

Isoprostanoids quantitative profiling of marine red and brown macroalgae

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Abstract

 With the increasing demand for direct human and animal consumption seaweed farming is rapidly expanding worldwide. Macroalgae have colonized aquatic environments in which they are submitted to frequent changes in biotic and abiotic factors that can trigger 22 oxidative stress (OS). Considering that isoprostanoid derivatives may constitute the most relevant OS biomarkers, we were interested to establish their profile in two red and four brown macroalgae. Seven phytoprostanes, three phytofuranes, and four isoprostanes were quantified through a new micro-LC-MS/MS method. The isoprostanoid contents vary 26 greatly among all the samples, the *ent*-16(*RS*)-9-*epi*-ST-∆¹⁴-10-PhytoF and the sum of 5- F2t-IsoP and 5-*epi*-5F2t-IsoP being the major compounds for most of the macroalgae studied. We further quantified these isoprostanoids in macroalgae submitted to heavy metal (copper) exposure. In most of the cases, their concentrations increased after 24 h of copper stress corroborating the original hypothesis. One exception is the decrease of *ent*-9-L1-PhytoP content in *L. digitata*.

Keywords

Macroalgae, isoprostanoids, heavy metal, copper stress, oxylipins, micro-LC-MS/MS

1-Introduction

 Macroalgae, also known as seaweeds, constitute a large group of coastal macro- organisms playing an important role in marine environment, both as food resource and engineer species for shaping coastal marine habitats (Hurd, Harrison, Bischof, & Lobban, 2014). Seaweeds have been also part of the human diet for thousands of years, based on archaeological evidence in Chile (Dillehay, Ramirez, Pino, Collins, Rossen, & Pinot- Navarro, 2008) and on several other reports (e.g., in China, 300 A. D.; in Ireland, 600 A.D; Aaronson, 1986; Craigie, 2010; Gantar & Svircev, 2008; Newton, 1951; Tseng, 1981; Turner, 2003). Nowadays, they are extensively cultivated in the Far East Asia to provide mainly high-quality food. Indeed, seaweeds are interesting natural sources of functional ingredients such as carbohydrates, proteins, minerals, vitamins, and present a low content of lipids with a high level of polyunsaturated ω-3 fatty acids (Holdt & Kraan, 2011; Plaza, Cifuentes, & Ibanez, 2008). In South East Asia and Eastern Africa, the seaweed biomass is harvested to extract phycocolloids such as carrageenans and agars. With the increasing demand for direct human and animal consumption, medicines, food additives, fertilizers, and cosmetics, seaweed farming is rapidly expanding worldwide.

 Most of the wild populations of macroalgae are thriving in the intertidal and near subtidal zone, a highly and frequently changing environment, and thus experience repeated biotic and abiotic (temperature, irradiation, salinity, …) fluctuations that require physiological plasticity for stress tolerance (Dittami, Gravot, Renault, Goulitquer, Eggert, Bouchereau, et al., 2011). Among potential stress factors, exposure to high level of heavy metals is very common, as illustrated by numerous studies conducted so far on different macroalgae (Collen, Pinto, Pedersen, & Colepicolo, 2003; Pinto, Sigaud-Kutner, Leitao, Okamoto, Morse, & Colepicolo, 2003; Roncarati, Sáez, Greco, Gledhill, Bitonti, & Brown, 2015; Saez, Roncarati, Moenne, Moody, & Brown, 2015).

 Among heavy metals, copper (Cu(II)) is an essential micronutrient to both land plants and macroalgae, notably for many electron carriers involved in photosynthetic electron transport, mitochondrial respiration or oxidative stress (OS) response (Yruela, 2005). However, above specific threshold concentration, it is considered as a pollutant and thus toxic. Copper is currently extensively used in antifouling marine paints, and in some coastal areas copper mining discharges are still very important. Therefore, both natural and farmed populations of seaweeds can be exposed to copper excess. To understand the mode of action leading to copper biological function (positive or negative), its chemical properties have to be considered.

72 Ritter and colleagues demonstrated that copper and H_2O_2 treatments lead to OS response in the model brown alga *Ectocarpus siliculosus* (Dillwyn) Lyngbye (A. Ritter, Dittami, Goulitquer, Correa, Boyen, Potin, et al., 2014). In these studies, the authors underlined a link between copper stress and fatty acid/lipid metabolism since they observed an increase of free fatty acid contents and oxylipins after exposure of *E. siliculosus* to this heavy metal. Similar conclusion were drawn with regards to the brown algal kelp *L. digitate* (A Ritter, Goulitquer, Salaun, Tonon, Correa, & Potin, 2008). In this context, it was relevant to complete these previous studies by assessing the potential production of isoprostanoid derivatives by non-enzymatic oxidation of lipids/fatty acids.

 Indeed, fatty acids, and more especially polyunsaturated fatty acids (PUFAs), are prone to 82 oxidation due to their highly reactive bis-allylic hydrogen atoms. This non-enzymatic lipid peroxidation generates series of lipid mediators such as phytoprostanes (PhytoPs), isoprostanes (IsoPs), and neuroprostanes (NeuroPs), derived from α-linolenic acid (ALA C18:3 n-3), arachidonic acid (AA, C20:4 n-6), and docosahexaenoic acid (DHA, C22:6 n-3) respectively. It is worth to mention that under high oxygen pressure, further transformations could occur, leading to the synthesis of furanic forms named phytofurans (PhytoFs), isofurans (IsoFs), and neurofurans (NeuroFs) (Table 1). All these compounds

89 are robust markers of oxidative stress in biological systems (Milne, Gao, Terry, Zackert, & Sanchez, 2013). They are also known to have functional roles in living organisms (Galano, Lee, Gladine, Comte, Le Guennec, Oger, et al., 2015; Galano, Lee, Oger, Vigor, Vercauteren, Durand, et al., 2017; Jahn, Galano, & Durand, 2008). Previous work by Barbosa et al. (Barbosa, Collado-Gonzalez, Andrade, Ferreres, Valentao, Galano, *et al.*, 2015) showed that macroalgae were able to synthesize ALA oxygenated metabolites, and among them, 9-F1t-PhytoP, 9-*epi*-9-F1t-PhytoP, 16-B1-PhytoP, and 9-L1-PhytoP. In view of these findings, and to go further in the study of potential production of isoprostanoids by non-enzymatic oxidation of lipids/fatty acids in macroalgae, we were interested we were interested in identifying and quantifying phytoprostanes potentially produced in macroalgae from other PUFAs, and also the possible synthesis of furanes in these organisms. We also forced the stress status with cupric exposure in order to observe an eventual change in amounts of detected compounds.

 To better understand the importance of isoprostanoids in seaweeds, we have considered two distinct groups of seaweeds, the brown (*Phaeophyta*) and the red (*Rhodophyta*) macroalgae, which belong to two independent eukaryotic lineages and therefore constitute very interesting biological models (Brodie, Chan, De Clerck, Cock, Coelho, Gachon, et al., 2017; Cock & Coelho, 2011). Among the brown algae, four species were considered: *Ectocarpus siliculosus* (Dillwyn) Lyngbye, *Laminaria digitata* (Huds.) Lamouroux, *Fucus spiralis* L., and *Pelvetia canaliculata* (L.) Decaisne & Thuret. Experiments were also conducted on two *Rhodophyta*, i.e. *Osmundea pinnatifida* (Hudson) Stackhouse, and *Grateloupia turuturu* Yamada. Isoprostanoid content was determined for all these species under normal control growth conditions, and after incubation under copper stress for 24h. To conduct such experiments, and because oxygenated metabolites were expected to be present at low concentrations, we first optimized the extraction protocol with *L. digitata* before applying it to all other algal matrices. In line with this, we developed a process to

 quantify PhytoPs/PhytoFs, based on micro-LC-MS/MS with increased speed, robustness, selectivity, and sensitivity of analysis (Medina, Miguel-Elizaga, Oger, Galano, Durand, Martinez-Villanueva, et al., 2015).

2-Material and methods

2.1 Chemicals and reagents

 The phytoprostane standard 16-(*RS*)-16-A1-PhytoP and the deuterated internal standard (IS) d4-15-F2t-IsoP were purchased from Cayman Chemicals (Ann Arbor, MI, USA). The two IS d4-10-F4t-NeuroP and C21-15-F2t-IsoP, as well as all the other standards, were synthesized according to previous procedures (Cuyamendous, Leung, Durand, Lee, Oger, & Galano, 2015; Thierry Durand, Cracowski, Guy, & Rossi, 2001; T. Durand, Guy, Vidal, & Rossi, 2002; El Fangour, Guy, Despres, Vidal, Rossi, & Durand, 2004; El Fangour, Guy, Vidal, Rossi, & Durand, 2005; Guy, Flanagan, Durand, Oger, & Galano, 2015; Guy, Oger, Hepekauzen, Signorini, Durand, De Felice, et al., 2014; Oger, Brinkmann, Bouazzaoui, Durand, & Galano, 2008; Oger, Bultel-Poncé, Guy, Balas, Rossi, Durand, et al., 2010). This concerns 9-F1t-PhytoP, 9-*epi*-F1t-PhytoP, *ent*-16-F1t-PhytoP, *ent*-16-*epi*-16-F1t-131 PhytoP, ent-16-B₁-PhytoP, ent-9-L₁-PhytoP, as PhytoPs, and ent-9(RS)-12-epi-ST-Δ¹⁰-13-132 PhytoF, ent-16(RS)-13-epi-ST-Δ¹⁴-9-PhytoF, and ent-16(RS)-9-epi-ST-Δ¹⁴-10-PhytoF as PhytoFs. Four IsoPs were also evaluated: 15-F2t-IsoP, 15-*epi*-15-F2t-IsoP, 5-F2t-IsoP and 5-*epi*-5-F2t-IsoP. Finally, three NeuroPs were considered: 10-F4t-NeuroP, 10-*epi*-10-F4t- NeuroP, and 4(*RS*)-4-F4t-NeuroP. Stock solutions of standards were prepared in methanol 136 to a concentration of 100 ng.µL⁻¹, and were stored at −20 °C. Appropriate dilutions from the mentioned stock were prepared for calibration purpose. Furthermore, two different 138 solutions of a Standard Mixture (SM) of the 18 compounds mentioned above (SM $_{32}$ = each 139 compound at 32 ng.ml⁻¹ or SM₂₅₆ = each compound at 256 ng.ml⁻¹) were made up for validation purpose (extraction yield and matrix effect).

 LC-MS methanol, acetonitrile, and HPLC chloroform were obtained from Fisher Scientific (Loughborough, UK). Hexane (CHROMASOLV, HPLC grade), absolute ethanol, formic and acetic acids, ammonia and potassium hydroxide (Fluka for mass spectrometry) were provided by Sigma-Aldrich (Saint Quentin Fallavier, France). Ethyl acetate (HPLC grade) was purchased from VWR (EC). Water used in this study was purified on a milliQ system (Millipore).

 The solid-phase extraction (SPE) cartridges were constituted of a mixed-mode ion-exchange sorbent (Oasis MAX; 3 mL, 60 mg; from Waters; Milford, MA, USA).

2.2 Macroalgal samples

2.2.1 Collection

 Of the six macroalgae used in this study, one *(E. siliculosus*) was cultivated in laboratory, and five (*F. spiralis*, *P. canaliculata*, *O. pinnatifida*, *L. digitata*, and *G. turuturu*) were collected during the summer 2015 at low-tide close to the Station Biologique of Roscoff, a site with no direct chemical influence from the shore.

 After collection, four algal species (*F. spiralis*, *P. canaliculata*, *O. pinnatifida*, and *G. turuturu*) were immediately transported to the laboratory where they were cleaned and then assigned in 40 L tanks with a permanent renewal of both seawater and bubbled air. After at least 24h of acclimatization, samples were submitted to copper stress (see section *2.2.2*).

 Young sporophytes of *L. digitata* (*ca* 10-20 cm in length) were also collected in the intertidal zone close to the Station Biologique of Roscoff, and maintained in 10 L flasks in autoclaved filtered seawater (FSW), at 13°C, under a photoperiod of 16 h of light (40 µmol 164 photons.m⁻².s⁻¹) and 8 h of darkness, and well-aerated with filtered (0.22 μ m) compressed air, up to one week before treatment.

 E. siliculosus (Dilwyn) Lyngbye, unialgal strain 32 (accession CCAP 13104, origin San Juan de Marcona, Peru, 2002) was cultivated in 10 L flasks as already described (A. Ritter, Dittami, Goulitquer, Correa, Boyen, Potin, et al., 2014).

2.2.2 Copper stress for the six species of macroalgae

 Each sample corresponded to a mixture of at least three to six individuals in the same stage of development (depending of the species) to reach a weight of 10 g of fresh algae. Copper stress was triggered by transferring the algal samples to FSW enriched with Cu(II) 174 as CuCl₂ (Titrisol, Merck) at nominal final concentration of 300 µg.L⁻¹ (15 µL of a 20 g.L⁻¹ stock solution) in 1 L glass flasks washed overnight with 1% HCl to limit Cu adsorption. Control treatment corresponded to another 10 g algal batch incubated without CuCl² 177 addition. After 24 hours in a culture room at 13°C under aeration with filtered (0.22 um) compressed air, control and stressed samples were washed with autoclaved FSW, briefly 179 dried using paper towel, immediately frozen in liquid nitrogen, and then stored at -80 °C until extraction.

2.2.3 Algal sample preparation

 Approximately 1 g of fresh algal weight was ground with grinding balls (50 mm diameter) in 184 liquid nitrogen using the Mixer Mill MM400 (Retsch[®]) bench top unit for 2 min at 20 Hz. After having evaluated the extraction methods suggested by Küpper (Küpper, Gaquerel, Boneberg, Morath, Salaün, & Potin, 2006), Barbosa (Barbosa, et al., 2015), and Leung (Leung, Chen, Zhong, Yu, & Lee, 2014) on *L. digitata*, we opted for the latter protocol since it allowed a better recovery of analytes and showed limited influence of the biological material (matrix effect) on the extraction procedure. Briefly, 0.10 g of each powdered sample was weighed in a flask, then added with (i) 25 µL of 1% (w/v) di-*tert-*butyl hydroxytoluene (BHT) in methanol, (ii) 2 mL of MeOH, and (iii) 1.5 mL of phosphate buffer

 (pH 2) prepared with saturated sodium chloride solution. At this step, the samples were spiked with 6 ng of each IS. This mixture was stirred with a vortex mixer for 30 sec, and then shaked at 100 rpm for 1 hour at room temperature with an IKA KS 4000 control shaker. Then, extracts were centrifuged at 5,000 rpm for 5 min at room temperature. The supernatant was separated, and 4.0 mL of cold chloroform were added. This mixture was stirred with a vortex mixer for 30 s and then centrifuged at 1,500 rpm for 5 min at room temperature. The lower organic layer was carefully removed, transferred into a Pyrex tube 199 and then evaporated under N₂ at 40 °C. To perform hydrolysis of samples, the dry extract 200 was dissolved into 950 µL of KOH (1 M in H₂O), incubated for 30 min at 40 °C into an IKA control shaker (100 rpm), and 1 mL of 40 mM formic acid was added. The solution was then ready for the clean-up step through a SPE process. Oasis mixed polymer phase cartridges were first conditioned with 2 mL of MeOH and equilibrated with 2 mL of 20 mM 204 formic acid (pH 4.6). After the SPE column had been loaded with samples, 2 mL of NH₃ 2% (v/v), followed by 2 mL of MeOH/20 mM formic acid (3:7; v/v), 2 mL of hexane, and 2 mL of hexane/ethyl acetate (7/3; v/v) were applied for removing undesired compounds. Target chemicals were eluted with 2 x 1 mL of a mixture constituted of hexane/EtOH/acetic acid (70:29.4:0.6; v/v/v), and then dried under nitrogen stream at 40°C. The dried residue was reconstituted with 100 µL of A/B LC-MS solvents (83:17; v/v). Then 5 μL of sample were injected and analysed using a micro-LC-MS/MS 5500 QTrap system.

2.3 Micro-LC-MS/MS analysis

213 All LC-MS analyses were carried out using an Eksigent[®] MicroLC 200 plus (Eksigent Technologies, CA, USA) on a HALO C¹⁸ analytical column (100*0.5 mm, 2.7 μm; Eksigent Technologies, CA, USA) kept at 40°C. The mobile phase consisted of a binary gradient of solvent A (water with 0.1% (v/v) of formic acid) and solvent B (ACN/MeOH; 8:2, v/v; with 217 0.1% (v/v) of formic acid). The elution was performed at a flow rate of 0.03 mL min⁻¹ using the following gradient profile: 17% solvent B at 0 min, 22% solvent B at 9.5 min, 30% solvent B at 11.5 min until 15 min and 95% solvent B at 16 for 2.3 min, and then returned to the initial conditions. Under these conditions, no sample contamination or sample-to-sample carry-over was observed.

 Mass spectrometry analyses were performed on an AB SCIEX QTRAP 5500 (Sciex Applied Biosystems, ON, Canada). The ionization source was electrospray (ESI), and it was operated in the negative mode. The source voltage was kept at −4.5 kV, and N² was used as curtain gas. Detection of the fragmentation ion products from each PhytoP, 226 PhytoF, or IsoP deprotonated molecule [M − H]⁻ was performed in the multiple reaction monitoring mode (MRM). The MS parameters were individually optimized for each compound.

2.4 Characterization method

 Parameters including extraction yield, matrix effect, sensitivity, linearity, accuracy and precision were determined to validate the methodology used for PhytoPs, PhytoFs and IsoPs quantification in *L. digitata* from an extractive and LC-MS analytical point of view.

2.4.1 Validation of sample preparation

 In order to determine the extraction yield and the matrix effect, experiments described below were performed in triplicate using the same algal powder. Briefly, three sets were prepared: 1) 100 mg of algal samples spiked with two different concentrations of a standard mixture (SM³² or SM256) before following the extraction procedure described in part 2.2.3; 2) 100 mg of algal samples treated according to the method described in 2.2.3, 241 and then spiked with $SM₃₂$ or $SM₂₅₆$; 3) $SM₃₂$ or $SM₂₅₆$ directly prepared into the mobile phase.

SPE extraction yield (EY) was evaluated for each compound (standards and internal

 standards) by comparing peak area of set 1 (spike before SPE) *versus* set 2 (spike after 245 SPE). Result is expressed in percentage by the following calculation: $EY = A_{set1}/A_{set2}$ *100. The matrix effect (ME), also expressed in percentage and evaluated for each compound, was determined as the difference between peak areas obtained for the standards added to the extracted samples (set 2) and pure standard (set 3). The calculation is: ME = Aset2/Aset3*100.

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- *2.4.2 Sensitivity linearity and quantification*

 In order to determine the sensitivity of the analytical method we evaluated the limit of detection (LOD) and the limit of quantification (LOQ) for each compound. These values corresponded respectively to 3 and 10 times the signal-to-noise ratio. The linearity of the response was evaluated using 15 concentrations of compounds (in triplicate). Calibration curves were calculated by the least-squares linear regression method, and linearity was 257 determined to range between $3.125x10^{-3}$ and 512 pg.uL⁻¹ for compounds injected in column. Analytes quantification was based on the analyte to IS ratio using the obtained calibration curves. Data processing was achieved using the MultiQuant 3.0 software (Sciex Applied Biosystems).

2.4.3 Accuracy and precision

 Trueness, precision and accuracy were determined by validation standard analysis performed in triplicate at defined concentrations, and on two different days. Intra-batch reflects intra-day precision or repeatability, and inter-batch the inter-day precision or reproducibility. These parameters express the error of the analytical measurement.

2.5 Statistical Analyses

Standard deviation (SD) and relative standard deviation (RSD) were used to determine

 significant differences of data. As mentioned above, algal samples corresponded to a mixture of individuals placed together in a same glass flask. Each flask thus represented one experimental condition, *i.e.* control or copper stress. Despite numerous individual algae being present in flasks, each individual cannot be considered as an independent biological replicate because all algae within a flask were harvested as a pool before preparation of powder for subsequent treatment. Three independent extractions were performed on each algal sample, thus the SD calculated reflected a technical triplicate and not a biological triplicate. Two-way ANOVA were calculated with GraphPad Prism 7. The level of significance was set at P < 0.05.

3-Results

 Before dealing with the analysis of the acquired data on various biological samples, an important part of this work consisted in the validation of the methodology presented below (section *3.1*).

3.1 Sample processing validation on **L. digitata**

 Sample validation was a pre-condition for extract preparation and analysis of the six macroalgae selected for this analysis. The aim was to verify that the work was done under favourable conditions for the detection and quantification of PhytoPs, PhytoFs, IsoPs, and eventually NeuroPs.

 First, the extraction yield and matrix effect determination assessed the efficiency of the sample processing (Table 2). The extraction yield, a parameter specific of each compound (standards and IS), allowed the evaluation of product losses that could happen by retention on the SPE cartridge and/or by partial elution during the washing steps. For the majority of analytes, the apparent loss of compounds during SPE was low (<10%), yielding recovery rates similar to as if they were added after SPE. Regarding the type of

 compounds (PhytoPs, PhytoFs, IsoPs or NeuroPs), no specific trend could be noticed, *i.e.* some PhytoPs exhibited good recovery ratio (*e.g. ent*-16-*epi*-16-F1t-PhytoP; EY32= 99.6%), while it was lower for other ones (*e.g.* 16(*RS*)-16-A1-PhytoP; EY32= 68.6%). The extraction yield calculated was more than 100% for some analytes, corresponding probably to the co- elution of a compound that presents the same MRM transition. It is the case for instance 301 for the mixture of 5-F_{2t}-IsoP and 5-epi-F_{2t}-IsoP with an EY of 144.4% at 32 pg.uL⁻¹. We could also notice that EYs were better at low than at high concentrations. To complete this validation, the matrix effect, corresponding to an ion-suppression/enhancement of co- eluted matrix compounds, was evaluated. As for EY, ME is specific to each isoprostanoids, and there was no similar behaviour across the same class of compounds. We observed a clearly marked effect at low concentration, for instance for 9-F1t-PhytoP and 9-*epi*-F1t- PhytoP between SM32 and SM²⁵⁶ conditions. Indeed, ME values were 169% (SM32) and 308 123% (SM₂₅₆) for the first compound, and 204% (SM₃₂) and 125% (SM₂₅₆) for the second one.

 In order to determine the linear range in the quantification process, 15 concentrations 311 ranging from 3.125x10⁻³ to 512 pg.µL⁻¹ and prepared in triplicate were injected. This allowed establishing calibration curves and calculating the linear regression equation. The detector response was linear across the range tested. LOD and LOQ were also determined and ranged from 0.16 to 0.63 pg injected for LOD and between 0.16 and 1.25 pg injected for LOQ. These values depended on the type of isoprostanoids but are quite homogenous.

 Finally, for testing the repeatability and precision of the method, the intra- and inter-day analysis of two selected concentrations (SM³² and SM256) was performed. Among the twenty compounds tested, the majority presented an intra-day variation lower than 2%, exceptions being 16(*RS*)-16-A1-PhytoP (2.2%), 5(*RS*)-5-F2t-I*s*oP + 5-*epi*-5-F2t-I*s*oP (2.7%), and 4(*RS*)-4-F4t-NeuroP (5.6%). Mean inter-day variation was 9.9%, with 7.8% and 13.7% as minimum and maximum values, respectively. In light of these results, we concluded on the robustness of the developed method that was reproducible and usable for the purpose of isoprostanoids quantification in macroalgae.

3.2. Profiling of isopropanoid in six species of brown and red algae

 It is well established that in seaweeds, the total fatty acid content and composition, as well as the proportions of the different lipid fractions, may vary during the algal cycle life and also according to the physiological state of the algae or growth conditions, and of the genetic status or taxonomic entity. Mean total lipid content for brown seaweeds (phylum *Phaeophyta*) is 3% of dry weight, and is comprised within a range of 0.1% to 20%. Based on published data reporting lipid composition in this phylum, no specific trend depending of the phylogenetic order could be inferred, and a similar conclusion was drawn for red algae (phylum Rhodophyta) (Wielgosz-Collin, Kendel, & Couzinet-Mossion, 2016). Analysis of fatty acid distribution allowed a better discrimination of phylogenetic order or sub-order. Indeed, many studies about the proportion of saturated fatty acids (SFAs), monounsaturated fatty acids (MUFAs) and PUFAs seemed to be in favour of a significant link between fatty acid signature and phylogenetic lineage (Galloway, Britton-Simmons, Duggins, Gabrielson, & Brett, 2012; P Kumari, M Kumar, C R K Reddy, & Bk Jha, 2013). In any cases, seaweeds are mainly characterized by a high content of PUFAs, such as α- linolenic acid (18:3, n-3, ALA), stearidonic (18:4, n-3, STA), arachidonic (20:4, n-6, AA) and eicosapentaenoic acids (20:5, n-3, EPA), but each phylum presented a characteristic PUFA signature as evidenced by clustering studies of algae belonging to the same phylum (Pereira, Barreira, Figueiredo, Custodio, Vizetto-Duarte, Polo, et al., 2012). In our work, we studied profiles of PUFA oxidized derivatives across two distinct phyla and tried to determine if such clustering could be observed. In other words, it was of interest to investigate selected species of two taxonomic groups to know if difference in PUFA

 composition subsequently resulted in occurence of different oxidized products. From the study of Ritter *et al.* on *E. siliculosus*, we already knew that a macroalga could produce PhytoPs (A. Ritter, et al., 2014). More recently, Barbosa *et al.* (Barbosa, et al., 2015) tested 24 different species belonging to *Chlorophyta*, *Phaeophyta* and *Rhodophyta,* and highlighted the presence of four oxygenated metabolites derived from ALA among ten available PhytoPs standards. These compounds were 9-F1t-PhytoP and 9-*epi*-9-F1t-PhytoP found in 13 species, 16-B1-PhytoP quantified in seven species among the 13 previous ones, and 9-L1-PhytoP detected only in two species. Considering that macroalgae do not contain exclusively ALA but also STA, AA, or EPA, it appeared interesting not to focus only on PhytoPs but to investigate also other oxygenated metabolites potentially originating from such PUFAs (P. Kumari, M. Kumar, C. R. K. Reddy, & B. Jha, 2013). Therefore, we were more interested in investigating the diversity of oxidised derivatives of PUFA containing 18 to 22 carbons rather than in conducting a study on a wide range of algal species among the *Phaeophyta* and *Rhodophyta*.

3.2.1 Laminaria digitata (Huds.) Lamouroux (Fig. 1; Table 3)

 It was worth considering this alga because its phytoprostane production had not been 365 investigated yet. We showed for the first time that it produces F_1 -, B_1 -, L_1 - and A_1 -PhytoPs. Identification of PhytoPs relied on retention times observed during spiked experiments, determination of molecular masses, and determination of specific MS/MS transitions. Among our results, F1-PhytoPs represented an interesting case. These metabolites are 369 characterized by the SRM transition (m/z) 327.2 \rightarrow 283.2, which is common to 9-F_{1t}- PhytoP (+ 9-*epi*-9-F1t-PhytoP) and to *ent*-16-F1t-PhytoP (+ *ent*-16-*epi*-16-F1t-PhytoP). In order to distinguish between these compounds, the second SRM transition was considered, which is usually more specific but less sensitive. The 9-F1t-PhytoP and 9-*epi*-373 9-F_{1t}-PhytoP presented the second SRM transition (m/z) 327.2 \rightarrow 171.2, whereas *ent*-16 F1t-PhytoP and *ent*-16-*epi*-16-F1t-PhytoP were observable by following the SRM transition 375 (m/z) 327.2 \rightarrow 151.2. Based on the combination of transitions 1 and 2, we were able to quantify 9-F1t-PhytoP and *ent*-16-*epi*-16-F1t-PhytoP. Unfortunately, due to matrix effect, the peaks separation corresponding to 9-*epi*-9-F1t-PhytoP and *ent*-16-F1t-PhytoP was ineffective, and allowed only integration of the two compounds together by following 379 transition 1, while transition 2 value was below the quantification threshold. For B_{1-} , L₁-380 and A₁-PhytoPs, the main transition of each series was already specific. A precursor ion at m/z 307 and a product ion at m/z 235 were observed for B₁-PhytoP; a precursor ion at m/z 382 307 and a product ion at m/z 185 for L₁-PhytoP; a precursor ion at m/z 307 and a product 383 ion at m/z 249 for A_1 -PhytoP. The content of these compounds reached values of 28.2 ng/g and 69.2 ng/g of fresh algae for *ent*-16-B1-PhytoP and 16(*RS*)-16-A1-PhytoP, respectively.

 PhytoPs were not the only compounds identified in *L. digitata*. Indeed, PhytoFs were detected for the first time in macroalgae. These compounds have recently been discovered in nuts, seeds, or melon leaves (Cuyamendous, Leung, Durand, Lee, Oger, & Galano, 2015; Yonny, Rodriguez Torresi, Cuyamendous, Reversat, Oger, Galano, *et al.*, 2016). *Ent*-9(*RS*)-12-*epi*-ST- ¹⁰-13-PhytoF, *ent*-16(*RS*)-13-*epi*-ST- ¹⁴ -9-PhytoF, and *ent*-391 16(*RS*)-9-*epi*-ST-∆¹⁴-10-PhytoF were three compounds found in quantities similar to those 392 observed for PhytoPs by following their specific SMR transitions: m/z 343.2 $\rightarrow m/z$ 237.1 393 for the first transition, m/z 343.2 \rightarrow m/z 201 for the second transition and m/z 343.2 \rightarrow m/z 209 for the last transition.

 Finally, we also succeeded in quantifying the AA derivatives 15-F2t-IsoP, 15-*epi*-15-F2t-396 IsoP, and the mixture of the two diastereoisomers of $5-F_{2t}$ -IsoP. These compounds were the most abundant in term of amounts measured, ranging from 79.1 to 342.6 ng/g of fresh algae.

 Considering these last results, it is possible to suggest that 5-F2t-IsoP and/or 5-*epi*-5-F2t- IsoP are particularly relevant as lipid OS biomarker. Indeed, a compound present in high quantity can be more easily and reliably quantified, any concentration change being more detectable. However, before making this simple observation in *L. digitata* a rule, it is necessary to carefully analyse data gathered for many other species of macroalgae.

3.2.2 Ectocarpus siliculosus (Dillwyn) Lyngbye (Fig. 1; Table 3)

 Analysis of *E. siliculosus* revealed the presence of PhytoPs different from those previously 407 described (A. Ritter, et al., 2014a). Indeed, this macroalga contained F₁-, L₁-PhytoPs, but also PhytoFs and IsoPs. It is worth to mention the high amount of *ent*-16(*RS*)-9-*epi*-ST- ¹⁴ -10-PhytoF, with a concentration of 332.9 ng/g of fresh algae. As for *L. digitata*, the content in 5-F2t-IsoP + 5-*epi*-5-F2t-IsoP was higher than for 15-F2t-IsoP and its epimer (106.3 versus 19.1 or 21.4 ng/g of fresh algae, respectively). Based on this observation, it 412 is possible to suggest that the two diastereoisomers of $5-F_{2t}$ -IsoP are better potential OS biomarkers than 15-F2t-IsoP for *E.siliculosus*, as already described for *L. digitata*. In *E. siliculosus*, after taking into account each class of compounds, PhytoFs seemed to be more relevant due to higher amounts with a total of 486 ng/g of fresh algae for three metabolites, against 310 ng/g of fresh algae for six PhytoPs, and 146 ng/g of fresh algae for three IsoPs.

 3.2.3 Fucus spiralis L., *Pelvetia canaliculata* (L.) Decaisne & Thuret, *Grateloupia turuturu* Yamada and *Osmundea pinnatifida* (Hudson) Stackhouse (Table 3)

 To complete the analysis on brown algae, isoprostanoids composition was also assessed in *F. spiralis* and *P. canaliculata*. These algae contained the same three PhytoFs, PhytoPs (except for series A1), and IsoPs as observed in *L. digitata* and *E. siliculosus*, but at lower concentrations.

 Fewer compounds were observed across the two investigated red algae, *i.e. G. turuturu* and *O. pinnatifida*. Indeed, only 8 or 4 compounds were respectively identified in these two organisms among the 16 compounds available. PhytoPs and PhytoFs were detected in low concentration, in contrast to IsoPs in *G. turuturu,* an alga known to be rich in AA. By looking at the heterogeneity of the results, a first suggestion to explain them could be related to the efficiency of the extraction method considering important differences between the algae investigated, *e.g.* in their cell wall composition, and the fact that the optimization process was carried out only on *L. digitata* (Jimenez-Escrig, Gomez-Ordonez, & P, 2012). However, if we place these results in a different context, *i.e.* by making correlation between isoprostanoids profile and phylogenetic classification, an additional hypothesis can be put forward. Indeed, a heatmap representing the levels of isoprostanoids identified across the six seaweeds considered in our study underlined the emergence of a phylogenetic clustering, in particular with all brown algae showing similar patterns of isoprostanoid composition, but with quantitative differences (Fig. 2). We observed that the closest evolutionary relationship between *E. siliculosus* and *L. digitata versus P. canaliculata* and *F. spiralis* was corroborated with the heatmap clustering. Thus, this part of the study suggests that isoprostanoids signature may be used as a chemotaxonomic tool to differentiate macrolagae at the taxonomic level. Obviously, this is an assumption that will need to be tested on a larger diversity of macroalgae.

3.3 Accumulation of isoprostanoids under copper stress condition

 The rationale supporting these experiments was based on previous reports describing that copper treatment induced oxidative stress in macroalgae, and was then expected to alter 448 the profile and content of isoprostanoids (A. Ritter, et al., 2014a).

 For *L. digitata*, we observed higher content for most of the detected compounds (excepted for *ent*-9-L1t-phytoP and *ent*-16-B1t-phytoP) under stress compared to control condition

 (Fig. 3, Table 3). Quantities of PhytoFs increased by +91%, +114% and +155% for *ent*-16(*RS*)-9-*epi*-ST- ¹⁴-10-PhytoF, *ent*-9(*RS*)-12-*epi*-ST- ¹⁰ -13-PhytoF, and *ent*-16(*RS*)-13- 453 epi-ST-∆¹⁴-9-PhytoF respectively, while this trend was less marked for other categories of compounds. Conversely, the content of *ent*-9-L1-PhytoP decreased under the stress condition, and this could be explained by physiological considerations. Production of PhytoPs has been suggested to occur in the same way as for IsoPs, through hydrogen 457 abstraction from ALA to give G_1 -PhytoPs isomers, which are subsequently metabolized to the detectable A-type to J-type PhytoPs. Under alkaline conditions, A- and J-types undergo isomerization of the double bond to form the thermodynamically more stable final metabolites (Jahn, Galano, & Durand, 2008) .Thus, the A-type isomerized into B-type, and the J-type led to the L-type. To explain the decrease of *ent*-9-L1-PhytoP under copper stress, a probable assumption would be the absence of alkaline conditions, making isomerization impossible, so stopping the PhytoPs pathway at the step of A- and J-types. The accumulation of 16(*RS*)-16-A1t-PhytoP could corroborate this hypothesis. Another way to explain this pattern is to consider that, due to the consumption of ALA for synthesis of all PhytoPs accumulated under copper stress, there is not enough of it left to support production of the B-type and L-type PhytoPs isomer precursors, which thus decrease. To be more precise in the mechanism, we can consider the biosynthetic pathways of PhytoPs as proposed by Galano and co-workers (GALANO 2017). If we consider that PhytoPs follow the same routes as IsoPs, the G2-IsoP intermediate (endoperoxide-hydroperoxide intermediate) could represent a key metabolite for PhytoPs production that may be modulated depending on physiological conditions. Indeed, G2-IsoP could be partially (i) or completely (ii) reduced. To date, no information about the prevalence of one way 474 compared to the other is known. In the first case (i), 15-D₂-hydroperoxide is formed, leading by dehydration to the compounds 14,15-epoxyde-15-D2-IsoP (single dehydration) or 14,15-epoxyde-15-J2-IsoP (double dehydration). If these compounds are produced

 (they were not quantified by our method), they limit the bioavailability of G2-IsoP for the 478 second pathway. When the level of G2-IsoP decrease, less H₂-IsoP can be formed and consequently less final products of this pathway accumulate. In the second case (ii), the $\,$ G2-IsoP is completely reduced to produce H₂-IsoP. This latter intermediate represents 481 also a key regulation point. Indeed, as for G2-IsoP, reduction of H₂-IsoP could be partial or complete. A partial reduction leads to the formation of E2-IsoP or D2-IsoP which are precursors of A2-IsoP and J2-IsoP respectively. These latter compounds are susceptible to be changed into B2-IsoP and L2-IsoP respectively under basic conditions. A complete reduction of H2-IsoP leads to the F2-IsoP family. We can suggest that copper stress induces the complete reduction of the H2-IsoP intermediate, leading to an accumulation of the F2 derivatives at the expense of B2 and L2 derivatives. So far, nothing is known about the conditions leading to a partial or total reduction of intermediates. We can only propose that high concentration of copper supports the way of a partial reduction of the G2-IsoP intermediate, and/or a complete reduction of H2-IsoP intermediate, which could explain the decrease in the formation of the derivatives B2 and L2. To finish on this, we can also suggest that copper stress, by altering the physiological status of the alga, may lead to changes in fatty acids and/or lipid metabolism that will affect the amount ALA available in algal cells, and thus influence the enzymatically and non-enzymatically production of its subsequent oxidized derivatives. In line with this, comparison between intact and wounded rice tissues has shown that ALA concentration, and not wounding by itself, was the key regulator of the octadecanoid pathway activity under stress condition(Christeller & Galis, 2014).

 Changes in isoprostanoids content between control and stress condition were more obvious in *E. siliculosus* than in *L. digitata*. All the isoprostanoids identified in *Ectocarpus* accumulated after copper treatment, fold changes ranging from 3 to 6 (Fig. 3, Table 3). For the two other brown algae and the two *Rhodophyta* investigated, similar observations were

 made, with variable increase depending on the alga considered and on the PUFAs oxygenated derivatives (Table 3).

 Interestingly, no alteration in the diversity of the molecules identified could be noticed between control and stress condition. Almost all the compounds observed under control condition were still identified after copper stress. The only exception was 16(*RS*)-16-A1- PhytoP in *E. siliculosus* that could not be quantified after heavy metal exposure due to the peak overlapping with overexpressed matrix compounds. Finally, no compound not detected under control condition was detected after copper stress. Thus, this treatment did not trigger the production of new isoprostanoids, but modified their relative quantities. It is important to draw attention to the fact that, in our targeted lipidomic approach, we have limited our analysis to non-enzymatically produced oxidized fatty acids that we were able to identify. Therefore, it cannot be ruled out that new non-targeted enzymatic and/or non- enzymatic oxylipids were produced during this treatment, and that our analysis has probably overlooked changes for some metabolites. Additional studies are necessary to deal with these aspects.

 In light of these results, *E. siliculosus* is, among those tested, the macroalgal species for which we observed the strongest response in term of isoprostanoid profile under copper stress. Based on previous observations in land plants, this may indicate that *E. siliculosus* is well suited to support heavy metals pollution. Indeed, several PhytoPs have been shown to activate plant defence and detoxification responses. In 2003, Thoma and co-workers demonstrated the ability of cyclopentenone PhytoPs, induced by Reactive Oxygen Species, to trigger expression of genes involved in defence mechanisms and the accumulation of phytoalexin in plant cells (Thoma, Loeffler, Sinha, Gupta, Krischke, Steffan, et al., 2003). Further research of the same group strongly suggest that PhytoPs may be an endogenous mediator capable of counteracting cell damages caused by various toxicants, especially those causing severe oxidative stress (Loeffler, Berger, Guy,

 Durand, Bringmann, Dreyer, et al., 2005; Mueller, Hilbert, Dueckershoff, Roitsch, Krischke, Mueller, et al., 2008). The ability to produce high amount of PhytoPs, compounds potentially involved in response against environmental stressors, may confer to *E. siliculosus* a protective role to alleviate copper-induced toxicity and thus a survival advantage.

 Interestingly, the high accumulation of isoprostanoids observed in this alga may also account for a higher sensitivity of *E. siliculosus* to OS in this species to the other ones investigated. Such potential lethality or phytotoxicity response suggests that isoprostanoid profiling in *E. siliculosus* may serve as a possible diagnostic tool for assessing potential heavy metal pollution in the marine environment. In a more comprehensive way, we observed that most of the isoprostanoids detected under control accumulated in this alga after exposure to copper. This supports a direct correlation between this stress and the non-enzymatic production of oxidized PUFA derivatives. Our observation corroborates results previously published by Ritter *et al.* demonstrating that copper stress induced OS in the model brown alga *E. siliculosus*, as illustrated by the overlapping of transcriptomic 544 response observed after copper and H_2O_2 treatments (A. Ritter, et al., 2014b). The proof that we bring today is not directly related to signalling pathway, but is quite relevant because it concerns end-products of oxidation also considered as "gold" OS biomarkers. Furthermore, in recent years, it has become accepted that these molecules not only serve as biomarkers but also exhibit a wide range of bioactivities (Galano, et al., 2017). Our observations lay the ground to determine the physiological role(s) of these lipid mediators in macroalgae, for instance in signalling and/or as effectors altering gene expression.

Conclusion

 To our knowledge, this is the first report of PhytoF production in macroalgae. Our analysis also allowed the detection of PhytoPs or IsoPs never reported so far. The *ent*-16(*RS*)-9-

555 epi-ST-∆¹⁴-10-PhytoF and the 5-F_{2t}-IsoP epimers are ubiquitous and the most abundant of the isoprostanoids identified and quantified. This study suggests the possible use of isoprostanoid signature as a potential chemotaxonomic tool to discriminate macroalgae. Our study is also the first to establish a link between significant changes in the isoprostanoid profiles of macroalgae and heavy metal stress. For instance, the total isoprostanoid concentration in *E. siliculosus* was in the range of 945.8 ng/g and 3957.8 ng/g of fresh algae before and after cupric treatment, respectively. Furthermore, these data could open prospects for the use of *E. siliculosus* as a model in the case of marine pollution and environmental emergencies. In addition, based on recent studies showing promising biological activities for PhytoPs, IsoPs and NeuroPs, (Minghetti, Salvi, Lavinia Salvatori, Ajmone-Cat, De Nuccio, Visentin, *et al.*, 2014; Noschka, Moore, Peroni, Lewis, Morrow, & Robertson, 2009; Roy, Fauconnier, Oger, Farah, Angebault-Prouteau, Thireau, *et al.*, 2017), and due to high amounts quantified in some of the tested macroalgae, it may be worth exploring these organisms as a potential natural bio-resource for extraction of these molecules, including as an alternative to their current production by complex chemical syntheses. In this context, further work should focus on assessing how manipulating culture conditions could enhance the production of isoprostanoids in macroalgae, notably by targeting the ALA biosynthetic pathway. Conditions to be tested may include nitrate depletion in the culture medium during acclimation before stress 574 treatment, and/or alternative oxidative stress (e.g. H₂O₂). Besides nutritional interests, additional studies will be necessary to unravel the biological effects of algal isoprostanoids in humans, since they show very similar structures to the relevant bioactive IsoPs and PGs.

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List of abbreviations

- AA: arachidonic acid
- ALA: linolenic acid
- BHT: butylated hydroxytoluene
- DHA: docosahexaenoic acid
- DW: dry weight
- EI: electron ionization
- EPA: eicosapentaenoic acid
- ESI: electrospray ionization
- EY: extraction yield
- FSW: filtered sea water
- FW: fresh weight
- IS: internal standard
- IsoFs: isofurans
- IsoPs: isoprostanes
- LC: liquid chromatography
- LOD: limit of detection
- LOQ: limit of quantification
- ME: matrix effect
- MRM: multiple reaction monitoring
- MS: mass spectrometry
- MUFA: monounsaturated fatty acid
- m/z: mass to charge ratios
- NeuroFs: neurofurans
- NeuroPs: neuroprostanes
- OS: oxidative stress
- PhytoFs: phytofurans
- PhytoPs: phytoprostanes
- PUFAs: polyunsaturated fatty acids
- ROS: reactive oxygen species
- SFA: saturated fatty acid
- SPE: solid phase extraction
- SM: standard mixture
- MRM: multiple reaction monitoring
- UV: ultraviolet
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Figure captions:

 Fig. 1: Isoprostane, phytoprostane and metabolite content in *Laminaria digitata* (Huds.) Lamouroux and *Ectocarpus siliculosus* (Dillwyn) Lyngbye. Results are expressed as means ± S.D. from three technical replicates per algal sample.

 Fig. 2: Hierarchical cluster analysis on isoprostanoid derivatives of the six seaweeds investigated. Results are expressed as means from three technical replicates per algal sample.

 Fig. 3: Qualitative and quantitative isoprostanoid profiles of *Laminaria digitata* (Huds.) Lamouroux and *Ectocarpus siliculosus* (Dillwyn) Lyngbye under control condition and copper stress. Results presented as box plot were obtained from three technical replicates per algal sample.

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Table captions:

 Table 1: Structures of some isoprostanoid isomers derived from α-linolenic acid (ALA) and arachidonic acid (AA), as well as of some of the internal standards considered in our

study.

 Table 2: Determination of matrix effect and extraction efficiency for isoprostanoid extraction from *Laminaria digitata* (Huds.) Lamouroux. Results are expressed as means ± S.D. from three technical replicates per algal sample.

 Table 3: Quantification of isoprostanes, phytoprostanes and metabolites in six algae incubated under control and copper stress condition based on the method described in 817 section 2. Results are expressed as means ± S.D. from three technical replicates per algal sample. Statistical differences between control and stress condition were tested by two-way ANOVA. The limit of statistical significance was set at p<0.05.

L. digitata

Group

