

Marine Sciences, University of Gothenburg,  
Strömstad 45296, Sweden

In terms of marine biodiversity, the Baltic Sea is a depauperated mass of water relatively isolated from the North Atlantic with a stable salinity gradient that poses a strong selective regime to any marine species willing to colonize it. The established populations of marine species that colonized it after the last glaciation are at their ecological and geographical limits. However, previous research in the Baltic Sea has shown adaptations to this environment that have produced an extremely rapid speciation event in *Fucus* seaweeds. Here, we used a population genomics approach with RAD-Seq to revisit this case and we found that what was previously believed to be a single case of speciation might be a cryptic radiation instead. Despite no apparent physical barriers, the permanent salinity and temperature regimes, combined with the water circulation patterns in this region may effectively isolate populations even at very short geographical distances, creating quick and large genetic differences among demes in many areas along the Baltic.

#### 1OR.14

##### **MATCHING NAMES AND CLADES IN THE BROWN ALGAL GENUS *LOBOPHORA* (DICTYOTALES, PHAEOPHYCEAE): AN EFFORT TO INTEGRATE TYPE SPECIMENS IN MODERN TAXONOMY**

Christophe Vieira<sup>1</sup> ([cvcarp@gmail.com](mailto:cvcarp@gmail.com)), Olga Camacho<sup>2</sup> ([olgacamacho76@yahoo.com](mailto:olgacamacho76@yahoo.com)), Michael J Wynne<sup>3</sup> ([mwynne@umich.edu](mailto:mwynne@umich.edu)), Lydiane Mattio<sup>4</sup> ([lydianemattio@gmail.com](mailto:lydianemattio@gmail.com)), Robert J Anderson<sup>5</sup> ([robert.anderson@uct.ac.za](mailto:robert.anderson@uct.ac.za)), John J Bolton<sup>6</sup> ([john.bolton@uct.ac.za](mailto:john.bolton@uct.ac.za)), Marta Sansón<sup>7</sup> ([msanson@ull.es](mailto:msanson@ull.es)), Sofie D'hondt<sup>8</sup> ([sofie.dhont@ugent.be](mailto:sofie.dhont@ugent.be)), Suzanne Fredericq<sup>2</sup> ([slf9209@louisiana.edu](mailto:slf9209@louisiana.edu)), Claude Payri<sup>9</sup> ([claud.payri@ird.fr](mailto:claud.payri@ird.fr)) and Olivier De Clerck<sup>8</sup> ([olivier.declerck@ugent.be](mailto:olivier.declerck@ugent.be))

<sup>1</sup>UMR ENTROPIE (IRD, UR, CNRS) LabEx-CORAIL, Institut de Recherche pour le Développement, Noumea B.P. A5, 98848, France; <sup>2</sup>Department of Biology, University of Louisiana at Lafayette, Lafayette LA 0504-2451, United States; <sup>3</sup>Department of Ecology and Evolutionary Biology and Herbarium, University of Michigan, Ann Arbor MI 48109, United States; <sup>4</sup>School of Plant Biology, University of Western Australia, Perth Crawley WA6919, Australia; <sup>5</sup>Fisheries Research, Department of Agriculture, Forestry and Fisheries, Roggebaai 8012, South Africa; <sup>6</sup>Department of Biological Sciences and Marine Research Institute, University of Cape Town, Cape Town 7701, South Africa; <sup>7</sup>Departamento de Botánica, Ecología y Fisiología Vegetal, Universidad de La Laguna, La

Laguna, Canary Islands 38271, Spain; <sup>8</sup>Phycology Research Group and Center for Molecular Phylogenetics and Evolution, Ghent University, Ghent 9000, Belgium and <sup>9</sup>UMR ENTROPIE, LabEx-CORAIL, Institut de Recherche pour le Développement, Noumea B.P. A5, 98848, France

The use of gene sequence data has profoundly altered our view on algal diversity on every taxonomic level. Most spectacularly, sequence data unveiled the existence of massive cryptic or pseudocryptic diversity at the species level. Cryptic diversity also makes linking DNA-based lineages to existing taxa exceedingly difficult, which results in a growing tendency to move from a formal algal taxonomy to a more informal system whereby clade-, specimen- or strain-based identifiers are used to communicate biological information. Counteracting the emergence of parallel taxonomies would require a better integration of historical collections into modern taxonomic research. Here we explore the feasibility of linking taxonomic names, often described decades before DNA-based species identification became the norm in phycology, to clades in modern phylogenies. The brown algal genus *Lobophora* forms an excellent test case to explore the feasibility of such efforts. Recent studies have demonstrated that the genus is far more diverse than traditionally assumed. For decades only a handful of species were recognized of which *L. variegata* (J.V.Lamour.) Womersley ex E.C.Oliveira was by far the most commonly reported. DNA-based species delineation methodologies, however, indicate that there may be at least over one 120 species. We reevaluated the identity of 17 taxa suspected to be representative of *Lobophora* species by attempting DNA amplification of historical herbarium material as well as specimens recently collected from the type locality (epitypes). Our results indicate that exclusive reliance on information preserved in type specimens is problematic. For several species, either the type could not be traced or we did not get permission to extract DNA from types. Epitype material proved a more successful way forward, but this route often comes with a considerable degree of uncertainty, especially in tropical regions where the degree of sympatry among *Lobophora* lineages is sometimes considerable.

#### 1OR.15

##### **BIODIVERSITY IN THE PLANKTONIC DIATOM FAMILY CHAETOCEROTACEAE**

Chetan Gaonkar<sup>1</sup> ([chetan.gaonkar@szn.it](mailto:chetan.gaonkar@szn.it)), Roberta Piredda<sup>1</sup> ([roberta.piredda@szn.it](mailto:roberta.piredda@szn.it)), Diana Sarno<sup>1</sup> ([diana.sarno@szn.it](mailto:diana.sarno@szn.it)), Marina Montresor<sup>1</sup> ([mmontr@szn.it](mailto:mmontr@szn.it)), Adriana Zingone<sup>1</sup> ([zingone@szn.it](mailto:zingone@szn.it)), David G Mann<sup>2</sup> ([d.mann@rbge.org.uk](mailto:d.mann@rbge.org.uk)), Carina Lange<sup>3</sup> ([clange@udec.cl](mailto:clange@udec.cl)) and Wiebe HCF Kooistra<sup>1</sup> ([kooistra@szn.it](mailto:kooistra@szn.it))