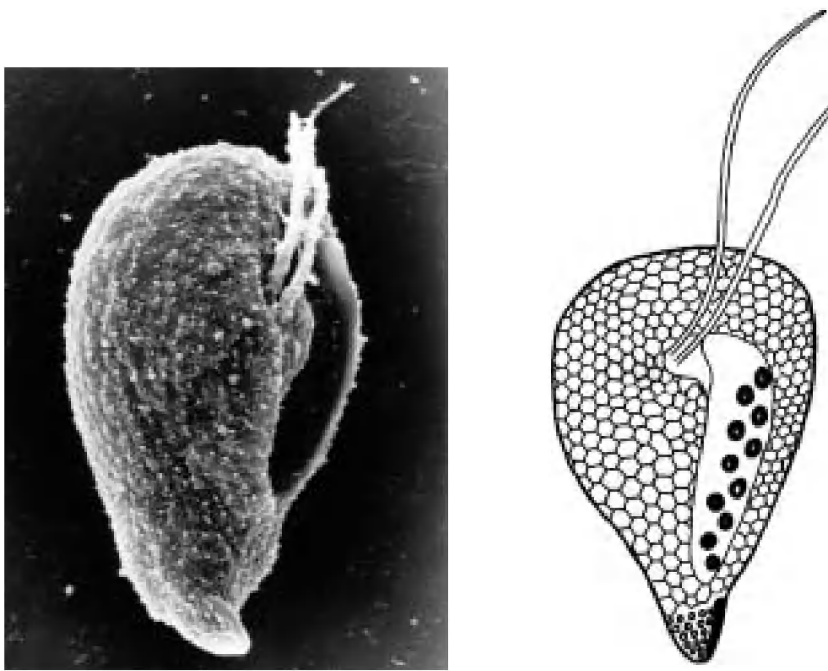


New Species

Cryptomonad flagellates

By Gianfranco Novarino

FREE-LIVING FLAGELLATE PROTISTS (flagellates for short) are arguably the most abundant and widespread eukaryotic microorganisms in the biosphere. As a group, flagellates are highly polyphyletic – they are defined simply by the possession of one or more flagella used for locomotion or feeding, or both. This “flagellate condition” has been a huge evolutionary success as shown by the presence of flagellate cells in the great majority of protistan, protozoological and algal phyla, as well as in many multicellular organisms – including ourselves.



Plagioselmis species inedita Novarino 2005 from the Mediterranean Sea.

Marine planktonic flagellates, especially the nanoplankton-sized (1-20µm) fraction, contribute significantly to marine primary production or carbon consumption, or both, and therefore play pivotal and intricate roles in the functioning of the marine ecosystem. Their diversity is far from having been described at both morphological and molecular levels. Improving our knowledge of nanoplankton diversity is a scientific imperative if we are to address such questions as the relationships between morphological, molecular, physio-ecological and geographical diversity, the occurrence of cryptic speciation, and ultimately the very nature and mechanisms of speciation and evolution in these organisms. These and other questions are being addressed in MarBEF within the MARPLAN Responsive Mode Project.

Cryptomonad flagellates, which are very abundant and widespread in the sea, are a moderately species-rich group (200 known species, possibly 300 to 1,200 species in total) on morphological grounds. Undescribed morphospecies of the genera *Cryptochloris*, *Hemiselmis* and *Plagioselmis* [see box] were found recently during ongoing investigations of nanoplankton diversity in the western Mediterranean. Despite being new, they have not been formally described, which may appear surprising but is becoming quite commonplace when dealing with protists. Previously undescribed species found in chemically-fixed water samples are often christened informally as species ineditae until they can be isolated in pure laboratory culture for further analysis, especially molecular sequencing.

The full names of these genera are *Cryptochloris* Schiller non Bentham non Shortridge & Carter, *Hemiselmis* Parke and *Plagioselmis* Butcher ex Novarino Lucas & Morrall.

Cryptomonad nomenclature is “ambiregna” because it falls under the dual jurisdiction of the Botanical and Zoological Codes. The long string of names constituting the authority reflects the ambiregna history of the generic name.

All species ineditae of cryptomonads were characterised using field-emission scanning electron microscopy. This revealed several ultrastructural features of taxonomic significance, especially the architecture of the cell surface (periplast) and the features of the vestibular region of the cell from which the flagella arise. *Plagioselmis* species inedita is particularly interesting owing to the superficial similarity to other cryptomonads – especially *Teleaulax* Hill – in terms of cell shape and pigmentation. It is a pear-shaped flagellate, slightly compressed along the perilateral axis, 6-9 x 4-5.5 x 3-4 µm in size, with equal or slightly unequal flagella inserted to the right-hand side of a broad ventral furrow reaching the median part of the cell. Its periplast allows it to be identified as a true member of its genus. Although the hexagonal plates on the cell body are very small (0.15-0.25µm) and barely perceptible, there is a non-plated periplast with a very short ventral band on the pointed cell posterior, as expected for a true member of *Plagioselmis*.

The Mediterranean species inedita brings the count of *Plagioselmis* morphospecies to five. The relationships between morphological, molecular, physio-ecological and geographical diversity within this genus are still unknown but these new discoveries add to the ongoing debate on the applicability of general biogeographical concepts to the protists.

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Genetic Diversity

Macrophytes as models

The emerging role of genetic diversity for ecosystem functioning

By Thorsten B.H. Reusch

DURING THE PAST decade, manipulative experiments have provided compelling evidence of the importance of biological diversity for ecosystem functioning and stability. Diversity at the species and functional-group level begets productivity, resistance and resilience in the face of disturbance and stability with respect to temporal fluctuations (overview in Loreau *et al*, 2002).

However, the emerging consensus is still incomplete. The majority of these studies have been performed in grassland communities or experimental micro- and mesocosms, while marine systems are clearly understudied. Moreover, a number of aquatic communities seem not to fall under the ‘species diversity is good’ consensus. What could be more uniform than endless meadows of reed, saltmarshes or seagrasses that are locally dominated by a canopy of a single species? Yet these macrophyte-based communities represent some of the most productive and stable shallow-water and estuarine ecosystems. Seagrasses in particular, a phylogenetically diverse group of 60 or so marine angiosperms, often form meadows that consist of only a few or even one species. Their low taxonomic diversity is in striking contrast to their ecological importance (Duarte, 2002). As foundation or ecosystem engineering species, seagrasses allow a rich invertebrate and fish community to thrive on otherwise barren sedimentary coastlines. Moreover, seagrass beds fix nutrients, stabilise the sediment and prevent coastal erosion. It has been estimated that the ecosystem services provided by macrophyte stands are among the highest for all ecosystems compared (Costanza *et al*, 1997).

The apparent uniformity of a seagrass canopy disappears when viewed through the eyes of molecular genetics. Modern molecular markers, in particular DNA microsatellites (see Box 1), tell a completely different tale, revealing hidden genotypic diversity resulting from the complex pattern of clonal reproduction of these plants (Fig 1, page 16). In many aquatic plants, including seagrasses, genetically identical shoots of a genotype proliferate in space and form clones of various sizes and spatial arrangement. The so-called ‘genets’ (clones) may comprise several thousands of morphological individuals, or ‘ramets’ that may be hundreds of years old.

Given striking differences in clonal diversity between seagrass populations on one hand, and the experimental evidence on the importance of species diversity on the other, marine ecologists have begun to address the role of genetic

diversity for ecosystem functioning. Recent experiments using the widespread seagrass species *Zostera marina* (eelgrass) indicate that genotypic (or clonal) diversity may replace the function of species diversity in ecosystems with few or a single foundation species. In an experiment in California by Hughes and Stachowicz (2004), mixtures of 1, 2, 4 and 8 eelgrass genotypes were planted into the intertidal zone of Bodega Bay. Diverse treatments colonised the area more rapidly, and recovered significantly faster, than monoculture plots after nearly destructive grazing by migrating Brant Geese (*Branta bernicla*). This effect, however, disappeared a few months after disturbance. In the southwestern Baltic (Germany), Reusch and colleagues combined six genotypes into diversity treatments of 1, 3 and 6 genotypes (Reusch *et al*, 2005). Their experiment coincided with a period of extreme water temperatures caused by the unparalleled heatwave that hit Europe in 2003 (Schär *et al*, 2004). These conditions can be viewed as a precursor for the predicted global warming in the coming decades. Water temperatures attained 25°C in the southwestern Baltic, leading to mortality among cold-temperate plant and animal species, including eelgrass. Similar to the response in the Californian experiment, the more diverse assemblages of seagrass genotypes showed faster recovery after the summer mortality. Moreover, there were more shoots, biomass and associated invertebrates in diverse plots at the end of the experiment. These findings should provide an additional motivation for conservation and restoration biology to protect and maintain genetic resources in addition to the diversity of species and functional groups.

Since Reusch and co-workers also transplanted all genotypes tested in mixtures as monocultures, the underlying mechanism of the positive biodiversity effect could be assessed (Reusch *et al*, 2005). Surprisingly, the enhancement of recovery and biomass at the end of the experiment were not due to a few dominant genotypes that happened to be the most resistant given the extraordinary conditions during the 2003 heatwave (the



Edge of an eelgrass (*Zostera marina*) bed in the southwestern Baltic on a sandy sediment in 3m depth.



Green crab (*Carcinus maenas*) feeding on juvenile blue mussels settling on eelgrass blades.



Mysiid shrimps (background) and isopod (*Idothea balthica*, white arrow) grazing on epiphytes of eelgrass leaves during a night dive.