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Natural biocontrol of a *Porphyra* sp. pest on farmed *Gracilaria chilensis* by a pythiosis outbreak

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Abstract

Gracilaria chilensis (a.k.a. pelillo) is the most produced seaweed in Chile and Latin America, yet its cultivation has historically faced lots of pest-associated constrains that threat its profitability and sustainability. Pests show temporal cycles of recruitment, growth and death/senescence, variation normally linked with sharp changes in environmental factors occurring in estuarine areas whereby *Gracilaria* is cultivated. Here we report the appearance of a bladed Bangiales species epiphytic on long-line farmed *Gracilaria* and identified as *Porphyra*. This species recruits to cover up to 50–72% of *G. chilensis* early in a suspended set-up in spring, until a filamentous fungal-like organism colonizes *Porphyra* blades, infecting a wide proportion of its tissue. After this outbreak, *Porphyra* recruits collapse, disappearing in few weeks from farmed *Gracilaria*. Observations of diseased individuals, and subsequent isolation and marker-assisted taxonomy of the pathogen, provide evidence for the identification of this organism as *Pythium porphyrae*, the aetiological agent for the red rot disease in commercial nori/gim in Asia. This is the first reported case for *P. porphyrae* in Chile and the Southeastern Pacific as well as for a disease-driven natural biocontrol of a *Gracilaria* pest alga, suggesting an unknown -yet considerable- cryptic biodiversity acting as natural regulators of natural pests during a *Gracilaria* cultivation cycle.

Keywords Algal parasite · Epiphyte · Oomycete · Pythium porphyrae · Red rot disease

Introduction

Gracilaria production has become a significant component of the global aquaculture industry. With its versatile applications in food, pharmaceuticals, cosmetics, and biofuel, *Gracilaria* cultivation has expanded worldwide (Ferdouse et al. 2018). Several countries have emerged as key players in *Gracilaria* production, including China, Indonesia, the Philippines, Vietnam, and Chile (Mantri et al. 2023). As global demand for seaweed products continues to rise, the production of *Gracilaria* is poised to play an increasingly vital role in meeting these growing needs while promoting economic development and environmental sustainability. Concomitantly, *Gracilaria* also represent a valuable resource for local communities, as its farming is carried out mainly by local fishermen, contributing directly or indirectly to meet at least five independent United Nations SDGs goals (goals 1, 5, 8, 12 and 14; see https://sdgs.un.org/goals).

Gracilaria chilensis (a.k.a. pelillo) is the most produced seaweed in Chile via aquaculture (Buschmann et al. 2017). Chilean farmers have adopted both traditional direct "offbottom" planting (Buschmann et al. 1995) and innovative farming methods, utilizing coastal ponds (Santelices and Doty 1989), long-lines (Westermeier et al. 1993), indoor (Caroca-Valencia et al. 2023) and integrated multi-trophic systems (Abreu et al. 2009) to grow this seaweed. Historically, pelillo farming in Chile has faced recurrent pest outbreaks which stagnate the expansion of the Chilean industry (Mendez et al. 2024). Pests such as epiphytic organisms, fouling species, grazers, and pathogens can compete with *Gracilaria* for resources, inhibit its photosynthetic efficiency, and cause physical damage to the seaweed fronds (Buschmann et al. 1997; Leal et al. 2020). As a result, the

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affected *G. chilensis* may exhibit stunted growth, decreased reproductive output, and increased susceptibility to diseases (Fletcher 1995). Moreover, pest and disease outbreaks can escalate rapidly, spreading between farms or wild stocks, exacerbating the ecological impact and posing a significant biosecurity risk to the surrounding marine environment (Murúa et al. 2023).

A poorly studied aspect on seaweed farming is the interaction of cultivated stocks with local ecosystems, for example pest ecology. In terms of Gracilaria pests, there is some knowledge of algal pests being controlled by grazers such as polychaetes controlled by foraging seabirds (Martínez-Curci et al. 2023). Nevertheless pathogen-mediated biocontrol is much as unclear as the general knowledge of algal disease in Latin America (Murúa et al. 2021). In recent observations within a G. chilensis suspended system, we identify a fungal-like outbreak that unexpectedly acts as a natural biocontrol agent, effectively suppressing a prevalent seaweed pest population of Porphyra. We identified the oomycete species responsible for such pest control, their interactions with the targeted pest, and the potential implications for sustainable Gracilaria farming. By exploring the ecological factors contributing to the fungal outbreak and its impact on pest populations, we hope to gain valuable insights into the natural biocontrol mechanisms in seaweed farming systems. This research not only highlights the potential of utilizing natural agents for pest management but also offers prospects for developing eco-friendly strategies to enhance the resilience and productivity of Gracilaria cultivation.

Materials and methods

Sampling

A suspended Gracilaria chilensis set-up was installed in Cariquilda estuary (41.624°S; 73.591°W: Fig. 1A) in spring 2022 (28-09-2022), in order to evaluate epiphyte succession of pests on a biweekly basis. Five 5 m long long-lines (n=5) seeded at ca.120 g m⁻¹ were installed superficially (1 m depth). From every long-line, 30 cm were harvested biweekly for Gracilaria biomass and pest load estimations. In particular, we focused on epiphytic Porphyra (Fig. 1B), which was estimated by i) its coverage on 50 randomly harvested Gracilaria filaments measured linearly on a millimeter paper and ii) the epiphyte weight in terms of 100 g of its basiphyte. As a matter of fact, both proxies are correlated (R2c=0.999; p=0.003; Fig. 2A), and coverage will be used for Porphyra abundance hereafter. Additionally, fifteen Porphyra individuals per sample were dissected for the estimation of the prevalence of the fungal-like disease.

Statistical analyses were carried out using R (R Core Team 2018). To demonstrate a potential link between

coverage and weight of *Porphyra* recruits, data were fit to a generalised linear mixed model (GLMM) with Poisson error structure using the {glmer} function of the "lme4" package, where long-line measured and time (n° week) were set-up as random effects (Bates et al. 2015). Likewise, to assess the association *Pythium* prevalence and *Porphyra* coverage or week, another GLMM was performed with Poisson error structure and long-line as random effect model. Pairwise comparisons were done applying a Tukey test on the GLMM models using the library "Ismeans" (Lenth 2016). Both conditional (r2c, fixed, and random effects) and marginal (r2m, fixed-factors effects) goodness of the fits were calculated to estimate the impact of our random effects (Johnson 2014).

Oomycete isolation

Porphyra blades symptomatic for the red rot disease were acquired from our *Gracilaria* farm facility by 10–11-2022. These samples were carefully stored in 50 mL Falcon tubes in a cooled container with ice packs and transported to the FICOPAT lab (UACh) in Puerto Montt, Chile. To isolate the pathogen, we placed infected tissues (ca. 3 mm diameter each) on 1.7% corn meal agar (CMA BBL) plates, prepared in filtered (0.2 μ m) and autoclaved seawater from the estuary with a salinity of 25 PSU. Additionally, before pouring the agar, we supplemented with 200 mg mL⁻¹ of penicillin and streptomycin sulphate to prevent bacterial contamination (Atami et al. 2009).

The agar dishes were sealed using Parafilm and then incubated at 12 °C in darkness. They were monitored daily for hyphal growth. After 14 days incubation, single hyphal tips were excised out the agar cultures and transferred to a fresh CMA in Petri dishes, to establish pure cultures. As these visible mycelia grew, we aseptically subcultured single hyphal tips by transferring them to Petri dishes with fresh medium. This process was repeated several times until the cultures were completely free of any visible bacterial or protist contamination.

Microscopy and molecular diagnoses

Microscopical observations of diseased *Porphyra* and oomycete isolates were performed on fresh material. Samples were mounted using a Calcofluor white (CFW) solutions (0.02 mg mL⁻¹ in seawater; Gachon et al. 2017), observed and imaged on a Zeiss Microscope Axioscope 5 DIC and epifluorescence microscope with a Axiocam 202 Color digital camera, under a Colibri 3 Illumination System.

For molecular diagnoses, samples were DNA-extracted using a commercial kit (GeneJet DNA extraction kit, Thermofisher). PCRs were performed to amplify 18S (primer pairs F139/R1233 complemented with EUK422-445/EUK1422-1440_R and TK18Sfwd/ TK18Srev,

Fig. 1 Identification of the red rot disease agent Pythium porphyrae on Gracilaria-epiphytic Porphyra sp. A: Gracilaria chilensis farmed on a suspended long-line in the Cariquilda estuary. B: macroscopic view of Gracilaria filaments colonized by Porphyra recruits (arrowheads). C: Porphyra sp. symptomatic for a Pythiosis (a.k.a. red rot disease in case of Bangiales, arrows). D: upon magnification, necrotic areas show the infection by filamentous fungal like structures, which introduce within Porphyra tissues and cells. Inset: after calcofluor white staining (CFW), pathogen cells can be easily spotted inside the host tissue under UV light. AUTO: Chlorophyll autofluorescence. E: in older cultures, P. porphyrae overgrew Porphyra blades (arrows) and cover most of the tissues. Inset: Pythium sporangia (arrowheads) in heavily infected tissues. F: A Pythium porphyrae isolate growing in CMA culture media



annealing = 55 °C), COI (primers TKCOIfwd -TKCOIrev, annealing = 55 °C) and COII (primers COX2-For3 – COX2-Rev3, annealing = 55 °C) regions (Sekimoto et al. 2007, 2008; Wang et al. 2014; Gachon et al. 2017; Klochkova et al. 2017b), using reagent concentrations established in Murúa et al. (submitted), and sequenced by Sanger (Macrogen). Phylogeny reconstructions were inferred by aligning Pythium clade I and II sequences available in NCBI in addition to those newly generated by this study (accessions: PP481400/ PP481401 for 18S, PP503415 for COI and PP493240/ PP493240 for COII). Alignments were performed using MAFFT (Katoh and Standley 2013) and modelled for phylogeny reconstruction using RaXML version 8.2.11 with 1000 bootstrap replications (Stamatakis 2014) and MrBayes version 3.2.6 using default settings four MCMC chains (Ronquist et al. 2012), implemented in Geneious v11 (Kearse et al. 2012). Analyses were made for each gene separately.

Results

Once the *Gracilaria* set-up was installed (Fig. 1A), *Porphyra* recruitment started right away after two weeks and progressively increased to reach a peak after 6 weeks of cultivation (50–72%) (Figs. 1B, 2B). At the 8th week, there was a collapse of epiphytic *Porphyra* on *Gracilaria* thalli, with no visible recruits or elongated *Porphyra* from previous months.

Concomitantly, *Porphyra* started to show changes in coloration over the course of cultivation. Whilst 2-weeks-old *Porphyra* looked dark red, 4- and 6-weeks old specimens show irregular pink areas across the thalli, of variable irregular areas (Fig. 1C). Under the microscope, such areas evidenced an intracellular hyphal organism infecting the host cells (Fig. 1D), which contained a cellulosic/quitinated



Fig. 2 Variations of *Porphyra* epiphytic load and *Pythium* prevalence during a *Gracilaria chilensis* suspended set-up. A: both *Porphyra* coverage and weight are strongly correlated, after a Generalised linear mixed model including the long-line sampled and the week as random effects. B: *Porphyra* abundance variation in 8-week *Gracilaria* farming. C: *Pythium* prevalence variation (% diseased *Porphyra* specimens) over the same 8-week course. Both weeks and and *Porphyra* coverage were significant for the GLMM model fit

cell walls and caused necrosis in neighbouring host cells. In very infected host tissues (ca. 6 weeks old), such hyphae emerged and formed extra-tissular complexes that included sporangia of 15–20 µm diameter in their tips (Fig. 1E). The prevalence of diseased *Porphyra* follows the same pattern of rise and fall of its recruitment (Fig. 2C), with symptomatic individuals detected after 4 weeks (up to 12%), reaching a peak of infection (60–100%) at 6 weeks, and no records at 8 weeks.

The symbionts were culturable in solid medium (CMA medium; Fig. 1F). We obtained two fungal-like strains from infected *Porphyra* (Pyt1 Cariq and Pyt2 Cariq), which were subjected to molecular phylogeny. Both isolates were identical for 18S sequences and differed in only two bases for COII nucleotide sequences. The phylogenetic analyses, under both RAxML and MrBayes, showed that Chilean samples formed a well-supported clade within *Pythium* clade A, using 18S, COI and COII (Figs. 3, 4 and 5). Within this clade, our isolates share monophyly with *Pythium chondricola*, *P. porphyrae*, and to a lesser extent *P. adhaerens*. Members of *P. porphyrae* includes specimens from Japan, China, Korea and New Zealand, suggesting a cosmopolitan distribution of the species.

Discussion

Pest outbreaks are keystone factors regulating profitability and sustainability in seaweed aquaculture (Brakel et al. 2021; Murúa et al. 2023). In G. chilensis farms, pests such as worms (Polychaeta), ceramialean blooms or green tides have historically had significant consequences on both the cultivated seaweed, the overall aquaculture operations, and the social acceptability of surrounding settlements (Mantri et al. 2023). For instance, these outbreaks end up with Gracilaria reduced biomass, mixed with contaminants (e.g., pests), stunted morphologies and sometimes diminished biochemical quality; thus, economic detriment for farmers (Fletcher 1995). Furthermore, major decomposing pest drifts may lead to human health problems. Such consequences underscore the importance of effective pest identification and management strategies, including early detection, proper sanitation measures, and the implementation of biosecurity protocols (Mendez et al. 2024). By preventing and mitigating the impact of pest outbreaks, farmers can safeguard the health and productivity of seaweed farms, ensuring the sustainability and success of valuable seaweed aquacultural species (Cottier-Cook et al. 2021, 2022).

In Chile, *G. chilensis* has been extensively farmed in systems with direct attachment to substrata (Buschmann et al. 1995). Nevertheless, suspended lines have drawn some attention, as the cultivable areas can be expanded from tidal-affected regions towards offshore. Suspended systems had suggested a lower epiphytic load than direct attachment (Westermeier et al. 1993), in contrast to abundant filamentous red and brown seaweeds that are very common in traditional systems (Leonardi et al. 2006). Nonetheless, a different bathymetrical level potentially incorporates new ecological interactions. For example, *Porphyra* species had



Fig. 3 Bayesian phylogenetic tree reconstruction of Chilean *Pythium por-phyrae* (in bold pink within the tree) and available *Pythium* SSU rDNA sequences. The tree contains a total of 23 sequences and 1834 nucleotide positions. Support values given are posterior probabilities (MrBayes)/

bootstrap support (RAxML). MrBayes settings: chain length 1.000.000, subsample frequency 1.000, burn in of 10%. The scale bar indicates the number of substitutions per site



Fig. 4 Bayesian phylogenetic tree reconstruction of Chilean *Pythium porphyrae* (in bold pink within the tree) and available *Pythium* COI mtDNA sequences. The tree contains a total of 26 sequences and 682 nucleotide positions. Support values given are posterior probabilities (MrBayes)/

bootstrap support (RAxML). MrBayes settings: chain length 1.000.000, subsample frequency 1.000, burn in of 10%. The scale bar indicates the number of substitutions per site





not been recognized in off-bottom systems as a significant epiphytic pest affecting *Gracilaria* farms (Candia et al. 2006). Nevertheless, in our study *Porphyra* was one of the most abundant epiphytes in suspended systems during 2022 and 2023 (unpublished). It is unknown how *Gracilaria* would be affected in terms of growth, survival or biochemical quality (e.g. agar composition) in case *Porphyra* would keep growing, although due to its superficial attachment (type 1–2 after Leonardi et al. 2006), it is presumed a significant competitive interaction only when blades are considerably larger. On the other hand, *G. chilensis* was not observed affected by *P. pophyrae*. Despite its initial abundance, *Porphyra* co-existence in *Gracilaria* farms is rather ephemeral, suggesting an outward disruption source during *Porphyra* recruitment and settlement during the initial weeks.

In this system we report a third party: a fungal-like organism inhabiting Porphyra, whose prevalence was directly linked with the demise of *Porphyra* recruits. Identified as Pythium porphyrae after marker-assisted taxonomy, the facultative parasitic oomycete caused pink lesions and massive mortality in Porphyra blades, resembling red rot disease symptoms (Klochkova et al. 2017a). Our molecular data suggests that Chilean Pythium is very similar genetically to those found on Pyropia plicata in New Zealand (Diehl et al. 2017) and Porphyra and Pyropia spp. in China, Korea and Japan (Kawamura et al. 2005; Kim et al. 2014; Qiu et al. 2019). Our phylogenetic analyses also suggest the conspecificity between P. porphyrae and P. chondricola (Diehl et al. 2017), with neither morphological nor genetic dissimilarity except for COII, which are rather different between them (Robideau et al. 2011; Lee and Lee 2022). Both species have been isolated primarily from algae (Lee et al. 2015), and can 100% identical using other sequences such as ITS1 (Lévesque and De Cock 2004). More powerful techniques (e.g., phylogenomic, phenomics) will be requested in order to pinpoint the specific genetic and phenotypic differences between both traits and to know whether they are currently under a speciation process.

The three-party interaction described here raises important questions about the utilization of microbes in seaweed pest biocontrol. Because of the fragility and dynamisms of the aquatic environment, it is highly non recommendable to use chemical methods for pest control as in terrestrial agriculture (Pawan Kumar et al. 2023). Managing pest suppression by the addition of specific microorganisms or complete microbial communities resulted as an eco-friendly alternative of controlling unwanted organisms (O'Hanlon et al. 2012). In forestry, it is increasingly common the use of native entomopathogenic fungi, bacteria and viruses for the natural biocontrol of insect pests (Dara et al. 2019). In aquatic systems, seaweed fitness has been improved by other accompanying organisms. For example, some mesograzers increased *Gracilaria foliifera* fitness by eating epiphytes that compete with their host (Brawley and Adey 1981). Similarly, amphipods reduced epiphytic biomass from the seaweed *Sargassum filipendula* (Duffy 1990). As bioengineers. *Gracilaria* also increase the invertebrate biodiversity in the faring area, increasing worm pests that are controlled by migratory birds (Martínez-Curci et al. 2023). In our study we describe a microorganism regulating a macroalgal pest management of a commercially important seaweed. In spite of its potential use for biocontrol in *Gracilaria* aquaculture, its use must be carefully assessed in terms of suitability and environmental impacts.

In contrast to long-lasting pests, *Porphyra* was quickly controlled by the naturally-occurring *P. porphyrae*, counteracting *Porphyra* prevalence to non-detectable levels and indirectly aiding farmed *Gracilaria*. Nevertheless, *P. porphyrae* has been described as a significant biosecurity threat on *Pyropia* and *Porphyra* farms in Asia (Badis et al. 2020). For the first time, we report this parasite in Chilean waters, proposing a widespread distribution alongside subantarctic ecosystems. These records add up to latest records of another pathogenic oomycete of Bangiales, such as *Olpidiopsis* (sensu lato) *porphyrae* in the Southeastern Pacific (Murúa et al. submitted). Both parasites affect farmed and cultivated specimens, whose impact in natural populations or incipient *Pyropia* aquaculture is yet to be assessed.

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Author contributions Original concept (LM, PM); field collections and sampling (LM, DJP); strain isolation and laboratory culturing (LM); microscopy (PM); phylogenetic analyses (PM, LM); drafting the manuscript (LM); editing the manuscript (All authors).

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Data availability Data obtained in the experiments herein can be available upon request.

Declarations

Competing interests The authors have no competing interest to declare.

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