



The Diagnostic Characteristics Are Highly Homoplasious Used in Cladonia gracilis and Cladonia cornuta

Jae Eun So^{1,2}, Ji Hee Kim¹, Soon Gyu Hong^{1,2}, Chae Haeng Park¹

¹Division of Life Sciences, Korea Polar Research Institute, KIOST, Incheon 406-840, Korea

²Department of Polar Sciences, University of Science and Technology, Incheon 406-840, Korea

Contact: jhalgae@kopri.re.kr (Ji Hee Kim), polypore@kopri.re.kr (Soon Gyu Hong)

Abstract

The genus Cladonia lives on many different habitat and more than 400 species hitherto have been documented. Traditionally, the genus was classified into 7 taxonomic sections by morphology. However, the taxonomical classification is not well accord with that of molecular phylogenetic research. The genus has high morphological diversity, yet there has not been a coherent agreement on the delimitation of species. The Cladonia gracilis group and allies in the section Cladonia show an extreme phenotypic variety. Cladonia cornuta which are members of the C. gracilis group have been identified by variable characteristics. This study deals with the taxonomic problem between C. gracilis and C. cornuta by confirming the consistent phenotypic characteristics again with molecular phylogeny at species level. About 150 specimen were analyzed by 36 morphological and chemical characteristics using the DNA sequences with three loci(ITS rDNA, mtSSU and LSU rDNA). Specimen were collected from various regions covering bipolar areas and Korea. Phenotypic data will be discussed with several statistical methods. The study indicates that the homogeneous clade did not form in these species at species level. The results show no clear distinction between the two species in terms of secondary metabolites and geographical distribution. The characteristics used for classical diagnosis may be highly homoplasious.

Lichen Flora around KGI



King George Island, the largest of the South Shetland Islands belonging to the maritime Antarctic zone, is located at the northern tip of the Antarctic Peninsula. There are two vascular plants and diverse bryophytes and lichens (Ø vstedal et al., 2001). This island is one of the most appropriate places for studying the evolution of lichenized fungi of Antarctica because of its geographical locality and diversity of lichens.

The taxonomy of Antarctic lichens, 427 species in Antarctica and South Georgia were reported. Kim et al (2006) reported 62 lichenized fungi around the Korean Antarctic Scientific Station(King Sejong St.) located on Barton peninsula, King George Island.

Cladonia gracilis group

The lichenized ascomycete Cladonia gracilis (L.) Willd. (Cladoniaceae, Lecanorales) and its allied species are morphologically similar to each other, and each species has a high intraspecific variation, they are considered as a quite difficult group to identify until the species level. Therefore, the combination of several charateristics geographical or distribution has been used as the criterion for identification. Corticated cortex and subulate podetial form are the key diagnostic characters. This group is treated as several infraspecific taxa under C. gracilis and the closely related sorediate taxa, *Cladonia cornuta* (L.) Hoffm.

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MATERIALS & METHODS

383 Cladonia specimen in this study were acquired from 4 regions (King George Island, Antarctica, Punta Arenas, Chile, Korea and Svalbard) from which the presence of *Cladonia* has been widely documented (Stenroos, 1995; Osyczka & Olech, 2005; Ø vstedal, 2009; Wang, 2011).

36 characters were coded for 13 taxa including an outgroup. Primary thallus or upper part of podetia were used to identify chemical substances. With Lethariella cladonioides as control, chemical analyses (thin-layer chromatography, TLC) were performed according to standardized methods (Culberson 1972; Orange et al. 2001) in solvent systems A and C, using Merck TLC silica gel 60.

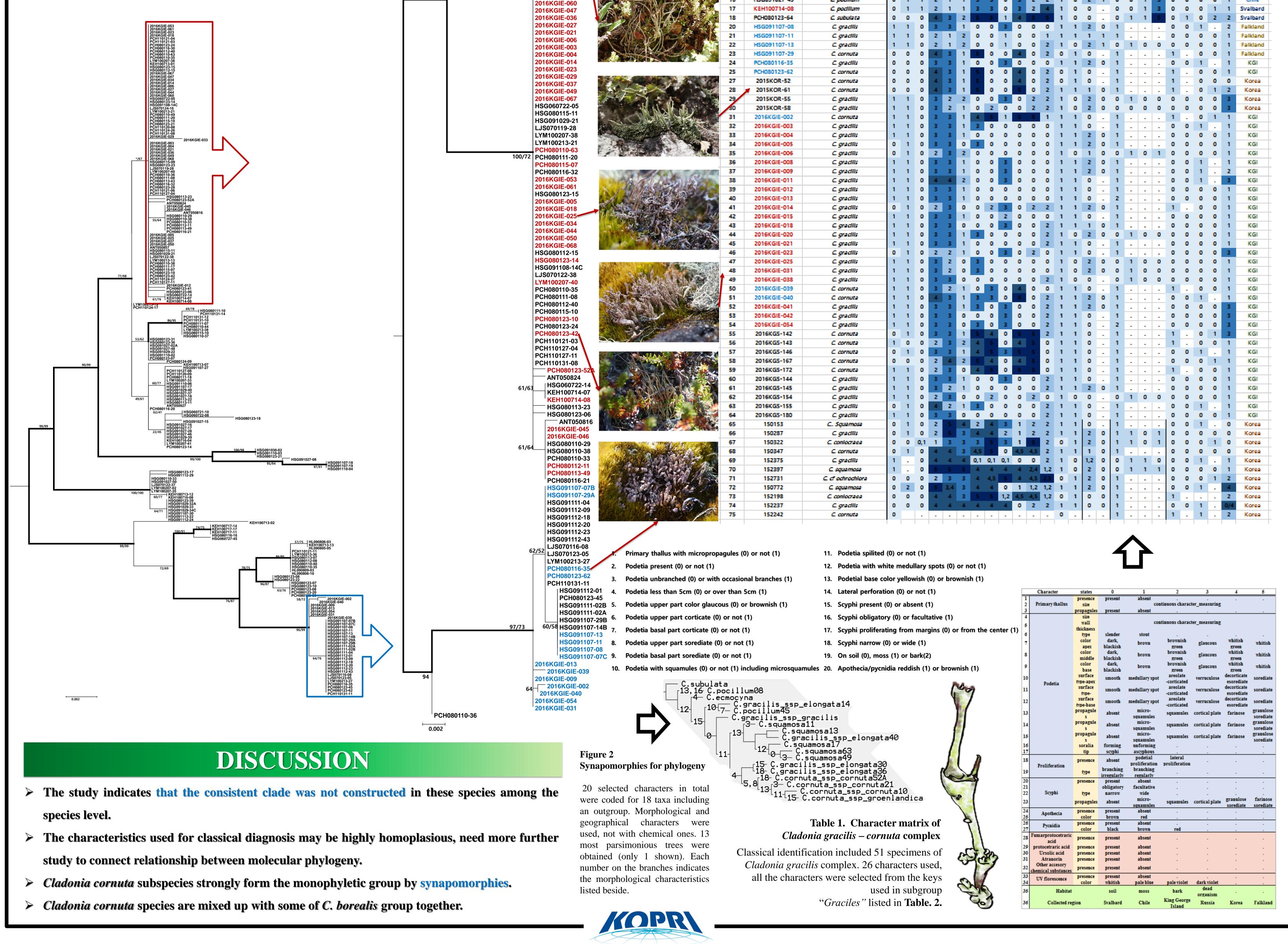
The phylogenetic analysis with phenotype was performed using TNT version 1.1. LSU rDNA, mitochondrial Small Subunit(mtSSU) rDNA and Internal transcribed spacer(ITS) rDNA sequences were incorporated into alignments. The analysis involved 383 nucleotide sequences(not shown) and reconstructed the phylogeny with 212 allied samples. Data for these samples were aligned manually with Jphydit. Evolutionary analyses were conducted in MEGA6 and PhyML.

RESULTS

Figure 1 Molecular Phylogeny of the *Cladonia gracilis-cornuta* complex.

Select several identified samples from each clade of whole tree (not shown), phylogeny of C. gracilis complex was reconstructed. Combine NJ and ML method on the base MP tree. Thick branches indicate well conserved to all trees over B.V. >70. (CI = 0.944000, RI = 0.922222)

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