



Title	Taxonomic and molecular phylogenetic studies of the genus <i>Colpomenia</i> (Scytosiphonaceae, Phaeophyceae) [an abstract of dissertation and a summary of dissertation review]
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Abstract of Doctoral Dissertation

Degree requested: Doctor of Science Applicant's name: Michael Jacob Cleto Dy

Title of Doctoral Dissertation

Taxonomic and molecular phylogenetic studies of the genus *Colpomenia* (Scytosiphonaceae,
Phaeophyceae)

【褐藻フクロノリ属 (カヤモノリ科) の分類学および分子系統学的研究】

The classification of the brown algal family Scytosiphonaceae still remains problematic because of their morphological plasticity and also the molecular phylogenetic inconsistencies among its genera. With the help of several phycologists, some of the issues have been addressed, but the problem is still there especially in the genus *Colpomenia*.

I attempted in this study to resolve taxonomic problems within this genus and its species by combining multi-gene molecular data with morphological observations and life histories. I assessed the taxonomy of all known globular species, using *Colpomenia* samples from Japan, Russia, Australia, and Portugal. Three molecular markers were used for phylogenetic analyses: mitochondrial *cox3* gene and plastidal *rbcL* and *psaA* genes. In all *cox3*, *rbcL* and *psaA* trees reconstructed, this genus revealed four major evolutionary lineages (Lineages I–IV). In addition, a new species has been discovered while conducting this research.

Colpomenia borea is characterized by its small globular to ovoidal thalli and thin thallus membrane and is epiphytic on the brown alga *Stephanocystis*. This species was found in the Pacific coast of Hokkaido, Japan, and Magadan, Far East Russia which are the coldest regions in the distributional range of *Colpomenia*.

This study revealed independence of each of Lineages I–IV, suggesting polyphyly of the genus *Colpomenia*. Lineage I consisted of *Colpomenia sinuosa* which is the generitype of the genus. Lineage II consisted of *C. claytoniae*, *C. expansa*, *C. peregrina* and *C. borea*, which have globose thalli. Since this Lineage was distantly related to the generitype *C. sinuosa*, a new genus name should be proposed for the Lineage II. Lineages III and IV were composed of *C. ecuticulata* and *C. ramosa*, respectively. These Lineages were also distantly related to *C. sinuosa* in *cox3* analyses.

In *cox3* trees, highly supported subclades were formed in *C. sinuosa* and *C. claytoniae*, suggesting multiple species within those species. *Colpomenia peregrina* also showed large intraspecific sequence differences. Four DNA-based species delimitation analyses (ABGD, ASAP, PTP, bPTP) were also conducted for *Colpomenia* species, using *cox3* sequences. Results of ABGD and ASAP were similar, suggesting two or four species within *C. sinuosa* and a single species for *C. claytoniae* and *C. peregrina*. In contrast, PTP and bPTP yielded nine species within *C. sinuosa* and five species within *C. claytoniae* while a single species for *C. peregrina*. Species boundaries that corresponded among all species delimitation analyses supported the current classification except for *C. sinuosa* which was divided into two by the boundary. *Colpomenia sinuosa* could include at least two species.

Because globose *Colpomenia* are similar in gross morphology, they may have been misidentified. In this study, molecular identification of *Colpomenia* species from Japan was conducted, and their more accurate distributional ranges were revealed in Japan.