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RECEIVED 26 September 2023 ACCEPTED 15 January 2024 PUBLISHED 07 February 2024

CITATION

Encinas-Yánez MF, Band-Schmidt CJ, Zenteno-Savín T, Leyva-Valencia I, Fernández Herrera LJ and Palacios-Mechetnov E (2024) Deleterious effects of free fatty acids and hydrogen peroxide towards the dinoflagellate *Gymnodinium catenatum. Front. Protistol.* 2:1302560. doi: 10.3389/frpro.2024.1302560

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Deleterious effects of free fatty acids and hydrogen peroxide towards the dinoflagellate *Gymnodinium catenatum*

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Allelopathy refers to biochemical interactions among competing microalgae, it involves a donor species that produces metabolites which can cause inhibitory effects on susceptible species. This phenomenon can participate in the regulation of harmful algal blooms. The dinoflagellate Gymnodinium catenatum is negatively affected by allelopathic interactions with co-occurring microalgae species, like Chattonella marina var. marina, which has been suggested to produce reactive oxygen species (ROS) and free fatty acids (FFA) as nocive and allelopathic agents. This study explored the effect of hydrogen peroxide (H_2O_2) and the main fatty acids produced by C. marina. An analysis of fatty acids content of C. marina in exponential phase detected 16:0 (12.5 ± 0.01%), $18:4\omega$ -3 (15.4 \pm 0.36%) and $20:5\omega$ -3 (35.4 \pm 0.71%) as the most abundant. These fatty acids along with H₂O₂ were used in dose-response bioassays with cultures of G. catenatum in exponential phase. Results suggest that these substances affect cell morphology, including the loss of motility and signs of chlorosis, as well as the chain forming qualities of G. catenatum. Toxicity among these substances varied, suggesting that the polyunsaturated fatty acid $18:4\omega$ -3 can potentially act as a more effective allelochemical (LD₅₀ = 1.7 ± 0.19 mg L⁻¹ at 24 h), followed by 20:5 ω -3 (LD_{50 =} 3.6 \pm 0.17 mg L⁻¹ at 24 h) and the saturated fatty acid 16:0 (LD_{50 =} 6.2 \pm 1.05 at 48 h). Our results suggest these substances can act, at least partially, as allelochemicals, with PUFA being the most effective metabolites. These results contribute in elucidating the potential role of ROS and FFA in allelopathy in marine phytoplankton communities.

KEYWORDS

allelopathy, dinoflagellate, phytoplankton, reactive oxygen species, fatty acids

1 Introduction

Harmful algae blooms (HABs) are natural phenomena regulated by diverse factors, including biological interactions, such as predation, competition, and parasitism (Solé et al., 2006; Mazzillo et al., 2011; Gleason et al., 2015). Allelopathy is a biochemical interaction in which metabolites are released to the surrounding environment by donor species, in this context called allelochemicals, that influence the growth and development of target species (Rizvi et al., 1992). This phenomenon has been described as concerning only chemical interactions among competing microalgae species in which one or various allelochemicals can cause inhibitory effects on susceptible species; it has been hypothesized that allelopathy encompasses adaptations that confer competitive advantages to some species over others (Keating, 1977; Legrand et al., 2003). In microalgae, the injurious effects of allelopathy on target species include the promotion of oxidative stress, by raising the endogenous production of reactive oxygen species (ROS) and inducing changes in the activity of antioxidant enzymes (Campos et al., 2013; Lu et al., 2017), photosystem II interference, electron transport chain blockage and subsequent photosynthesis inhibition (Weir et al., 2004; Qian et al., 2009; Zhu et al., 2010), disruption of cell membranes and nucleic acids which lead to high mortality in susceptible cells (Granéli et al., 2008).

The allelopathic potential of marine toxins has been explored. It has been reported that okadaic acid produced by Prorocentrum lima can contribute partially to allelopathy with co-occurring species (Windust et al., 1996; Sugg and VanDolah, 1999). Also, karlotoxins produced by dinoflagellates of the genus Karlodinium have been reported as allelochemicals capable of negatively affecting competitors and prey (Adolf et al., 2006; Wang et al., 2020). Continuous efforts to describe the mechanisms of these interactions has demonstrated that allelopathy is mediated by a great diversity of metabolites (Chaïb et al., 2021). The mechanisms of allelopathy are diverse and remain largely unknown (Śliwińska-Wilczewska et al., 2021). Nonetheless, research efforts have demonstrated that various types of secondary metabolites such as alkaloids like fischerellin (Hagmann and Jüttner, 1996; Gantar et al., 2008) and cyclical peptides like microcystins and portoamide (Kearns and Hunter, 2001; Leão et al., 2010) are associated with allelopathy in microalgae. Particularly, fatty acids in their pure form, also known as free fatty acids (FFA) have been suggested as allelochemicals produced by freshwater phytoplankton species like Botryococcus braunii, Chlorella vulgaris and Peridinium bipes (Uchida et al., 1988; Chiang et al., 2004; Song et al., 2017). In marine microalgae, the potential herbicidal qualities of fatty acids produced by the cyanophyte Lyngbya aestuarii have been explored 10.3389/frpro.2024.1302560

(Entzeroth et al., 1985). Wang et al. (2023) studied the inhibitory effects of linoleic acid (18:2 ω -3, LA) on the marine dinoflagellate *Karenia mikimotoi* which caused the reduction of photosynthetic pigments and an increase in ROS in the organism.

Laboratory studies have suggested that the chain-forming paralytic shellfish toxin (PST) producing dinoflagellate Gymnodinium catenatum can be negatively affected and dominated by the dinoflagellates Gymnodinium impudicum, Margalefidinium polykrikoides, and the raphidophyte Chattonella marina var. marina (Fernández-Herrera et al., 2016; Band-Schmidt et al., 2020; Fernández-Herrera et al., 2021; Fernández-Herrera et al., 2022). The co-occurrence and the dominance of C. marina over G. catenatum was previously reported in the Gulf of California during a HAB event (López-Cortés et al., 2011). Although the identity of the allelochemicals involved in these interactions remains unknown, C. marina and M. polykrikoides, both competitors of G. catenatum via allelopathy, have been hypothesized to produce compounds, including FFA and ROS that can act as allelochemicals (Marshall et al., 2003; Marshall et al., 2005; Tang and Gobler, 2010). The toxicity of FFA and ROS has been previously explored in microalgae, suggesting that susceptibility can vary among species, type of substance and laboratory conditions (Wu et al., 2006; Vale, 2018).

With the aim to document the effects of FFA and ROS towards *G. catenatum*, a strain of *C. marina* from Bahía de La Paz, Gulf of California, was isolated and its fatty acid profile was determined to pinpoint the FFA that can potentially act as allelochemicals towards *G. catenatum*. The response to the most abundant fatty acids in *C. marina* in their pure form was evaluated, as well as H_2O_2 under laboratory conditions. Changes in cell density, chain length and morphology were evaluated.

2 Materials and methods

2.1 Strains and culture conditions

Monoalgal strains of *G. catenatum* and *C. marina* isolated from Bahía de La Paz, Mexico, were cultured in modified GSe medium (Bustillos-Guzmán et al., 2015). Strain details are shown in Table 1. Culture conditions remained constant throughout this study at $24 \pm$ 1°C, salinity of 34, 12/12 h light/dark cycle and an irradiance of ~150 µmol photons m⁻¹ s⁻¹.

For fatty acid analysis, strains were grown in triplicate 1 L cultures in 2 L Erlenmeyer flasks. Each strain was harvested by centrifugation (1000 rpm, 5 min, 4°C) during mid exponential growth phase. For the dose-response bioassays, sterile, polystyrene flat bottom six welled (5 mL) culture plates were employed.

TABLE 1 Origin and isolation of strains.

Species	Strain designation	Origin	Isolation date	Isolated by
Gymnodinium catenatum	GCBAPAZ-10	Bahía de La Paz, Gulf of California, Mexico	June 2017	C. J. Band Schmidt
Chattonella marina	CMBAPAZ-2	El Mogote, Bahía de La Paz, Gulf of California, Mexico	June 2019	L. J. Fernández-Herrera

2.2 Growth curves

To determine the exponential growth rate, strains were grown in triplicate in batch cultures in 150 mL of modified GSe medium (Bustillos-Guzmán et al., 2015) within 300 mL Erlenmeyer flasks. Samples of each strain were taken every 48 h. Samples of *G. catenatum* were fixed in Lugol's iodine solution and samples of *C. marina* were fixed with hepes buffered paraformaldehyde (Katano et al., 2009). Cell densities were obtained by counting in a 1 mL Sedgewick-Rafter chamber with an optic microscope (Primo Star, Carl Zeiss). Specific growth rates were calculated using the following equation: $k = \ln (N_2/N_1)/(t_2 - t_1)$; considering the ratio of the cell counts (N_2/N_1) at times t_2 and t_1 (Guillard and Ryther, 1962).

For fatty acid analysis, strains were grown in triplicate 1 L cultures in 2 L Erlenmeyer flasks. Each strain was harvested by centrifugation (1000 rpm, 5 min, 4° C) in the mid exponential growth phase. For the dose-response bioassays, sterile, polystyrene flat bottom six welled (5 mL) culture plates were employed.

2.3 PCR, DNA sequencing and phylogenetic analysis

A 2 mL sample of the raphidophyte *C. marina* was harvested in exponential growth phase. The supernatant was removed by gentle aspiration. DNA extraction was carried out using the Quick-DNA Miniprep Plus Kit (Zymo Research). The genomic DNA samples were amplified by polymerase chain reaction (PCR) using a thermal cycler (MJ Mini, Bio-Rad, Hercules, CA). The reaction was carried out in 50 μ L, employing PCR master mix 2X solution (ThermoFisher) and primers 28S F (5'-TATGCTTAAATTC AGCGGGT-3') and 28S R (5'-GTGAACCTGCAGAAGGATCA-3') (Hosoi-Tanabe et al., 2006). PCR conditions are the following: denaturation at 94°C for 1 min, 35 cycles at 94°C for 30 s, annealing at 55°C for 2 min, extension at 72°C for 3 min, and final extension at 72°C for 10 min.

The PCR products were purified using the ZymocleanTM Gel DNA Recovery Kit (Thermo Fisher). Sequencing was carried out by MCLAB (San Francisco, CA) using an automated DNA sequencer ABI 3730XL (Thermo Fisher). The sequence was analyzed using the software BioEdit (ver. 7.2.) and the software Molecular Evolutionary Genetics Analysis (MEGA, ver. 10.1.7.). Existing Chattonella sequences (Supplementary Table S1) were obtained using NCBI Blast (https://blast.ncbi.nlm.nih.gov/Blast.cgi). Sequence alignment was performed with the MUSCLE algorithm. To select the best nucleotide substitution model, a comparison between 24 models was carried out using the Bayesian Information Criterion. Consequently, a phylogenetic analysis with Maximum Likelihood Algorithm was carried out. A sequence of Heterosigma akashiwo was used as an outgroup. The sequence of the strain of Chattonella from Bahía de La Paz was submitted to Genbank (Accession number: OR642744).

2.4 Fatty acids extraction and analysis

Lipid extraction and analysis was carried out using ~100 mg of biomass of each strain, samples were placed in thick-walled glass tubes, 6 mL of Folch's solution (chloroform/methanol, 2:1 v/v), 10 μ L of the antioxidant butylated hydroxytoluene (BHT) and 10 μ L of the internal standard fatty acid 23:0 were added to each sample. Samples were sonicated during 15 min and kept at -20°C for 24 h.

Samples were dried under nitrogen gas (N₂), 1000 μ L of Boron trifluoride-methanol (BF₃ 10%) were added to the samples and were incubated at 85-95°C during 5 min. After cooling for 5 min at room temperature, 1000 μ L of hexane was added to each sample to extract fatty acid methyl esters (FAME). Samples were centrifuged at 2000 rpm for 5 min at 5°C. The hexane phase was washed with deionized water.

Sample analysis was performed in a gas chromatograph (6890 N, Agilent Technologies, Santa Clara, CA) employing a DB-23 silica column (30 m \times 0.25 mm internal diameter \times 0.25 µm film thickness, 50% Cyanopropyl; 50% Methylpolysiloxane, Agilent J&W, USA), using helium as the carrier gas and a temperature ramp from 110 to 220°C. Identification of FAME was carried out by comparing retention times from the samples and the known standards (47885-U, Supelco, Bellefonte, USA). The concentration of each fatty acid was corrected by the response of the corresponding known standard and the internal standard (23:0). Results were presented as the proportion of each fatty acid out of the total fatty acids.

2.5 Dose-response bioassays

The three most abundant fatty acids from C. marina were acquired as pure analytic standards (Sigma Aldrich). Preliminary bioassays were carried out to determine the range of final concentrations where the inhibitory effect could be observed for each fatty acid. A range of final concentrations was prepared for each fatty acid analyzed by diluting with dimethyl sulfoxide (DMSO): from 0 to 32 mg L⁻¹ for palmitic acid (PA), from 0 to 10 mg L⁻¹ for stearidonic acid (SDA), and from 0 to 15 mg L⁻¹ for eicosapentaenoic acid (EPA). For H₂O₂, a range of concentrations from 0 to 200 µM was prepared by diluting a 30% w/v solution. For bioassays with fatty acids, DMSO was used as carrier solvent (0.4% of the total volume). Treatments were done in triplicate with an initial cell density of 500 cells mL⁻¹ of G. catenatum. Cultures of G. catenatum in GSe medium and of G. catenatum in GSe medium with the addition of DMSO (0.4%) were used as negative controls. In addition, mixed cultures of G. catenatum and C. marina in a 1:2 cell density proportion were used to compare the effects on G. catenatum.

2.6 Statistical analyses

All statistical analyses were carried out in R software (ver. 4.2.1, R Core Team, 2021). Normality and homogeneity of the data was

tested by Shapiro-Wilk and Levene tests, respectively. When parametric conditions were met, Welch's t test was used in the comparison of two treatments and one-way ANOVA was used for comparisons between three or more treatments followed by a *posthoc* Tukey's test. Data on the proportions of chain lengths did not meet the parametric criteria; therefore, non-parametric Kruskal-Wallis tests followed by Conover-Iman tests were performed. For lethal dose estimation, the drm function from the "dose response curve" package (Ritz et al., 2015) was employed to model the effect of the potential allelochemicals on the cell density of *G. catenatum*. Several fitted models were compared and the most adequate were chosen based on the Akaike's information criterion.

3 Results

3.1 Phylogenetic analysis of the raphidophyte strain

The amplification of a partial sequence of the 28S region in *Chattonella* sp. strain resulted in a product of approximately 625 bp. A phylogenetic tree was constructed from sequences of 28S region of rDNA from 11 isolates of the *Chattonella* genus (Figure 1). Phylogenetic analysis placed *Chattonella* sp. strain within the *C. marina* cluster with a bootstrap support of 100%. Sequences of *C. subsalsa* were placed in a separated clade at bootstrap support of 97%, both clades were separated from the *H. akashiwo* sequence used as an outgroup.

3.2 Growth

The maximum cell density for *G. catenatum* in monoalgal cultures was $6,289 \pm 375$ cells mL⁻¹ which was reached at day 14,

while for *C. marina* $39,209 \pm 2,489$ cells mL⁻¹ were reached at day 16 (Figure 2). The specific growth rates were 0.26 and 0.15 for *G. catenatum* and *C. marina*, respectively; doubling times were 0.21 div day⁻¹ and 0.38 div day⁻¹ for *G. catenatum* and *C. marina*, respectively.

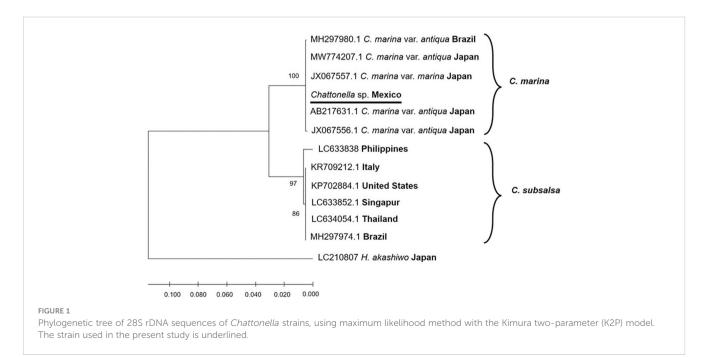
3.3 Fatty acids

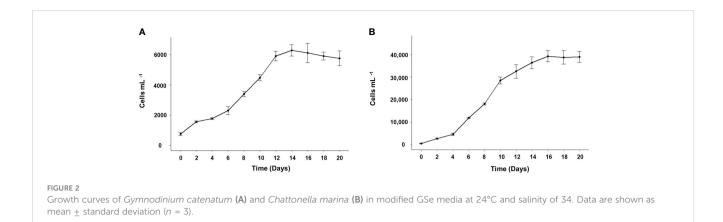
The fatty acid composition obtained for *G. catenatum* and *C. marina* is shown in Table 2. The most abundant saturated fatty acid was PA (16:0) in both species; *C. marina* in a proportion of 12.5 \pm 0.01%, and in *G. catenatum* of 27.4 \pm 0.93%. The proportion of total saturated fatty acids was 21.9 \pm 1.02% for *C. marina* and 36.2 \pm 2.64% for *G. catenatum*. The most abundant monounsaturated fatty acids were palmitoleic acid (16:1 ω -7, 4.2 \pm 0.13) in *C. marina* and oleic acid (18:1 ω -9, 2.3 \pm 0.45%) in *G. catenatum*. Both strains had a low percentage of monounsaturated fatty acids (12.4 \pm 1.4% in *C. marina* and 7.1 \pm 0.28% in *G. catenatum*).

The most abundant polyunsaturated fatty acids (PUFA) in *C.* marina were EPA (20:5 ∞ -3, 35.4 ± 0.71%) and SDA (18:4 ∞ -3, 15.4 ± 0.36%). In contrast, the most abundant PUFA in *G. catenatum* were docosahexaenoic acid (22:6 ∞ -3, 23.5 ± 1.72%) and EPA (19.22 ± 0.51%). Additionally, octadecapentaenoic acid (18:5 ∞ -3) was detected in *G. catenatum* as the third most abundant PUFA (9.0 ± 0.18%). The total proportion of PUFA was 65.62 ± 1.46% for *C. marina* and 56.6 ± 2.50% for *G. catenatum*.

3.4 Effect of free fatty acids on the cell density and chain length of *G. catenatum*

Addition of FFA in the culture medium caused mortality in *G. catenatum* (Figure 3A). A mortality higher than 90% was observed





with 32 mg L⁻¹ of PA starting from 48 h and continued increasing at 72 h (> 95%). The lowest PA concentration (1 mg L⁻¹) at 48 h showed a cell density of *G. catenatum* higher than the mixed culture with *C. marina* (ANOVA $F_{3,8} = 5.32$, p < 0.05). In contrast, there were no significant differences in cell density between the control, the control with DMSO, and the mixed culture with *C. marina*.

Exposure to the free polyunsaturated fatty acids SDA and EPA caused mortalities above 90% at 24 h (Figures 3B, C) with the highest concentrations analyzed (15 mg L^{-1} and 5 mg L^{-1} , respectively). Exposure to SDA at 24 h caused a decrease in cell density at concentrations above 1 mg L^{-1} ; an apparent increase in cell density was observed at concentrations from 3 to 5 mg L^{-1} SDA at 48 h and 72 h. Mortalities were also higher than 90% at 48 h and 72 h in experiments with EPA with the highest concentrations used (9 to 15 mg L^{-1}).

Changes in chain length of *G. catenatum* after exposure to the fatty acids is shown in Figure 4. When exposed to the highest concentration of PA (32 mg L⁻¹) at 48 h, the proportion of individual cells (91.9 ± 10.80%) was significantly higher than in the control (56.7 ± 3.16%), the control with DMSO (62.9 ± 1.00%), and the mixed culture with *C. marina* (58.7 ± 1.58%, Kruskal-Wallis $\chi^2 = 22.54$, p < 0.005). The proportion of individual cells of *G. catenatum* at 72 h was also higher with 32 mg L⁻¹ of PA (91.9 ± 10.80%) than in the control (44.4 ± 6.10%), the control with DMSO (47.1 ± 3.86%), and the mixed culture with *C. marina* (39.2 ± 3.06%, Kruskal-Wallis $\chi^2 = 22.99$, p < 0.005).

Exposure to 2 mg L⁻¹ of SDA at 24 h (Figure 4) resulted in a higher proportion of individual cells of *G. catenatum* (55.7 ± 5.10%) than in the control (36.1 ± 4.82%), the control with DMSO (42.6 ± 3.01%), and the mixed culture with *C. marina* (32.7 ± 2.78%), as well as with treatments with the highest concentrations of SDA (3 mg L⁻¹, 40.1 ± 2.50%; 4 mg L⁻¹, 41.9 ± 3.04%; 5 mg L⁻¹, 35.2 ± 2.34%; (Kruskal-Wallis $\chi^2 = 22.81$, p < 0.005). In contrast, at 72 h after exposure to SDA, individual cells of *G. catenatum* were higher in the control (50.7 ± 7.87%) than in the treatments with the highest concentrations of SDA (3 mg L⁻¹, 27.4 ± 1.48%; 4 mg L⁻¹, 28.2 ± 1.57%; 5 mg L⁻¹, 28.4 ± 2.74%), (Kruskal-Wallis $\chi^2 = 20.37$, p < 0.01). At 48 h of exposure, the proportion of two-cell chains was higher in the treatment with 5 mg L⁻¹ SDA (50.06 ± 0.38%) than in the control with DMSO (37.28 ± 1.53), the mixed culture (35.61 ±

6.45) and the treatment with 1 mg L $^{-1}$ (30.44 \pm 4.5, Kruskal-Wallis χ^2 = 19.926, p < 0.05).

When *G. catenatum* was exposed to the highest concentration of EPA (15 mg L⁻¹) at 24 h the proportion of individual cells (67.2 ± 24.88%) was significantly higher than the control (31.8 ± 2.30%), the control with DMSO (38.0 ± 3.59%) and the mixed culture (41.0 ± 1.27%) with *C. marina* (Kruskal-Wallis $\chi^2 = 32.87$, p < 0.05). Furthermore, single cells of *G. catenatum* were also higher with 15 mg L⁻¹ EPA at 72 h (41.7 ± 5.01%) than in the control with DMSO (16.8 ± 0.64%, Kruskal-Wallis $\chi^2 = 28.78$, p < 0.01). At 72 h the proportion of 2-cell chains was significantly higher in treatments with 9 to 15 mg L⁻¹ (> 30%) than in the control (22.06 ± 2.01%), the control with DMSO (21.80 ± 2.49%) and the mixed culture (20.28 ± 1.36%, Kruskal-Wallis $\chi^2 = 33.662$, p < 0.05). chains of 5 or more cells disappeared from the treatment with 15 mg L⁻¹ EPA from 24 to 72 h.

The toxicity of FFA to *G. catenatum* is shown in Table 3. The toxicity of the three FFA tested varied throughout the sampling times. The LD_{50} of the free saturated fatty acid PA was calculated after 48 h to be 6.2 ± 1.05 mg L⁻¹. The LD_{50} of the two free PUFA tested, EPA and SDA, was calculated to be 3.6 ± 0.17 mg L⁻¹ and 1.7 ± 0.19 mg L⁻¹, respectively at 24 h. In addition, the Cedergreen-Ritz-Streibig model (Supplementary Figure S1) suggests a stimulatory response in the surviving cells of *G. catenatum* exposed to concentrations between 3 to 5 mg L⁻¹ SDA at 48 h (p < 0.05).

3.5 Effect of hydrogen peroxide on the cell density and chain length of *G. catenatum*

Exposure to H_2O_2 in the culture medium caused mortality in *G. catenatum* (Figure 5A). A mortality higher than 80% was observed with the highest concentrations of H_2O_2 used (180 µM and 200 µM) at 12 h of exposure. At 24 h of exposure to 180 µM and 200 µM of H_2O_2 a mortality higher than 90% was observed. Moreover, at 12 h of exposure, the cell density of *G. catenatum* was significantly lower in the mixed culture with *C. marina* than in the control (ANOVA, F (7,16) = 29.95, *p* < 0.05). However, at 24 h of exposure no differences between cultures were observed. Additionally, a higher cell density of *G. catenatum* compared to the control was observed at 6 h of exposure to 60 µM H_2O_2 (t (2.44) = -4.8654, *p* < 0.05).

TABLE 2 Fatty acid composition of *Chattonella marina* and *Gymnodinium catenatum* strains from Bahía de La Paz, Gulf of California, Mexico.

Fatty acid	C. marina (%)	G. catenatum (%)		
12:0	0.2 ± 0.06	0.0 ± 0.00		
13:0	0.5 ± 0.04	0.3 ± 0.02		
14:0	7.1 ± 0.26	1.9 ± 0.06		
15:0	0.3 ± 0.01	0.05 ± 0.02		
16:0	12.5 ± 0.01	27.4 ± 0.93		
18:0	1.1 ± 0.76	4.14 ± 1.70		
20:0	0.0 ± 0.00	1.8 ± 0.13		
22:0	0.1 ± 0.05	0.0 ± 0.00		
24:0	0.1 ± 0.02	0.2 ± 0.04		
Σ Saturated	21.9 ± 1.02	36.2 ± 2.64		
14:1 ω-8	0.5 ± 0.02	0.3 ± 0.56		
15:1 ω-8	0.1 ± 0.05	0.0 ± 0.00		
16:1 ω-9	2.2 ± 0.23	1.3 ± 0.50		
16:1 ω-7	4.2 ± 0.13	1.3 ± 0.30		
16:1 ω-5	2.4 ± 0.09	0.4 ± 0.01		
18:1 ω-9	1.9 ± 0.05	2.3 ± 0.45		
18:1 ω-7	0.8 ± 0.29	0.7 ± 0.01		
Σ Monounsaturated	12.4 ± 1.4	7.1 ± 0.28		
18:2 ω-6	1.7 ± 0.05	2.8 ± 0.00		
18:3 ω-6	0.9 ± 0.03	0.0 ± 0.00		
18:3 ω-3	3.7 ± 0.15	0.8 ± 0.09		
18:4 ω-3	15.4 ± 0.36	0.6 ± 0.01		
18:5 ω-3	0.0 ± 0.00	9.0 ± 0.18		
20:2 ω-6	0.1 ± 0.01	0.0 ± 0.00		
20:3 ω-3	0.1 ± 0.01	0.0 ± 0.00		
20:4 ω-6	3.1 ± 0.07	0.0 ± 0.00		
20:4 ω-3	0.0 ± 0.00	0.0 ± 0.00		
20:5 ω-3	35.4 ± 0.71	19.2 ± 0.51		
21:4 ω-6	0.2 ± 0.01	0.03 ± 0.01		
22:5 ω-6	0.0 ± 0.00	0.08 ± 0.14		
22:6 ω-3	5.1 ± 0.37	23.5 ± 1.72		
Σ Polyunsaturated	65.6 ± 1.46	56.6 ± 2.50		

Data are shown as mean \pm standard deviation (n = 3).

Changes in chain length of *G. catenatum* after exposure to H₂O₂ is shown in Figure 5B.When *G. catenatum* was exposed to H₂O₂ for 6 h, the proportion of individual cells was significantly higher in the treatments with 20 μ M (55.6 ± 10.65%), 120 μ M (39.4 ± 13.48%), 180 μ M (71.9 ± 0.56%), and 200 μ M H₂O₂ (61.6 ± 2.24%) than in the control (27.7 ± 0.91%, Kruskal-Wallis χ^2 = 29.565, *p* < 0.05). After 24 h, the proportion of individual cells was higher in the

treatments with 180 µM (57.0 ± 7.43%) and 200 µM H₂O₂ (48.0 ± 14.72%) than in the treatment with 20 µM H₂O₂ (17.9 ± 5.06%), the control (17.0 ± 3.17%) and the mixed culture (17.2 ± 6.49%, Kruskal-Wallis χ^2 = 26.482, *p* < 0.05). The toxicity of H₂O₂ to *G. catenatum* is shown in Table 3. The LD₅₀ of H₂O₂ decreased from 161.2 ± 4.69 µM at 6 h to 103.1 ± 8.14 µM at 24 h.

3.6 Changes in the morphology of G. catenatum after exposure to FFA and H_2O_2

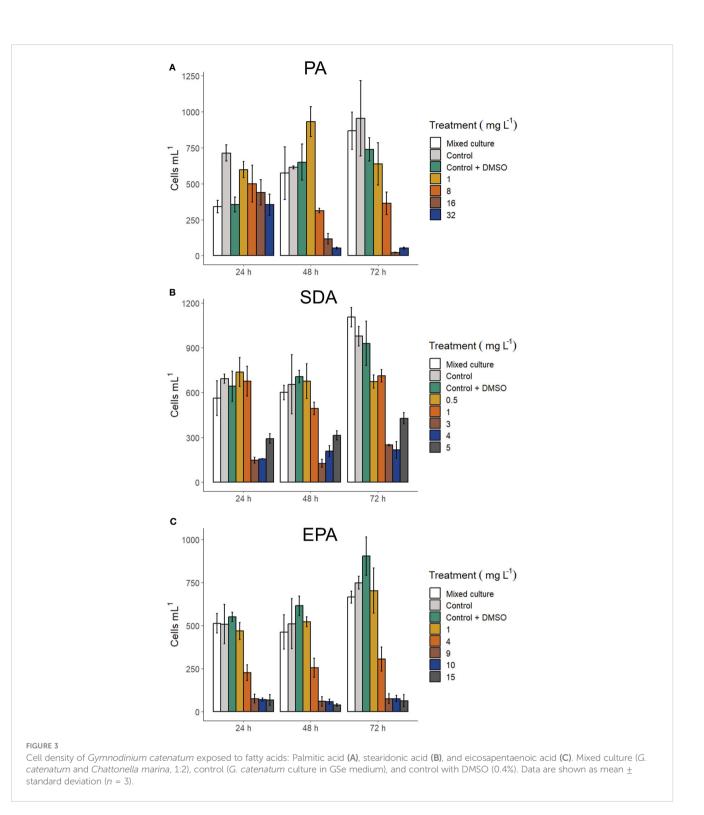
Morphological changes were observed in *G. catenatum* after exposure to the FFA and H_2O_2 (Figures 6–9). Evident changes were observed at 48 and 72 h exposure at concentrations above 4 mg L⁻¹ PA, which included swelling, loss of motility and flagella, detachment of the external membrane, lysis, and apparent chlorosis at the highest concentrations (32 mg L⁻¹ PA, Figure 6).

Exposure to concentrations above 2 mg L^{-1} EPA also caused evident changes in cell morphology at 24 h including swelling and vacuolization, the loss of motility and increased signs of cell lysis (Figure 7). Similar changes were observed in *G. catenatum* after exposure to SDA at 24 h, where the general loss of motility, the appearance of orange-brown accumulation bodies and swelling were also observed. Signs of lysis were more apparent at concentrations above 2 mg L^{-1} SDA; the presence of cells forming chains was also observed (Figure 8).

Cells of *G. catenatum* exposed to H_2O_2 showed similar effects on cell morphology as FFA, including the loss of motility, swelling, membrane detachment, lysis and chlorosis when exposed to the highest concentrations (180 – 200 μ M H_2O_2 , Figure 9). Few *G. catenatum* cells showing a similar deformation pattern were also found in mixed cultures with *C. marina*. These changes in cell morphology included swelling and vacuolization, loss of motility, presence of internal accumulation bodies and detachment of the external membrane.

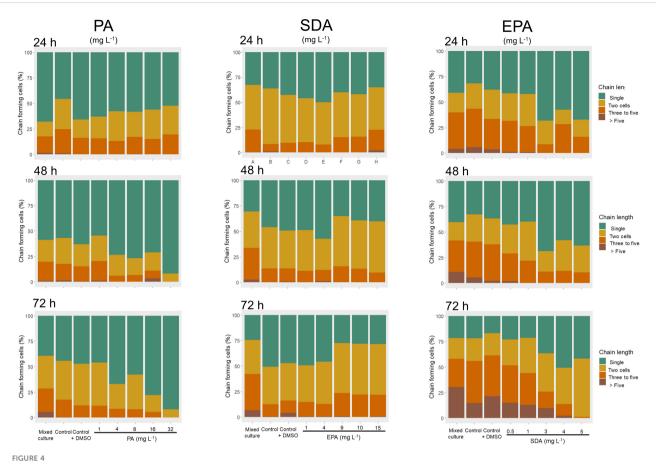
4 Discussion

The results of this study show that PA, EPA, and SDA were the most abundant fatty acids in the strain of C. marina in exponential growth phase. Previous studies suggested these fatty acids are among the most abundant in raphidopyte strains of the species H. akashiwo, Fibrocapsa japonica, and C. marina from different geographic regions (Nichols et al., 1987; Marshall et al., 2002; Giner et al., 2008; Band-Schmidt et al., 2012; Dorantes-Aranda et al., 2013). The C. marina strain employed in the present study showed EPA as the most abundant fatty acid. This is in agreement with Band-Schmidt et al. (2012) who also suggested that EPA was the most abundant fatty acid (19.8 - 34.9%) in four strains of Chattonella and F. japonica from the Gulf of California, Mexico in exponential growth phase. Furthermore, Dorantes-Aranda et al. (2013) suggested the relative abundance of FFA in C. marina can vary; while some strains showed a higher abundance of FFA in the stationary phase, the strain CMCV-1 of C. marina from Bahía de La Paz showed a higher abundance in the exponential growth phase.



The dinoflagellate *G. catenatum* contained a high proportion of PA (27.4 \pm 0.93%), EPA (19.2 \pm 0.51%), 22:6 ω -3 (DHA, 23.5 \pm 1.72%) and 18:5 ω -3(9.0 \pm 0.18%). A similar profile was reported by Hallegraeff et al. (1991) for laboratory cultures of *G. catenatum* and field samples, although the fatty acid 18:5 ω -3 was reported in low proportions (from 1.2 to 2.3%). This fatty acid has been reported to be quite variable among dinoflagellates (Mansour et al., 1999).

Negative effects of FFA and H_2O_2 on *G. catenatum* were observed in this study. Changes in cell density and signs of lysis in the experiments suggest the toxicity of these substances varies with the concentration and exposure time. Also, exposure to the highest concentrations of PA and H_2O_2 caused an apparent chlorosis in *G. catenatum* cells. It has been suggested that FFA are capable of interfering with the electron transport chain in chloroplasts (Venediktov and Krivoshejeva, 1983). It has also



Chain length of *Gymnodinium catenatum* exposed to free fatty acids: Palmitic acid (16:0, PA), stearidonic acid ($18:4\omega-3$, SDA), and eicosapentaenoic acid ($20:5\omega-3$, EPA). Mixed culture (*G. catenatum* and *Chattonella marina*, 1:2), control (*G. catenatum* culture in GSe medium), and control with DMSO (0.4%). Data are shown as mean \pm standard deviation (n = 3).

been suggested that FFA can cause membrane disruption and the detachment of pigments in freshwater microalgae (Wu et al., 1998; Wu et al., 2006). However, further studies are needed to elucidate the mechanisms involved.

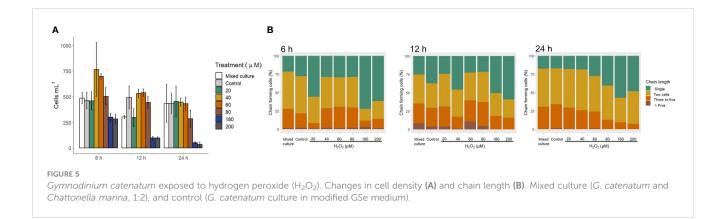
TABLE 3	Toxicity of fatty	v acids and hydrogen peroxide towards			
Gymnodinium catenatum in modified GSe medium.					

Fatty Acid	24 h		48 h		72 h	
	LD ₅₀	LD ₂₀	LD ₅₀	LD ₂₀	LD ₅₀	LD ₂₀
PA	>32	>32	6.2 ± 1.05	3.1 ± 0.54	8.0 ± 0.59	5.8 ± 0.79
EPA	3.6 ± 0.17	2.9 ± 0.18	3.8 ± 0.17	3.0 ± 0.23	3.5 ± 0.13	1.2 ± 0.53
SDA	1.7 ± 0.19	1.3 ± 0.15	-	-	-	-
	6 h		12 h		24 h	
H ₂ O ₂	LD ₅₀	LD ₂₀	LD ₅₀	LD ₂₀	LD ₅₀	LD ₂₀
	161.2 ± 4.69	159.2 ± 3.62	112.8 ± 7.51	90.1 ± 5.94	103.1 ± 8.14	73.4 ± 8.59

 $\rm LD_{50}$ and $\rm LD_{20}$ indicate the concentration that caused a decrease of 50% and 20% in cell abundance, respectively.

Data are shown as mean \pm standard deviation (n = 3).

Chattonella marina and M. polykrikoides have been suggested to produce ROS and FFA as metabolites involved in their ichthyotoxicity (Marshall et al., 2003; Dorantes-Aranda et al., 2009; Dorantes-Aranda et al., 2013). The role of ROS and FFA as potential allelochemicals produced by raphidophytes has been previously suggested by Marshall et al. (2003). Their results showed that ROS production is density dependent in raphidophytes. Additionally, the behavior of different strains of raphidophytes towards ROS production varied, including observations of autolysis in a strain of C. marina due to its ROS production, while other strains were resistant to higher concentrations of ROS. Their results also showed that EPA in its free form can be an allelochemical towards bacteria, an effect that is enhanced by the presence of superoxide. It has been reported that H₂O₂ production in C. marina takes place in the intracellular medium, while the production of O2 - takes place at the cell surface (Kim et al., 2007). The intracellular accumulation of H₂O₂ in raphidophyte cells has been suggested, as the measured H₂O₂ is higher in ruptured C. marina cell suspensions compared to intact cell suspensions (Oda et al., 1994; Oda et al., 1995). A mechanism for the exogenous release of FFA to the marine environment has not been suggested for C. marina. Cell rupture has been identified as a key factor in C. marina ichthyotoxicity, and an increase in FFA proportion has been observed in the profile of ruptured cells,



suggesting that dying cells are more toxic due to the increased release of FFA and ROS (Dorantes-Aranda et al., 2013; Dorantes-Aranda et al., 2015). It is, therefore, possible that *C. marina* populations can benefit from their dying conspecifics upon releasing putative allelochemicals from ruptured cells. This hypothesis can be explored in future studies.

Supplementary Table S2 shows differences in measurements of H_2O_2 in *Chattonella* reported in the literature. *Chattonella marina* strains show substantial variability in H_2O_2 production. Laboratory culture conditions are suggested to play a significant role in ROS production in raphidophytes; particularly, different light intensities have been reported to cause differences in H_2O_2 production among *C. marina* strains (Dorantes-Aranda et al., 2013; Li et al., 2015). According to these measurements, an exceedingly high cell density of *C. marina* cells would be needed to reach the LD_{50} H_2O_2

concentrations estimated for *G. catenatum* in this study. Indicating that the release of H_2O_2 alone cannot be responsible for the allelopathic effects towards *G. catenatum*. Previous studies have suggested that the role of ROS on the ichthyotoxicity of harmful algae is not a direct one, and experiments that involve the chemical addition of ROS substances do not mimic the toxicity of live isolates (Marshall et al., 2003; Tang et al., 2005).

The effects of the FFA on *G. catenatum* in this study, suggest that the PUFA, EPA and SDA cause mortality at lower concentrations and in a shorter time than the saturated fatty acid PA. Particularly, SDA showed the most effective inhibitory capacity at 24 h of exposure. It has been previously suggested that fatty acid carbon chain length is related to the algicidal potential of these substances (Zhu et al., 2021). These observations are also in accordance with previous studies on the effect of FFA on

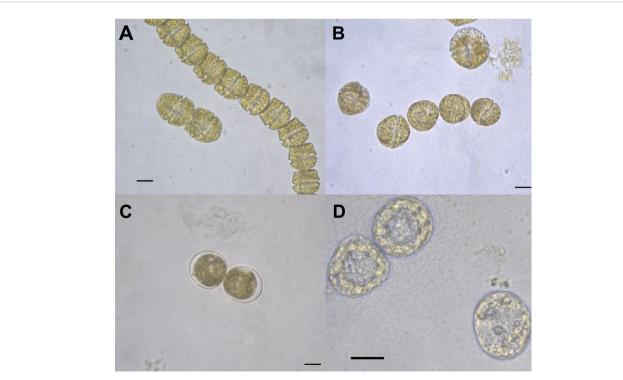


FIGURE 6

Gymnodinium catenatum cells exposed to palmitic acid (PA) at 72 h. Cell swelling (A, B), cells surrounded by detached external membrane (C), dead cells (D). Scale bar = $20 \ \mu m$.

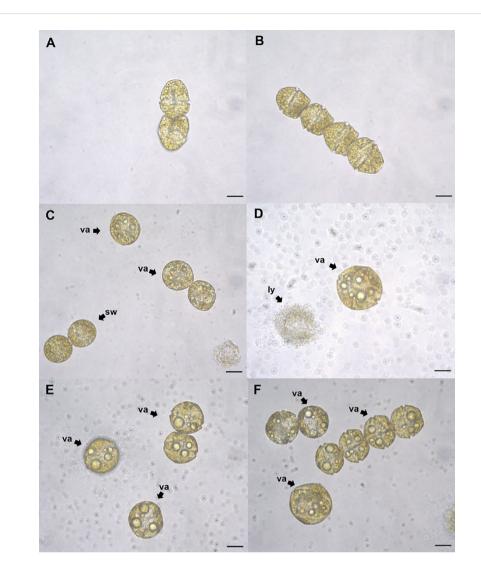


FIGURE 7

Gymnodinium catenatum cells exposed to eicosapentaenoic acid (EPA) at 24 (h) Control with dimethyl sulfoxide (DMSO) (A), cells exposed to 1 mg L⁻¹ (B), 3 mg L⁻¹ (C), 6 mg L⁻¹ (D), 8 mg L⁻¹ (E), and 10 mg L⁻¹ (F). Swollen cells (sw), vacuolization (va), lysis (ly). Scale bar = 20 μ m.

freshwater microalgae. Chiang et al. (2004) reported that *B. braunii* can produce and release a mixture of FFA as allelochemicals, including PA which showed lower toxicity than the PUFA 18:3 ω -3, 18:2 ω -7 and 18:1 ω -9. Moreover, Wu et al. (2006) reported that the toxicity of PA and EPA can vary among different species of microalgae, suggesting cells that lack an external covering structure beyond a thin mucilage layer are more susceptible to the effects of FFA. While it is suggested that *G. catenatum* has amphiesmal vesicles, it is generally recognized as a naked planktonic dinoflagellate that lacks cellulose plates (Morey-Gaines, 1982). This characteristic could explain its susceptibility to the effects of FFA.

The observed toxicity of FFA could suggest a relevant participation of the oxidized products from these substances (Aliotta et al., 1990). Previous experiments on the ichthyotoxicity of *C. marina* and other microalgae reported that the negative effects of fatty acids, particularly PUFA, can be enhanced by the presence of ROS (Marshall et al., 2003; Marshall et al., 2005; Mardones et al., 2015). Also, it has been suggested that the ichthyotoxicity among strains of *C. marina* is influenced mainly by differences in ROS production rather than by differences in fatty acid composition (Shikata et al., 2021). A synergistic role of different allelochemicals has also been reported in experiments with *Cochlodinium geminatum* (Wu et al., 2021). In this study, the strain of *C. marina* (CMBAPAZ-2) employed in mixed cultures with *G. catenatum* did not cause a significant decrease in cell density at the end of the experiments, as opposed to the *C. marina* var. *marina* strain previously reported to induce high mortalities of *G. catenatum* (Fernández-Herrera et al., 2016; Fernández-Herrera et al., 2021; Fernández-Herrera et al., 2022) which suggests that the allelopathic capabilities of *C. marina* can vary between strains or taxonomical varieties.

Our results show that low concentrations of PA (1 mg L^{-1}) and H_2O_2 (60 μ M) caused an increase in cell density of *G. catenatum* at punctual sampling times (48 h for PA; 6 h for H_2O_2). The presence of an initial stimulating phase has been reported in experiments

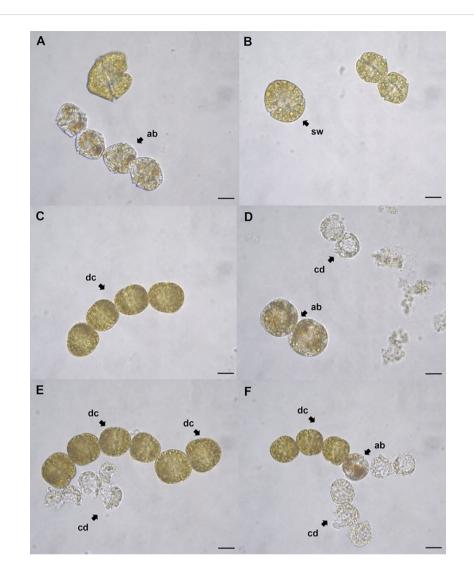


FIGURE 8

Gymnodinium catenatum cells exposed to stearidonic acid (SDA) at 48 h. Affected cells exposed to 0.5 mg L⁻¹ (A), 1 mg L⁻¹ (B), 2 mg L⁻¹ (C) 3 mg L⁻¹ (D), 4 mg L⁻¹ (E), and 5 mg L⁻¹ (F). Cell with orange-brown accumulation bodies (ab); cell swelling (sw); deformed chain-forming cells (dc); dead cells (cd). Scale bar = 20 μ m.

with chlorellin exposure on freshwater species (DellaGreca et al., 2010). Vale (2018) also reported the presence of an initial stimulating phase in the cell density of *G. catenatum* exposed to low concentrations of H_2O_2 . It has been suggested that ROS can have cell signaling capabilities related to growth processes at low concentrations (Holmström and Finkel, 2014). Additionally, Wang et al. (2023) reported that at low concentrations of the PUFA linoleic acid (0.1 mg L⁻¹) promotes the growth of *K. mikimotoi* while higher concentrations (0.5 mg L⁻¹) cause inhibitory effects on growth, carotenoid and polysaccharide biosynthesis, porphyrin, and sphingolipid metabolism, as well as an increase in ROS production.

Exposure to FFA and H_2O_2 in our experiments also produced changes in chain formation of *G. catenatum*, in which the decrease in cell density often coincided with an increase in single cell proportions. A similar response was also reported in the experiments by Vale (2018), in which concentrations above 245 μ M of H_2O_2 under halogen light caused single cells to dominate in cultures of *G. catenatum*. It has been suggested that high irradiance conditions can enhance the toxicity of H_2O_2 in consequence to an increase in its transformation into hydroxyl radical (OH) (Drábková et al., 2007).

It has been reported that a low number of *G. catenatum* cells can survive the allelopathic effect of *C. marina*, among these, chain forming cells show a higher growth rate, suggesting the survival strategy of *G. catenatum* involves chain formation (Fernández-Herrera et al., 2022). Our results also show that a low number of *G. catenatum* cells can survive exposure to the highest concentrations used of fatty acids and H_2O_2 . In addition, treatments with the highest concentrations of SDA in our experiments showed an apparent growth stimulation at 48 h and 72 h. This was observed after a significant decrease in cell density at 24 h. Additionally, a decrease in single cells concomitant with an increase in chain formation was observed in treatments with concentrations of SDA above 2 mg L⁻¹ at 48 h and 72 h, which suggests growing cells favor chain formation. An apparent stimulatory phase in a

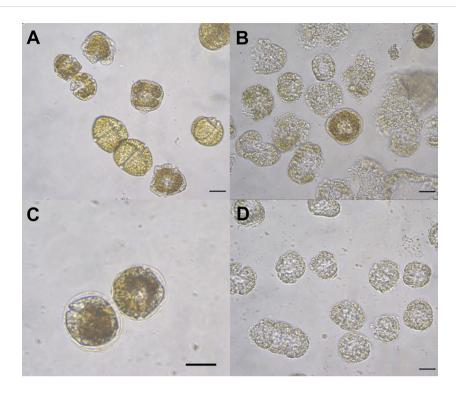


FIGURE 9

Gymnodinium catenatum cells exposed to hydrogen peroxide H_2O_2 at 24 h. Affected cells exposed to 100 μ M showing deformation and membrane detachment (A), affected cells exposed to 200 μ M showing deformation, chlorosis and cell death (B–D). Scale bar = 20 μ m.

dose response curve may suggest that the surviving cells, after exposure to toxic agents, increase their growth rate in response to the inhibitory potential of the substances (Calabrese and Baldwin, 2001). The surviving cells exposed to the highest concentrations of SDA may be showing a compensatory response related to growth and chain formation which is observable at 48 h and 72 h after exposure.

The allelopathic effect of C. marina var. marina towards G. catenatum was reported by Fernández-Herrera et al. (2016). Their results showed that inhibition of G. catenatum was higher in mixed co-cultures of both species than in co-cultures with no direct contact and exposure to cell filtrates of C. marina. This suggested that C. marina can inhibit the growth of G. catenatum through the release of allelochemicals, although cell contact or proximity between the cells of both species can cause a higher inhibition towards G. catenatum. The changes observed in G. catenatum cells after exposure to FFA and H₂O₂ are similar, coinciding mainly in the loss of motility, swelling, detachment of the external membrane, and alterations in the length of chain formation. These effects are in accordance with the previous allelopathy experiments with C. marina var. marina, and the dinoflagellates M. polykrikoides and G. impudicum (Fernández-Herrera et al., 2016; Band-Schmidt et al., 2020; Fernández-Herrera et al., 2021; Fernández-Herrera et al., 2022).

Previous studies suggested that *Chattonella marina* var. *antiqua* can affect *Akashiwo sanguinea* via allelopathy (Qiu et al., 2011). Similar negative effects of allelopathy have been reported between other species; cells of *Heterocapsa triquetra* and *Scrippsiella trochoidea* exposed to cell-free filtrates of *Alexandrium ostenfeldii*,

showed loss of motility (Tillmann et al., 2007; Hakanen et al., 2014). Studies in different species exposed to allelochemicals from *Alexandrium leei* reported that *M. polykrikoides* can be negatively affected showing alterations in chain formation, cell deformations and lysis, while the naked dinoflagellates *G. catenatum*, *Karlodinium veneficum* along with the haptophyte *Isochrysis galbana* were not dominated by *A. leii* (Shang et al., 2021). The precise identity of the allelochemicals produced by *Alexandrium species* remains unknown. However, *Alexandrium tamarense* has been suggested to produce lytic compounds targeting membrane related sterols (Ma et al., 2011).

Chain formation in dinoflagellates such as *G. catenatum* may constitute a survival strategy by enhancing motility and allowing displacement of cells (Doblin et al., 2006) out of the reach of allelochemicals in the marine environment; however, this strategy may be limited by the spatial restrictions of laboratory cultures. While being stressed, naked dinoflagellates could employ alternative defense mechanisms facing allelopathy, including chain formation or separation (Vale, 2018; Shang et al., 2021; Fernández-Herrera et al., 2022). Due to the spatial constraints of the experimental setup, the strategy of chain cell formation of *G. catenatum* as a means of escape to allelochemicals was not clearly observed in the presence of FFA and H_2O_2 . Therefore, the effects on chain cell formation were not conclusive.

In conclusion, results from this study suggest that the fatty acids PA, EPA, and SDA along with H_2O_2 can individually cause deleterious effects on *G. catenatum*. Alterations in chain formation and cell morphology are similar to the expected effects of allelopathy towards *G. catenatum* by competing species, and

suggest that these substances can be, at least partially, involved with allelopathic interactions in marine environments. Toxicity among the fatty acids varies, suggesting that PUFA with shorter carbon chains can potentially act as more effective allelochemical substances, causing a decrease in cell density at lower concentrations and within a shorter time than saturated fatty acids. However, the overall allelopathic effect of *C. marina* towards *G. catenatum* may be caused by a mixture of various compounds including ROS and FFA. It remains to be seen if other uncharacterized metabolites participate in this effect.

Data availability statement

The original contributions presented in the study are publicly available. This data can be found here: https://www.ncbi.nlm.nih. gov/; OR642744.

Author contributions

ME-Y: Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Visualization, Writing – original draft. CB-S: Conceptualization, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Validation, Visualization, Writing – review & editing. TZ-S: Conceptualization, Data curation, Methodology, Resources, Supervision, Validation, Writing – review & editing. IL-V: Data curation, Formal analysis, Investigation, Methodology, Supervision, Validation, Writing – review & editing. LFH: Methodology, Visualization, Writing – review & editing. EP-M: Data curation, Methodology, Resources, Validation, Writing – review & editing.

Funding

The author(s) declare financial support was received for the research, authorship, and/or publication of this article. ME-Y was a recipient of a student fellowship CONACyT-1106788 and BEIFI.

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Acknowledgments

We are grateful for the technical support of O. Arjona-López for the analysis of fatty acids, O. Lugo-Lugo for assistance in analyses for oxidative stress indicators, and D.I. Rojas-Posadas for the molecular taxonomy methods.

Conflict of interest

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Supplementary material

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