

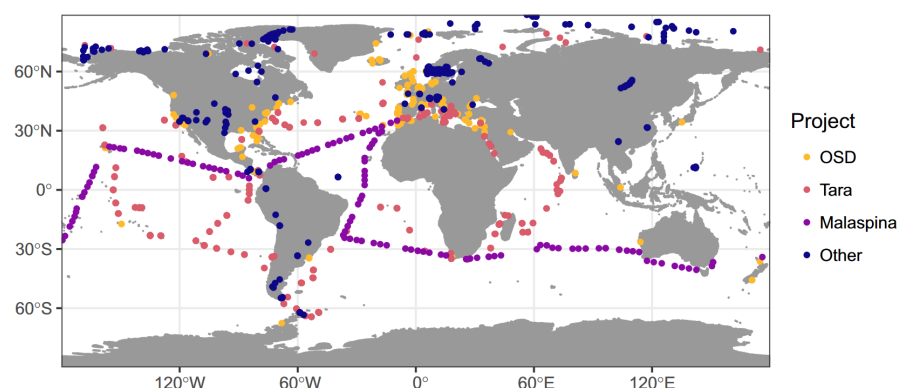
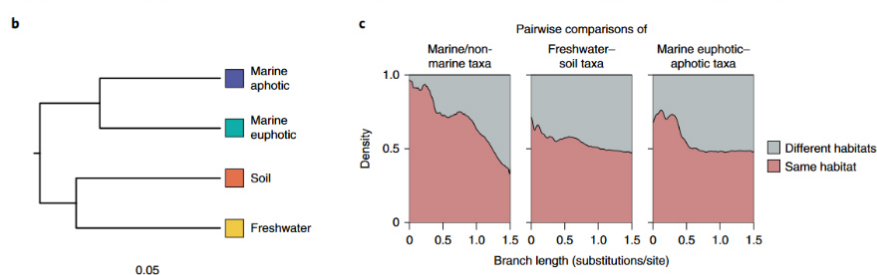
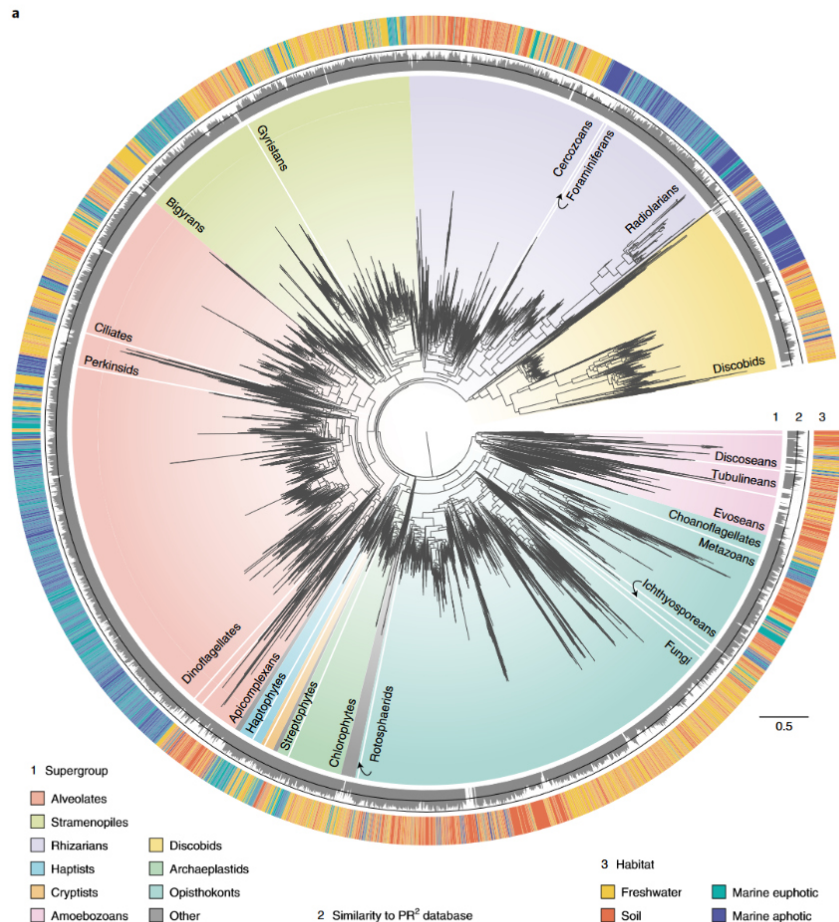


OPEN

Global patterns and rates of habitat transitions across the eukaryotic tree of life

Mahwash Jamy¹, Charlie Biver¹, Daniel Vault², Aleix Obiol³, Hongmei Jing⁴, Sari Peura^{5,6}, Ramon Massana³ and Fabien Burki^{1,6}✉

The successful colonization of new habitats has played a fundamental role during the evolution of life. Salinity is one of the strongest barriers for organisms to cross, which has resulted in the evolution of distinct marine and non-marine (including both freshwater and soil) communities. Although microbes represent by far the vast majority of eukaryote diversity, the role of the salt barrier in shaping the diversity across the eukaryotic tree is poorly known. Traditional views suggest rare and ancient marine/non-marine transitions but this view is being challenged by the discovery of several recently transitioned lineages. Here, we investigate habitat evolution across the tree of eukaryotes using a unique set of taxon-rich phylogenies inferred from a combination of long-read and short-read environmental metabarcoding data spanning the ribosomal DNA operon. Our results show that, overall, marine and non-marine microbial communities are phylogenetically distinct but transitions have occurred in both directions in almost all major eukaryotic lineages, with hundreds of transition events detected. Some groups have experienced relatively high rates of transitions, most notably fungi for which crossing the salt barrier has probably been an important aspect of their successful diversification. At the deepest phylogenetic levels, ancestral habitat reconstruction analyses suggest that eukaryotes may have first evolved in non-marine habitats and that the two largest known eukaryotic assemblages (TSAR and Amorphea) arose in different habitats. Overall, our findings indicate that the salt barrier has played an important role during eukaryote evolution and provide a global perspective on habitat transitions in this domain of life.



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RESOURCE ARTICLE

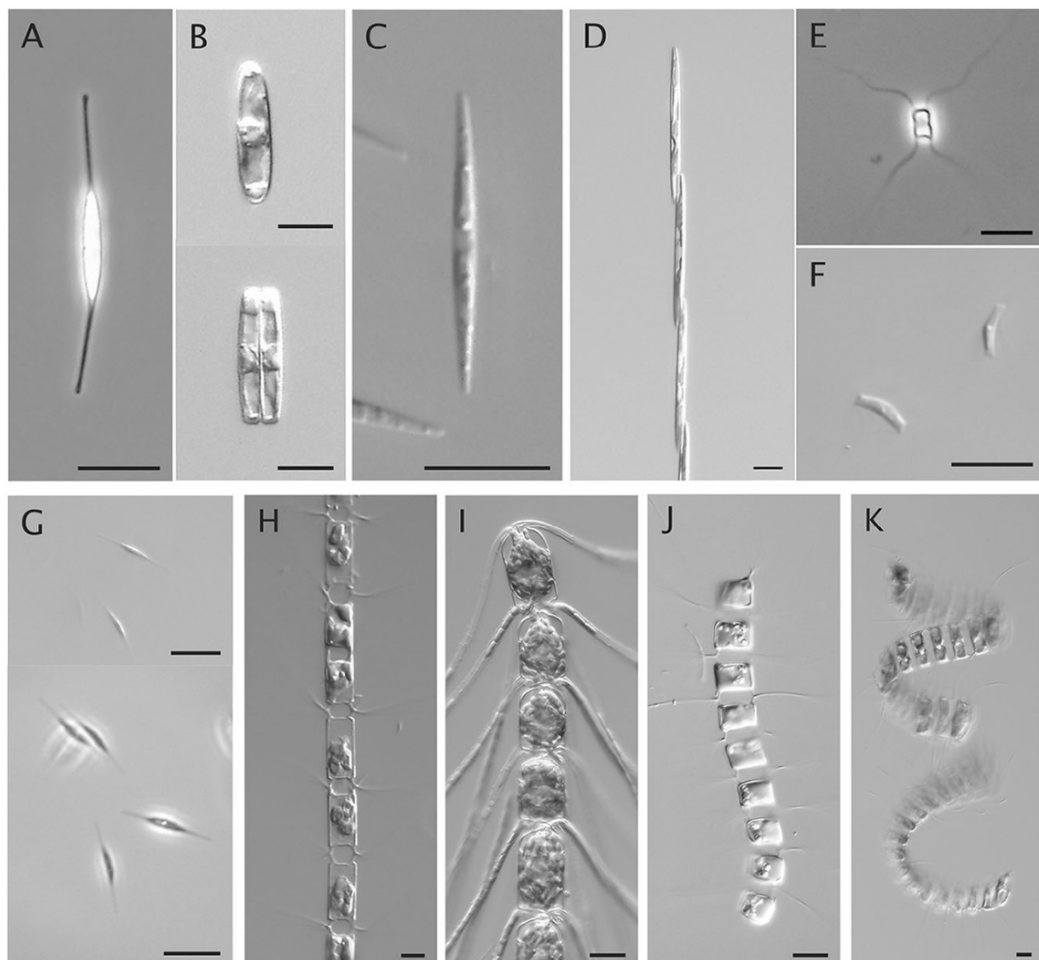
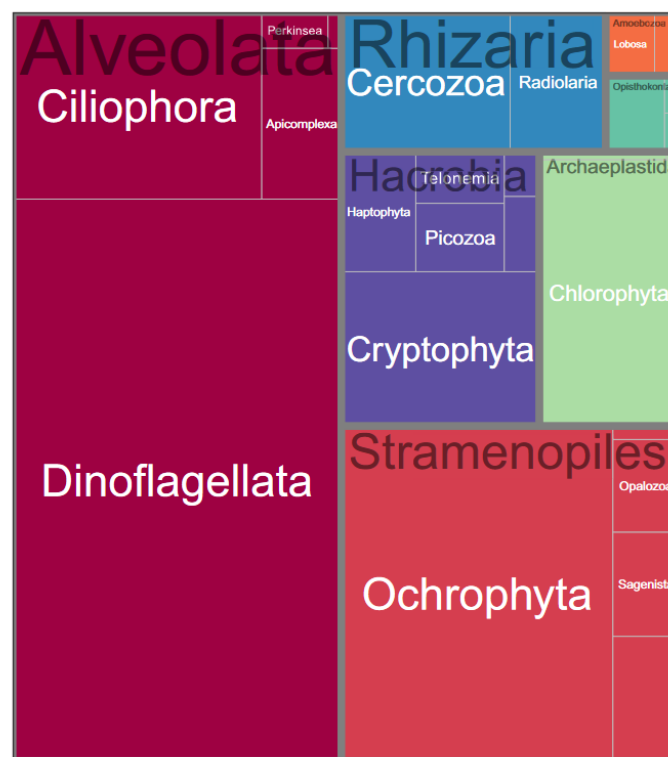
MOLECULAR ECOLOGY
RESOURCES WILEY

metaPR²: A database of eukaryotic 18S rRNA metabarcodes with an emphasis on protists

Daniel Vault¹ | Clarence Wei Hung Sim² | Denise Ong² | Bryan Teo² | Charlie Biver³ | Mahwash Jamy³ | Adriana Lopes dos Santos²¹UMR 7144, ECOMAP, CNRS, Sorbonne Université, Station Biologique de Roscoff, Roscoff, France²Asian School of the Environment, Nanyang Technological University, Singapore³Department of Organismal Biology (Systematic Biology), Uppsala University, Uppsala, Sweden

Abstract

In recent years, metabarcoding has become the method of choice for investigating the composition and assembly of microbial eukaryotic communities. The number of environmental data sets published has increased very rapidly. Although unprocessed sequence files are often publicly available, processed data, in particular clustered se-

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RESEARCH ARTICLE

Diversity and biogeography of planktonic diatoms in Svalbard fjords: The role of dispersal and Arctic endemism in phytoplankton community structuring

Luka Šupraha^{1,*}, Kerstin Klemm², Sandra Gran-Stadniczeňko¹, Cora Hörstmann², Daniel Vault³, Bente Edvardsen¹, and Uwe John^{2,4,*}

Understanding the processes that shape the community structure of Arctic phytoplankton is crucial for predicting responses of Arctic ecosystems to the ongoing ocean warming. In particular, little is known about the importance of phytoplankton dispersal by the North Atlantic Current and the prevalence and maintenance of Arctic endemism. We investigated the diversity and biogeography of diatoms from five Svalbard fjords and the Hausgarten observatory (Fram Strait) by combining diatom cultivation and 18S rRNA gene metabarcoding. In total, 50 diatom strains were isolated from the area during the HE492 cruise in August 2017. The strains were identified taxonomically using molecular and morphological approaches, and