



**A variety of interactions
in the marine environment**

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trophozoite-infected intestines showed that the anterior end of *Selenidium* sp. was stretched (6–8 µm in length) and anchored between folds of the host intestinal epithelium. A direct contact between the host cell and attached parasite was not observed. Subcellular organization of the elongated anterior end was the same as that of the rest part of the parasite cell (pellicle, micropores, microtubules, mitochondria). In addition, several rhoptries and multiple groups of micronemes were present in the anterior end of *Selenidium* sp. We found no traces of the conoid and apical polar ring that might be a consequence of reduction of some apical organelles during trophozoite development. We can also suggest that the reason of this was our failure to obtain complete serial ultrathin sections. Thus, the fate of apical organelles is another subject for further investigation in this parasite. ML and Bayesian analysis of 18S rDNA data showed that *Selenidium* sp. from *Pygospio elegans* belonged to one of the archigregarine branches including four other parasites of polychaetes Sabellariidae and Spionidae: *Selenidium serpulae*, *S. boccardiella*, *S. cf. mesnili*, *S. idanthysae*. Unexpectedly, the analysis proved the full identity of sequences from specimens collected from different hosts and places: *Selenidium* sp. from *Pygospio elegans*, the White Sea, and *Selenidium* sp. from *Polydora glycymerica*, the Sea of Japan. This evidences that biogeographical distribution of archigregarines is probably more extensive than usually assumed, and that the traditionally used for gregarines systematic principle 'new host – new species' should be revised. To highlight the taxonomic status of the archigregarine involved in the present study, further investigations are needed including the comparison with other parasites from Spionidae polychaetes.

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FINE STRUCTURE OF *POLYRHABDINA* SP. (APICOMPLEXA: EUGREGARINIDA), WITH EMPHASIS ON THE TAXONOMIC POSITION OF POLYRHABDINES

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Apicomplexans form a large and diverse group of unicellular parasites inhabiting invertebrates and vertebrates. Gregarines are mostly extracellular apicomplexan parasites that occur in the intestine, coelom and reproductive organs of marine, freshwater and terrestrial invertebrates. Most gregarines infecting the intestine of marine invertebrates have been described within the family Lecudinidae and the type genus *Lecudina*. The diversity of these 'marine' parasites is vast and still poorly understood. Moreover the family Lecudinidae is probably a taxonomic mixture; some species considered to be 'lecudinids' may well belong to other families of aseptate eugregarines. The genus *Polyrhabdina* (= *Polyrhabdina* by Caullery & Mesnil, 1914, presently accepted) was established by Mingazzini, 1891 for *Gregarina spionis* Kolliker, 1848 from polychaetes *Malacoceros fuliginosus*. To date this genus comprises six species of parasites inhabiting marine worms of the family Spionidae; *Polyrhabdina spionis* is the type species. The identification of *Polyrhabdina* species is very difficult, as all of the original descriptions are based solely on line drawings. Furthermore, the descriptions are limited to the trophozoite stage with special attention to attachment organelles. In attached cells of *Polyrhabdina*, this globular organelle is embedded in a depression of the host intestinal epithelium cell. Some authors mentioned hook-like processes on the apical surface in addition to the cirlet of tiny teeth at the base of the attachment organelle (AO). In contrast, other scientists described the AO without hooks on its surface, but with a collar at its base. There was no consensus on the definition of the AO: mucron or epimerite. Here, we present results of the fine structure study of an aseptate eugregarine *Polyrhabdina* sp., a parasite of the spionid polychaete *Pygospio elegans*. About 50% of marine worms sampled at the silt-sand littoral zone near the White Sea biological station of St. Petersburg state university were infected with this gregarine. Both attached and non-attached parasites were found in the host intestine. The detached individuals measured about 28 – 288.4 µm (av. 123.3 µm, n=40) x 14 – 50.4 µm (av. 34.8 µm, n=40). As a rule, they were of ellipsoid shape and circular in cross section. Pear-shaped, slightly elongated or curved cells also occurred. Parasites had a large nucleus with one nucleolus. The non-attached cells demonstrated gliding motility. The cell surface of parasites was covered with numerous longitudinal epicytic folds. Some folds were straight, some ones were slightly undulated. Ultrathin cross-sections of gregarines showed that the organization of each fold was typical of that of eugregarines: a three-membrane pellicle (plasmalemma + inner membrane complex [IMC]), an electron-dense fibrillar layer (internal lamina) underlying the innermost membrane of the IMC. The internal lamina formed an additional loop between adjacent folds, but no connection at the base of each fold. In this case, the cytoplasm of each fold connects freely with the bulk of the cell cytoplasm. At the fold tip, 10–12 apical arcs could

be seen between the plasmalemma and IMC as well as 10–12 apical filaments under the IMC. Typical micropores were located on side surfaces of the epicytic folds. The attached trophozoites were anchored in the intestinal epithelium by a globular AO (9 µm in diameter). The AO formed a skirt-like circular fold (2.6 µm in length) at the base. This circular fold was localized epicellularly and limited the zone of AO penetration to the host cell. The AO was very rarely observed in non-attached parasites. Trophozoites released accidentally from the intestinal epithelium during material preparation had attachment organelles with damaged surfaces. Longitudinal ultrathin sections through the attachment site of the host and parasite cells demonstrated that the AO was only covered by a plasma membrane. There was a close contact between the plasma membrane of the AO and the plasmalemma of the host epithelial cell. The skirt-like circular fold represented a thin cytoplasmic extension of the AO covered by the host membrane and parasite plasma membrane. The cytoplasm of the AO exhibited obvious zonation: a finely granular cortical zone located peripherally under the plasma membrane and filled the circular fold; a vesicular cytoplasm of the central part with occasional organelles typical for the rest of the parasite body (e.g., amylopectin granules). No septum was observed between the AO and the rest of the cell. However, at the base of the AO there was an annular membrane junction formed by the plasmalemma of the host cell and the plasma membrane with IMC of the parasite. In this region, the cytoplasm was organized as a ring enriched by some fibrillar material. From the annular membrane junction a thin fibrillar layer extended to the cell body being spread under the pellicle; then it transformed to the internal lamina of the pellicle. There is a need to add that several gregarines *Polyrhabdina* sp. were infected with microsporidia *Metchnikovella spiralis* and *M. incurvata*. Interestingly, the microsporidian stages also occupied the AO of the host. We believe that the AO of *Polyrhabdina* sp. represents an epimerite. Its structure resembles that in some septate eugregarines, but differs from the mucron in leucinids. Additionally we compared scanning electron microphotographs of *Polyrhabdina* sp. and *P. spionis* isolated from polychaetes *Malacoceros fuliginosus*, which were sampled at the littoral zone near the Biological station of Roscoff. Gregarines of both species share the same attachment apparatus: the globular epimerite with the circular fold around its base. At the end of the attached stage, polyrhabdines separate from the host epithelium. The alternative possible ways of the separation mechanism can be considered: throwing the epimerite away from the parasite cell or retracting the epimerite inside the parasite body as a result of the contraction of the fibrils located at the epimerite base. Following Kamm (1922) and her successors we propose to exclude the genus *Polyrhabdina* from the family Lecudinidae and place it in its own family Polyrhabdinidae.

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SEAWEEDS IN THE FJORDS REGIONS OF SOUTHERN CHILE: BIODIVERSITY INCLUDING ANTIOXIDANT COMPOUND PROFILES AS AN ADDITIONAL PARAMETER

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The fjord region of southern Chile is characterized by a high biodiversity due to the subantarctic water, equatorial subsurface water and western Pacific subsurface water it receives, together with the fact that in the interior zone, all these are mixed with freshwater from precipitation, river flow, and meltwater from Cordilleran glaciers. Several studies of the Comau fjord, for example, report this biodiversity particularly considering anemones and corals. However, the distribution of seaweed in this ecosystem has not previously been reported. Seaweeds are very rich in different compounds that may exhibit significant biological activity, including a class of phenolic antioxidant compounds, the phlorotannins, not found in other natural products. The potential applications of these bioactive compounds make it especially interesting to characterize seaweed according to its antioxidant compound profile. The aim of the work reported here was to characterize the biodiversity of seaweeds in Comau Fjord, considering not only taxonomy, but also antioxidant compound profiles. To that end, seaweed samples were collected from the submareal and intermareal areas surrounding the Huinay Scientific Field Station, at Comau Fjord, in October 2013. The samples were identified according to morphological characteristics, dried in an oven at 60°C for 2 h and the following analyses were carried out according to procedures previously described for seaweeds: total polyphenol content (extractable and hydrolysable), polyphenol profile by HPLC-DAD, antioxidant capacity by FRAP (ferric reducing antioxidant power assay) and ABTS (2,2'-azino-bis(3-ethylbenzo-thiazoline-6-sulfonic acid) assays. The six most abundant seaweeds in the area were finally selected for analysis: 2 brown (*Macrocystis* and *Scytosiphon*), 2 green (*Ulva* and *Enteromorpha*) and 2 red (*Gracilaria* and *Callophyllis*) seaweeds. *Scytosiphon* showed the highest extractable polyphenol content (1,297 mg/100 g