



“Scientific Opportunities for a Global Algal Revolution”

Program and Book of Abstracts

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Microcoleus genomes in our dataset could be differentiated into 13 putative species, forming a speciation continuum. The morphology was relatively stable within the putative species but varied highly between species. Some species could be identified by distinct apomorphies or by a combination of morphological traits, while others are morphologically cryptic and could not be differentiated without the use of molecular data. We were able to match 6 species to a previously described unrevised species, including 2 species with available herbarium specimens, while 7 species are likely new species. This approach combining population genomic and morphological data with herbarium genomes allows to bridge the centuries of cyanobacterial taxonomy and peek into the true biodiversity of cyanobacteria.

Is structural colour in the red algal genus *Chondria* (Rhodomelaceae, Chondriales) taxonomically significant?

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Some species in the red algal genus *Chondria* (Ceramiales, Rhodomelaceae) have structural colour, the phenomenon created by nano-structures of a material splitting up light into the colours of the spectrum and causing iridescence. There are four species of *Chondria* recorded in Britain: *Chondria coerulescens* and *C. scintillans*, which are well-known for their strikingly iridescent fronds, *C. capillaris*, which has recently been seen with iridescent reproductive structures, and *C. dasyphylla* which has no structural colour. In order to see whether there is an evolutionary signal between those species with structural colour and those without, it is necessary to confirm their identity and determine phylogenetic relationships within *Chondria*. Systematic studies on the Chondriales tribe show the need for taxonomic clarification. Molecular phylogenies inferred from COI-5P and *rbcL* gene regions were constructed to map the structurally coloured species and understand where samples collected from Britain relate to those from other regions of the world. The resulting trees show that *C. scintillans* consists of more than one species and structural colour in *Chondria* appears to be spread throughout the genus but is not monophyletic. This has led to additional morphological analyses to complement the results. These results support previous studies pointing to the need for a revision of the Chondriales.

Assessing the molecular diversity of *Sargassum* (Phaeophyceae) in the NE Atlantic Ocean

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Sargassum plays a key role as habitat-forming species in benthic and pelagic ecosystems in tropical and subtropical regions, and has recently become a global environmental issue due to the societal impact of its massive blooms. With about 1000 taxa described and ca. 350 taxonomically accepted species, *Sargassum* represents almost one-sixth of Phaeophyceae and a prime example of a troublesome

taxonomy. Species identification has traditionally been hampered by the phenological plasticity exhibited in response to environmental conditions and life history. The advent of DNA phylogenies has challenged the taxa circumscription of this genus and have proven critical in delimiting the species. However, the molecular diversity of the Atlantic species of *Sargassum* remains poorly understood, and recently a few studies have shown a low genetic diversity between the species in the NW Atlantic. Here, we aim to assess the molecular diversity of *Sargassum* in the NE Atlantic Ocean using a multigene approach, combining markers commonly used in delineating species of this genus (*rbcLS*, *ITS2*, *cox3*, *mtsp*) and exploring new markers (*cox2*, *nad6*, *psbC*, *clpC*, *atpB*) to determine the phylogenetic relationships between the different morphospecies. Both single-gene and multigene phylogenies confirmed the low genetic variability and did not support distinct species in *Sargassum* sect. *Sargassum* in the N Atlantic benthic species, probably due to a recent colonization and radiation of this basin. These findings contrast with the morphological and ecological diversity of *Sargassum* in the Atlantic, and showcase the need for further analyses, including population genetics and the use of high-throughput DNA technologies.

KEYNOTE

The future challenges of seaweed systematics

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With an estimate of 9,600 described extant species, seaweeds are a diverse and taxonomically challenging group of eukaryotes. Seaweed systematics has come a long way, and represents a vast body of work that has accumulated over the past two and a half centuries. Advances in seaweed taxonomy have often been accompanied by technological or analytical progress, including improved microscopy and culture techniques. Unquestionably, the main revolution in recent decades has come with the application of molecular data, which has profoundly reshaped our understanding of algal diversity and relationships. However, this progress has not been uniform geographically. New methods have also created taxonomic challenges, such as how to deal with cryptic diversity, non-monophyly, and old taxon names. The field of seaweed systematics is transitioning into the genomic era, which will provide further insights into diversity and classification. A second ongoing revolution comes with digital access to collections. Herbarium specimens have long been the cornerstone of taxonomic research. Their digitization is increasing access and is transforming them into new dynamic digital research tools. Digital collections likely will be targeted by machine learning for automated species discovery and delimitation. Together with other digital sources such as literature and DNA sequences, Linked Open Data will further revolutionize the way taxonomic data is managed, shared, and integrated.

ORALS

On the Application of European Binomials for Western Atlantic Marine Macroalgae by 19th Century Taxonomists

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