

Stramenopiles

	Название вида	GC	Среда обитания
Екатерина Гришина	<i>Aureococcus anophagefferens</i>	69.5	Водоемы, море, 20-25 °C
Полина Шайдурова	<i>Phytophthora sojae</i>	54.5	Паразит растений
Илья Герман	<i>Blastocystis hominis</i>	45	Human parasite
Ян Аникиев	<i>Nannochloropsis gaditana</i>	54	Водоемы, море, 24-26 °C
Михаил Сизов	<i>Tetraparma gracilis</i>	66	western North Pacific at 5 °C
Ульяна Ключникова	<i>Aphanomyces astaci</i>	50	Паразит у раков
Георгий Караваев	<i>Thalassiosira pseudonana</i>	47	Водоемы, море, 10-30 °C
Денис Михайлов	<i>Phytophthora nicotianae</i>	49.5	Паразит растений, 29-32 °C
Егор Попов	<i>Phaeodactylum tricornutum</i>	49	Водоёмы, море, 10-25 °C

Stramenopiles (Страменопилы)

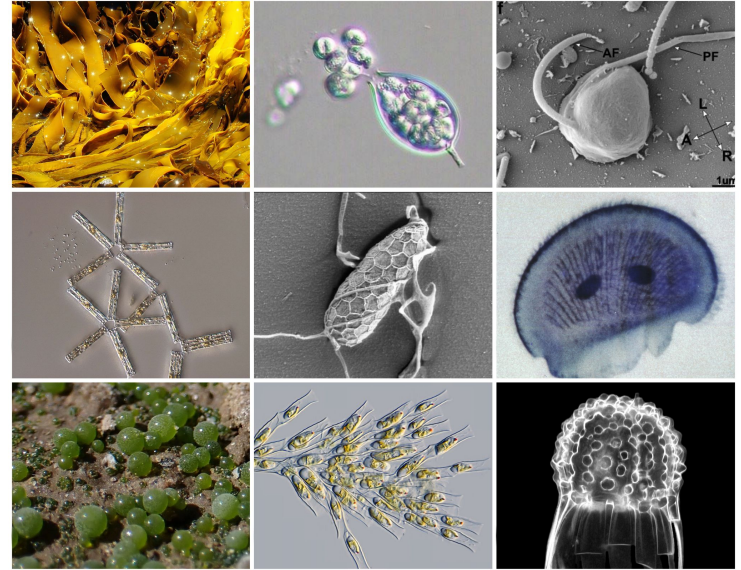
The **Stramenopiles**, also called **Heterokonts**, are a clade of organisms distinguished by the presence of stiff tripartite external hairs.

In most species, the hairs are attached to flagella, in some they are attached to other areas of the cellular surface, and in some they have been secondarily lost.

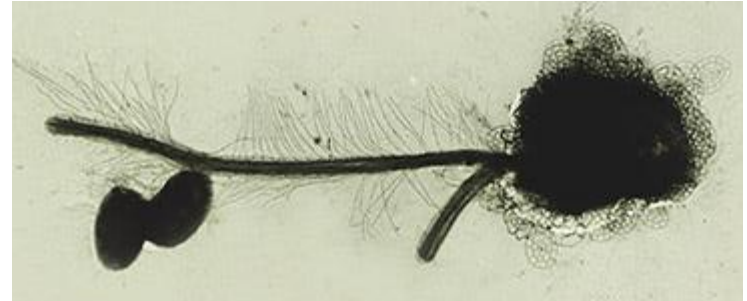
Stramenopiles are eukaryotes; most are single-celled, but some are multicellular including some large seaweeds, the brown algae.

Stramenopiles represent one of the three major clades in the SAR supergroup, along with Alveolata and Rhizaria.

Some stramenopiles are significant as autotrophs (diatoms) and as heterotrophs in natural ecosystems; others are parasitic.



Paraphysomonas butcheri.



Stramenopiles epigenetics

The *T. pseudonana* and the *P. tricornutum* genomes contain

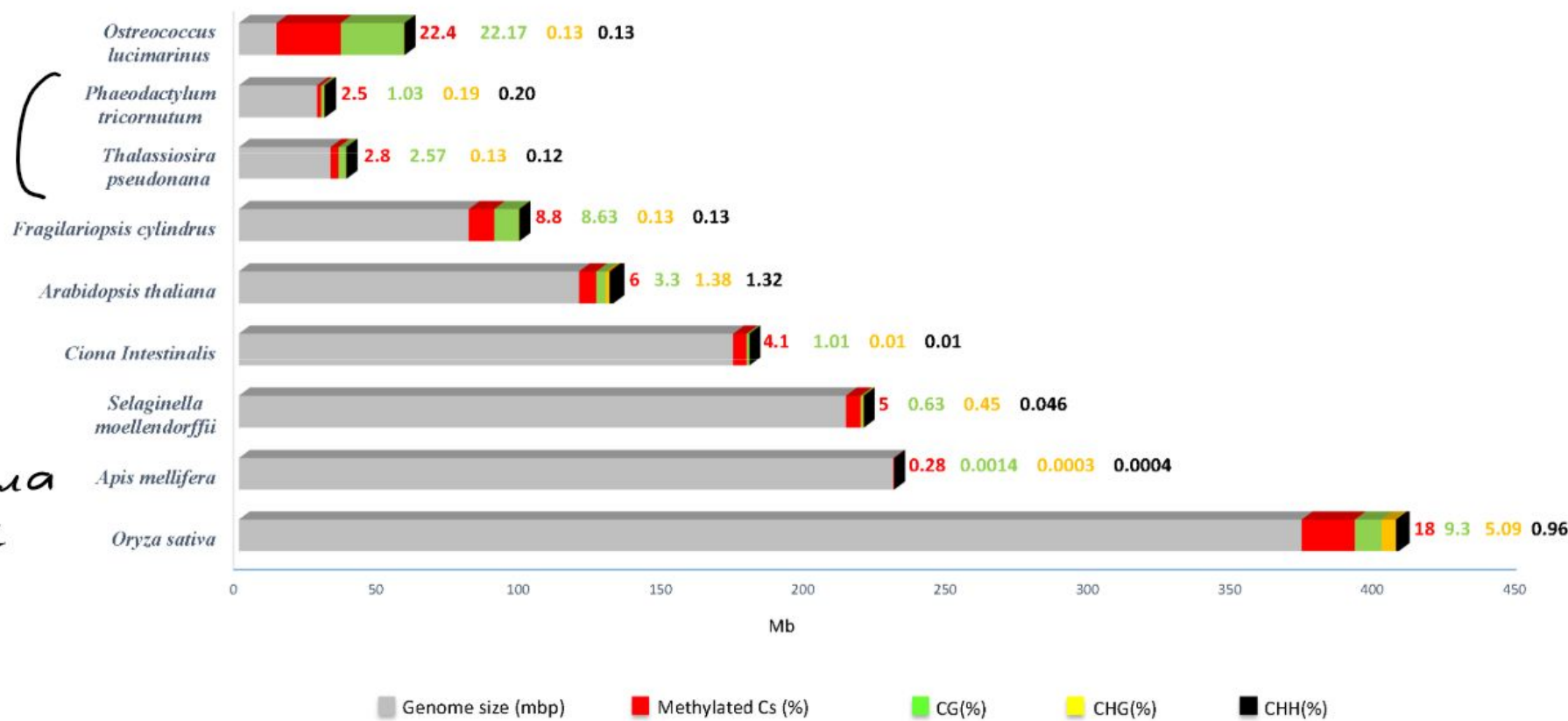
- four gene models with C5-MTase domain
- predicted proteins similar to members of the DNMT2, DNMT3, DNMT5 gene families
- DNMT1 homologs were not found in diatom genomes. Both diatom genomes contain predicted
- RNAi-based silencing system in *P. tricornutum*

Aureococcus anophagefferens and the green algae *Ostreococcus tauri*, *Ostreococcus lucimarinus*, *Micromonas pusilla* contain

- proteins similar to members of the DNMT5 family

In the *E. siliculosus*

- **no** putative DNA C5-MTase could be detected. Only a DNMT2 homolog was found therefore suggesting that this organism may lack cytosine methylation in nuclear DNA completely.
- a canonical Dicer-like protein as well as one AGO and two RdRP homologs



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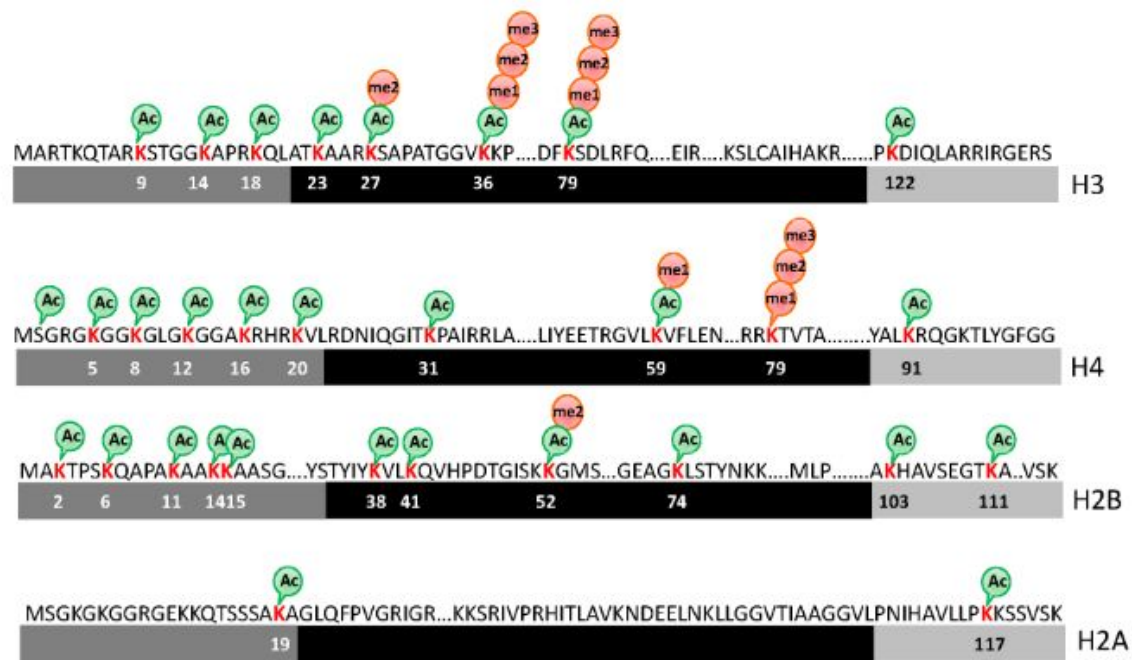


Figure 5. Histone PTMs in *T. pseudonana*. Diagram showing sites of PTMs of core and variant histones identified in *Thalassiosira pseudonana* by mass spectrometry. Amino acid residue number is indicated below the peptide sequence. Dark gray, black and light gray boxes indicate N-terminal, globular core and C-terminal domains, respectively. Acetylation and methylation are indicated in green and red respectively.

Aureococcus anophagefferens

(Катя)

Scaffold N50	1.4 Mb
GC percent	69.5
Genes	11522
Genome size	56.7 Mb
Pubmed publications	90



A. anophagefferens generates harmful algal blooms, known as ‘brown tides’ in estuaries both in South Africa and the eastern United States.

This genome contains:

- 1.5–3 times more LHC (light-harvesting complex) genes than other eukaryotic phytoplankton genomes that have been sequenced. The LHC proteins confer a higher ability to capture photons.
- genes suggesting an evolutionary adaptation to bacterial attack. Over 163 genes that are involved in the synthesis of putative compounds to deter competitors and predators, including ABC transporters, multi-drug ABC transporters and chloroquine transporters.

Phytophthora sojae

(Полина)

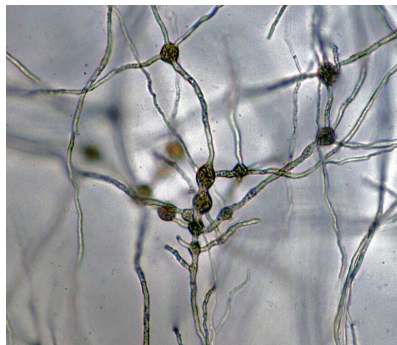
Scaffold N50	7.6 Mb
GC percent	54.5
Genes	28142
Genome size	82.6 Mb
Pubmed publications	6159

Phytophthora sojae is an oomycete and a soil-borne plant pathogen that causes stem and root rot of soybean. This is a prevalent disease in most soybean growing regions, and a major cause of crop loss.

Phytophthora sojae favor fields that are poorly drained or highly-susceptible to flooding. The optimum temperature for its disease development is above **16 °C**.

Qutob et al. show non-Mendelian interactions between naturally occurring *Phytophthora sojae* alleles that result in transgenerational gene silencing and gain of virulence in soybean plants.

Elevated levels of histone H3K27me3 were observed at the Avr1b locus in a naturally occurring Avr1b-silenced strain but not in an Avr1b-expressing strain, suggesting a **correlation between this epigenetic modification and silencing of Avr1b**.



Transgenerational gene silencing causes gain of virulence in a plant pathogen. Dinah Qutob, B. Patrick Chapman and Mark Gijzena.

Effector gene silencing mediated by histone methylation underpins host adaptation in an oomycete plant pathogen. Liyuan Wang, Han Chen, JiangJiang Li, Haidong Shu, Xiangxue Zhang, Yuanchao Wang, Brett M Tyler, Suomeng Dong

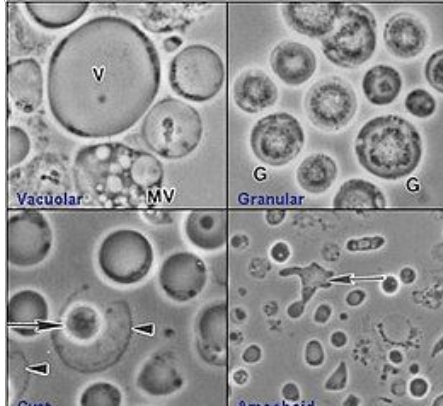
Blastocystis hominis

(Илья)

Scaffold N50	900.6 kb
GC percent	45
Genes	6020
Genome size	18.8 Mb
Pubmed publications	1102

Blastocystis is a genus of single-celled [parasites](#) belonging to the [Stramenopiles](#). There are several species, living in the [gastrointestinal tracts](#) of species as diverse as humans, farm animals, birds, rodents, reptiles, amphibians, fish, and cockroaches. *Blastocystis* has low host specificity, and many different species of *Blastocystis* can infect humans, and by current convention, any of these species would be identified as ***Blastocystis hominis***.

Blastocystis is one of the most common human parasites in the world and has a global distribution. It is the most common parasitic infection in the United States, where it infected approximately 23% of the total population during year 2000. In [less developed](#) areas, infection rates as high as 100% have been observed. Symptoms associated with the infection are diarrhea, constipation, nausea, abdominal cramps, bloating, excessive gas, and anal itching.

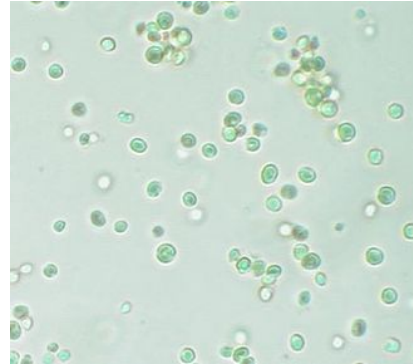


Nannochloropsis gaditana

(ЯН)

Nannochloropsis is a genus of [algae](#) comprising six known species. The [genus](#) in the current [taxonomic classification](#) was first termed by Hibberd (1981). The species have mostly been known from the marine environment but also occur in fresh and brackish water. All of the species are small, nonmotile spheres which do not express any distinct morphological features that can be distinguished by either [light](#) or [electron microscopy](#). The characterisation is mostly done by [rbcL gene](#) and [18S rRNA](#) sequence analysis.

Nannochloropsis is actually in use as [food additive](#) for human nutrition and it is also served at Restaurant "A Poniente" of [El Puerto de Santa María \(Cádiz, Spain\)](#) close to the natural environment where **Nannochloropsis gaditana** was first isolated and still grows. A 2020 study suggests it could be used for a highly performant, [sustainable fish-free feed for farmed fish](#).



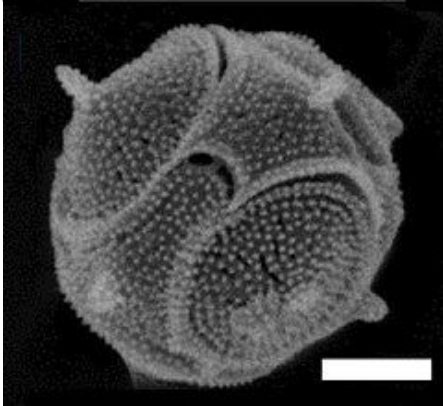
Scaffold N50	1052 kb
GC percent	54.47
Genes	3465
Genome size	30.7 Mb
Pubmed publications	184

Tetraparma gracilis

(Миша)

Scaffold N50	10.7 kb
GC percent	66
Genes	15310
Genome size	43.6 Mb
Pubmed publications	8886

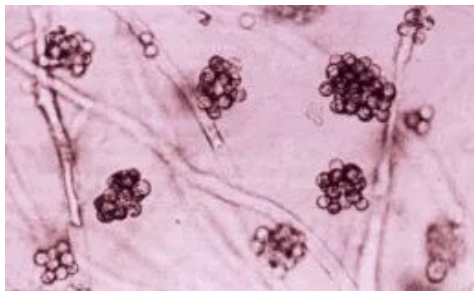
Tetraparma is a genus of unicellular algae in the family **Triparmaceae** in the order **Parmales**. They form siliceous plates on the cell surface that aid in identification. *Tetraparma* is distinguished by its possession of three shield plates that may have everted rims, three triradiate girdle plates, a triradiate dorsal plate with notched ends, and a large ventral plate. They are typically 2-5 μm in size and generally spherical or heart-shaped. They inhabit mainly in western North Pacific at 5 °C.



(Ульяна)

Aphanomyces astaci (чума раков)

Crayfish plague is a water mold that infects crayfish, most notably the European *Astacus* which dies within a few weeks of being infected.



victim



Scaffold N50	657.5 kb
GC percent	50
Genes	19 584
Genome size	75.8 Mb
Pubmed publications	90
Primary habitat	North America
Optimal temperature	4-25°C

Thalassiosira pseudonana

Подготовил Г. К.

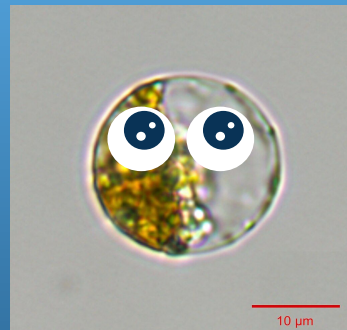
Этот вид диатомовых водорослей — первый фитопланктон, для которого сделали секвенирование полного генома!

Они имеют радиальную симметрию и разделены на две части, имеющие цилиндрическую форму. По периметру каждой половины расположены поры, иногда в центре также есть пора.

Во время созревания у клетки начинает формироваться тонкая пластинка по краям, придающая цилиндрическую форму клетке. Затем начинают формироваться окремнённые рёбрышки и обод клетки, а также формируются поры. Примечательно, что у клетки невысокий уровень окремнения, сконцентрированный в области рёбрышек, который делает водоросль прочной, но лёгкой! В процессе окремнения участвуют около 150 генов, а сам процесс регулируется с помощью мРНК.

Основное требование данного планктона к окружающей среде — высокий уровень содержания углекислого газа для его типа метаболизма.

Данный вид отличается невысоким уровнем метилирования (около 2% С-оснований). Около $\frac{2}{3}$ генома являются кодирующими белки.



Длина генома	32.4 Mb
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Количество генов	11771
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N50	2Mb
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GC	47%
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Публикаций на Pubmed	489
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Phytophthora nicotianae (Денис)

Phytophthora nicotianae has a broad host range comprising 255 **genera** from 90 **families**. Hosts include **tobacco**, **onion**, **tomato**, **ornamentals**, **cotton**, **pepper**, and **citrus** plants. This pathogen can cause **root rot**, **crown rot**, fruit rot, leaf infection, and stem infection.

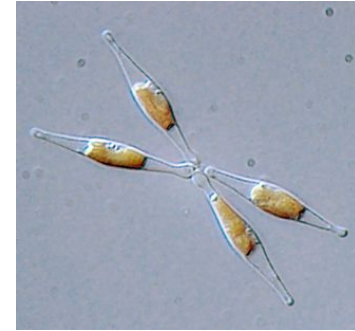
Scaffold N50	888.3 Kb
GC percent	49.5
Genes	23240
Genome size	82.4 Mb
Pubmed publications	1019

This pathogen thrives in temperatures ranging from 84–90 °F (29–32 °C). Disease is prominent in many agricultural productive regions and therefore is a major host to many warm environment crops. Black shank needs water for germination and movement. Saturated soil optimizes disease spread because water is used for dissemination of motile zoospores and sporangia.

Phaeodactylum tricornutum

Phaeodactylum tricornutum is a diatom, though does not have typical silicone shell. P. tricornutum can change cell form on different environment conditions. Commonly found in marine ecosystems, prefers temperature 20°C.

P. tricornutum and T. pseudonana genome sequencing revealed a long list of histone modifying and demodifying enzymes. P. tricornutum possesses 14 histone genes encoding 9 histone proteins that belong to the five known classes, histone H1, H3, H4, H2A and H2B. They are dispersed throughout five chromosomes with most in clusters of two to six genes as seen for most Eukaryotes.



(Erop)

Genome size	27.5 Mb
Scaffold N50	945 kb
GC%	49
Pubmed publications	139
Genes	10 398

References

<https://www.sciencedirect.com/topics/agricultural-and-biological-sciences/aureococcus-anophagefferens>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3145265/>

<https://www.nature.com/articles/s42003-023-05002-x>