

ABSTRACTS

SYMPOSIA TALKS

PROGRESS REPORT OF REDTOL: THE RED ALGAL TREE OF LIFE

Yoon, H. S.

Sungkyunkwan University, Republic Of Korea,
hsyoon2011@skku.edu

Bhattacharya, D.

Rutgers University, USA,
bhattacharya@aesop.rutgers.edu

Boo, S. M.

Chungnam National University, Republic Of Korea,
sboo@cnu.ac.kr

Fredericq, S.

University of Louisiana at Lafayette, USA,
slf9209@louisiana.edu

Hommersand, M.

University of North Carolina, USA,
hommersand@bio.unc.edu

Vis, M.

Ohio University, USA, vis-chia@ohio.edu

Lopez-Bautista, J.

University of Alabama, USA, jlopez@ua.edu

Saunders, G.

University of New Brunswick, Canada, gws@unb.ca

Red algae (Rhodophyta) are important aquatic primary producers that are one of the most anciently diverged eukaryotic phyla. The red algal plastid is widespread in the Tree of Life (ToL) among photosynthetic chromalveolates. In spite of its obvious importance, the Rhodophyta is under-studied. To fill this gap in eukaryote phylogeny, we assembled a research team of eight red algal taxonomy and genomics experts to address fundamental questions in red algal evolution and their place in the ToL. Since 2009, the RedToL team has made significant progress in: 1) generating a multi-gene phylogeny using eight gene markers from 500 red algal species, and 2) generating genome and transcriptome data from 16 key taxa that represent the phylogenetic (e.g., class- and order-level) breadth of red algae. Here we will introduce the aims and strategies of RedToL with highlights of recent research results.

GENOME-WIDE TRANSCRIPTOMICS OF PORPHYRA

Stiller, J. W.

East Carolina University, USA, stillerj@ecu.edu

This presentation provides an overview of collaborative analyses carried out by researchers from the *Porphyra* Genome Project through the Joint Genomics

Institute, and the National Science Foundation sponsored *Porphyra*/Algal Genomics Research Collaboration Network, on a large expressed sequence tag (EST) data set from two closely related species of *Porphyra* (Bangiales, Rhodophyta). Approximately 4.7 million EST reads were assembled into 36,276 and 68,506 contigs for *Porphyra umbilicalis* and *P. purpurea*, respectively. About 20% of these contigs are inferred to encode proteins of known function, and these have been the subject of comprehensive investigations of various protein families and metabolic pathways. Comparative bioinformatics indicate that 482 contigs encode membrane transporters, most of which can be assigned to one of 57 distinct transporter families. These and other sequences suggest a complex history, including evidence for vertical descent, endosymbiotic gene transfer and associations that are not easily explained by current phylogenetic models. Paralogs of major developmental (MADS-box and Homeodomain) gene families are present, and several exhibit differential expression between the *Porphyra* blade (gametophyte) and conchocelis (sporophyte); however, there is no evidence that these or other key developmental families have expanded substantially in the transition from unicellular to multicellular forms in red algae. Most expected genes for histones and ribosomal proteins also were identified and, as with developmental regulators, some show evidence for differential regulation between the life history stages. These and other major findings will be presented. Overall, the EST data provide novel insights into *Porphyra* and red algal biology, and point to exciting new directions for further experimental research.

RECENT ADVANCES IN THE CALLIARTHRON GENOME: CLIMATE RESPONSES AND CELL WALL EVOLUTION

Chan, C. X.

The University of Queensland, Institute for Molecular Bioscience, and ARC Centre of Excellence in Bioinformatics, Brisbane, Australia

Martone, P. T.

Department of Botany, University of British Columbia, Vancouver, Canada

Corallines are a distinct group of calcifying red algae that are important ecological components of marine communities around the world, inducing settlement and providing habitat for invertebrates and other organisms. According to the fossil record, corallines have been abundant on Earth and perhaps ecologically central for millions of years. The recent discovery of secondary cell walls enriched with cellulose and lignin in *Calliarthron* has prompted a

Pterocladia capillacea, one of the sources for agar production in East Asia, is suitable for studying phylogeography of marine organisms since it commonly occurs in temperate to tropical waters around the planet. In order to understand its current distribution pattern, more than 340 specimens from Korea, Japan, Brazil, France, Italy, Mexico, New Zealand, Spain, and USA were analyzed using three molecular markers: plastid *rbcL* for identifying the species, and mitochondrial *cox1* and *cob* for phylogeography. The *rbcL* analysis resolved all *P. capillacea* samples within a single monophyletic clade. Analyses of mitochondrial *cox1* and *cob* sequence data revealed six subclades within *P. capillacea*: group I from Korea and Japan; II from USA (California) and Mexico; III from New Zealand and Korea; IV from France, Italy and Spain; V from Brazil, and VI from USA (Hawai'i). Forty seven *cox1* haplotypes were detected among the samples. Haplotype and nucleotide diversities were compared between clades. Despite geographical structure of most populations, the finding of clade III suggests a genetic connectivity *P. capillacea* between Korea and New Zealand.

ASSESSMENT OF CRYPTIC RHODYMENIA SPP. (RHODYMENIACEAE, RHODOPHYTA) IN BRITISH COLUMBIA, CANADA: AN INTEGRATIVE TAXONOMIC APPROACH

Filloramo, G. V.

Centere for Environmental & Molecular Algal Research,
Dept. of Biology, University of New Brunswick, Canada,
gina.filloramo@gmail.com

Saunders, G. W.

Centere for Environmental & Molecular Algal Research,
Dept. of Biology, University of New Brunswick, Canada,
gws@unb.ca

Combined with morphological assessments, DNA barcoding has revolutionized our ability to delimit red algal species. A recent survey in British Columbia, Canada used the DNA barcode to reveal new and previously overlooked species within the genus *Rhodymenia*. Although two species of *Rhodymenia* were recognized in British Columbia (*R. pacifica* and *R. californica*), our molecular data resolved four distinct species groups. Analysis of vegetative and reproductive features confirmed the presence of *R. pacifica* and *R. californica*. Some samples field identified as *R. pacifica*, resolved as a separate genetic species and were determined to be *R. rhizoïdes*, which consequently resurrected this species. Additionally, some samples field identified as *R. californica* were found to be genetically distinct. To accommodate these samples we investigated synonyms of *R. californica* as well

as *Rhodymenia* species from the west coast of North America, Japan and Russia. Among those species we could not find a good match to our collections and we thus propose *R. bamfieldiensis* sp. nov. for this group. In recognizing these four species we have doubled the number of species for this genus in British Columbia.

MOLECULAR DIVERSITY OF MAËRL-FORMING CORALLINES (CORALLINALES, RHODOPHYTA)

Hernandez-Kantun, J. J.

National University of Ireland, Galway, Ireland,
j.hernandez2@nuigalway.ie

Rindi, F.

Università Politecnica delle Marche, Italy,
f.rindi@univpm.it

Riosmena-Rodriguez, R.

Universidad Autonoma de Baja California Sur, Mexico,
riosmena@uabcs.mx

Maggs, C. A.

Queen's University, United Kingdom, c.maggs@qub.ac.uk
Hall-Spencer, J. M.

University of Plymouth, United Kingdom,
jason.hall-spencer@plymouth.ac.uk

Peña, V.

Museum National d'Histoire Naturelle, France,
vpena@udc.es

Maërl-forming corallines are calcareous red algae with unattached thallus. Despite their ecological and economic importance, to date there are few molecular data concerning these algae, and the present knowledge of their taxonomy and biogeography is mostly based on morphological information. The molecular diversity of maërl-forming species was investigated using SSU, *psbA*, *rbcL*, *cox1*, *cox2-3* and ITS sequences. The phylogenies recovered showed that these organisms belong to several separate clades, in which they co-occur with crustose corallines of the genera *Lithophyllum*, *Hydroolithon*, *Phymatolithon*, *Lithothamnion* and *Mesophyllum*; four maërl-forming species of *Neogoniolithon* form a monophyletic group. A large number of cryptic species was observed in *Lithophyllum* for Europe (in the morphospecies *Lithophyllum incrustans* and *L. dentatum*) and Gulf of California (*L. margaritae*). Some species that were previously believed to exist only as encrusting forms (*Lithophyllum incrustans* and *Phymatolithon purpureum*) are shown to occur also as maërl. Our results suggest that the diversity of maërl-forming species has been considerably underestimated and additional studies are required to clarify the evolutionary history and phylogeography of this group.