

who had not been previously infected were almost twice as likely to develop HCV infection compared with people who had been infected in the past. Approximately 170 million people worldwide are chronically infected with HCV and many will develop liver cirrhosis or cancer. Although the use of injected drugs and unscreened blood transfusions are major methods of transmission, in developing countries there is also a risk of infection from using improperly sterilized tools for body piercing, tattooing, circumcision and other traditional practices. The source of 10% of acute cases of HCV infection in the United States is unknown. AV <http://www.who.int/emc/diseases/hepatiti/index.html>
<http://www.hopkinsmedicine.org>

Close relatives

Camelpox virus appears to be even closer to smallpox virus than originally thought, a finding that heightens concern about its

possible development and use as a biological weapon, particularly as Iraq is believed to be working on the virus. The central region of the genome of poxviruses contains genes essential for virus replication and thus does not vary much between species. Peripheral regions of the genome harbor genes controlling characteristics such as host range, infectivity and means of evading host immunity. Normally these parts of the genome show variation between species but camelpox virus has now been shown to have similarities to smallpox virus in these areas. Disturbingly, this implies that camelpox virus might already possess some of the genes required for human pathogenesis. CK <http://www.newscientist.com/news>

HIV and TB in Europe

HIV infection and tuberculosis (TB) are rising rapidly in Eastern Europe, placing the whole of Europe at risk of a major health crisis, according to Knut Ipsen,

president of the German Red Cross. Speaking at the April European Regional Red Cross and Red Crescent Conference in Berlin, Ipsen said that although Africa and Asia have the highest number of AIDS cases, Eastern Europe has the fastest growth rate, with 250 000 new cases in 2001. Approximately 30 000 people die each year from TB in Russia, which, in 2000, had a rate of 90.7 cases per 100 000 people, double the European average. Large numbers of economic migrants from the East could pose a major problem for the countries of Western Europe. Ipsen estimates there could be as many as 2 million deaths from HIV and TB across Europe in the coming years, unless preventive action is taken. CK <http://www.medscape.com/infectiousdiseaseshome>

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Letters

Are autotrophs less diverse than heterotrophs in marine picoplankton?

In a recent *Trends in Microbiology* review [1], Moreira and López-García highlighted the very large diversity that has recently been unveiled among marine protists, especially in the wake of several studies performed on oceanic picoplankton, that is, the organisms with an average size <2–3 μm [2–4]. This diversity is comparable to that now well established for bacteria following the pioneering work of Giovannoni *et al.* [5]. Surprisingly, although the biomass of autotrophic prokaryotes in the euphotic zone of the ocean is of the same order of magnitude as that of heterotrophic ones [6], their diversity is strikingly low. In fact, there are only four genera of marine cyanobacteria that are globally significant: *Prochlorococcus*, *Synechococcus*, *Trichodesmium* and the recently discovered N_2 -fixing *Synechocystis* [7]. To these, one could add two types of newly recognized facultative phototrophs of potential

significance, belonging respectively to the α - and γ -proteobacteria [8,9]. This contrasts with the puzzling diversity of marine heterotrophic bacteria observed within many groups such as the Proteobacteria, the *Cytophaga-Flavobacterium-Bacteroides* cluster or the Actinobacteria [10].

In the euphotic zone of oceanic waters, the abundance and biomass of pico- and nano-planktonic heterotrophic eukaryotes is commensurate with that of the autotrophic ones. However, analysis of published data and work in progress in the framework of the European program PICODIV reveals that the diversity of the former could be much wider than that of the latter, as observed for prokaryotes. In the equatorial Pacific at 75 m depth [4], the number of unique 18S rDNA sequences that could be attributed to heterotrophic organisms was almost twice as large as those from autotrophic organisms (Table 1). At a coastal site in the English Channel, we recovered only 21 autotrophic sequences among 145 different partial sequences obtained from seven different clone libraries (Table 1; Romari unpublished). A significant fraction of these sequences corresponded to previously described

genera belonging in particular to the Prasinophyceae, such as *Bathycoccus*, *Micromonas* or *Ostreococcus*. The low diversity of autotrophic eukaryotes at this coastal site was also supported by fluorescent *in situ* hybridization (FISH) data. Based on the analysis of seven samples taken throughout the summer, a probe targeting a single species, *Micromonas pusilla*, recognized between 36% and 63% of eukaryotic cells (Not, unpublished). By contrast, we recovered 108 sequences that could be linked to groups that are most likely heterotrophic, in particular to novel lineages within the stramenopiles and alveolates [1]. Moreover, within these groups, diversity is apparently high. For example, the average similarity among stramenopile sequences was only 83% compared with 90% among Prasinophyceae.

Why would the diversity of autotrophs be lower than that of heterotrophs? The diversity of heterotrophic prokaryotes can be explained by the fact that they are involved in the degradation of the numerous organic molecules produced in the marine environment, in particular as a result of photosynthesis by phytoplankton: each taxonomic entity is

Table 1. Diversity of photosynthetic vs non-photosynthetic eukaryotes in coastal and open ocean picoplankton clone libraries^a

Sequence affiliation	Coastal	Oceanic
Photosynthetic		
Chlorophyta	8	3
Cryptophyta ^b	6	0
Haptophyta	1	4
Stramenopiles (Eustigmatophyceae)	1	0
Stramenopiles (Pelagophyceae)	0	1
Stramenopiles (Dictyochophyceae)	0	1
Alveolates (Dinophyceae ^b)	5	3
Total	21	12
Non-photosynthetic		
Stramenopiles (Thraustochytrids)	2	0
Stramenopiles (<i>Cafeteria</i>)	1	0
Stramenopiles (unidentified)	23	5
Cercozoa	20	0
Alveolates group I	7	6
Alveolates group II (<i>Amoebophrya</i>)	32	6
Ciliophora (<i>Strombidium</i>)	2	0
Ciliophora (Choanoflagellates)	3	2
Ciliophora (others)	18	0
Acanthareans	0	2
Total	108	21
Others ^c	16	0

^aFor the coastal site (English Channel off Roscoff; Romari, unpublished), seven clone libraries of 18S rDNA were constructed at different times of the year and partial 500 bp sequences were obtained in a variable region (roughly at positions 528–1028). Open ocean data (full-length sequences) originate from a single clone library from a 75 m deep sample in the equatorial Pacific and are described in Moon-van der Staay *et al.* [4]. The table gives the number of different sequences (i.e. presenting <98% similarity) recovered from these libraries.

^bSome members of the Cryptophyta and Dinophyceae are non-photosynthetic and therefore the diversity of photosynthetic sequences might be overestimated.

^cIt is not known whether these sequences correspond to autotrophic or heterotrophic organisms.

probably more or less specialized for a given substrate. The niches available to autotrophs are probably much fewer and only a small number of taxa are adapted to given levels of light and nutrients. In the current concept of the microbial loop [11], heterotrophic pico- and nano-eukaryotes are considered to be mainly predators (often referred to as HFLAG or heterotrophic flagellates) feeding on bacteria, with little discrimination, except based on cell size [12]. According to this view, the diversity of heterotrophic eukaryotes should not be very high. We argue, in contrast, that the diversity of heterotrophic eukaryotes is a hint that they play complex roles in the microbial food web. Predation might be much more dependent on prey type than has been assumed until now and heterotrophic eukaryotes might also be involved in the degradation of organic molecules, a role solely attributed to bacteria in current models [13]. The latter hypothesis is supported by the higher diversity of heterotrophic eukaryotes in coastal waters (Table 1), where organic matter is more abundant and diverse.

Analyzing these complex interactions is absolutely necessary to understand the functioning of marine ecosystems and will require extensive use of molecular tools, such as FISH, coupled with techniques that allow the detection of the activity of these organisms, such as micro-autoradiography [14].

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Two different open reading frames named *slyA* in the *E. coli* sequence databases

It has been reported that the *Escherichia coli slyA* gene encodes a transcriptional activator protein that confers a hemolytic phenotype by activating expression of the cryptic hemolysin ClyA [1,2]. Homologs (SlyA/Hor/Rap/RovA) of this protein are found in several Enterobacteriaceae, where they play a role in pathogenesis, being involved in invasion and intracellular survival in host cells. Moreover, this protein is distantly related to a broad family of bacterial regulatory proteins that affect diverse functions crucial for bacterial survival, for example, microcin production, multiple antibiotic