

# TEM investigation of FD 95, Aphelid parasite of Scenedesmus

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LM Images by Sal Lopez

FD 95 is a typical member of class Aphelidea, in the genus *Amoeboaphelidium*, and sister to FD 01 *A. protococcarum*.

The *Scenedesmus* host is infected not only with FD 95, but also with a bacterium:

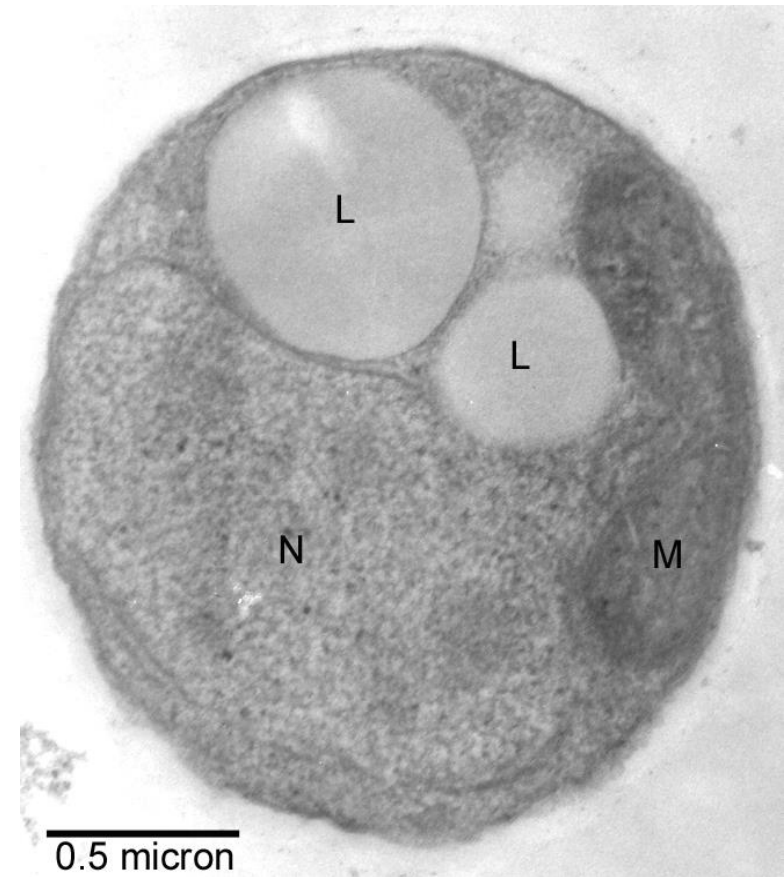
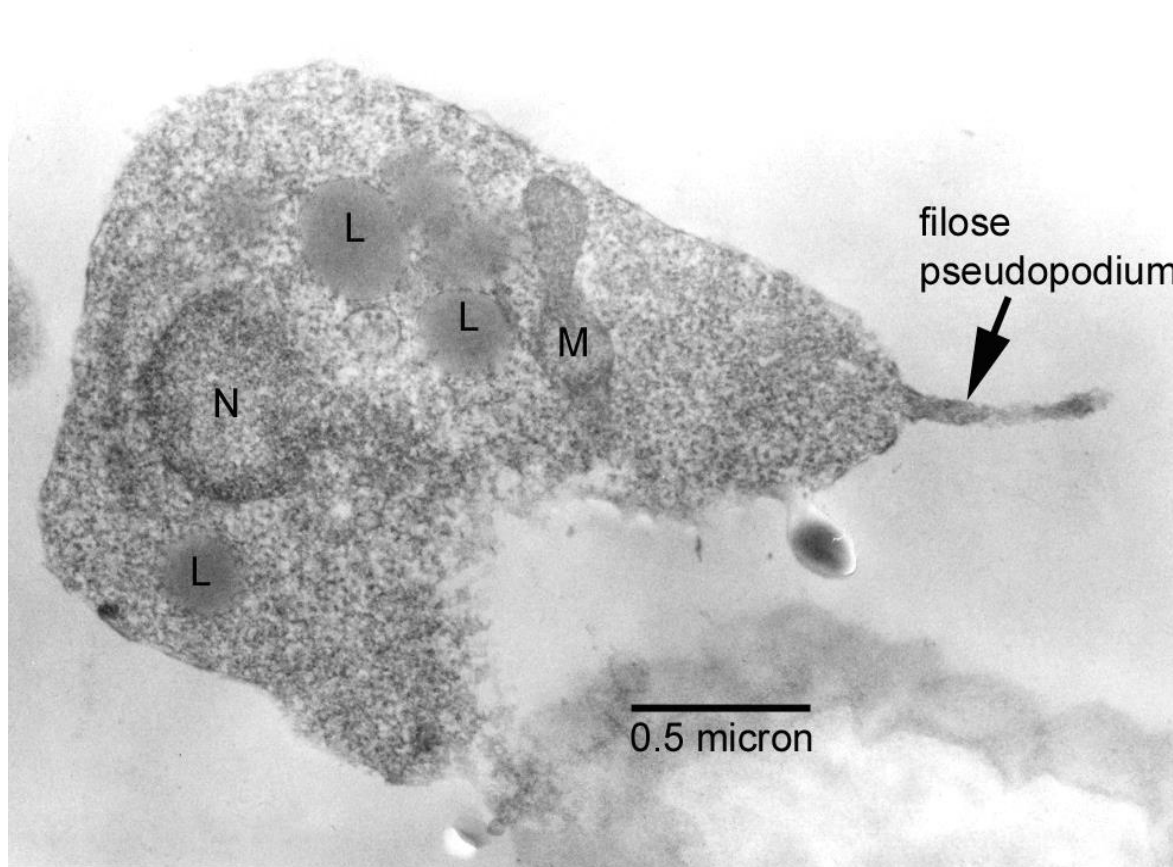
FD 95 is a typical eukaryote with organelles;

The bacterium is a typical “bacillus” prokaryote, with no discernable organelles, but with a cell wall and capsule, probably gram positive (no outer membrane)

Day 1 of infection is characterized by:

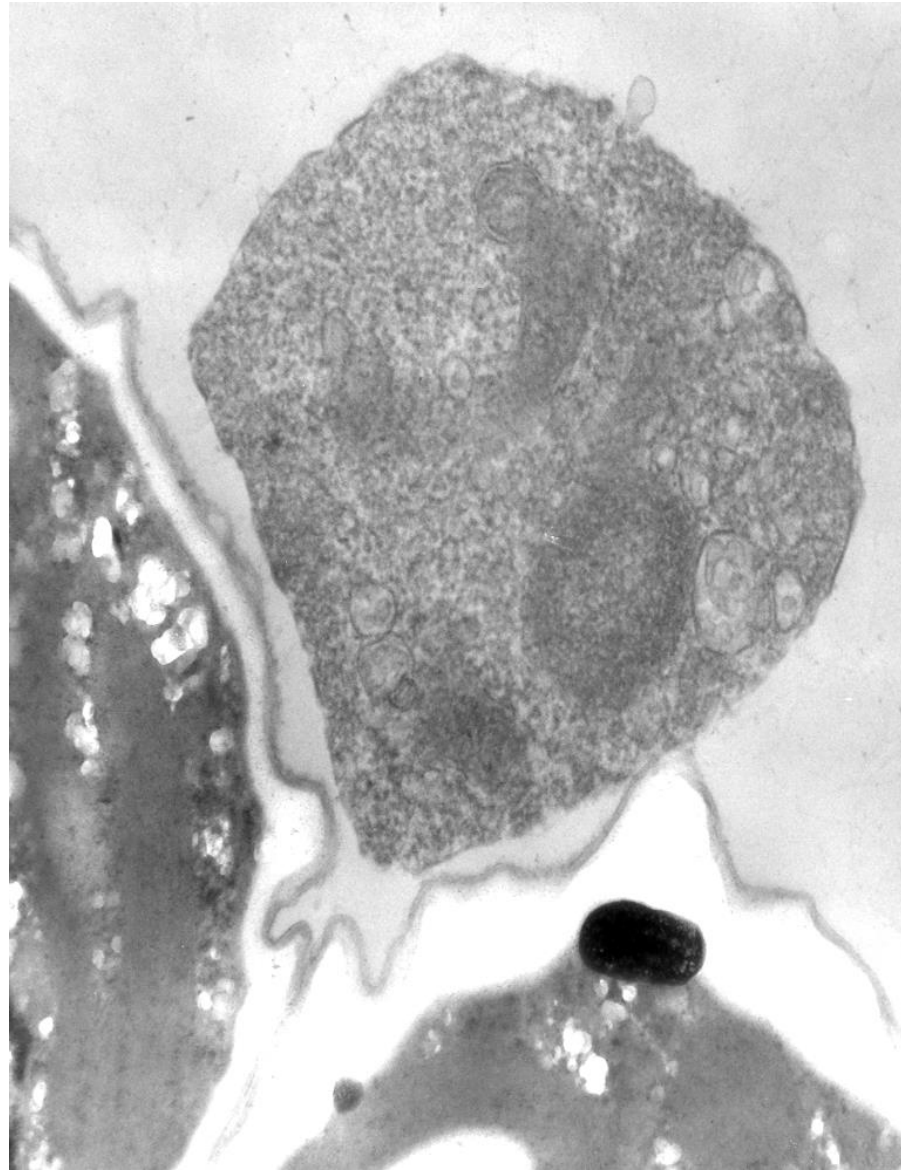
- abundant healthy algal cells;
- presence of motile filopseudopodiate aplanospores;
- aplanospores “docking” with algal cells;
- aplanospore cysts on host;
- rod-shaped bacteria on host.

Day 1: aplanospores, 1.3-2.7 microns diam.

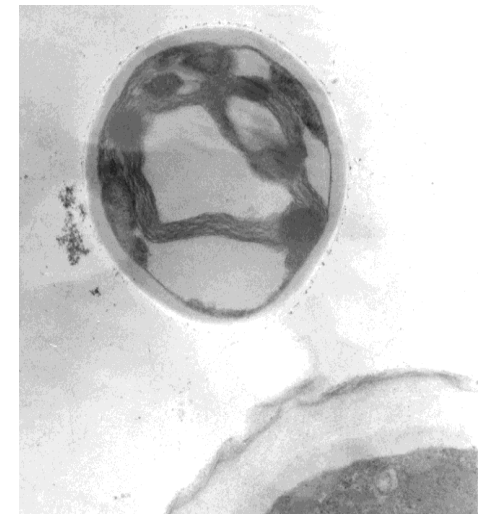
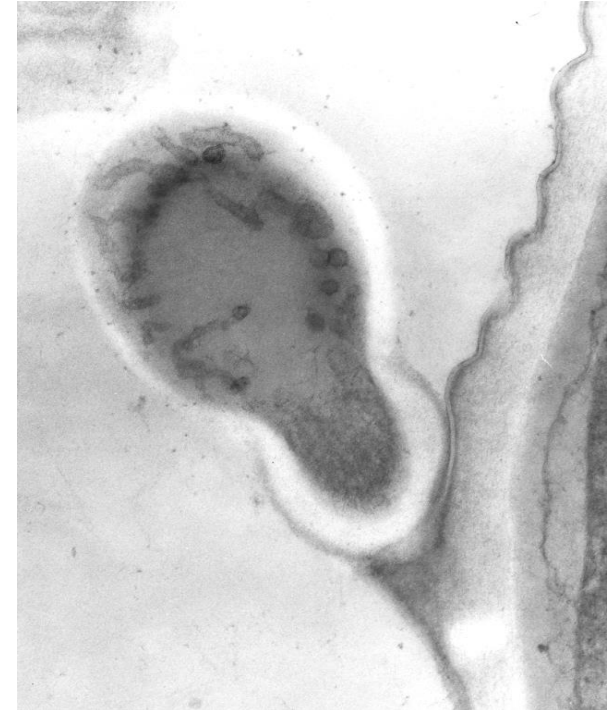
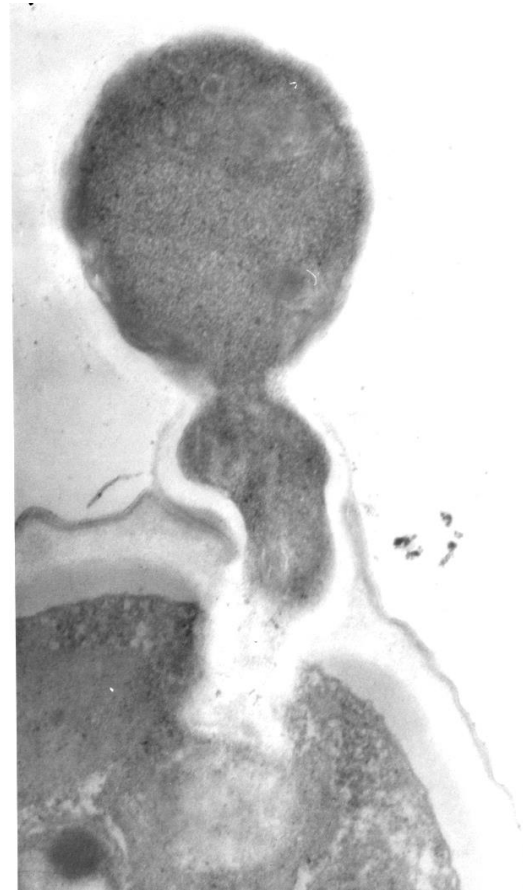
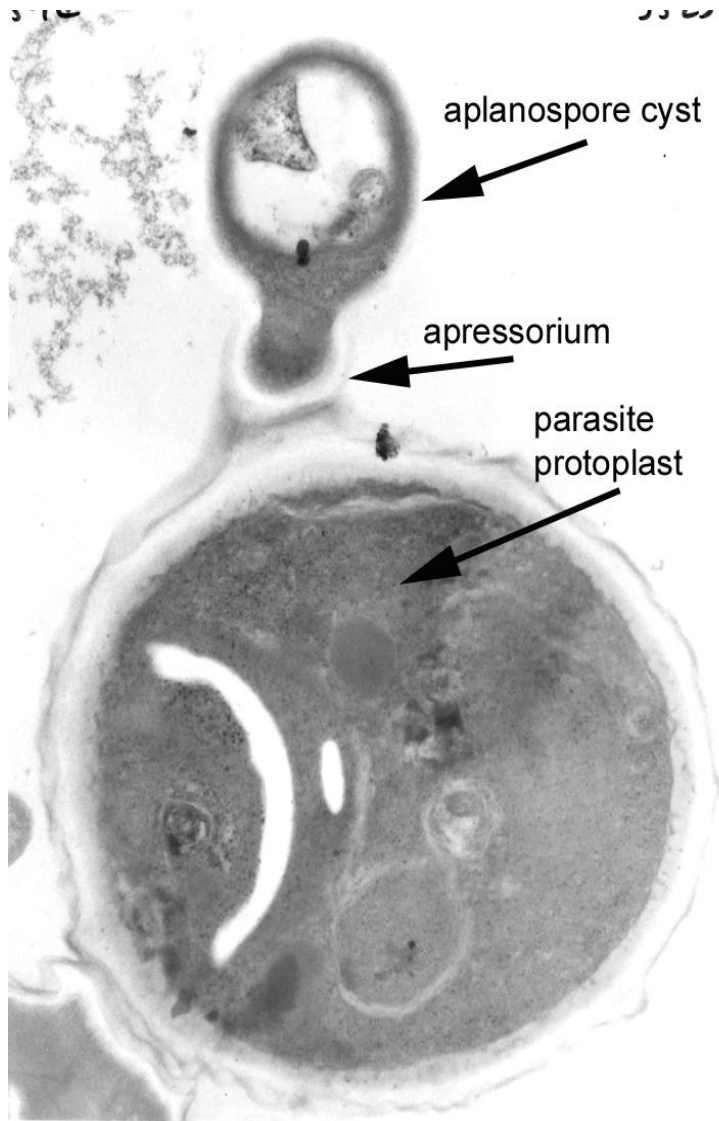


L: motile aplanospore contacting an algal cell; R: encysting aplanospore, producing a wall.

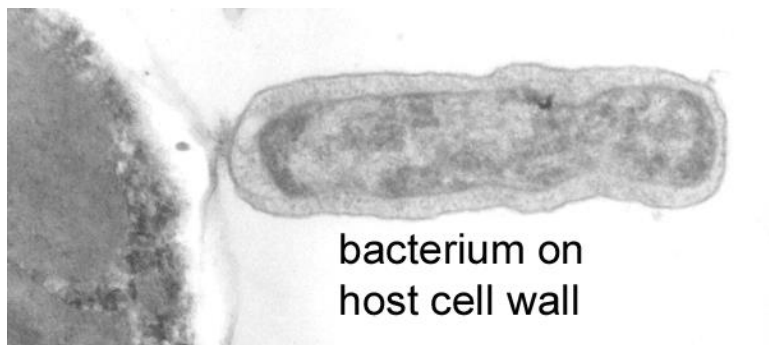
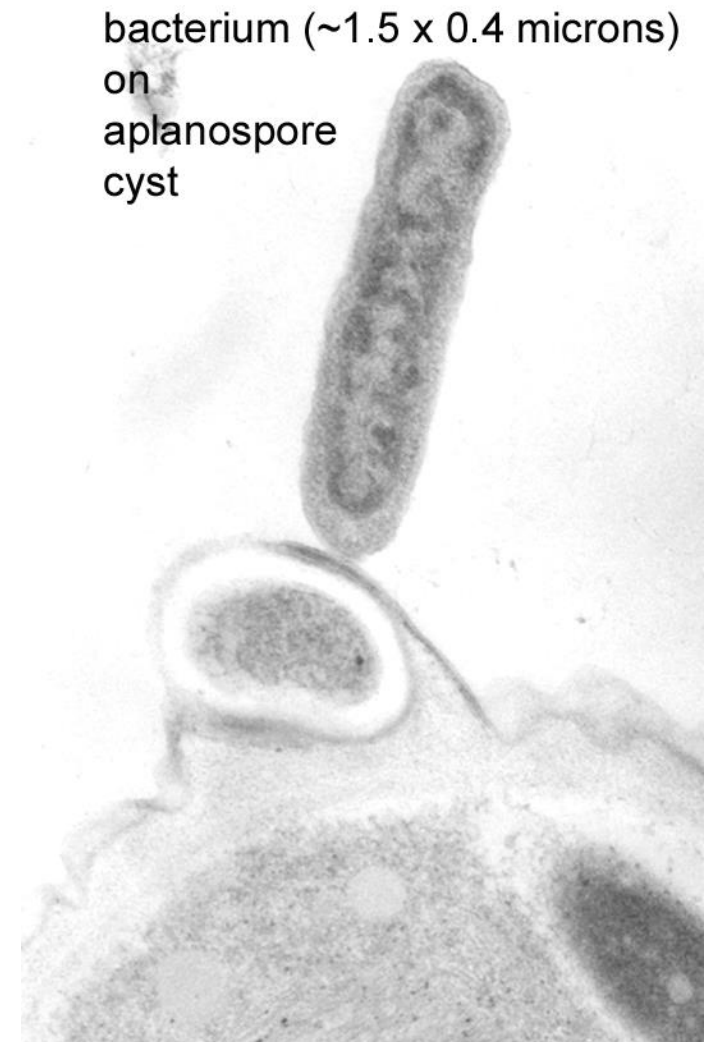
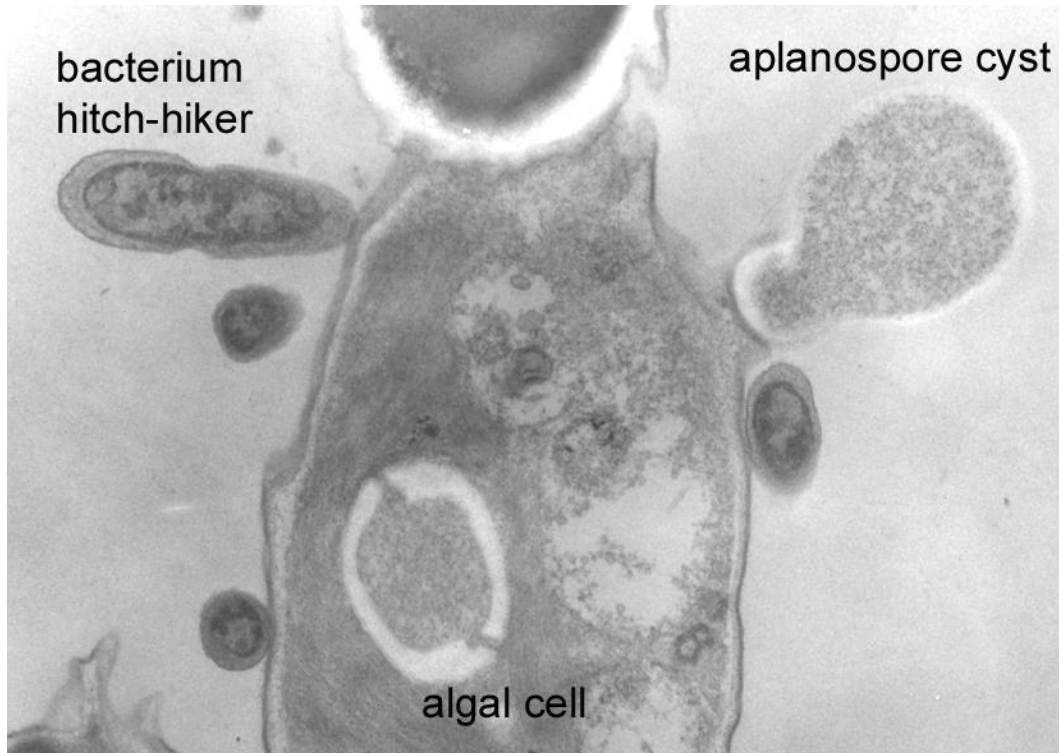
# Day 1: aplanospore “docking” with algal cell



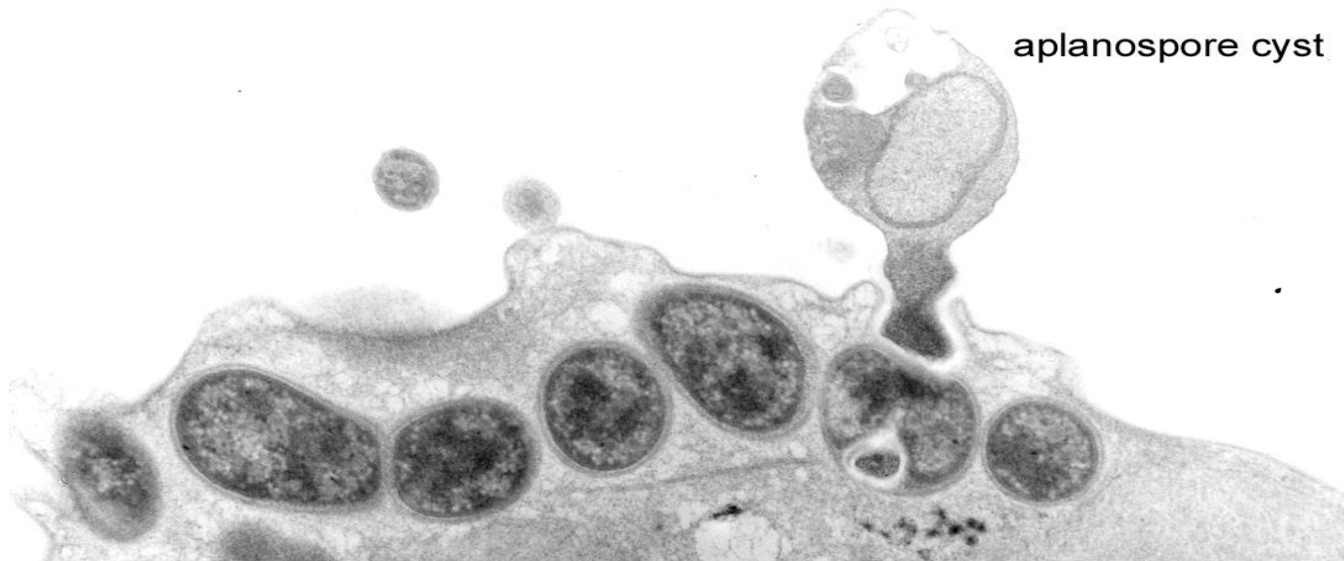
# Day 1: aplanospore cysts on host cells



# Day 1: aplanospore cyst and bacterium on host



Day 1: bacteria on host surface (epibiotic) and within host (endobiotic), both epibiotic and endobiotic stages presumed to be of same organism



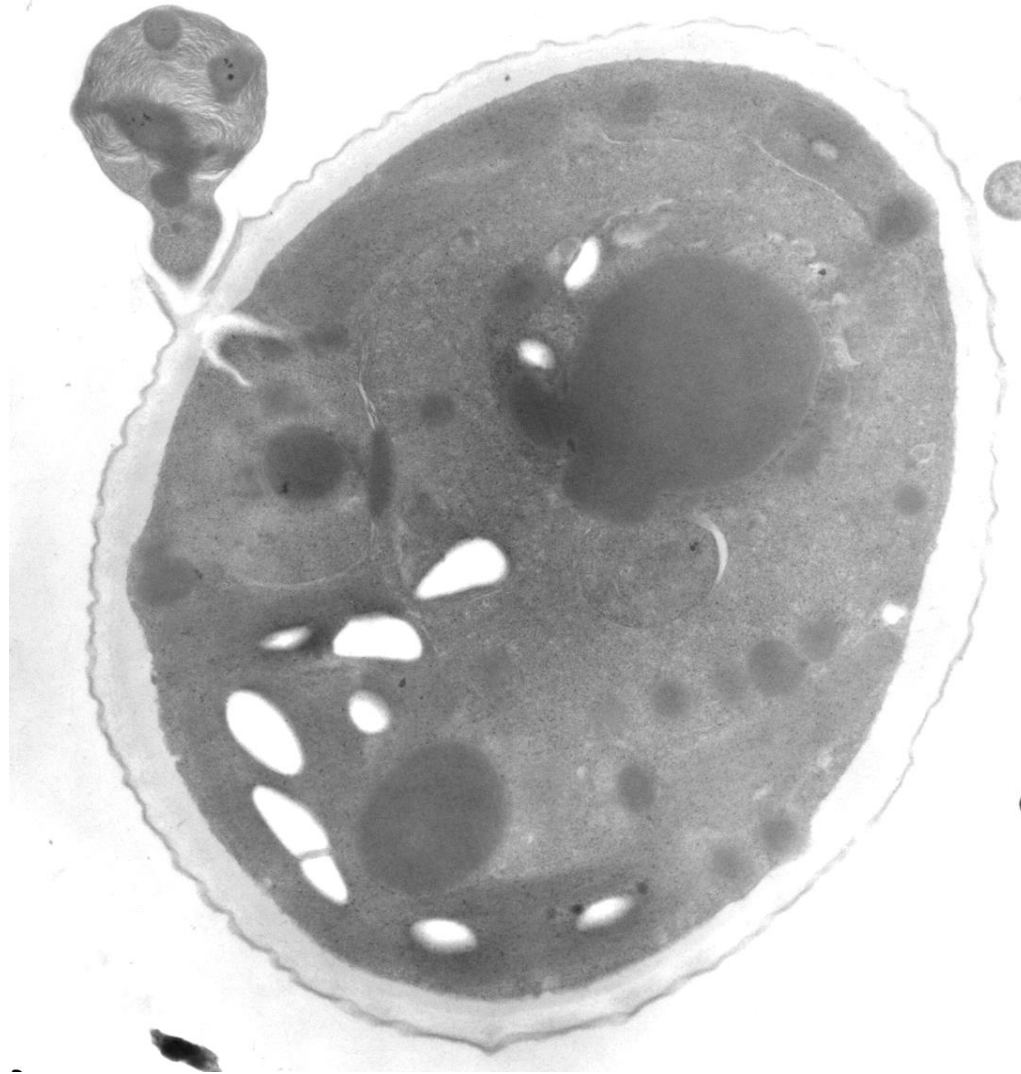


Day 2 of infection characterized by:

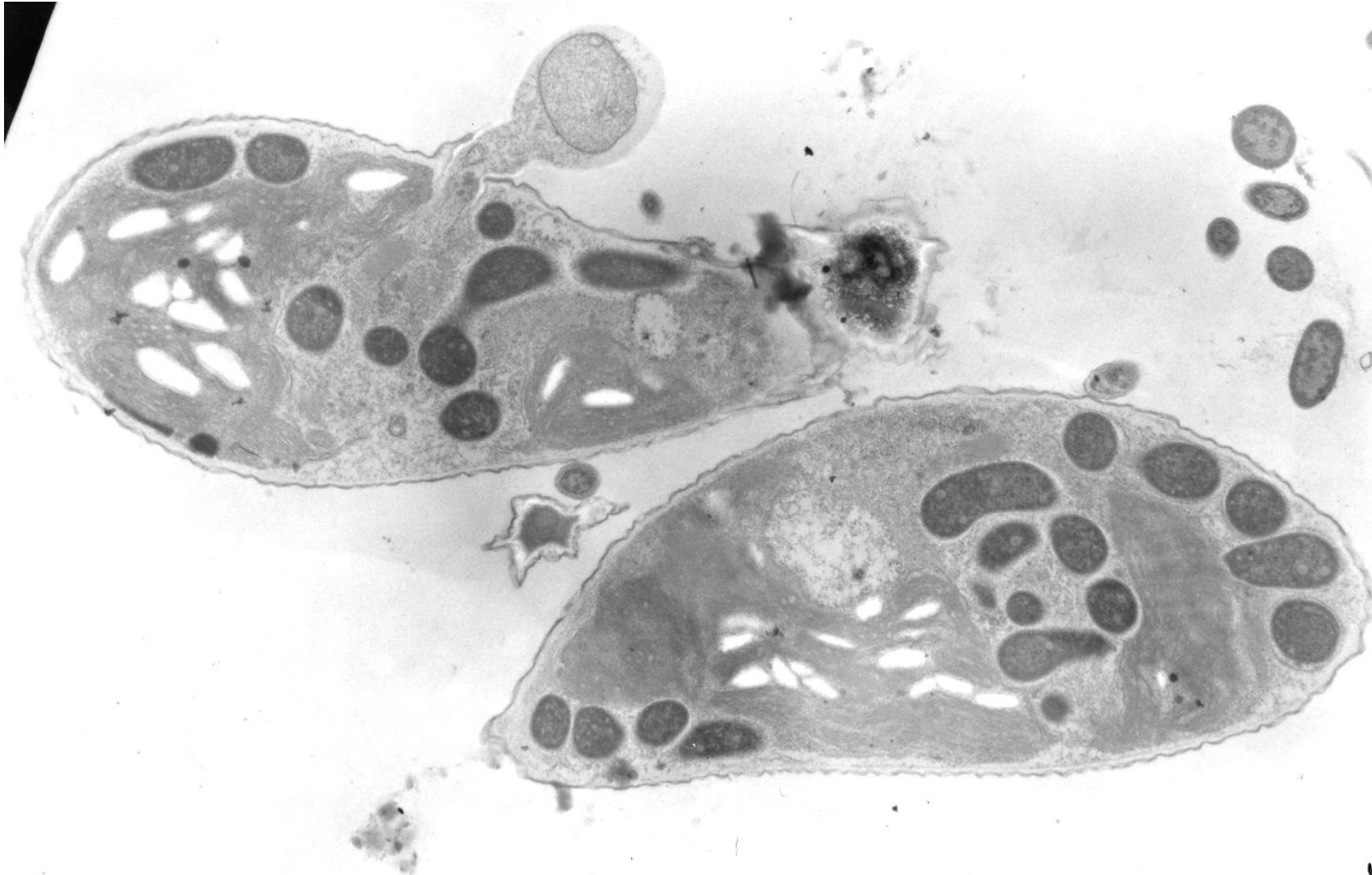
- typical progression of Aphelid infection;

almost all algal cells infected with both the Aphelid and the endobiotic prokaryotic pest

## Day 2: typical Aphelid infection



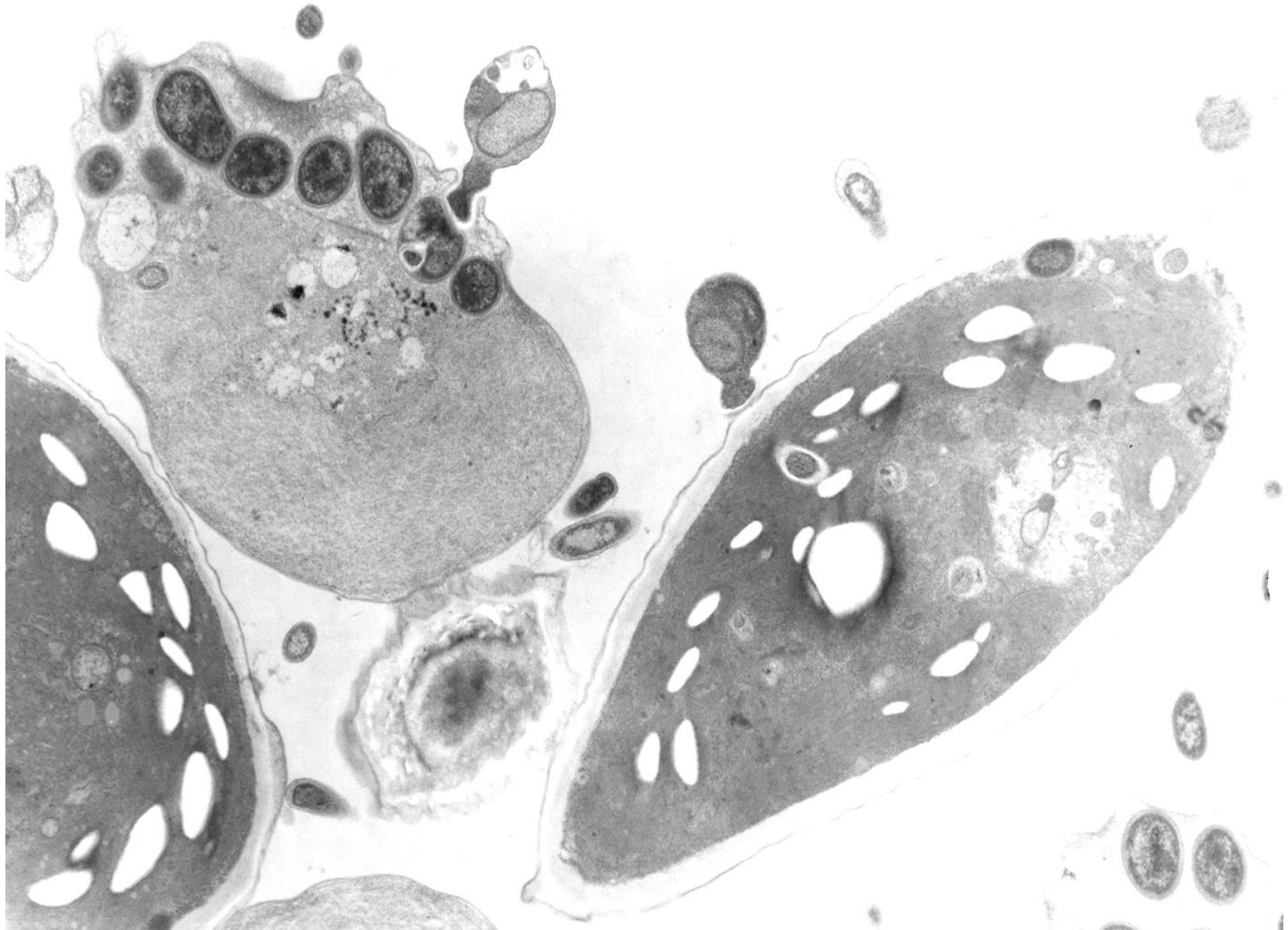
## Day 2: Aphelid and endobiotic prokaryote infection



Day 3 characterized by:

- continued progression of Aphelid infection;
- mitotic division of Aphelid parasite nucleus;
- aplanospore cleavage; no flagellar sections observed

## Day 3: typical infection

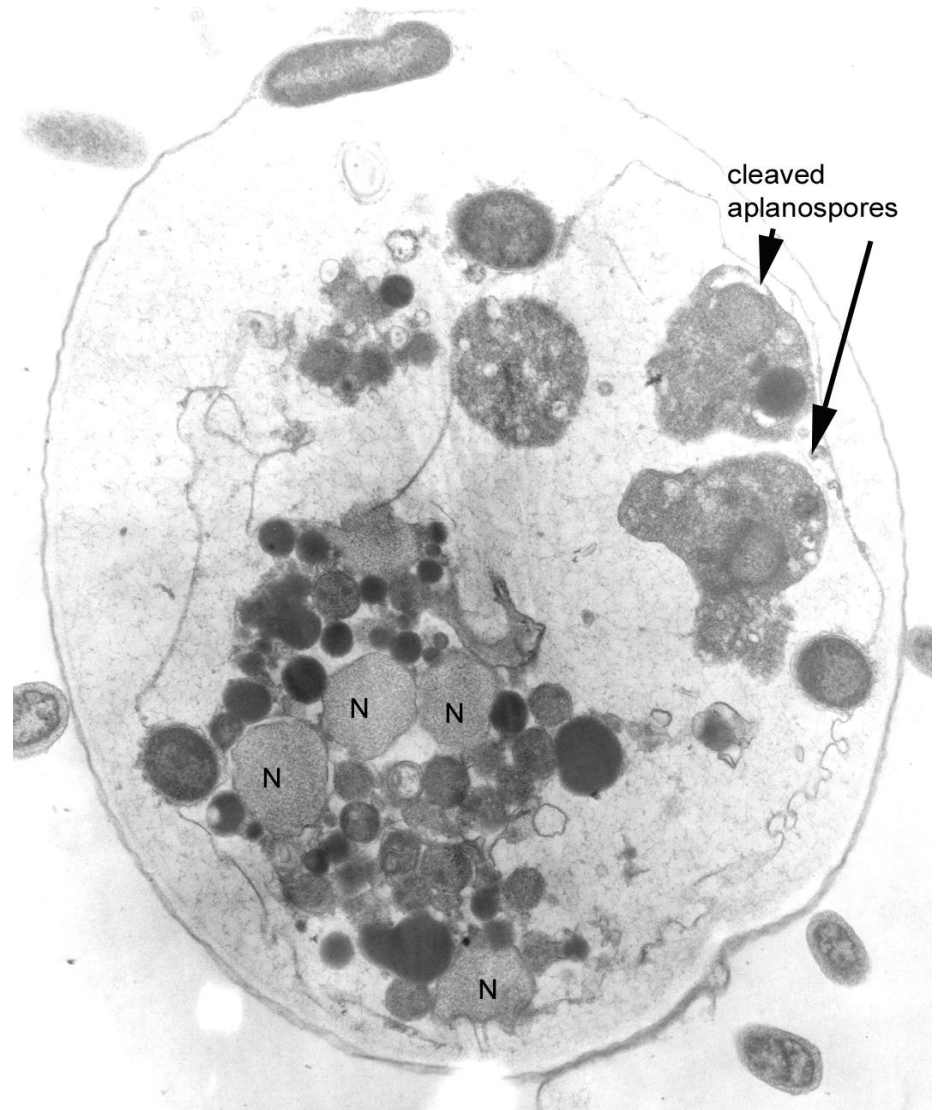
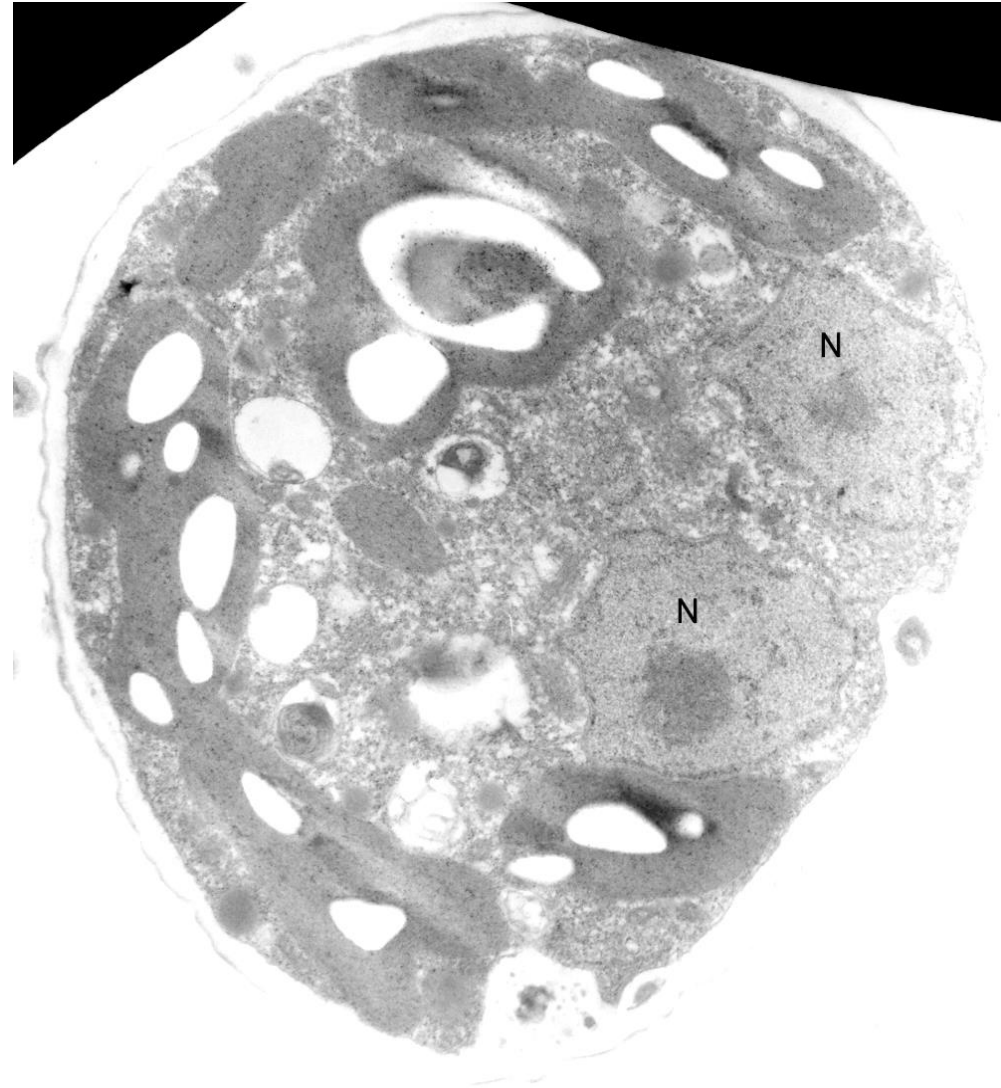


FD 95

## Day 3: mass endobiotic infection by prokaryote

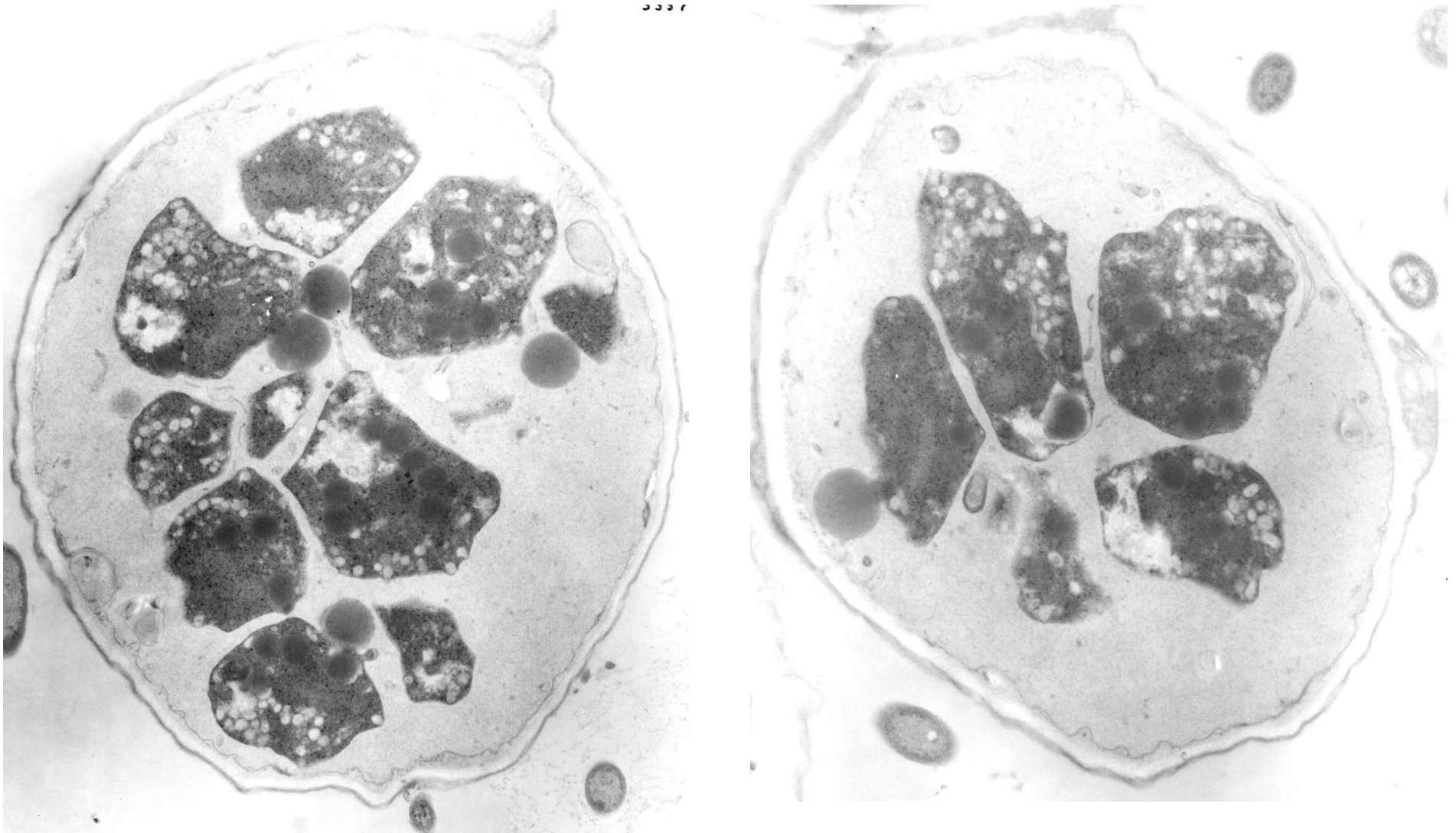


## Day 3: Aphelid mitosis





# Day 3: Aphelid aplanospore cleavage; no flagellar cross-sections/longitudinal sections evident

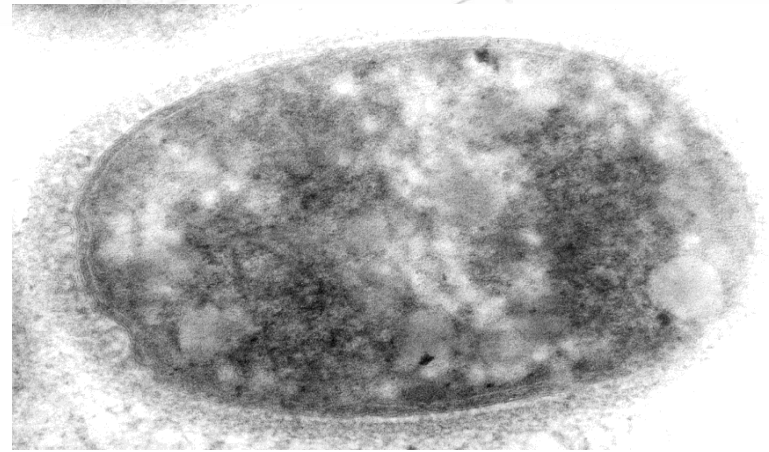
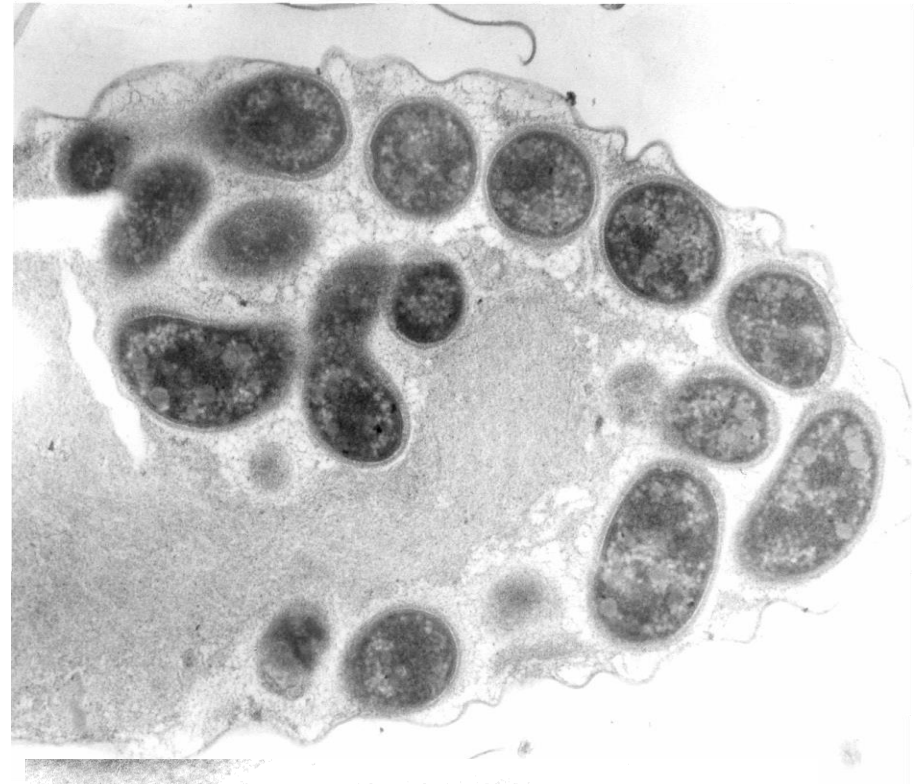
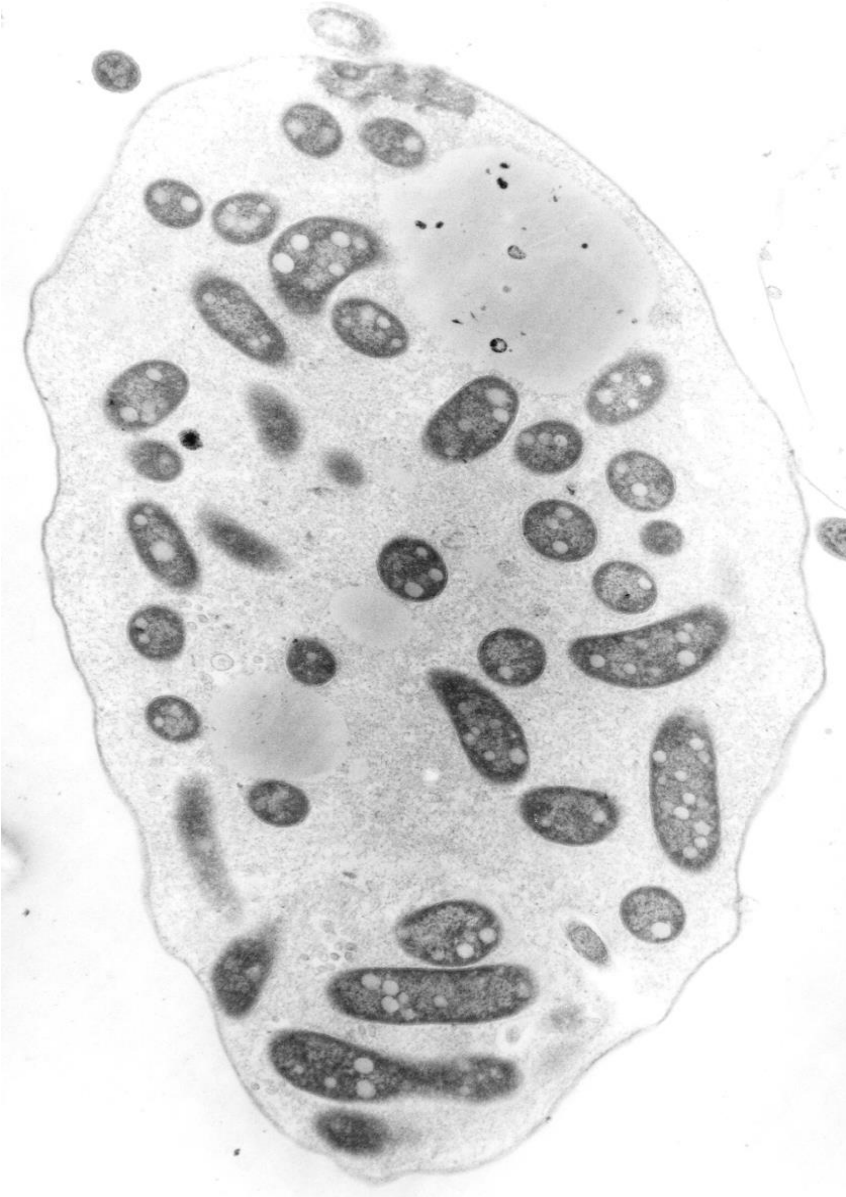




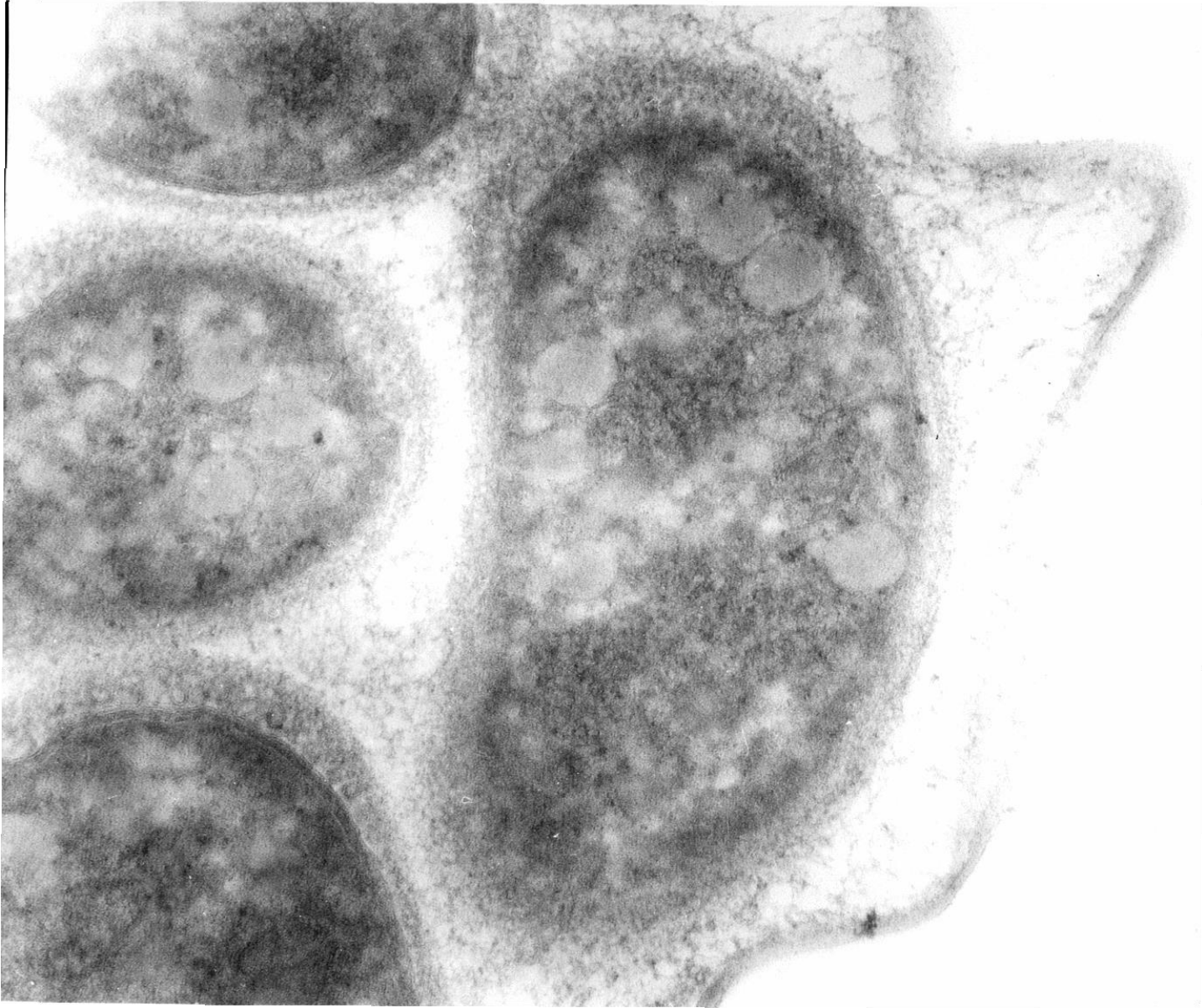
Day 4 characterized by:

- majority of algal cells with full-throttle infection by prokaryotic pest;
- some empty, senesced algal cells;
- motile aplanospores

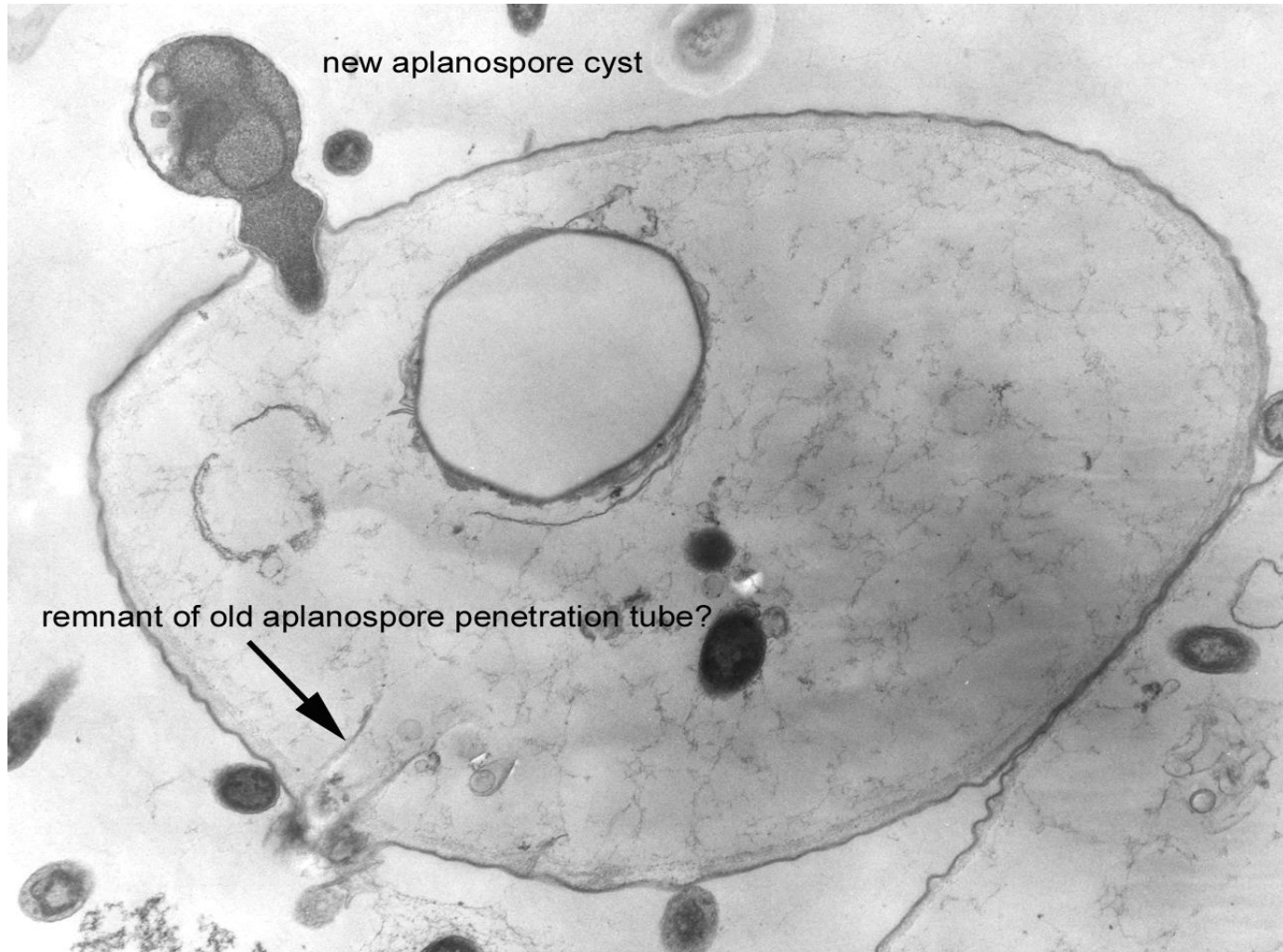
## Day 4: prokaryotic infection rampant



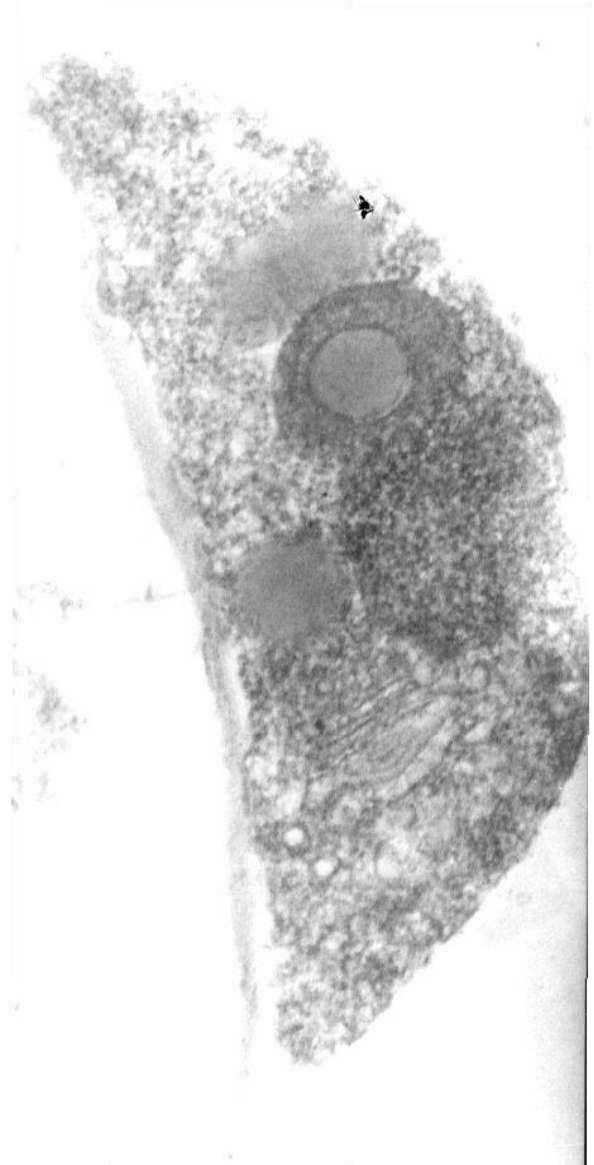
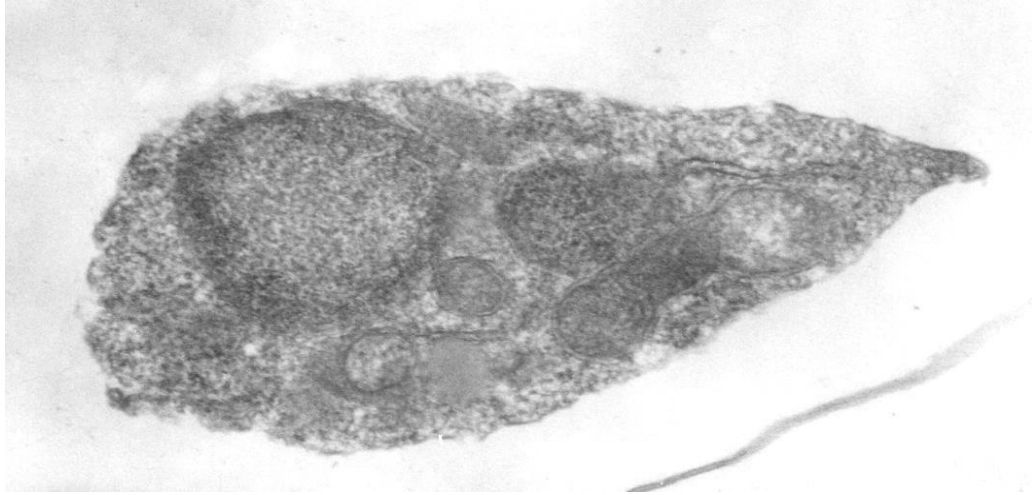
## Day 4: endobiotic prokaryote parasite



# Day 4: senesced algal cell with aplanospore cyst(s)



## Day 4: motile aplanospores



## Bacterial infection

- I think the bacterial component of this infection is secondary and opportunistic; when the alga gets hit with the Aphelid, the bacteria gets in for a free lunch.
- It might be interesting and informative to try to sequence the bacterium.

## FD 95 vs. Karpov X-5

RDNA sequence similarity:

18S: 99%

28S: 99.6%

ITS1-5.8S-ITS2: 95%

Ultrastructure:

FD 95: flagellum absent; pseudopodiate  
aplanospore

X-5: rudimentary flagellum present; non-  
pseudopodiate zoospore

## FD 95 vs. Karpov X-5

High genetic similarity suggests closely related organisms;

Ultrastructural dissimilarity suggests more distantly related organisms;

X-5 appears to represent an undescribed genus;

FD 95 is a typical *Amoeboaphelidium*, but is not *A. protococcarum*, because.....



## FD 95 vs. FD 01, *Amoeboaphelidium protococcarum* (Letcher et al. 2013)

RDNA sequence similarity:

18S: 65%

28S: 77%

ITS1-5.8S-ITS2:

Thus, FD 95 is probably a new species of *Amoeboaphelidium*, on *Scenedesmus* (as is *A. protococcarum*).

We do not have to address what Karpov X-5 is, only what FD 95 is. All this is indicative of “unrealized diversity” among the Aphelids.

# What is FD 95?

- Morphologically, FD 95 is an *Amoeboaphelidium*, quite similar (but not identical) to FD 01 *Amoeboaphelidium protococcarum*.
- Genetically, it is very distant from FD01 *A. protococcarum*.
- For now, I suggest simply referring to isolate FD 95 as *Amoeboaphelidium* sp.
- If we really want to find out what *Amoeboaphelidium* is, we should obtain strain X-1 *A. protococcarum* from ATCC, sequence it, and compare that with our FD01 and FD95. Any takers?