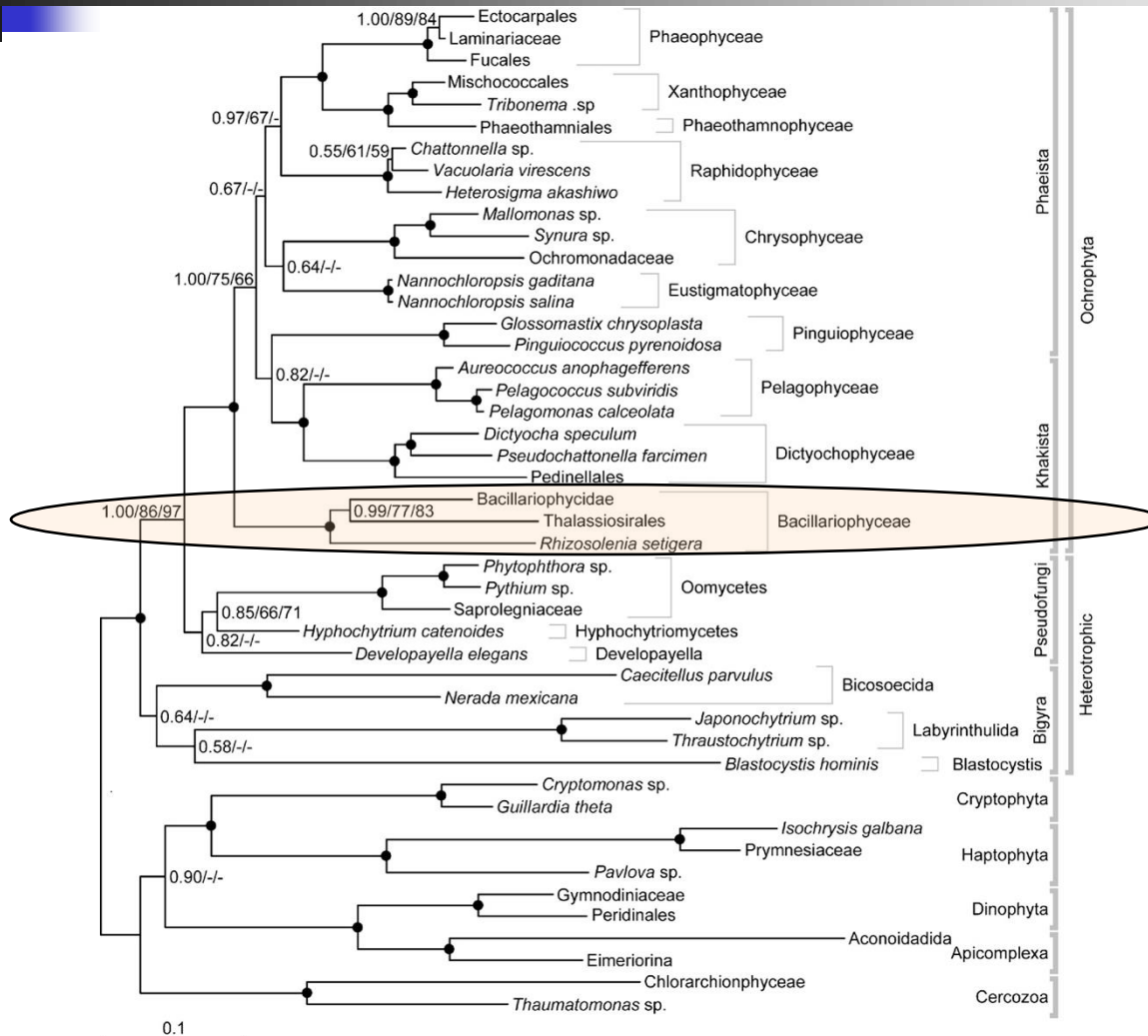
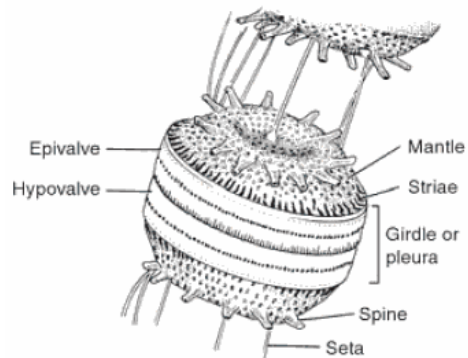


Lineage *Heterokonts*



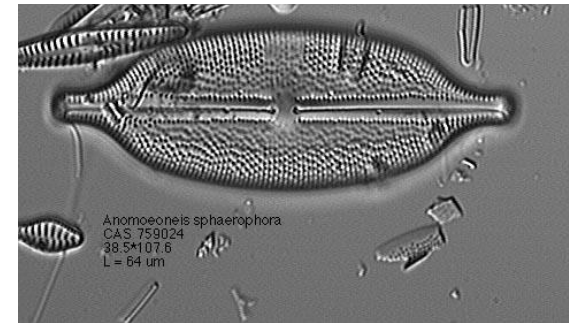
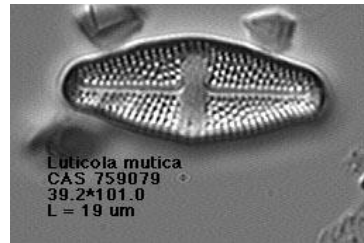
Diatoms (Bacillariophyceae)

- Microalgae with valves of pectinous material impregnated with silicates

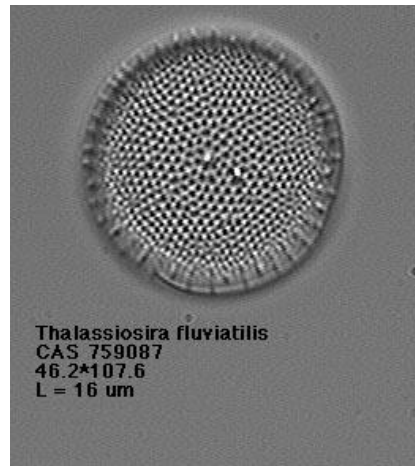


Diatoms (Bacillariophyceae)

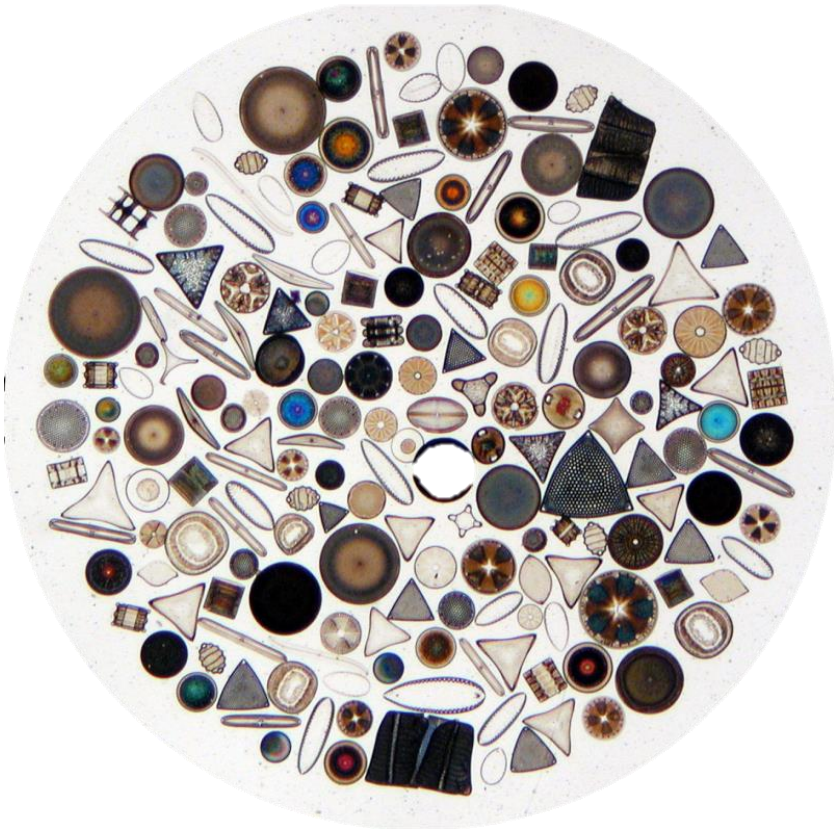
- Pennatae



- Centricae

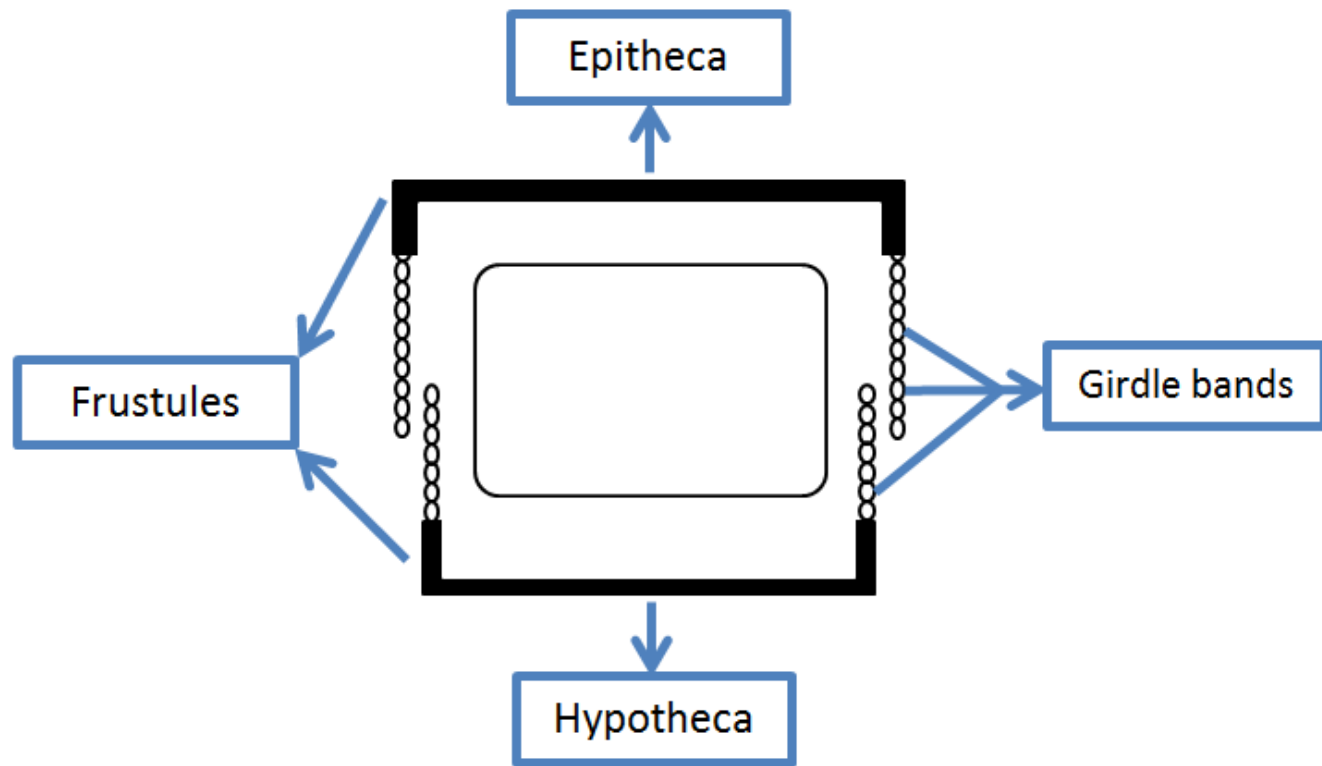


Diatoms (Bacillariophyceae)

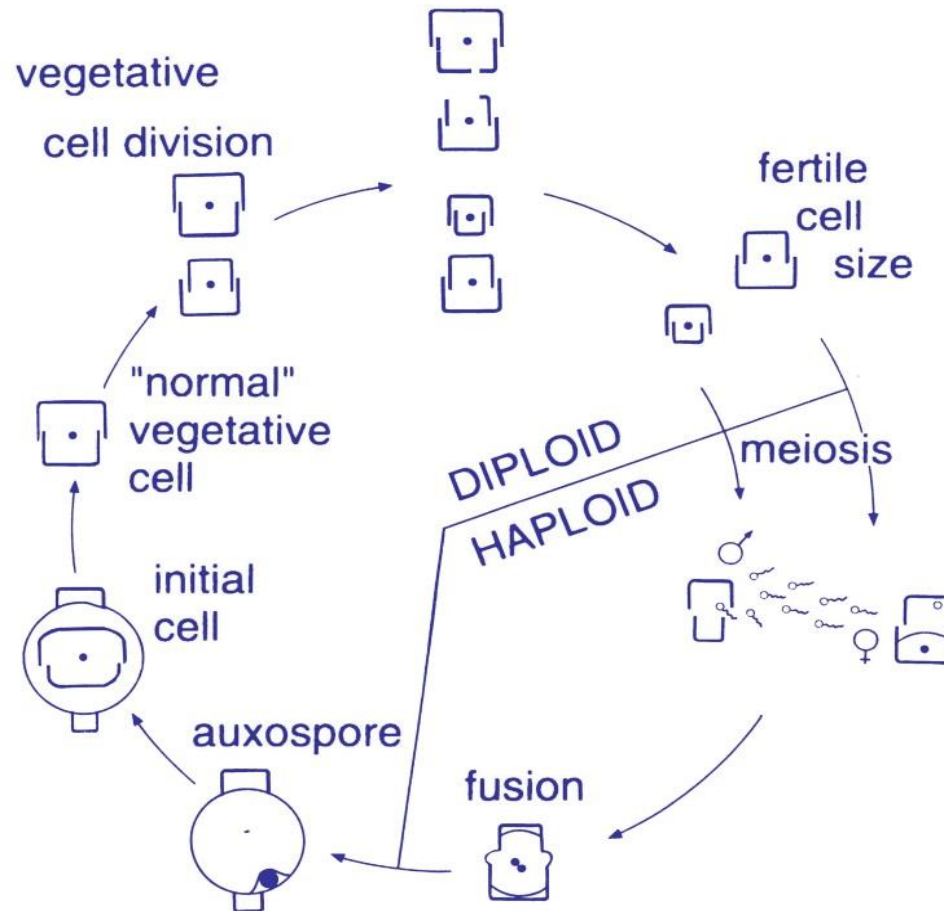


- Unicellular;
- Photoautotrophic, heterotrophic, symbionts;
- Exoskeleton with silicates;
- Essential in the marine trophic chain;
- Contribute to 45% of the primary ocean productivity and 20% of global productivity

Diatoms (Bacillariophyceae)



Diatoms (Bacillariophyceae)



Diatoms (Bacillariophyceae)

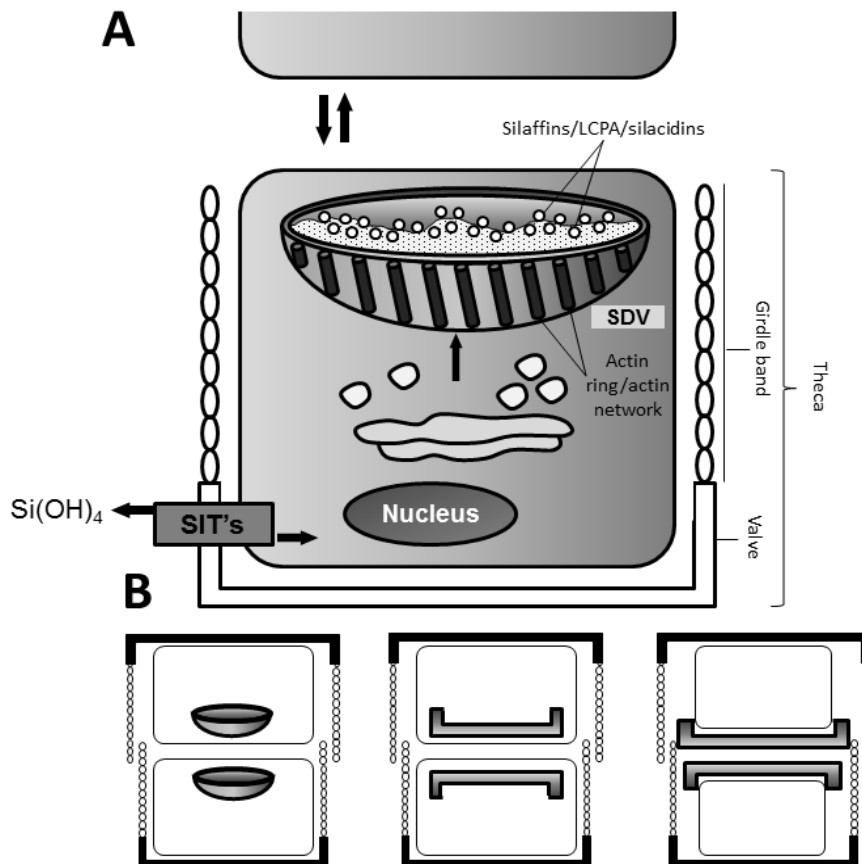
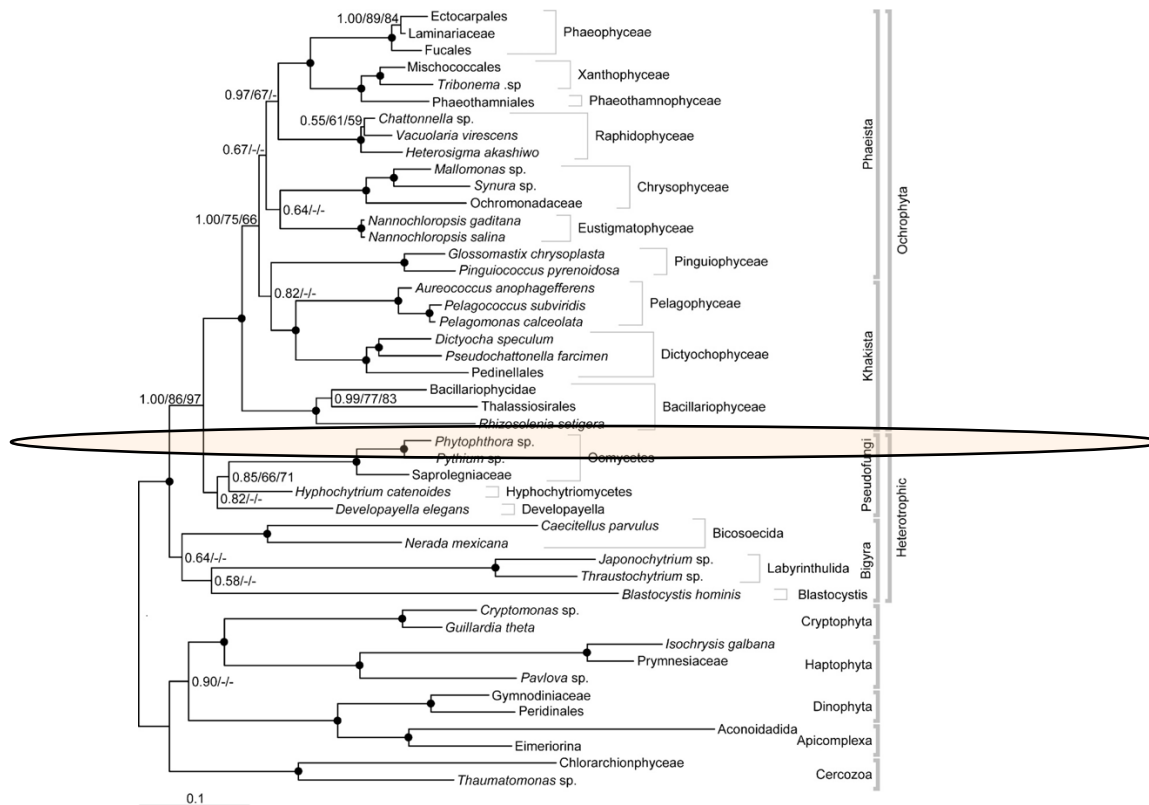


Fig.6 – Adapted representation of the frustules formation [8]. A) Internal illustration of a diatom, silica in-take via SIT proteins and polymerization in SDV. B) Frustule formation in SDV, fusion of SDV membrane with plasma membrane and exocytosis of newly formed exoskeleton.

Lineage *Heterokonts*



Riisberg et al. (2009)

Heterotrophic Heterokonts: Pseudofungi

Class *Oomycetes*

Phytophthora infestans

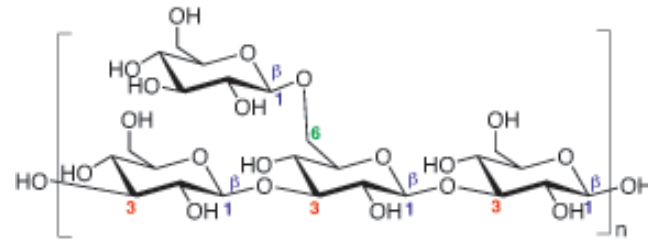


Mildew (lettuce)



Mildew (potato)

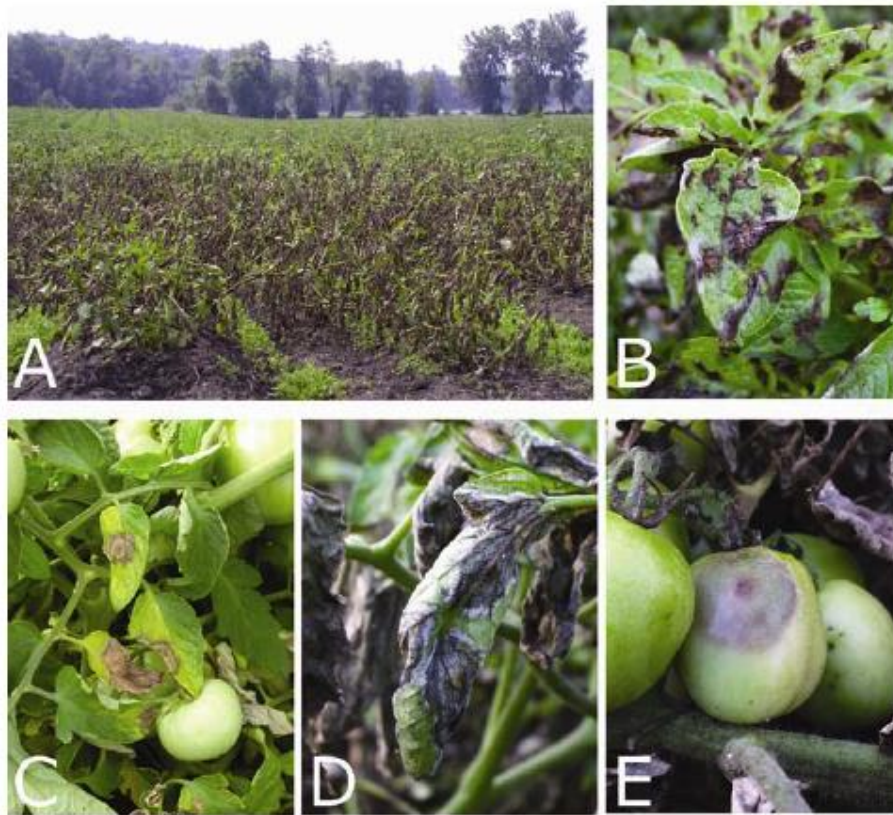
Phytophthora infestans



Laminarin (β -1,3-glucan with β -1,6 cross-links)

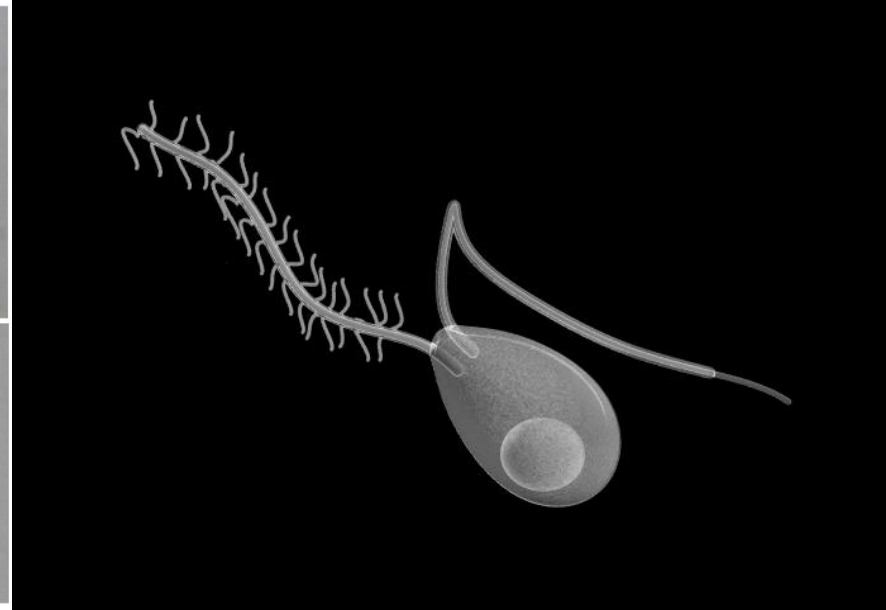
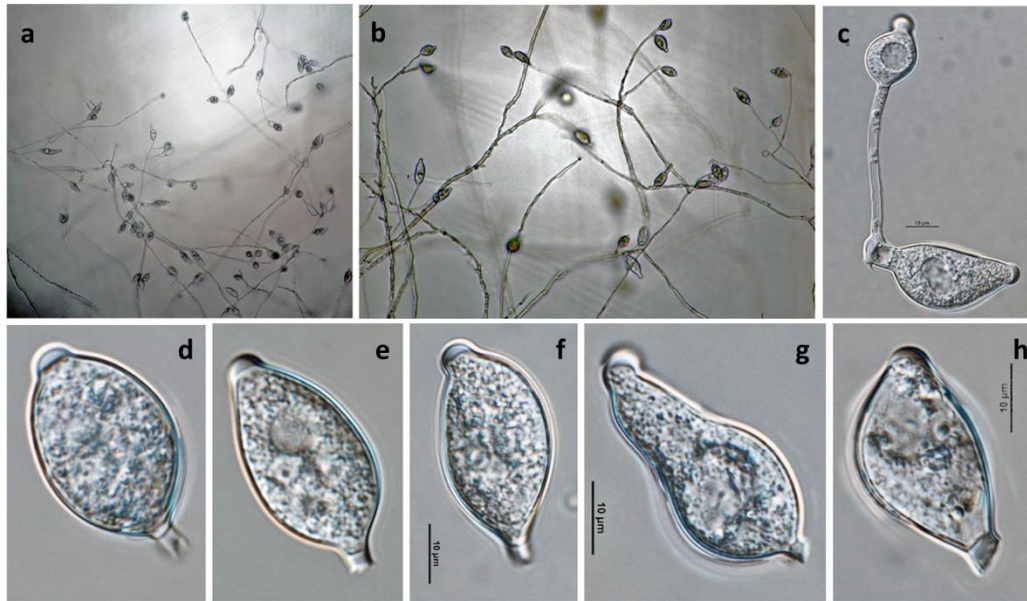
- Similar to fungi: hypha-like structures
- They are diploid: the true fungal hyphae are haploid
- Cell wall: essentially composed of cellulose instead of chitin
- Reserve polysaccharide: laminarin (β -1,3-glucan with β -1,6 linkages)

Phytophthora infestans





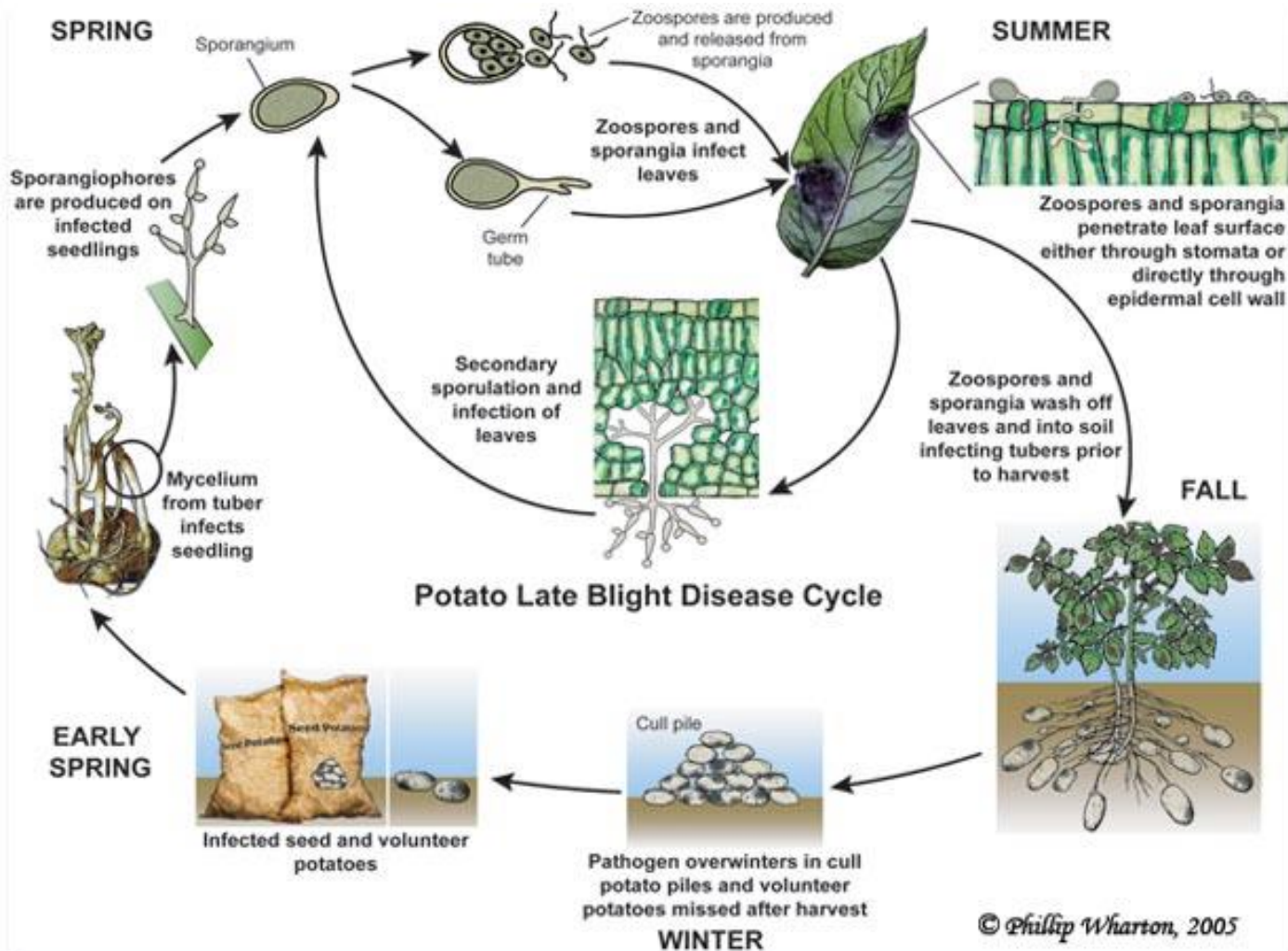
Phytophthora infestans



Sporangia in sporangiophores

Zoospores

Phytophthora infestans





Phytophthora infestans and fungi use similar infection strategies

Large-Scale Gene Discovery in the Oomycete *Phytophthora infestans* Reveals Likely Components of Phytopathogenicity Shared with True Fungi

Thomas A. Randall,¹ Rex A. Dwyer,¹ Edgar Huitema,² Katinka Beyer,³ Cristina Cvitanich,⁴ Hemant Kelkar,¹ Audrey M. V. Ah Fong,⁴ Krista Gates,¹ Samuel Roberts,⁴ Einat Yatzkan,¹ Thomas Gaffney,¹ Marcus Law,¹ Antonino Testa,² Trudy Torto-Alalibo,² Meng Zhang,⁵ Li Zheng,¹ Elisabeth Mueller,⁶ John Windass,⁶ Andres Binder,⁷ Paul R. J. Birch,⁸ Ulrich Gisi,⁷ Francine Govers,⁹ Neil A. Gow,¹⁰ Felix Mauch,¹¹ Pieter van West,¹⁰ Mark E. Waugh,¹² Jun Yu,⁵ Thomas Boller,³ Sophien Kamoun,² Stephen T. Lam,¹ and Howard S. Judelson⁴

To overview the gene content of the important pathogen *Phytophthora infestans*, large-scale cDNA and genomic sequencing was performed. A set of 75,757 high-quality expressed sequence tags (ESTs) from *P. infestans* was obtained from 20 cDNA libraries representing a broad range of growth conditions, stress responses, and developmental stages. These included libraries from *P. infestans*-potato and -tomato interactions, from which 963 pathogen ESTs were identified. To complement the ESTs, onefold coverage of the *P. infestans* genome was obtained and regions of coding potential identified. A unigene set of 18,256 sequences was derived from the EST and genomic data and characterized for potential functions, stage-specific patterns of expression, and codon bias. Cluster analysis of ESTs revealed

major differences between the expressed gene content of mycelial and spore-related stages, and affinities between some growth conditions. Comparisons with databases of fungal pathogenicity genes revealed conserved elements of pathogenicity, such as class III pectate lyases, despite the considerable evolutionary distance between oomycetes and fungi. Thirty-seven genes encoding components of flagella also were identified. Several genes not anticipated to occur in oomycetes were detected, including chitin synthases, phosphagen kinases, and a bacterial-type FtsZ cell-division protein. The sequence data described are available in a searchable public database.

Convergent evolution

