Variations in monosaccharides (Rha (rhamnose), Gal (galactose), Ara (arabinose), Glc (glucose), Man (mannose), Fuc (fucose), Xyl (xylose), Rib (ribose)) and uronic acids (UA), given in % of the total composition) in EPS of Charophyta (▪), Chlorophyta (▪), Rhodophyta (▪), Ochrophyta (▪) and Haptophyta (▪) (16, 23, 13, 20 and 9 monosaccharides compositions, respectively). Data obtained from the literature and those included in this study are shown. Miozoa were not included in this analysis, since only two monosaccharide compositions were available. Miozoa were not included in this analysis, since only two monosaccharides compositions were available. Results are given as box-plots such as the central lines represent the medians, boxes the lower 25 % to the upper 75 % quartile, and the whiskers the range excluding outliers, that are given as open circles and stars. For each monosaccharide, Kruskal-Wallis tests were performed. When a significant difference was found ($p < 0.05$), this test was followed by multiple pairwise comparisons (Mann-Whitney tests), with significance levels adjusted according to the Benjamini and Hochberg method (1995) [28]. Different letters indicate statistically significant differences between phyla. NS: Non-Significant results.The classification was done according to the AlgaeBase database [29]. Different letters indicate statistically significant differences between phyla. ○ and ★: outliers. NS: Non-Significant.

sp. (RCC2684)), and iii) in the genus *Glossomastix* (RCC3685, RCC3688 and RCC3707) (Pinguiophyceae, Ochrophyta phylum). The compositions were extremely variable even if all EPS were heteropolysaccharides. They are mainly composed of three or five monosaccharides including neutral sugars and uronic acids apart for the biopolymers produced by *Pavlova* sp. (RCC4120) and *Tetraselmis globosa* (RCC1564) mainly composed of two monosaccharides representing 81 and 75 % of the total monosaccharides, respectively. EPS of *Tetraselmis rubens* (RCC133) and *Prasinococcus* sp. (RCC2684) are galactans since Gal represents 74 and 89 % of the total monosaccharides compositions, respectively. Table 3 shows that all the neutral sugars usually detected in the composition of microalgae/cyanobacteria EPS (Fuc, Ara, Rha, Gal, Glc, Gal, Xyl and Man) were present in the composition of biopolymers analyzed in this study. After analysis of the 17 EPS compositions, Gal, Rha, Xyl, Fuc, Ara, Glc and Man were respectively identified as the main monosaccharide in 7, 4, 2, 2, 1, 0 and 0 EPS (meaning for example Gal was the main monosaccharide in 7 EPS compositions). Similarly, Gal, Rha, Xyl, Fuc, Ara, Glc and Man were quantitatively the second monosaccharide in 6, 2, 2, 0, 3, 1 and 1 EPS compositions. The EPS of *Exanthemachrysis* sp. (RCC1544) was distinguished by its richness in GlcA representing around 35 % of its composition. Note that PS mainly composed of glucuronic acids and called glucuronans are poorly detected in natural biomass and are very attractive for their biological and rheological properties [51]. In addition, most of the EPS identified in this study (with the exception of *Synechococcus* sp. (RCC2380)) contained at least one uronic acid (GlcA or GalA) and most of the time both. They are present in variable content, sometimes in trace amounts (EPS from RCC6688), in small quantities (EPS from *Tetraselmis* sp. (RCC4435) and *Pavlova* sp. (RCC4120 and RCC4037)) or in very large quantities as previously described in EPS from *Exanthemachrysis* sp. (RCC1544) and to a lesser degree in that of *Pavlova gyrans* with 35 % and 11 % of GlcA, respectively. Overall, this work confirmed that EPS from microalgae have very complex compositions, probably evolved in response to biotic and/or abiotic conditions.

3.3. Relationship between phylogeny and exopolysaccharides compositions

We performed a metanalysis on the EPS compositions of 81 strains of microalgae from bibliographic data and experimental results obtained in this study in order to determine whether they could vary according to their taxonomic affiliation. This metanalysis was not done on the composition of EPS from cyanobacteria as their specificity is the systematic presence of Glc as main (63 %) or second monosaccharides (18 %) (Table 2). Levels of some monosaccharides varied significantly between phyla ($p < 0.05$ in Kruskal-Wallis tests for Gal, Ara, Man, Fuc, Xyl, Rib and Uronic acids) while Rha and Glc levels were relativement constant across phyla (Fig. 1, $p = 0.117$ and $p = 0.058$, respectively). Such differences appear also on the phylogenetic tree presented on Fig. 2.

Clear differences, between the 3 phyla of the plantae kingdom included in the analysis (Charophyta, Chlorophyta and Rhodophyta), have been detected. EPS from Charophya have the most distinct composition profile, with higher Fuc levels compared to Chlorophyta and Rhodophyta. Fuc was the first or second monosaccharide in 10/16 profiles, while it was only 4/23 profiles of the Chlorophyta and none in the Rhodophyta ($p < 0.001$ for each comparison). They also contain significantly higher levels of uronic acids compared to EPS from the two other Plantae phyla ($p = 0.013$ and $p = 0.01$ when compared to Chlorophyta and Rhodophyta, respectively). They can represent up to 28 and 29 % in EPS of *Netrium interruptum* and *Netrium oblongum*, respectively [52]. In EPS from *Spondylosium panduriform*, uronic acids were only represented by GlcA which represents 24 % of the total composition [53], and it is even the major monosaccharide in EPS from *Closterium* sp. and *Hyalotheca dissiliens* [54,55]. EPS from Charophya were also characterized by the presence of Rib (8/16 profiles) which contrasts with those of Chlorophyta and Rhodophyta profiles (1/23 and 1/13, respectively). This characteristic seems to be specific of the Zygnematophyceae (8/13 profiles) since Rib was not found in Klebsormidiophyceae. More specifically, it is systematically present in traces in *Netrium*, *Cosmarium*, *Penium*, *Tetmemorus*, *Pleurotaenium* genus [52]. A large majority of Charophyta EPS contain sulphate groups, except EPS from *Klebsormidium flaccidum* (749B) [56]. The sulphate content of some EPS can reach up > 10 % as for those of *Tetmemorus brebissonii* and *Pleurotaenium trabecula* [52].

EPS from Rhodophya are characterized by high levels of Xyl ($p = 0.005$ and $p = 0.001$ when compared to Charophyta and Chlorophyta, respectively). This monosaccharide is the first or second in 11/13 profiles, which contrasts with those from Chlorophyta (2/23) and Charophyta (5/16). The Porphyridiaceae familly (including *Porphyridium* and *Flintiella* genera) was characterized by the production of galactoxylans, whereas EPS from the Glaucosphaeraceae familly were rhamnoxylans and/or galactoxylans, depending on the species. All these EPS were sulphated (excepted for *Flintiella sanguinaria*), sometimes with a content > 10 % [49,50].

High levels of Gal were often observed in EPS from Chlorophyta (this monosaccharide being the first or second in 18/23 profiles) which differs from Charophyta ($p = 0.025$) but not from Rhodophyta ($p = 0.15$), which have also Gal as a first or second monosaccharide in 9/13 profiles.

The second kingdom analysed is the Chromista. Results presented part 3.2 have highlighted Haptophyta producing EPS. Thus, there are 3 phyla involved in EPS production, including Ochrophyta, Haptophyta, and Miozoa phyla. As only two monosaccharide compositions were available for Miozoa, comparaison analyses were only performed on

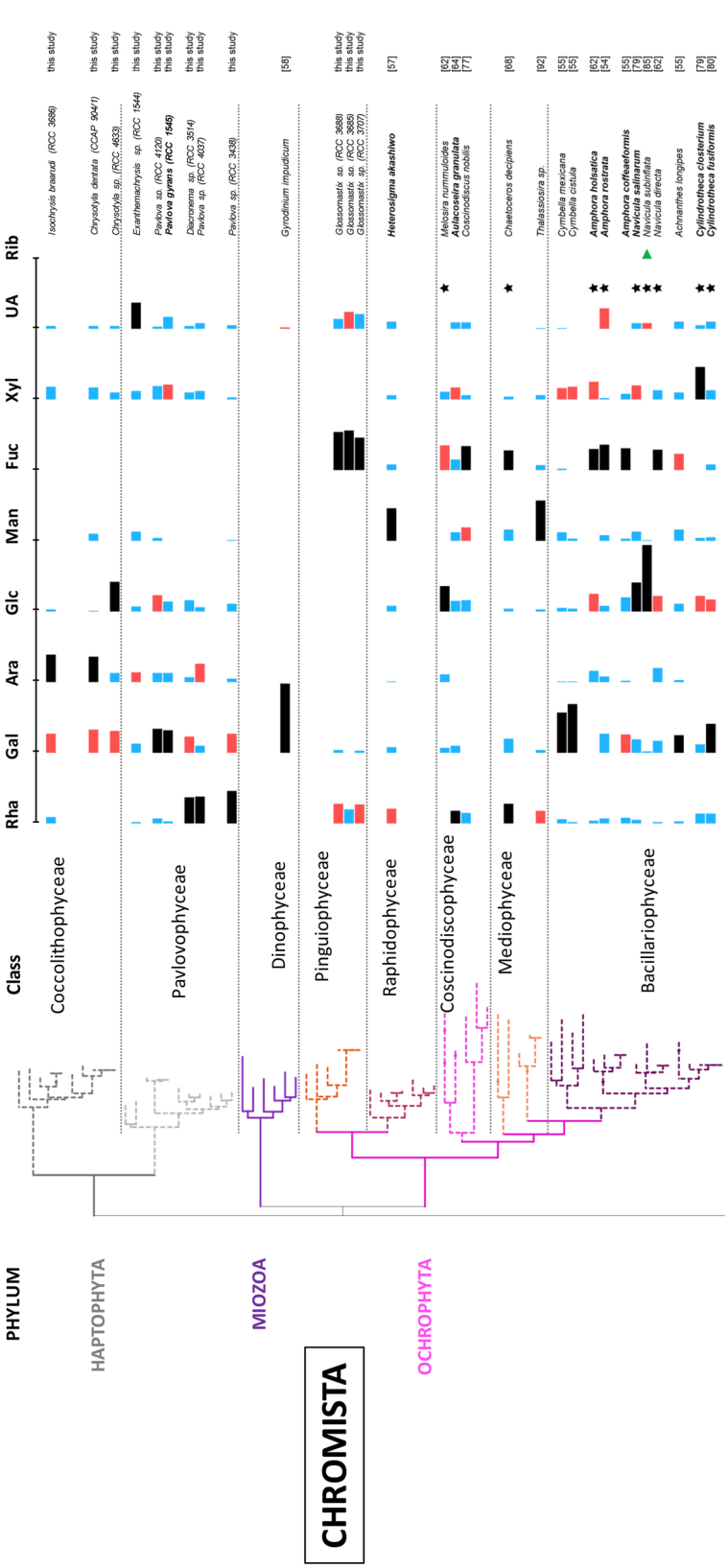

Fig. 2. parts 1 and 2: Composition in neutral sugars (Rha (rhamnose), Gal (galactose), Ara (arabinose), Glc (glucose), Man (mannose), Fuc (fucose), Xyl (xylose), Rib (ribose)) and uronic acids (UA) (in % of the total composition 0–100 % scale) of EPS from 81 microalgae (16 Charophyta, 23 Chlorophyta, 13 Rhodophyta, 20 Ochrophyta and 9 Haptophyta) placed on a Neighbor-Joining phylogenetic tree based on 18S rDNA sequences. ■: 1st major monosaccharide, ■: 2nd major monosaccharide, ■: secondary monosaccharides, ★: % of UA was obtained by colorimetric assay, ▲: presence of Rib. The positions of the strains written in bold were determined from sequences corresponding to the right species. For the other species, sequences from a representative of the same genus were used. The classification was done according to the AlgaeBase database [29].

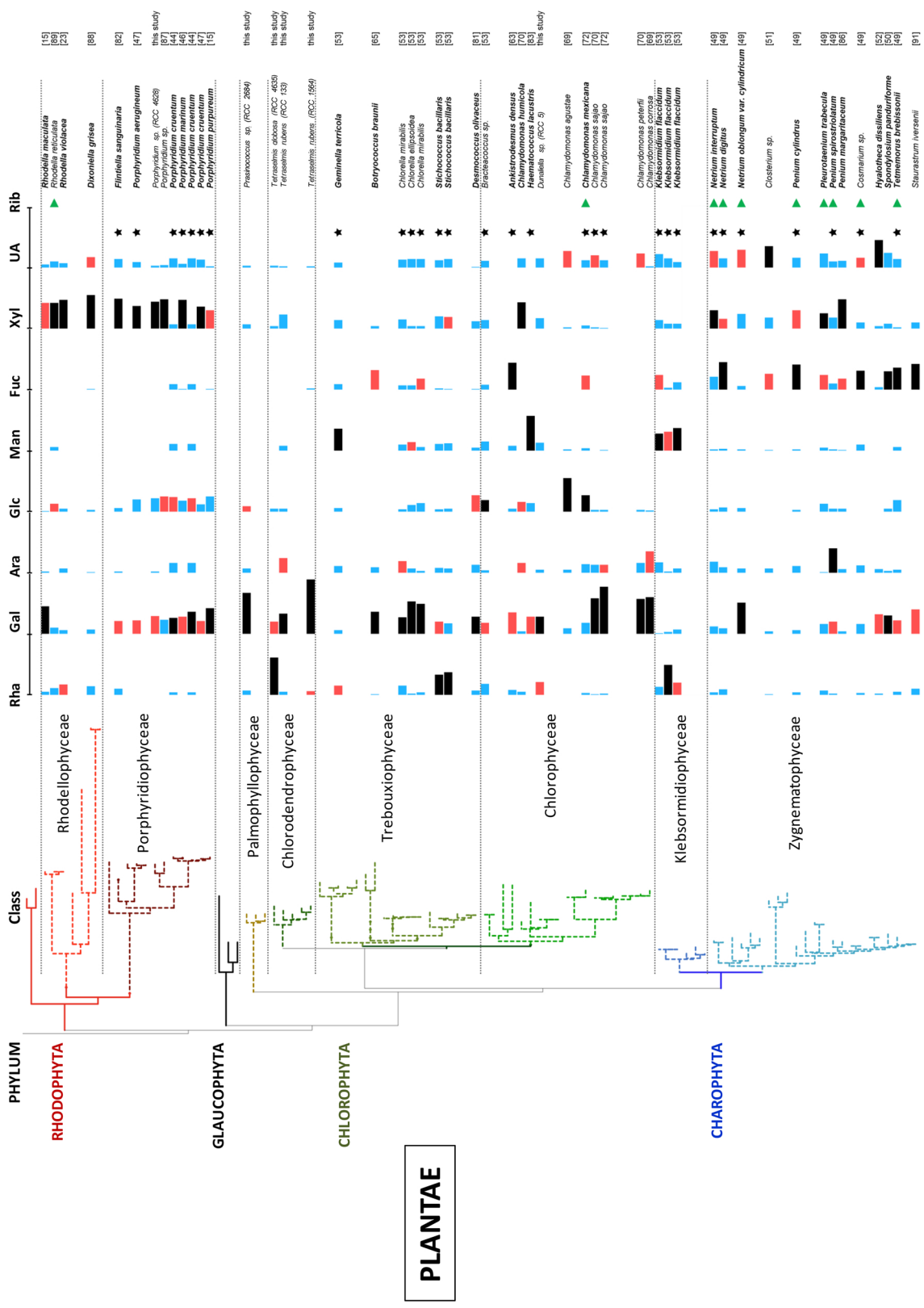

Fig. 2. (*continued*)

Ochrophyta and Haptophyta. The main differences between Ochrophyta and Haptophyta lie in the differences in Fuc contents ($p < 0.001$) (Fig. 2). Indeed, Fuc is present in most EPS of Ochrophyta (17/20 profiles), as the first or second monosaccharide (11/20 profiles) whereas it is present in only 2 species of Haptophyta on the 10 analyzed. In the genera *Amphora* and *Glossomastix* in particular, Fuc represents respectively more than 30 and 46 % of the total monosaccharide composition [57,58]. Differences in Ara levels can also be observed ($p < 0.001$). While most of the Ochrophyta EPS contain, at best, traces of Ara (content > 3 % of the composition in only 4/20 profiles), this monosaccharide is present at significantly higher levels in Haptophyta (content >7 % in 8/10 profiles).

Although the analysis was focused on the distinctions of EPS compositions between phyla, it was contested that in the Chromista some species belonging to the same genus had very varied compositions, as *Pavlova* species for example. These differences could be explained by the fact that *Pavlova* is a polyphyletic genus [59]. Specific composition was found for the EPS of *Heterosigma akashiwo* which was the sole example of microalgae EPS containing ManA [60]. The composition of *Gyrodinium impudicum* EPS is also special because this is a homopolysaccharide: a sulphated galactan [61].

Finally, the last kingdom and also phylum is the cyanobacteria. EPS production by these photosynthetic microorganisms has been abundantly published, maybe because of their ecological abundance and easy growing. All these data make it possible to view the large diversity of composition of the exopolymers resulting from this phylum (Table 2). The main characteristic of cyanobacteria is the systematic presence of Glc, with the exception of *Nostoc carneum* [62]. It is the principal or second monosaccharide in 65 (50/78 profils) and 18 % (14/78 profiles) EPS, respectively. In comparison, Xyl appearing as main monosaccharide just after Glc is 7 times less present (7/78 profiles). Some specific compositions have been highlighted. Osamines (GlcN and or GalN) were found in 21 compositions. In addition, GlcN is the first and second monosaccharide in EPS of *Rhabdoderma rubrum* and *Synechocystis aquatilis*, respectively [63,64]. Moreover, similar EPS compositions were found between strains belonging to the same genus, as *Synechocystis* [98,113], *Phormidium* [109], *Oscillatoria* [64,98,109], *Leptolyngbya* [56,107] and *Plectonema* [56,64,107].

4. Conclusions

One hundred and sixty-six microalgae and cyanobacteria were screened and 45 of them were detected as producers of a soluble EPS based on colorimetric assays. The composition analyses performed on 20 of them confirmed they were EPS. This allowed to highlight 8 new genera of microalgae and to characterize 17 new monosaccharide compositions. Overall, all the microalgae and cyanobacteria EPS are heteropolymers. They are produced by 49 and 29 genera in microalgae and cyanobacteria, respectively, which represent 134 species. Some common points in composition can be established according to the phylogenetic affiliation.

EPS from Charophya contain high Fuc and uronic acids levels and were characterized by the presence of Rib in the half part on EPS compositions available. Moreover, a large majority of their EPS contain sulphate groups. EPS from Rhodophya were characterized by high levels of Xyl, and the Porphyridiaceae and Glaucosphaeraceae families produce compositions that were specific to them. High levels of Gal were often observed in EPS from Chlorophyta. In Chromista, Fuc is present in most EPS of Ochrophyta compare to Haptophyta but Ara levels were significantly higher in Haptophyta compare to EPS of Ochrophyta. To conclude, EPS produced by cyanobacteria were mainly composed Glc, and this monosaccharide is always present.

Thanks to the growing number of studies and the 132 compositions available, the metanalysis on the EPS compositions by statistical tests made it possible to distinguish specific compositions between phyla. This finding is clearly the proof that evolution has conserved some complex biosynthesis pathways inside specific phyla to give an advantage to strains having the ability to produce some exopolysaccharides in some environments. However, the current lack of knowledge on the physiological function of EPS despite the abundance of literature on this subject makes it difficult to correlate some polysaccharidic structures with their biological roles. Nevertheless, there are still a lot of microalgae to study and only a tiny part of the phylogenetic tree has been concerned (insufficient data on Miozoa phylum for example).

Authors' contributions

Philippe Michaud conceived the project and reviewed the manuscript. Céline Laroche designed the experiments for microalgae screening and culture in PBR; Guillaume Pierre, Cedric Delattre and Pascal Dubessay have setup methods for sugars analysis and molecular biology. Clément Gaignard has done the screening of microalgae and polysaccharides analysis, interpreted the results and wrote the manuscript. Christine Gardarin realised analysis by ionic chromatography; Aurore Dubuffet conducted the phylogenic analysis and interpreted the results; Priscillia Gourvil and Ian Probert have chosen the microalgae strains considering their phylogeny and phenotypes. All authors approved the final manuscript.

Statement of informed consent, human/animal rights

No informed consent, human or animal rights applicable

Declaration of Competing Interest

The authors declare that they have no conflict of interest.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.algal.2019.101711.

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