of chlorophylls. A phototrophic euglenoid *Euglena gracilis* exhibited that chloroplasts underwent dismantled when incubated in the dark, leaving brown-colored granules. The brown granules were massive structures of membranes generated after degraded thylakoids. Chlorophylls are converted to CPEs in an early stage of dismantling, and proteins were removed during the dismantling. Macroautophagy of chloroplasts was not apparent, and the dismantling chloroplasts seem not to undergo acidification; instead, large acidic vacuoles commonly formed beside the dismantling chloroplasts. This would be comparable to digestion of chloroplasts by phycophagic euglenoids, where also accumulated CPEs. However, the digestive degradation proceeds within acidified phagosome hence being apparently non-homologous to the dismantlement in the phototrophs. We infer that the CPE-metabolism, which has not been reported for green algae, might have been inherited from ancestral heterotrophs to phototrophs, and is now adapted into a novel mechanism to dismantle the secondary chloroplasts.

**COMPARISON OF FRESH WATER CILIATED PROTIST COMMUNITIES FROM TWO LOCATIONS ALONG NAJAFGARH DRAIN, DELHI, INDIA, AND THEIR CORRELATION WITH PHYSIO-CHEMICAL PARAMETERS**

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There are 18 sewage drains traversing the National Capital Region (NCR) of Delhi, India, that flow into the River Yamuna. Najafgarh Drain is the largest with a catchment area of around 400 km². It picks up domestic and industrial wastes from 38 secondary drains coming from over 2/3 of the city. It carries a total flow of over 2100 million litres per day of which 30% is treated. Sewage treatment plants and effluent treatment plants discharging into the drain are inadequate and not working to full capacity. Ciliated protist communities were assessed (with appropriate morphological, morphometric and morphogenetic descriptions) at two locations along the drain: the mid-point of the drain (D1) and at the end of the drain before it empties into the river Yamuna (D2). Various physico-chemical parameters were also measured. Sampling was carried out weekly for 3 weeks during the pre-monsoon season. Compared to D1, substantially higher levels of free CO₂, chloride, phosphates and hardness were observed in D2 indicating the water here is more polluted. The ciliate communities at the two sites differed significantly. The results of detailed analyses, showing correlations between physico-chemical parameters (including heavy metals), and ciliate communities, will be presented. The significance of such data collected over a period of time along the drains, the river, and at water treatment plants, shall benefit ecologists in developing strategies to help mitigate river pollution as ciliates are known to clarify waste water and act as bio-indicators of specific pollutants.

**OLIGOTROPHIC LAGOONS OF THE SOUTH PACIFIC OCEAN ARE HOME TO A SURPRISING NUMBER OF NOVEL EUKARYOTIC MICROORGANISMS**

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The diversity of microbial eukaryotes was surveyed by metagenomic sequencing from tropical lagoon sites of the South Pacific, collected through the American Museum of Natural History (AMNH)’s Explore21 expedition to the Solomon Islands in September 2013. The sampled lagoons presented low nutrient concentrations typical of oligotrophic waters, but contained levels of chlorophyll α, a proxy for phytoplankton biomass, characteristic of meso- to eutrophic waters. Two 18S rDNA sites that include the V4 and V8-V9 regions were amplified from the total of eight lagoon samples and sequenced on the MiSeq system. After assembly, clustering at 97% similarity, and removal of singletons and chimeras, a total of 2,741 (V4) and 2,606 (V8-V9) operational taxonomic units (OTUs) were identified. Taxonomic annotation of these reads, including phylogeny, was based on a combination of automated pipeline and manual inspection. 18.4% (V4) and 13.8% (V8-V9) of the OTUs could not be assigned to any of the known eukaryotic groups. Of these, we focused on OTUs that were not divergent and possessed multiple sources of evidence for their existence. Phylogenetic analyses of these sequences revealed more than ten branches that
might represent new deeply-branching lineages of microbial eukaryotes, currently without any cultured representatives or morphological information.

THE PLASTID GENOMES OF THE CRYPTO-MONAD ALGAE REVEAL LINEAGE-SPECIFIC GENE LOSS
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Cryptophytes are an enigmatic group of photosynthetic unicellular eukaryotes with plastids derived from red alga through secondary endosymbiosis that contains four different genomes (host nuclear, mitochondrial, plastid, and nucleomorph) in a cell. They are comprised of brown-, red-, or blue/green photosynthetic species, as well as colorless nonphotosynthetic species. Although its complex evolutionary history, the origins of the host and endosymbiotic components in cryptophyte algae are poorly understood. Here, we report a comparative analysis of plastid genomes from six cryptophyte genera. Three newly determined cryptomonads plastid genomes of Chroomonas, Cryptomonas, and Storeatula share a number of features including gene arrangement and gene content with previously reported ones of Rhodomonas, Teleaulax and Guilhardia. The plastid genomes of cryptomonads reveal lineage-specific gene loss and intron insertion in eight significant gene syntenic positions. The chlL/chlN/chlB genes, which is the light-independent (dark active) protoclorophyllide oxidoreductase (LIPO), show the evolutionary changes across the cryptomonad lineages. We will discuss phylogenetic relationships of the red-derived lineages using 93 plastid genes showing a strong monophyletic group of the cryptophytes and haptophytes.

A NEW SOIL CILIATE, BIOJIMIA SOYAEN-SIS NOV. SPEC. (CILIOPHORA: UROSTYLI-DA) FROM SOUTH KOREA
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A new soil urostylid ciliate, Biojimia soyaensis nov. spec., was discovered from Soya Island, Incheon, South Korea. It is described the species based on live and stained specimen observation, and 18S ribosomal RNA gene sequence analyses. Biojimia soyaensis nov. spec. is characterized by the following features: body slender elongate and somewhat twisted; 170–200 µm × 40–50 µm body size in vivo; contractile vacuole located at middle of left cell margin; cortical granules present; 37–48 adoral membranelles; 3 frontal and 2 frontoterminal cirri present; III/2 and buccal cirrus present; midventral pairs only; pretransverse ventral and transverse cirri present; 1 left and 4 right marginal rows, including 3 compound rows; 5 complete dorsal kineties with additional 3 shortened kineties which are anteriorly of compound rows; 8–11 caudal cirri; 53–69 macronuclear nodules; and 2 or 3 micronuclei. Biojimia soyaensis nov. spec. is similar to B. terricola, but is distinguished by cortical granules (present vs. absent), number of caudal cirri (8–11 vs. 2–7) and number of dorsal bristle rows (8 vs. 6, on average). Biojimia muscorum is separated from B. terricola and B. soyaensis; sp. by midventral row present (vs. absent, midventral pairs only) which is an important key of the Bakuellidae. Furthermore, in phylogenetic tree, Biojimia soyaensis has widely distance from the bakuellids. Thus, we agree with Berger (2006) that the new genus needs to establish for B. muscorum. Phylogenetic tree suggests this new species is the most closely related to the genus Hemicyclistyla.

FIRST MARINE PHOTOSYNTHETIC TEST-TATE AMOEBA CONTAINING THE CHROMATOPHORE: PAULINELLA LONGICHROMATOPHORA
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Of 10 formally described species in the genus, all species are marine heterotrophic species, except for one freshwater species, Paulinella chromatophora which is the sole species to have plastids termed the “chromatophores” of a Synechococcus/Prochlorococcus-like cyanobacterial origin. Here, we report the first marine phototrophic species, Paulinella longichromatophora sp. nov., using light and electron microscopy and molecular data. This new species contains two blue-green U-shaped plastids reaching up to 40 µm in length. Further, the new Paulinella species is characterized by having five oral scales.