

ESTIMATION OF CARBON FLUX SED ON ECOSYSTEM DUCTION IN THE NORTHEASTERN KWANGYANG BAY

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To understand carbon flux in vegetation-dominated coastal system, the present study was conducted at Kwangyang Bay (an estuary in southern coast of Korea) in June 2007. Community production was measured using the classical ^{14}C tracer and oxygen microprofiling methods which were undertaken of all autotrophic components, i.e., eelgrass beds, macroalgal vegetation, phytoplankton and micro-phytobenthos. For calculating gross ecosystem production (GEP), intensity of ambient light was measured during the field experiments conducting in two eelgrass beds (EG1 and EG2), a rocky macroalgal vegetation (AG) and an unvegetated sediment (UNV). Macroalgal vegetation (AG) had the highest GEP ($32.4 \pm 3.59 \text{ g C m}^{-2} \text{ d}^{-1}$) due to high biomass and productivity of macroalgae, whereas the lowest GEP was found outside of macroalgal vegetation (AG-out; $1.2 \pm 0.02 \text{ g m}^{-2} \text{ d}^{-1}$) where only the phytoplankton community was considered. All study sites had a net autotrophic environment except for EG2. The P:R (GEP:GER) ratio was high in unvegetated sites (EG1-EG2-out, AG out and UNV) showing low respiration compared to vegetative sites. Based on CO_2 gas exchange calculation (net ecosystem exchange; NEE), eelgrass beds acted as a CO_2 sink during periods of high light (10:00–11:00 AM). High rates of CO_2 sink observed in eelgrass beds by comparing the GEP or NEP (net ecosystem production) to NEE. In this study, we first elucidated that a conceptual model of carbon flux in a bay system having both macroalgae and eelgrass beds has been designed based on results of GEP, NEP and NEE. We also compared the potential capacity for carbon uptake among macroalgae, eelgrass, microphytobenthos and phytoplankton from various habitats.

SYSTEMATICS OF *EUGLENA DESES* COMPLEX (EUGLENACEAE) USING MOLECULAR AND MORPHOLOGICAL EVIDENCE

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Euglena deses complex is common species in freshwater and comprised of *E. adhaerens*, *E. carterae*, *E. deses*, *E. mutabilis* and *E. satelles*. They are characterized by elongated cylindrical worm-like cell body and numerous discoid chloroplasts with naked pyrenoid. To understand

taxonomy and phylogenetic relationships among these species, we analyzed morphological data using light and scanning electron microscope and molecular data based on combined SSU, LSU and *psbA* gene in plastid, including two *Phacus* species and two *Lepocinlis* species as an outgroup. Bayesian and Maximum-likelihood (ML) analyses resulted in tree of two major clades. The first clade was composed of two subclade; *E. mutabilis* subclade and *E. carterae* and *Euglena* sp. Songdang042007A subclade. *E. mutabilis* subclade was characterized by a lateral canal opening at the anterior end and single pellicular stria. *E. carterae* and *Euglena* sp. Songdang042007A subclade was characterized by an apical anterior part of the cell and double pellicular striae. The other clade was consisted of ten strains of *E. deses*, including one *E. deses* var. *mesnii*. *E. deses* clade has shared common characteristics such as subapical canal opening at the anterior end and double pellicular striae but showed a various genetic diversity.

PHYLOGEOGRAPHY OF *GELIDIUM* *ELEGANS* (GELIDIALES, RHODOPHYTA)

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Recently Korean company exhibited the production of high quality pulp from endofibers of the gelidioid species. *Gelidium elegans* Kützinger, previously named as *G. amansii*, is the most common species in the Gelidiales in northeast Asia and is harvested for agar production in May in Korea. We collected more than 200 samples on the west, south, Jeju and east coast in Korea, seven localities in Japan and four localities in China. We analyzed plastid *rbcL* and mitochondrial *cox1* genes in order to elucidate diversity and phylogeny of the species. Both data sets were congruent in topology. However, eight haplotypes of *rbcL* were found in 55 specimens, while 29 haplotypes of *cox1* occurred in 155 specimens. The same *cox1* haplotype occurred in Korea, China and west of Japan. The haplotype diversity was 0.766 ± 0.035 and the nucleotide diversity was 0.001 ± 0.0001 . It is interesting that Japanese populations had high haplotype diversity ($h = 0.894 \pm 0.078$) and low nucleotide diversity ($\pi = 0.014 \pm 0.003$). On-going analysis of the remaining specimens will give us a better understanding of the distribution pattern of *G. elegans*.

PRIMARY STRUCTURE OF THE 11.5 KDA LECTINE, BPL3, FROM THE MARINE GREEN ALGA *BRYOPSIS PLUMOSA*

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The *N*-acetyl-D-galactosamine and *N*-acetyl-D-glucosamine recognizing lectin (BPL3) from *Bryopsis plumosa* was purified by affinity chromatography. The recombinant protein was constructed based on cloned cDNA sequence. Purified native BPL3 had a molecular weight of 11.5 kDa on SDS-PAGE, also a molecular mass of 11533.85 Da by MALDI-TOF-MS. The hemagglutinating activity using human erythrocytes (types A, B, O) was inhibited by *N*-acetyl-D-galactosamine and *N*-acetyl-D-glucosamine. BPL3 consists of 106 amino acid residues including two cystein moieties and two N-glycosylation sites by prediction based on cDNA sequence. A primary structure was identified using MALDI-TOF-MS peptide mapping method in combination with specific peptidase (trypsin and carboxypeptidase Y), which was confirmed by the peptide sequences with MALDI-TOF-MS. In order to characterize the number and location of free Cys and disulfide bonds in the protein, chemical modification and MALDI-TOF-MS were used. C-terminal residues were determined by analyzing the molecular masses of the truncated peptides. The result show that BPL3 was composed of 103 amino acids and three amino acids in the C-terminal were cleaved. The peptide masses containing of N-glycosylation site were not changed in comparison with calculated peptide mass. This result suggested that the native BPL3 was not glycosylated. Our results also showed that presence of two cystein residues and two free sulfhydryls without disulfided bond in the amino acids sequence of BPL3. We will try to predict a complete primary structure of BPL3 through study of other types of post-translation modification.

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DIFFERENCE OF ELIMINATION TIMING IN MALE MITOCHONDRIA AND MITOCHONDRIAL DNA AFTER FERTILIZATION BETWEEN ISOGAMOUS AND OOGAMOUS BROWN ALGAE

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In brown algae, there are three types of sexual reproduction patterns, isogamy, anisogamy and oogamy. Maternal

inheritance of mitochondria has been reported in isogamous and oogamous members. We examined the selective elimination systems of mitochondria derived from the male gametes in isogamous and oogamous members. First, we examined when mitochondrial DNA (mtDNA) derived from the male gamete disappeared, and observed the number and morphology of mitochondria during the zygote development after fertilization in *Scytosiphon lomentaria* (isogamy). We clarified that the paternal mtDNA disappeared during four to seven-celled stages of sporophytes. The number of mitochondria did not change until two-celled stage of zygotes. During the zygote development, mitochondria did not fuse each other and were not digested in lysosomes. In the four-celled stage of sporophyte, we observed mitochondria of which the inner structure was disrupted. These mitochondria would be the destructing male mitochondria. While, in the oogamous brown alga, *Undaria pinnatifida*, it became clear that the sperm mtDNA was disappeared at the later stages of one-celled zygote using the single cell PCR. Furthermore, we confirmed that the sperm mitochondria were digested in this stage by TEM. Therefore, the sperm mitochondria and mtDNA were eliminated at the one-celled zygotes. From these results, timings of disappearance of the male mitochondria were different between isogamous and oogamous members. For examining how these differences are caused in these algae, we are now performing TEM observations on the mitochondrial behavior during zygote development in the isogamous and the oogamous brown algae.

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THE IDENTITY OF AN ENDOZOIC RED ALGA, *RHODOCHORTONOPSIS SPONGICOLA* YAMADA (ACROCHAETIALES, RHODOPHYTA)

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An unusual, endozoic red alga, *Rhodochortonopsis spongicola* Yamada (Acrochaetiales, Rhodophyta) was re-examined using its type specimens (TNS). This species was described by Yamada (1944) based on the plants within the tube materials of polychaete, which were collected by the Emperor Showa (1901–1989) in the sea off Hayama, Sagami Bay, Japan. Yamada (1944) established also the new monotypic genus *Rhodochortonopsis* for this species because of the “very peculiar stichidia” with long tetrasporangia divided zonately. After his original description this alga has not been collected from Japan over the 60 years. Only Norris (1991) recorded this rare algal species from Natal, South Africa and suggested a possible relationship of *Rhodochortonopsis* with the order Gigartinales not Acrochaetiales because of the cystocarpic structures of his female plants and Yamada’s “stichidia”. In this research on the type materials, however, it was revealed that the structures was not real stichidia because its axis was formed from many sponge spicules covering by uniseriate filaments. Cells of the