THE STUDY OF TROPICAL PLANKTON APPEARANCE IN EAST SEA, KOREA

J. Lee, M. R. Kim and M. Chang
(jylee0409@hanmail.net)
KIOST, Republic of Korea

Global warming has resulted in lots of environmental changes. This study was conducted to determine the biological adjustment to changes in the ocean ecosystem such as new tropic plankton appearances in a temperate climate area. Therefore, in this study, we focused on appearance of tropical plankton and the extent of adaptations for increases in water temperature. We conducted sampling at 16 stations from 28 May to 3 June and 35 stations from 5 August to 10 August 2012. Several tropic species were found near the Dokdo, which is located in the eastern part of Korea. Their presence near the Dokdo is probably related to the Kuroshio Current, which affected their influence from spring to the summer in East Sea. The 5 species, Cochlodinium sp., Dinophysis caudata, Gonyaulax spinifera, Ostreopsis sp., Phalacroma mitra were observed at 9 of the 16 stations. The 4 species other than Cochlodinium sp. were observed at 7 of the 35 stations. 8 genera were observed during May but only 4 genera were observed; most of the observed species in August were diatoms. When we compared biomass based on the cell counting, the numbers were similar in spring (30.6~252.6 cells L^{-1}) and summer (35.0~260.0 cells L^{-1}) in 2012. The dominant species were Chaetoceros curvisetus, Chroomonas sp., Corymbellus aureus, Leptocylindrus minimus, Proboscia alata, and Prorocentrum balticum in spring and Chaetoceros affinis, Ch. curvisetus, Gymnodinium sp., Leptocylindrus minimus, Nitzschia sp., Rhodomonas sp., Thalassiosira sp. in summer. Based on this study, even though, the water temperatures were higher in summer than in spring in this general temperate climate area, a similar number of tropical species were observed spring season. It could be the explanations of the seasonal effect of Kuroshio Current in East Sea, Korea.

CHARACTERIZATION OF PHOTORECEPTORS AND THEIR MACHINERIES INVOLVED IN TWO TRACK PHOTOMOVEMENT OF SPIROGYRA VARIANS

J. W. Lee, J. W. Han and G. H. Kim
(ljw86@kongju.ac.kr)
Kongju National University, Republic of Korea

The filamentous green alga Spirogyra varians shows two track photomovement; a positive phototropic movement to blue light and an irregular twisting movement to red light. The reversal of red light movement by a short exposure (<30s) to far-red light implied that phytochrome is involved in photomovement too. Two phototropin genes and three phytochrome isoforms were isolated and characterized for the first time in Spirogyra. Both photoreceptor genes showed high homology with land plants but each isoforms of phototropin and phytochrome contained some unique structures. Real time PCR analysis showed that the expression level of each isoform was differently affected by the prolonged exposure of filaments to blue and red light. Previous studies showed that the blue and red light responsive movements are controlled through different signaling pathways. Seven different GTPase genes were isolated and the expression level was compared before and after exposure to red and blue light. Among them, the Rop (Rho small GTPase of plants) family of small GTPase genes showed dramatic response to change of light condition. The potential molecular mechanisms of Rop GTPase signaling involved in cell motility were discussed together with the role of actin and tubulin as machineries.

THE GEOGRAPHIC SCALE OF SPECIATION IN THE MARINE RED ALGA PORTIERIA

F. Leliaert, D. A. Payo and O. De Clerck
(frederik.leliaert@gmail.com)
Ghent University, Belgium

The role of geographic isolation in marine speciation has been contested because of the high dispersal potential of marine species and the apparent lack of dispersal barriers in the sea. Compared to marine invertebrates and fish, most seaweed species are considered poor dispersers. This limited dispersal capacity may reflect on diversity patterns and the
spatial scale at which speciation takes place. We assessed species diversity, distribution patterns and phylogenetic relationships within the marine red algal genus *Portieria* based on multilocus data and analyses combining phylogenetic and population genetic principles. In stark contrast with the current morphology-based assumption that the genus includes about seven species, including one widely distributed species in the Indo-West Pacific (*P. hornemannii*), DNA-based species delimitation resulted in the recognition of more than 90 species. Species distributions were found to be highly structured with most species having narrow ranges. Our results indicate that speciation in the marine environment may act at much smaller geographical scales than is commonly assumed. The most likely explanation to account for the observed diversity is a peripatric model of speciation, involving founder events resulting from long distance dispersal and subsequent differentiation of the established populations. Temporal analyses of diversification indicate a gradual pattern since the Eocene, and long term persistence of ancient lineages within confined regions of the Indo-Pacific. The Indo Malay archipelago (IMA or Coral Triangle) was found to be particularly diverse. Our phylogenetic data indicate that this diversity resulted from a combination of species accumulation via island integration through tectonic movement, in combination with speciation within the IMA as a result of increased geographical complexity of the region from the Miocene to Pleistocene.

160 BIOINDICATORS OF MARINE ENVIRONMENTS: USING SEAWEEDS AS A TOOL FOR BIOMONITORING THE QUALITY OF COASTAL WATERS RESPONSE TO A PROBLEM OF MASSIVE SEAWEED BEACHING

S. Lemesle, I. Mussio, A. M. Rusig and P. Claquin (stephanie.lemesle01@unicaen.fr) 
*Université de Caen Basse-Normandie, France*

In the context of massive seaweed beaching during summer along the French coast of the English Channel in the region of Calvados, the aim of this study was to use the seaweeds to understand the environmental conditions responsible for this phenomenon. The evaluation of eutrophication of coastal waters is based on the use of delta-15N signatures in seaweed tissues to identify the sources of nitrogen. Five naturally occurring seaweeds (*Ulva* sp., *Fucus vesiculosus*, *F. serratus*, *Chondrus crispus* and *Porphyra* sp.) were collected at two sites (Baie des Veyes and Courseulles-sur-Mer) at two-monthly intervals in 2012. Isotopic signatures ranged from 5.79 ±1.13‰ to 14.16 ±0.38‰ at the 17 sampling points distributed between the two sites. Seasonal variations in isotopic signatures were observed with low delta-15N values in spring (5.79 ±1.13‰ to 9.37 ±0.39‰) and high delta-15N values in summer, autumn and winter (8.18 ±0.19‰ to 14.16 ±0.38‰). Differences in delta-15N signatures were detected between sampling points and in the different species of seaweeds.

161 EXTENSIVE CHLOROPLAST GENOME REARRANGEMENTS AMONG SPECIES OF THE GENUS ELLIPTOCHLORIS (TREBOUXIOPHYCEAE, CHLOROPHYTA)

M. R. Letsch and L. A. Lewis (molly.letsch@gmail.com) 
*University of Connecticut, USA*

Chloroplast genomes of green algae are highly variable in architecture within and across major taxonomic groups. To investigate the evolution of chloroplast genomes at a shallow phylogenetic depth, we used a nextgen approach to sequence the chloroplast genomes of *Elliptochloris marina* and *Elliptochloris reniformis*. The two genomes vary in size, the *E. reniformis* genome is 110 kb and *E. marina* is 145 kb. Extensive chloroplast gene rearrangements are found between the two species. In contrast, these taxa have very low pairwise sequence divergence in orthologous genes. Like the majority of published trebouxiophyte chloroplast genomes, these species have no inverted repeats. They also share similarities with the published genome of *Coccomyxa subellipsosidea*, having large spacer regions, and a high GC-bias. Pairwise sequence divergence of *Coccomyxa* and the two *Elliptochloris* species is twice as great as that found between the *Elliptochloris* species. However, the amount of chloroplast genome rearrangement is relatively consistent among all three species. This study demonstrates extensive chloroplast architectural rearrangements among congeneric Chlorophyta, while also illustrating of some shared