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## Comparative Morphology and Molecular Phylogeny of *Apicoporus* n. Gen.: A New Genus of Marine Benthic Dinoflagellates Formerly Classified within *Amphidinium*

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25 The composition of the dinoflagellate genus Amphidinium is currently polyphyletic and includes several species in need of re-evaluation using modern morphological and phylogenetic methods. We investigated a broad range of uncultured morphotypes extracted from marine sediments in the 27 Eastern Pacific Ocean that were similar in morphology to Amphidinium glabrum Hoppenrath and Okolodkov. To determine the number of distinct species associated with this phenotypic diversity, we 29 collected LM, SEM, TEM and small subunit ribosomal DNA sequence information from different morphotypes, including the previously described A. glabrum. Both comparative morphological and 31 molecular phylogenetic data supported the establishment of a new genus, Apicoporus n. gen., including at least two species, A. glaber n. comb., and A. parvidiaboli n. sp. Apicoporus is 33 characterized by having amphiesmal pores and an apical pore covered by a hook-like protrusion: neither of these characters has been observed in other athecate dinoflagellates. The posterior end of 35 Apicoporus parvidiaboli possessed varying degrees of "horn formation", ranging from slight to prominent. By contrast, the posterior end of Apicoporus glaber was distinctively rounded and lacked 37 evidence of horn formation. Although these species were previously interpreted to be obligate heterotrophs, TEM and epifluorescence microscopy demonstrated that some cells of both species 39 had unusually small but otherwise typical dinoflagellate plastids. The number and density of plastids in any particular cell varied significantly in the genus, but the plastids were almost always 41 concentrated at the posterior end of the cells or around the nucleus. The presence of cryptic photosynthetic plastids in these benthic species suggests that photosynthesis might be much more 43 widespread in dinoflagellates than is currently assumed. © 2008 Elsevier GmbH. All rights reserved.

**Key words:** *Amphidinium glabrum*; apical pore; *Apicoporus glaber*; *Apicoporus parvidiaboli*; dinoflagellate; pellicle; heterotrophic; plastid; SSU rDNA.

Introduction

The genus *Amphidinium* Claparède and Lachmann is among the largest and most diverse of all marine benthic dinoflagellates and has long been recognized as being polyphyletic (Dodge 1982;

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Hoppenrath 2000a: Larsen 1985: Larsen and 1 Patterson 1990: Murray and Patterson 2002). One reason for this is the overly generalized 3 criteria used for distinguishing Amphidinium from 5 other athecate genera, such as episome dimensions (shorter than 1/3 of the cell length) and the 7 displacement of the cingulum (Steidinger and Tangen 1997). Over the last 10 years, modern methods have been used to re-investigate the q type species of different athecate genera, such as 11 Gvmnodinium Stein and Gvrodinium Kofoid and Swezy (Daugbjerg et al. 2000; Hansen et al. 2000; Hansen and Daugbjerg 2004; Takano and Hor-13 iguchi 2004). More precise re-definitions of these genera have caused many of the species formerly 15 assigned to them to be considered "sensu lato 17 taxa"; accordingly, several new genera have been described, such as Akashiwo Hansen and Moestrup, Karenia Hansen and Moestrup, Karlo-19 dinium Larsen, and Takayama de Salas, Bolch, Botes and Hallegraeff (Daugbjerg et al. 2000; De 21 Salas et al. 2003). Amphidinium has also been re-23 defined in recent years after reinvestigations of A. operculatum Claparède and Lachmann, the type species, and putative relatives (Flø Jørgensen et 25 al. 2004a: Murrav et al. 2004). The genus was subsequently split into Amphidinium sensu stricto 27 and Amphidinium sensu lato. Amphidinium sensu 29 stricto are dorso-ventrally flattened, athecate dinoflagellates with a minute epicone that overlays the anterior ventral part of the hypocone and 31 deflects to the left (Flø Jørgensen et al. 2004a). The epicones can be irregular, triangular-shaped 33 or crescent-shaped. Cells may or may not be photosynthetic. Some of the former Amphidinium 35 species that do not fit the above description have 37 been classified into new genera, such as the marine benthic Togula Flø Jørgensen, Murray and 39 Daugbjerg (Flø Jørgensen et al. 2004b) and the freshwater Prosoaulax Calado and Moestrup 41 (Calado and Moestrup 2005).

In an effort to improve our understanding of 43 marine athecate dinoflagellates and the composition of Amphidinium sensu stricto, we reinvestigated Amphidinium glabrum Hoppenrath and 45 Okolodkov (Hoppenrath and Okolodkov 2000) and several similar morphotypes. These uncul-47 tured morphotypes were isolated form marine sand collected near Vancouver and Bamfield, 49 British Columbia, Canada. All of the morphotypes, 51 including the type species, shared many morphological characteristics. However, we observed a 53 great deal of morphological variability at the posterior end of the cells. We evaluated the number of distinct species associated with this 55

phenotypic diversity and whether these species belonged to the Amphidinium sensu stricto, or a 57 different genus altogether, using light and electron microscopy and molecular phylogenetic methods 59 based on small subunit ribosomal DNA (SSU rDNA) sequences. Moreover, our ultrastructural 61 studies led to some unexpected discoveries, such as the presence of cryptic photosynthetic plastids 63 in these benthic marine dinoflagellates. 65 67 Results 69 **Taxonomic Descriptions** 71 Alveolata Cavalier-Smith 1991 73 Dinozoa Cavalier-Smith 1981 emend. Cavalier-Smith and Chao 2004 75 Dinoflagellata Bütschli 1885 emend. Fensome et al. 1993 77 Apicoporus Sparmann, Leander and Hoppenrath n. gen. 79

Description: Athecate, dorso-ventrally flattened cells with a small, low and wide, beak-shaped, asymmetrical episome with an apical pore beneath a hook-shaped apical protrusion. Descending cingulum with its distal end not connected to the sulcus. Narrow and shallow sulcus on the hyposome, extending as deeper furrow onto the episome and running down to the posterior cell end where it terminates into a semicircular posterior cell indentation (notch). Posterior ventral 'flap' partly covering the notch. With or without cryptic photosynthetic plastids. Vegetative cells with internal dinoflagellate-pellicle.

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*Type species: Apicoporus glaber* (Hoppenrath and Okolodkov) Sparmann, Leander and Hoppenrath n. comb. (designated here)

*Etymology:* Latin *apic*, from apex = top end; Latin *porus* = opening/pore; due to the presence of an apical pore which has so far only been reported in thecate dinoflagellates.

*Apicoporus glaber* (Hoppenrath and Okolodkov) Sparmann, Leander and Hoppenrath n. comb.

Basionym: *Amphidinium glabrum* Hoppenrath and Okolodkov 2000, Eur J Phycol 35, p. 62

Lectotypification of *Apicoporus glaber*: Hoppenrath and Okolodkov 2000, Eur J Phycol 35, p. 63, Figure 4, here first designated

Paratype: present study Figures 3C, 4A (same specimen)

Morphology and Molecular Phylogeny of Apicoporus n. gen. 3

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Figure 1. Line drawings of Apicoporus glaber (A) and morphological variation in Apicoporus parvidiaboli (**B**-**F**) (bar = 10 µm).

17 Only one morphotype of Apicoporus glaber (Figs 1A, 2A, 3C) was found. Its size varied from 30 to 50  $\mu$ m in length and 16 to 30  $\mu$ m in width. It 19 was observed to move with the apical end leading while rotating around its longitudinal axis, but was mostly attached to the bottom of the Petri dish. 23 Most studied cells showed golden brown coloration especially at the posterior end (Figs 2A, 3C). 25 Many specimens also showed food bodies in the apical half of the cell (Figs 2A, 3C). All cells 27 demonstrated an almost guadrangular, elongated shape with almost parallel sides, were dorso-29 ventrally compressed and had a symmetrically rounded posterior end (Fig. 3A). The beak-shaped asymmetrical episome took up about one eights of the cell length (Fig. 3A, C). On the ventral side, 33 the sulcus reached into the episome (Fig. 3A, C) and continued to the antapical end where it 35 terminated at the indentation (Fig. 3A). The sulcus was displaced to the right by about one quarter 37 cell width (Fig. 3A). At the apex, an apical hooklike protrusion was present where the sulcus 39 ended (Fig. 3A). The apical protrusion sat above an apical pore (Fig. 3F; picture taken of Apico-41 porus parvidiaboli sp. nov., but the apical pore was observed in both species). The cingulum was 43 descending by about six cingulum width and the distal end did not connect to the sulcus (Fig. 3A, C). A semicircular indentation was found at the 45 antapex and sat symmetrically along the centre line of the cell (Figs 1A, 3A, 4C). A protrusion 47 ('flap') at the antapical end of the sulcus covered 49 most of the indentation (Figs 3A, 4A). The nucleus was located in the lower cell half (Figs 3C, 4A). 51

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The general features discovered with TEM and SEM (Figs 5-7) could be observed in both species, but pictures displayed are only of Apicoporus parvidiaboli n. sp. Descriptions can

be found in the next section about the morphology of Apicoporus parvidiaboli n. sp.

Epifluorescence was used to relate the presence of brownish golden coloration in the posterior end of cells with the location of plastidautofluorescence in the same specimen (Fig. 7C, D). The area that showed coloration with light microscopy (Fig. 7C) also displayed autofluorescence (Fig. 7D).

Apicoporus parvidiaboli Sparmann, Leander and Hoppenrath n. sp.

Holotype/type micrograph: Figure 3D

Paratypes: Figures 2B-I, 3B, 4B, D

Type locality: Brady's Beach, Bamfield, British Columbia, Canada,

parvus = small:Etymology: Latin diabolus = devil; due to the presence of at least one but mostly two horns at the posterior end.

Description: Athecate, dorso-ventrally flattened cells with a small, low and wide, beak-shaped, 91 asymmetrical episome with an apical pore beneath a hook-shaped apical protrusion. Cells 93 are  $27-65 \,\mu\text{m}$  long and  $18-40 \,\mu\text{m}$  wide. Episome about one-eighth of the cell length. Cingulum 95 descending by about four cingulum widths, with its distal end not connected to the sulcus. Narrow 97 and shallow sulcus on the hyposome, extending as deeper furrow onto the episome and running 99 down to the posterior cell end where it terminates 101 into a semicircular posterior cell indentation (notch). Posterior ventral 'flap' partly covering 103 the notch. With a few or without cryptic photosynthetic plastids. Nucleus in the posterior cell 105 half. Cells with dinoflagellate-pellicle. Three morphotypes: (1) cells with a more or less tapered and 107 oblique posterior end and little horn formation: (2) cells with parallel sides and two more or less equal sized horns at the antapex; and (3) cells with a 109

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Morphological Diversity of Apicoporus

preeminent than the other.

sack-like appearance and one horn (left) more

Three main morphotypes of Apicoporus parvidia-7 boli n. sp. were observed at sites in Bamfield and Vancouver, BC, Canada (Fig. 1B-F). The cell size a ranged from 27 to 65 µm long and 18 to 40 µm wide. Cells were either swimming in an apical 11 direction while rotating around their longitudinal axis or attached to the bottom of the Petri dish. No 13 vegetative cyst formation was observed. Some specimens possessed golden brown pigments 15 near the posterior end of the cell or around the nucleus, while others were completely colorless. 17 This variation in pigmentation was evident even within the same morphotype (Fig. 2B-I). All 19 morphotypes of this species showed some level of horn formation at the posterior end of the cell 21 (Fig. 1B-F) and could be categorized into one of three groups: (1) "oblique antapex" - smaller 23 cells (approx, 19 µm wide, 29 µm long) with a more or less tapered antapex, oblique posterior ends 25 and very little horn formation (Fig. 2B-D); (2) "horned antapex" - cells that displayed parallel 27 sides and a more symmetrically arranged antapex with two horns of equal length (Fig. 2E, F); and (3) 29 "sack-shaped" - larger cells (approx, 50 um wide, 78 µm long) with a sack-like appearance, a 31 more or less obligue antapex and one horn that is more prominent than the other (Fig. 2G-I). 33 However, variation in cell morphology within each morphotype overlapped in a way that eliminated 35 discrete discontinuities between the three categories.

All Apicoporus cells were dorsoventrally compressed, and many specimens also contained food bodies (Fig. 2F). The beak-shaped episome was asymmetrical and extended to about one eighth of the cell length (Figs 2B-I, 3B, D). An apical pore positioned beneath an apical hook-like protrusion was evident at the anterior end of the cell (Figs 3B,E,F). The sulcus extended into the episome and terminated at the apical hook (Figs

3B. D. E). Toward the posterior end, the sulcus was displaced towards the right (ventral view) by about one guarter of the cell width and ended at the posterior indentation (Fig. 3B). The cingulum descended by about four cingulum widths and did not join with the sulcus at its distal end (Fig. 3B, D, E). A protrusion ('flap') formed where the sulcus terminated at the posterior end of the cell, which covered most of the indentation (Figs 3B, 4B, E, F). In some specimens, the protrusion formed an extension that only covered part of the sulcus (Fig. 4E), while in others the sulcus was not hidden at all (Fig. 4F). The posterior indentation was positioned symmetrically in the middle of the cell (Figs 3B, 4D-F). The nucleus was located in the posterior end of the cell (Figs 2B, C, F, 3D, 4B).

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71 LM and TEM demonstrated a large dinokaryotic nucleus that took up most of the posterior end of 73 the cell and a food body positioned closer to the apical end (Figs 5A, 6A, D). TEM through the 75 episome clearly showed the apical hook-like protrusion. The cingulum had a thick dinoflagel-77 late-pellicle that subtended the alveoli (Fig. 5B). The general surface of the cells consisted of a 79 double laver of plasma membrane that covered empty alveolar vesicles that were subtended by a 81 dinoflagellate-pellicle; the pellicle was subtended by a single row of microtubules (Fig. 5C-F). 83 Mucocysts and trichocysts were present beneath distinct pores in the cell surface (Fig. 5G, H, I). The 85 nuclear envelope contained nuclear pores and 87 vesicular regions where the envelope split to form different sized swellings that were devoid of material (Fig. 6B). Moreover, gaps in the envelope 89 were also formed in some areas, where the two membranes of the envelope were folded over and 91 remained connected (Fig. 6C). The pusule (Fig. 6A), a Golgi apparatus (Fig. 6E) and mitochondria 93 (Fig. 6A, E, F) were present. Plastids were not found in every cell examined with TEM. However, 95 plastids, when present, ranged in size from about 1 to  $2\mu m$  and were arranged in clusters around 97 the nucleus and the posterior end of the cell (Fig. 7A). The plastids were mostly flattened and some 99 contained a distinct pyrenoid (Fig. 7A). Three outer 101

47 Figure 2. Light micrographs (LM) of Apicoporus glaber (A) and different morphotypes of Apicoporus 103 parvidiaboli (B-I). A. Cell with evenly rounded posterior end (star), food body (fb) and plastids (p). B. Cell with 49 oblique posterior end (star), nucleus (n) and plastids (p). C. Cell with oblique posterior end (star) and nucleus 105 (n), D. Cell with oblique posterior end (star) and two horns of uneven length. E. Dorsal view of a cell showing 51 the cingulum (arrow) and two posterior horns of even length (star). F. Cell showing two posterior horns of even 107 length (star), plastids (p), the nucleus (n) and a food body (fb). G. Cell with a more rounded shape and two 53 posterior horns of unequal length extending from an oblique posterior end (star). H. Cell with a more rounded 109 shape and one posterior horn extending further than the other (star); plastids (p) are also present. I. Cell with a 55 more rounded shape and one posterior horn extending even further (star). (A–I, bar = 10  $\mu$ m).

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#### Morphology and Molecular Phylogeny of *Apicoporus* n. gen. 7

membrane lavers could be distinguished and the 1 inner membranes showed a thin-thick-thick-thin pattern, which is indicative of the typical pattern 3 for plastids with thylakoids stacked in three (Fig. 5 7B).

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Several specimens of Apicoporus parvidiaboli also contained golden-brown pigmentation that coincided with the area of plastid autofluorescence observed using epifluorescence microscopy (Figs 7R, F). Cells without pigmentation did not show autofluorescence.

## Molecular Phylogeny of Apicoporus

15 We generated new SSU rDNA sequences from A. glaber and three uncultured morphotypes that 17 represent the morphological variability observed in our samples, namely "oblique antapex", 19 "horned antapex" and "sack-shaped". The SSU rDNA sequences from these three morphotypes 21 were derived from cells that were either pigmented or entirely clear. The sequence from "oblique 23 antapex" was intentionally derived from selected cells that were completely colorless; the 25 sequences from "horned antapex" and "sackshaped" were derived from cells containing 27 differing levels of pigmentation. The SSU rDNA sequences from "oblique antapex" (clear cells) 29 and "sack-shaped" (pigmented cells) were only 8/ 1805 bases different. The sequence derived from 31 "horned antapex" was 21/1805 and 24/1805 bases different from "sack-shaped" and "oblique 33 antapex", respectively. The sequence derived from A. alaber differed more significantly from 35 the other three sequences: 73/1805 different bases when compared to "oblique antapex", 84/ 37 1805 different bases when compared to "horned antapex" and 64/1805 different bases when 39 compared to "sack-shaped".

The phylogenetic position(s) of these four sequences within the dinoflagellate clade was 57 analyzed with a 45-taxon alignment consisting 59 mainly of athecate taxa representing all available genera (1614 unambiguously aligned base positions). The inferred phylogenetic framework 61 demonstrated that Apicoporus glaber and the three morphotypes were only distantly related to 63 Amphidinium sensu stricto (Fig. 8). Sequences from the three morphotypes showing different 65 degrees of posterior horn formation clustered together with strong statistical support; this clade 67 consisted of the three sequences representing the morphological variation observed in Apicoporus 69 parvidiaboli (Fig. 8). The sequence from Apicoporus glaber did not cluster strongly with this well 71 supported A. parvidiaboli clade. The phylogenetic 73 analyses of SSU rDNA did not provide sufficient signal to address this relationship and was unable to confirm or refute the monophyly of this 75 dinoflagallate genus. A more global dinoflagellate alignment (63 taxa) including the diversity of 77 thecate dinoflagellates was also analyzed. The 79 branching pattern was unchanged in showing two separated clades for Apicoporus (not shown). 81

## Discussion

## Comparative Morphology of Apicoporus

All species within Apicoporus have a relatively 87 small, asymmetrical, beak-shaped episome (about one-eighth of the total cell length), with the sulcus extending onto it. Moreover, the cells are dorsoventrally compressed and possess an 91 apical hook-shaped protrusion with a subtending apical pore. Apicoporus parvidiaboli can be dis-93 tinguished from Apicoporus glaber by the presence of some level of horn formation or asym-95

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41 Figure 3. Scanning electron micrographs (SEM) and light micrographs (LM) of Apicoporus glaber (A, C) and 97 Apicoporus parvidiaboli (B, D, E, F) showing morphological similarities between the species. A. SEM of the 43 ventral side of A. glaber showing the apical hook (ah), the sulcus reaching into the episome (single black 99 arrow head), the descending cingulum (double headed arrow) reaching around the cell transversely at the 45 apical end, the sulcus (double arrow head), the protrusion (star) and the indentation (single white arrow head) 101 of the cell. **B**. SEM of the ventral side of *A*. parvidiaboli showing the apical hook (ah), the sulcus extending into 47 the episome (single black arrow head), the descending cingulum (double headed arrow) reaching around the 103 cell transversely at the apical end, the sulcus (double arrow head), the protrusion (star) and the indentation 49 (single white arrow head) of the cell. C. LM of the ventral side of A. glaber displaying the sulcus extending into the episome (single arrow head), a descending cingulum (double headed arrow), a food body (fb), the nucleus 105 51 (n) and plastids (p). D. LM of the ventral side of A. parvidiaboli showing the sulcus extending into the episome (single arrow head), a descending cingulum (double headed arrow) and the nucleus (n). E. LM of the apical 107 end of A. parvidiaboli showing the apical hook (ah), the sulcus extending into the episome (single arrow head) 53 and a descending cingulum (double headed arrow). (A-E, bar = 10  $\mu$ m). F. High magnification SEM of the 109 apical hook (ah) and apical pore (ap) found in both species (bar =  $1 \mu m$ ). 55



**Figure 4.** Light micrographs (LM) of *Apicoporus glaber* (**A**, **C**) and *Apicoporus parvidiaboli* (**B**, **D**), as well as scanning electron micrographs (SEM) of *Apicoporus parvidiaboli* (**E**, **F**) showing variation of the posterior end of the cell within *Apicoporus parvidiaboli*. **A**. LM of ventral view showing sulcus (double arrow head), protrusion (star) and nucleus (n). **B**. LM of ventral view showing sulcus (double arrow head), protrusion (star) and longitudinal flagellum (single arrow head). **C**. LM displaying the indentation at the posterior end (double headed arrow). **D**. LM displaying the indentation at the posterior end (double headed arrow). **D**. LM displaying the indentation at the posterior end (double headed arrow). **E**. SEM of the ventral, antapical end displaying a large protrusion (star) forming a flap that is covering the sulcus and an indentation (single arrow head). **F**. SEM of the ventral, antapical end displaying a smaller protrusion (star) that does not cover the sulcus and an indentation (single arrow head). (**E**, **F**, bar = 5 µm).

Figure 5. Transmission and scanning electron micrographs (TEM and SEM, respectively) of Apicoporus parvidiaboli showing details of surface structures. A. Low magnification TEM montage of the whole cell showing a food body (fb) and the nucleus (n) (bar =  $7.5 \,\mu$ m). **B**. TEM through the episome displaying the apical hook (ah) and cingulum (double headed arrow) (bar =  $3 \,\mu$ m). C. TEM through the plasma membrane (single arrow head), alveoli (double arrow head) and dinoflagellate-pellicle (triple arrow head); (bar =  $0.5 \,\mu$ m). D. High magnification TEM showing the arrangement of microtubules subtending the dinoflagellate-pellicle (arrow) (bar =  $0.3 \,\mu$ m), E. High magnification TEM through the alveoli (double arrow head) (bar =  $0.5 \,\mu$ m), F. SEM showing alveoli (double arrow head) on the surface of the cell (bar =  $2.5 \,\mu$ m). G. TEM through a mucocyst (single arrow head) sitting beneath the alveolar layer and piercing the dinoflagellate-pellicle (bar = 1  $\mu$ m). H. High-magnification TEM of a trichocyst (bar = 0.75  $\mu$ m). I. SEM showing pores (single arrow head) and the sulcus (double arrow head) on the cell surface (bar = 1  $\mu$ m).

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**Figure 6.** Transmission electron micrographs (TEM) of *Apicoporus parvidiaboli* showing the nucleus, mitochondria and Golgi apparatus. **A.** Transverse section through the cell showing a dinokaryotic nucleus with permanently condensed chromosomes (single arrow head), nucleolus (double arrow head) and nuclear envelope (triple arrow head); a pusule can also be seen (arrow) (bar =  $1.5 \,\mu$ m). **B.** High magnification of the nuclear envelope (triple arrow head) displaying nuclear pores (double arrow head) and intra-nuclear envelope swellings (single arrow head) of varying size (bar =  $0.5 \,\mu$ m) **C.** Nuclear envelope (triple arrow head) and discontinuity of the envelope (single arrow head) (bar =  $0.75 \,\mu$ m). **D.** Striation pattern of the permanently condensed chromosomes (single arrow head) (bar =  $0.5 \,\mu$ m). **E.** Mitochondrion (star) enveloped by endoplasmic reticulum and a Golgi apparatus (arrow) (bar =  $0.5 \,\mu$ m). **F.** Mitochondrion (arrow) (bar =  $0.75 \,\mu$ m).

metry at the posterior end of the cells. The cells of
 Apicoporus glaber have parallel sides and lack
 horn formation altogether; the posterior end of the
 cells are distinctively rounded and more symmetrical.

The presence of an apical pore in both species105of Apicoporus is quite unusual for athecate107dinoflagellates, because these pores have only107been described for thecate dinoflagellates so far109





**Figure 7.** Transmission electron micrographs (TEM) and epifluorescence micrographs of plastids in *Apicoporus parvidiaboli* and *Apicoporus glaber*. **A.** Low magnification TEM of *A. parvidiaboli* showing a cluster of small plastids (arrow) with pyrenoids (p) (bar =  $1.5 \mu m$ ). **B.** High magnification TEM of *A. parvidiaboli* showing a plastid with thylakoids arranged in stacks of three, which can be seen by the membrane pattern 'thin-thick-thick-thin' (between single arrow heads) (bar =  $0.3 \mu m$ ). Also note the three outer membranes (between arrows) **C.** LM of *A. glaber* showing the presence of plastids in the posterior end of the cell (arrow). **D.** Plastid autofluorescence in *A. glaber* present in the same posterior end of the cell (arrow). **F.** Plastid autofluorescence in *A. parvidiaboli* present in the same posterior part of the cell (arrow). (**C**-**F**, bar =  $10 \mu m$ ).

1993; Toriumi and Dodge 1993). Most species of the family Peridiniaceae form a tubular rim around the apical pore (Toriumi and Dodge 1993), a structure that has also been observed in *Apicoporus* (Fig. 3F; Hoppenrath and Okolodkov 2000, Figs 17, 18). Species of the athecate genus *Karlodinium* have a ventral pore (e.g., Bergholtz

et al. 2005; Daugbjerg et al. 2000; De Salas et al.1032005), a character also known for thecate dino-<br/>flagellates like Alexandrium Halim or Thecadinium105Kofoid and Skogsberg (e.g., Balech 1995; Hop-<br/>penrath 2000b). More common apical surface<br/>structures found in athecate dinoflagellates are<br/>"acrobases" (apical grooves) of different shapes103



Figure 8. Gamma-corrected maximum likelihood tree (-ln L = 11935.70254, α = 0.324, proportion of invariable sites = 0.163, 8 rate categories) inferred using the GTR model of substitution on an alignment of 45 SSU rDNA sequences and 1614 unambiguously aligned sites. Numbers at the branches denote bootstrap percentages using maximum likelihood – HKY (top) and Bayesian posterior probabilities – GTR (bottom). Black dots on branches denote robust bootstrap percentages and posterior probabilities of 95% or higher.
 The sequences derived from this study are highlighted in the shaded boxes.

(Biecheler 1952; Daugbierg et al. 2000; De Salas 43 et al. 2003; Takayama 1985). Acrobases are furrows that are shallower and narrower than the cingulum and sulcus and are usually not con-45 nected to either of these grooves (Takayama 47 1985). However, in a few cases, a connection between the acrobase, cingulum and sulcus was 49 observed, such as in Polykrikos species (Hoppenrath and Leander 2007b; Takayama 1985). An 51 acrobase was not present in Apicoporus. The furrow that extended from the cinculum to the 53 episome and towards the apical pore in Apicoporus was interpreted to be the sulcus, because 55

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of its deep incision (Fig. 3A-E). Nonetheless, 97 Apicoporus had novel apex characteristics for athecate dinoflagellates: (1) the sulcus reaches the 99 apex, (2) an apical pore is surrounded by a rim-like structure (so far only found in thecate dinoflagel-101 lates), and (3) a hook-like protrusion partly covers the apical pore. Apical hooks covering the apical 103 pore are only known from thecate benthic dinoflagellates like Herdmania litoralis Dodge emend. 105 Hoppenrath (Hoppenrath 2000c) and Rhinodinium broomeense Murray, Hoppenrath, Yoshimatsu, 107 Toriumi and Larsen (Murray et al. 2006). These morphological features are significant and justify 109

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1 the erection of the new athecate genus, namely *Apicoporus*.

Athecate motile dinoflagellates with a dinofla-3 gellate-pellicle as the principal structural element 5 in the amphiesma are rarely discussed in the literature and are, to the best of our knowledge, not well studied at the ultrastructural level. The 7 Ptvchodiscaceae, Amphitholaceae, Brachvdiniaceae, and Noctiluciphyceae have been shown to a have a dinoflagellate-pellicle (Fensome et al. 11 1993). Some of these pelliculate taxa show distinctive extensions ("arms"), like those found in Brachydinium Taylor and Asterodinium Sournia 13 (Fensome et al. 1993; Gómez 2006). These extensions seem to be highly variable in size and 15 relative proportion (Gómez 2003, 2006), which is 17 similar to the variability in horn-formation observed in Apicoporus parvidiaboli. Other pelliculate taxa are good candidates for discovering 19 additional athecate dinoflagellates with an apical 21 pore. The genus Berghiella Kofoid and Michener, for instance, has a truncated apical horn that 23 resembles the morphology of the apical pore complexes found in thecate dinoflagellates (Kofoid and Michener 1911: Taylor 1976). 25

The nucleus of the specimens observed with TEM was a typical dinokaryon with permanently 27 condensed chromosomes and a nucleolus (Fig. 6A). However, the splits in the nuclear envelope 29 (Fig. 6B) were unlike any other structures found in athecate dinoflagellates, such as Actiniscus pen-31 tasterias (Ehrenberg) Ehrenberg, Polykrikos, Gymnodinium and Gyrodinium (Bradbury et al. 1983; 33 Hansen 1993, 2001; Hansen and Daugbjerg 2004; 35 Hansen et al. 2000; Hoppenrath and Leander 2007b). Interestingly, these dinoflagellates do 37 possess vesicular or nuclear chambers in the nuclear envelope in which the nuclear pores are 39 situated. In these cases, both membranes of the nuclear envelope either invaginate or evaginate. 41 We did not observe these features in the TEM sections of Apicoporus (Fig. 6B). Instead, the two 43 membranes of the nuclear envelope actually split and created a space mostly void of electron dense material. Nuclear pores were not found within the 45 split membranes, but only in the parts of the nuclear envelope where the two membranes were 47 in close proximity to each other. Splits could also be found in varying sizes, unlike the nuclear 49 chambers reported from other dinoflagellates (Bradbury et al., 1983; Hansen 1993, 2001; 51 Hansen and Daugbierg 2004; Hansen et al. 53 2000; Hoppenrath and Leander 2007b). It cannot be completely ruled out, however, that the splits represent an artifact caused by a suboptimal 55

fixation. Nonetheless, another peculiar structure was the discontinuities within the nuclear envel-57 ope that formed relatively large openings about 0.35 um wide. They did not seem to be sections 59 through nuclear pores, since these discontinuities measured only about 0.05 µm across. They also 61 were not likely to be preparation artifacts since the two membranes of the nuclear envelope folded 63 towards each other and remained connected. It is 65 not clear at this point what the relevance of the split membranes or the interruptions of the envelope are, but they have not been observed 67 in any dinoflagellates studied so far.

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# Cryptic Photosynthetic Plastids in *Apicoporus*

73 Golden-brown pigmentation in dinoflagellates is indicative of the presence of photosynthetic 75 plastids. It is generally accepted that dinoflagellates acquired plastids early in their evolution and 77 that heterotrophic dinoflagellates have lost photosynthesis secondarily (Schnepf and Elbrächter 79 1999; Saldarriaga et al. 2001). The plastids most commonly found in dinoflagellates are inferred to 81 be ancestral for the group and can be recognized by a surrounding layer of three membranes, 83 thylakoids in stacks of three, a primary pigment consisting of peridinin and usually the presence of 85 pyrenoids (Schnepf and Elbrächter 1999). The 87 plastids in Apicoporus had all of the ultrastructural characteristics listed above and are therefore inferred to be the usual peridinin-containing 89 plastids of dinoflagellates (Fig. 7A, B). Because only some of the cells observed with LM and TEM 91 showed evidence of photosynthetic plastids, it is possible that the diversity of Apicoporus repre-93 sents an intermediate stage associated with the secondary loss of photosynthesis. This is consis-95 tent with the fact that even cells with pigmentation contained food bodies, suggesting that Apico-97 porus is mixotrophic and does not obligately rely on photosynthesis for nutrition. 99

Autofluorescence was consistent with the location of golden-brown pigmentation within cells of 101 Apicoporus glaber and Apicoporus parvidiaboli 103 and was completely absent in cells that lacked pigmentation. This further confirmed that both 105 species contain some cells that have photosynthetic plastids and some cells that do not. Interestingly, although cells of these species 107 reported from the North Sea and Arctic were 109 described as being completely colorless (Hoppenrath 2000a; Hoppenrath and Okolodkov 2000;

Larsen 1985), "dark granulation" is visible in the 1 posterior part of two specimens described from Denmark (Larsen 1985, p. 27, Figs 54, 57). The 3 discovery that the tiny brownish granules observed in these benthic specimens are in fact 5 plastids is especially interesting because nearly all dinoflagellates that show this minimum degree of 7 pigmentation have been assumed to be heterotrophic and to lack plastids altogether. For a instance, Amphidinium bipes Herdman is another 11 "heterotrophic" benthic dinoflagellate with brown pigmentation in the antapex (Herdman 1924; Hoppenrath 2000a); TEM investigations of this 13 species, and others, will very likely demonstrate the presence of photosynthetic plastids. 15

Nonetheless, the SSU rDNA sequences from 17 the three morphotypes of A. parvidiaboli were derived from cells that were either pigmented or 19 entirely clear. On one hand, the sequence from "oblique antapex" was intentionally derived from 21 selected cells that were completely colorless. On the other hand, the sequences from "horned antapex" and "sack-shaped" were derived from 23 cells containing different levels of pigmentation. Despite the presence or absence of pigmentation 25 in the isolated cells of each morphotype, the SSU 27 rDNA sequences from all three morphotypes were very similar (Fig. 8). In fact, the sequence derived 29 from "oblique antapex" (colorless) and "sackshaped" (pigmented) were only 8 of 1805 bases different. This result indicates that the presence or 31 absence of photosynthetic plastids does not necessarily reflect different species. This conclu-33 sion is significant because it stands in contrast to 35 the expected pattern of speciation demonstrated in other benthic dinoflagellates, such as Polykrikos herdmanae (heterotrophic) and P. lebourae (photo-37 synthetic) (Hoppenrath and Leander 2007b). This result also suggests that photosynthesis is facul-39 tative in A. parvidiaboli and that plastid develop-41 ment and photosynthetic ability might change in response to specific changes in environmental 43 conditions.

## <sup>45</sup> Taxonomy of *Apicoporus*

47 Several authors have suggested that the genus Amphidinium encompasses a polyphyletic assem49 blage of morphologically diverse groups (e.g., Daugbjerg et al. 2000; Flø Jørgensen et al. 2004a;
51 Murray and Patterson 2002). The redefinition of Amphidinium sensu stricto (s.s.) by Flø Jørgensen
53 et al. (2004a) necessitates the reinvestigation of several sensu lato species. This has already been
55 accomplished for Amphidinium britannicum (Herdman) Lebour and related taxa, which are now classified in the genus Togula (Flø Jørgensen 57 et al. 2004b). Likewise, all Apicoporus morpho-59 types have novel episome characteristics that are different from Amphidinium s.s. or any other athecate genus for that matter. Phylogenetic 61 analyses of small subunit rDNA (SSU rDNA) sequences from both species of *Apicoporus* also 63 demonstrate that these species are not closely related to Amphidinium s.s. (Fig. 8). However, not 65 surprisingly, the SSU rDNA marker offered only weak phylogenetic signal and was relatively silent 67 on many relationships among dinoflagellates, which is consistent with previous results (e.g. 69 Saldarriaga et al. 2004, Hoppenrath and Leander 2008). Moreover, like other species of dinoflagel-71 lates (e.g. Polykirkos spp.), the rate of sequence evolution in the three morphotypes of A. parvidia-73 boli was relatively high when compared to other species (e.g. Gyrodinium spp.), which indicates 75 that substitution-rate heterogeneity does not correspond directly with morphological diversity 77 in dinoflagellates. Nonetheless, even though Api-79 coporus glaber did not cluster strongly with the morphotypes of A. parvidiaboli in the molecular phylogenetic analyses, these species are classi-81 fied in the same genus because of several distinct morphological synapomorphies: the apical hook-83 like protrusion, the apical pore, the sulcal and 85 cingular characteristics, the posterior indentation and the posterior protrusion ('flap') covering the 87 indentation (Figs 3, 4).

Hoppenrath and Okolodkov (2000) described the new species Amphidinium glabrum, including 89 mostly guadrangular-elongated cells with evenly rounded posterior ends. A few of the published 91 micrographs however, represented specimens 93 with a more rounded body shape and an oblique antapex that is more consistent with A. parvidiaboli (Hoppenrath and Okolodkov 2000, Figs 3, 9, 95 10, 11, 13, 14). According to the data available from this study, it is likely that the two Apicoporus 97 species were described as one in the previous report because of their distinctive morphological 99 similarities. However, Hoppenrath and Okolodkov (2000) did not show any cells with strong horn 101 formation, as can be seen in the present study 103 (Figs 1B-F, 2B-I). Our phylogenetic analyses of SSU rDNA demonstrated that cells with different 105 degrees of horn formation (Fig. 1B-F) cluster together strongly and are more distantly related to 107 cells that lack horn formation, namely A. glaber (Fig. 1A). Although all of the morphotypes shared 109 many characteristics, the phylogenetic analyses are most consistent with the presence of two

distinct species, one of which is quite variable in 1 horn morphology (i.e. A. parvidiaboli). The presence of both species in the North German 3 Wadden Sea is likely, as inferred from the known 5 morphological variation known from this habitat. but this remains to be confirmed with molecular data. The taxon described from Arctic waters is 7 most probably A. parvidiaboli because of the oblique posterior end present in these cells q (Hoppenrath and Okolodkov 2000). Lastly, speci-11 mens described from the Danish Wadden Sea are A. glaber, except for one cell (Larsen 1985, Fig. 56), which has an oblique posterior end like that 13 found in A. parvidiaboli (Larsen 1985). 15

## Methods

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Organisms and light microscopy: Collections of marine sand began in the summer of 2006 at sites in Vancouver (Spanish Banks) and in Bamfield (Brady's Beach and Pachena Beach), B.C., Canada. A spoon was used to collect the top five centimeters of sand exposed during low tides. Samples were then brought back to the laboratory and the melting seawater-

**Q1** ice method (Uhlig 1964) was used with a 45 μm mesh size filter to extract organisms from the sand. Dinoflagellates were gathered in a Petri dish and then investigated at 40 to 250 × magnification. *Apicoporus glaber* was only found in samples from the sites in Bamfield, while *Apicoporus parvidiaboli* was present in all locations. Micropipetting was used for further processing of the cells as described below.

For documentation with differential interference contrast (DIC) light microscopy, the cells of interest were micropipetted onto glass specimen slides and covered with cover slips. A Zeiss Axioplan 2 imaging microscope connected to a Leica DC500 color digital camera was used to capture images. Autofluorescence micrographs of plastids in living cells were captured with the same microscope and digital camera using an excitation wavelength of 568 nm.

Scanning electron microscopy: Environmental samples extracted from the sand that included *Apicoporus* cells were first fixed with evaporating  $OsO_4$  for about 25 min and then by directly adding five drops of 4%  $OsO_4$  (v/v) to the sample for about 20 min. Following this the cells were transferred onto a 5-µm polycarbonate membrane filter (Corning Separations Div., Acton, MA), first washed with distilled water and then gradually dehydrated with increasing amounts of ethanol. After the final step with 100% ethanol the filter was critically point dried using  $CO_2$ , mounted on stubs, sputter-coated with gold and looked at under a Hitachi S4700 Scanning Electron Microscope. Some SEM images were put on a black background with the use of Adobe Photoshop 6.0 (Adobe Systems, San Jose, CA).

*Transmission electron microscopy:* The cells of interest were accumulated in Eppendorf tubes by micropipetting and slow centrifugation. The first fixation step was done by adding 2% (v/v) glutaraldehyde (in unbuffered seawater) at 4 °C for 30 min. Three washing steps with filtered seawater followed before post-fixation with 1% (w/v) OsO<sub>4</sub> (in unbuffered seawater) for 30 min at room temperature. The sample was then gradually dehydrated with increasing amounts of ethanol and then infiltrated with acetone-resin mixtures. Finally the cells were embedded in Epon 812 resin that was polymerized

at 60 °C. A diamond knife on a Leica Ultracut UltraMicrotome was used to cut ultrathin sections, which were then stained with uranyl acetate and lead citrate. The sections were viewed with a Hitachi H7600 Transmission Electron Microscope.

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DNA extraction, PCR amplification, and sequencing: The Epicentre MasterPure complete DNA & RNA Purification Kit was used for the DNA extraction. Between five and ten cells of each suspected morphotype of *Apicoporus* were micropipetted separately into filtered (eukaryote free) autoclaved seawater and then added together (each morphotype seperately) into  $2 \times$  lysis (cell tissue) solution that was mixed with proteinase K. After the addition of distilled autoclaved water, the manufacturer's protocol for cell samples was followed.

The isolated genomic DNA was then used for the following PCR amplification protocol: with universal eukaryotic primers, as reported previously (Leander et al. 2003). PCR consisted of an initial denaturing period (95 °C for 2 min); 35 cycles of denaturing (92 °C for 45 s), annealing (50 °C for 45 s), and extension (72 °C for 1.5 min); and a final extension period (72 °C for 5 min). PCR products of the right size were gel isolated and cloned into pCR2.1 vector with the use of a TOPO TA cloning kit (Invitrogen). New sequences from *A. glaber* and the three morphotypes of *A. parvidiaboli* were completely sequenced with ABI big-dye reaction mix using both vector primers and two internal primers oriented in both directions (GenBank accession codes EU293235, EU293236, EU293237, EU293238).

Alignment and phylogenetic analyses: The four new SSU rDNA sequences were aligned with other alveolate sequences using MacClade 4 (Maddison and Maddison 2000), forming a 45-taxon alignment and a 63-taxon alignment (including thecate dinofalgellates). Because the backbone of overall dinoflagellate phylogeny is poorly resolved (see Hoppenrath and Leander 2007a), outgroup selection for the *Gymnodinium* s.s. clade was somewhat arbitrary. Our main concerns in choosing our taxon sample were to ensure that (1) all known clades of the athecate dinoflagellates were represented and (2) the outgroup taxa did not represent unusually long branches. The alignments are available on request.

Maximum likelihood (ML), ML-distance and Bayesian methods under different DNA substitution models were 89 performed. All gaps were excluded from the alignments prior to phylogenetic analysis. The alpha shape parameters were 91 estimated from the data using the General Time Reversible (GTR) model for base substitutions, a gamma distribution with invariable sites and eight rate categories, respectively (45-93 taxon alignment:  $\infty = 0.324$ , i = 0.163). Gamma-corrected ML trees (analyzed using the parameters listed above) were 95 constructed with PhyML (Guindon and Gascuel 2003; Guindon et al. 2005) using the GTR model for base 97 substitutions (Posada and Crandall 1998). ML bootstrap analyses were performed on the 45-taxon alignment with PhyML on five hundred re-sampled datasets using HKY and 99 the alpha shape parameter and transition/transversion ratio estimated from the original dataset ( $\infty = 0.353$ , i = 0.220, Ti/ 101 Tv = 5.288). ML bootstrap analyses were done using HKY (rather than GTR) in order to help reduce the computational burden required. 103

We also examined the SSU rDNA dataset with Bayesian analysis using the program MrBayes 3.0 (Huelsenbeck and Ronquist 2001). The program was set to operate with GTR, a gamma distribution and four Monte-Carlo-Markov chains (MCMC) (default temperature = 0.2). A total of 2,000,000 generations were calculated with trees sampled every 100 generations and with a prior burn-in of 200,000 generations (2000 sampled trees were discarded). A majority rule 16 S.F. Sparmann et al.

consensus tree was constructed from 18.000 post-burn-in trees with PAUP\* 4.0. Posterior probabilities correspond to the frequency at which a given node is found in the post-burn-in trees.

## **Acknowledaments**

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