Marine plankton support global biological and geochemical processes. Surveys of their biodiversity have hitherto been geographically restricted and have not accounted for the full range of plankton size. We assessed eukaryotic diversity from 334 size-fractionated photic-zone plankton communities collected across tropical and temperate oceans during the circumglobal *Tara* Oceans expedition. We analyzed 18S ribosomal RNA sequences across the intermediate plankton-size spectrum from the smallest unicellular eukaryotes (protists, >0.8 micrometers) to small animals of a few millimeters. Eukaryotic ribosomal diversity saturated at ~150,000 operational taxonomic units, about one-third of which could not be assigned to known eukaryotic groups. Diversity emerged at all taxonomic levels, both within the groups comprising the ~11,200 cataloged morphospecies of eukaryotic plankton and among many other deep-branching lineages of unappreciated importance in plankton ecology studies. Most eukaryotic plankton biodiversity belonged to heterotrophic protistan groups, particularly those known to be parasites or symbiotic hosts.

**A global metabarcoding approach**

To explore patterns of photic-zone eukaryotic plankton biodiversity, we generated ~766 million raw rDNA sequence reads from 334 plankton samples collected during the circumglobal *Tara* Oceans expedition (17). At each of 47 stations, plankton communities were sampled at two water-column depths corresponding to the main hydrographic structures of the photic zone: subsurface mixed-layer waters and the deep chlorophyll maximum (DCM) at the top of the thermocline. A low-shear, nonintrusive peristaltic pump and plankton nets of various mesh sizes were used on board *Tara* to sample and concentrate appropriate volumes of seawater to theoretically recover complete local eukaryotic biodiversity from four major organisational size fractions: piconanoplankton (0.8 to 5 μm), nanoplankton (5 to 20 μm), microplankton (20 to 180 μm), and mesoplankton (180 to 2000 μm) (see (22) for detailed *Tara* Oceans field sampling strategy and protocols).

We extracted total DNA from all samples, polymerase chain reaction (PCR)-amplified the hypervariable V9 region of the nuclear gene that encodes 18S rRNA (8), and generated an average of 1.73 ± 0.65 million sequence reads (paired-end Illumina) per sample (17). Strict bioinformatic quality control led to a final data set of 580 million reads, of which ~2.3 million were distinct,