PHYLOGENETIC RELATIONSHIPS OF THE BANGIALES FROM KING GEORGE ISLAND, ANTARCTICA

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ABSTRACT

Members of the Bangiales (Rhodophyta) are distributed worldwide from tropic to Antarctic and Arctic waters. Three species of the Bangiales; Bangia sp. (as B. atropurpurea), Porphyra plocamiestris and Pyropia endiviifolia (as Porphyra endiviifolium), have been reported in the Antarctic. Morphological and molecular data were investigated for the Bangiales from the Antarctic and its adjacent waters. Each six sequences of SSU rDNA, plastid rbcL and mitochondrial cox1 gene were newly determined in this study. Molecular data from over 72 taxa of the Bangiales worldwide including previously published sequences, indicated that the genera Bangia, Dione, Pyropia, Porphyra, Wildemania and other related genera be recognized in the Bangiales as in the previous molecular study. Bangia fuscopurpurea from the Antarctic was different from B. fuscopurpurea from north Pacific (Korea and Japan) by 12 bp in cox1 gene sequence. Porphyra plocamiestris growing on other macroalgae in sub-tidal zone grouped into the genus Wildemania with the species having one or two cell layers in molecular data. Pyropia endiviifolia is olive green in color and it allied to a clade with P. aeodis from South Africa, P. cinnamomea and P. viridiidentata from New Zealand. The taxonomic issues and phylogenetic relationships of the Antarctic members of the Bangiales were discussed.

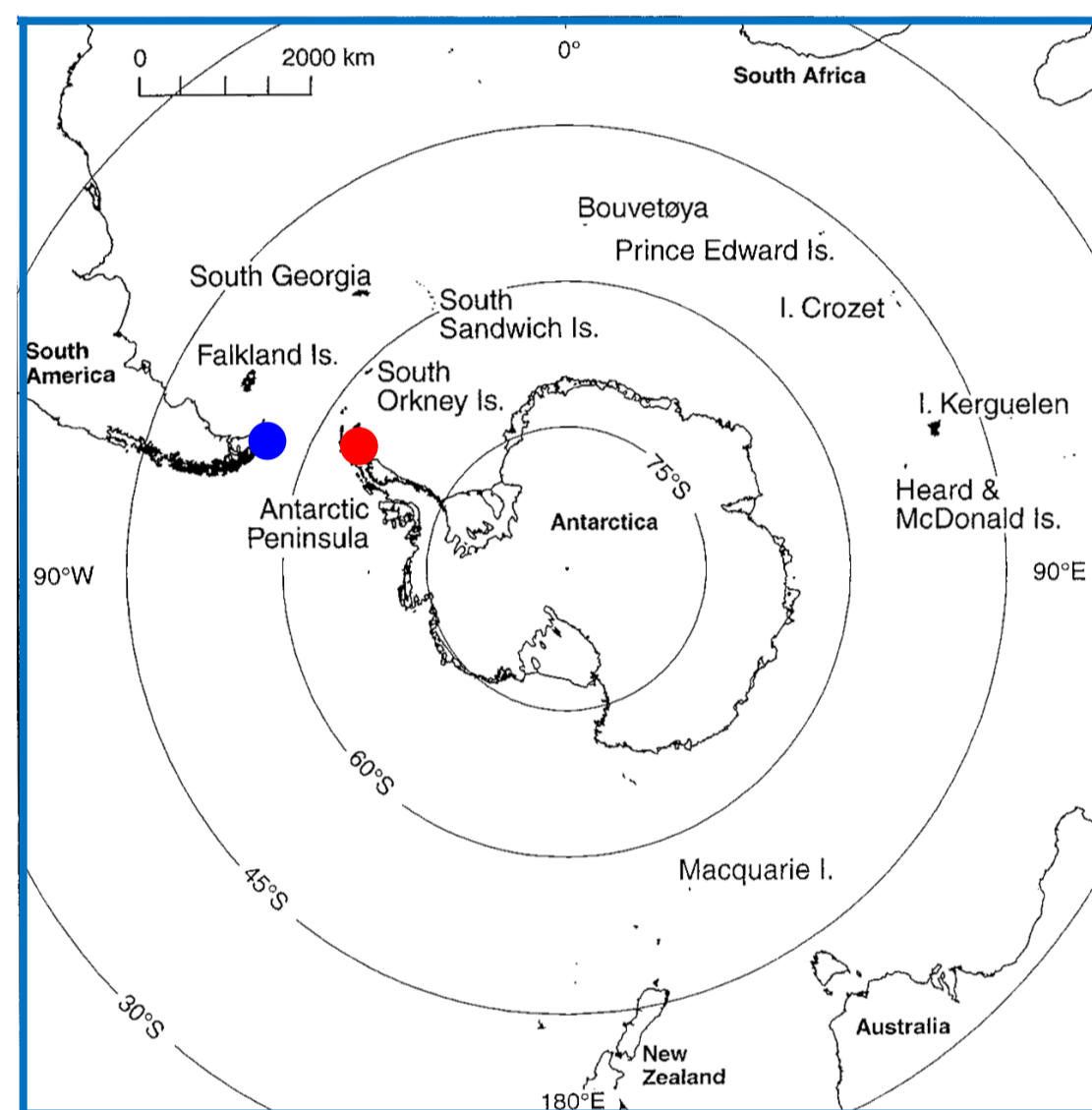## INTRODUCTION

Bangia and Porphyra belonging the order Bangiales are distributed world wide from the Arctic or Antarctic to tropical waters. Three species of the Bangiales have been reported from the Antarctica: Bangia sp. (as B. fuscopurpurea), Porphyra endiviifolium and P. plocamiestris, and several species have been added from sub-Antarctic islands (Clayton et al. 1997, Kim et al. 2001). Recently, the studies of materials from New Zealand, South Africa and sub-Antarctic islands have revealed unexpectedly high generic diversity in members of the Bangiales from the southern hemisphere regions (Nelson et al. 2006, Sutherland et al. 2011). In this study, nuclear SSU rDNA, plastid rbcL and mitochondrial cox1 gene sequences were examined for six entities of Bangia and Porphyra collected from the Antarctica and Chile in order to get some implications for the phylogenetic relationships with other members.

Fig. 1. Sampling sites of the Bangiales
●: King George Island, Antarctica for Bangia sp., Pyropia endiviifolia (KC105) and Porphyra plocamiestris
●: Punta Arenas, Chile for Porphyra woolhousiae and Pyropia sp.

GENERIC REVISION OF THE BANGIALES BY THE BANGIALES CONSORTIUM

Bangia-type 7 genera

Minerva W.A. Nelson in Nelson et al. 2005

Dione W.A. Nelson in Nelson et al. 2005

Pseudobangia K.M. Müll. et Sheath in Müller et al. 2005

Bangia Lyngb. 1819

'Bangia' 1

'Bangia' 2

'Bangia' 3

Porphyra-type 9 genera

Miuraea N. Kikuchi, S. Arai, G. Yoshida, J.A. Shin et M. Miyata gen. nov.

Clymene W.A. Nelson gen. nov.

Porphyra C. Agardh 1824

Sorora W.A. Nelson & J. Brodie gen. nov.

Lysithea W.A. Nelson gen. nov.

Fuscifolium S.C. Lindstrom gen. nov.

Boreophyllum S.C. Lindstrom, N. Kikuchi, M. Miyata and Neefus gen. nov.
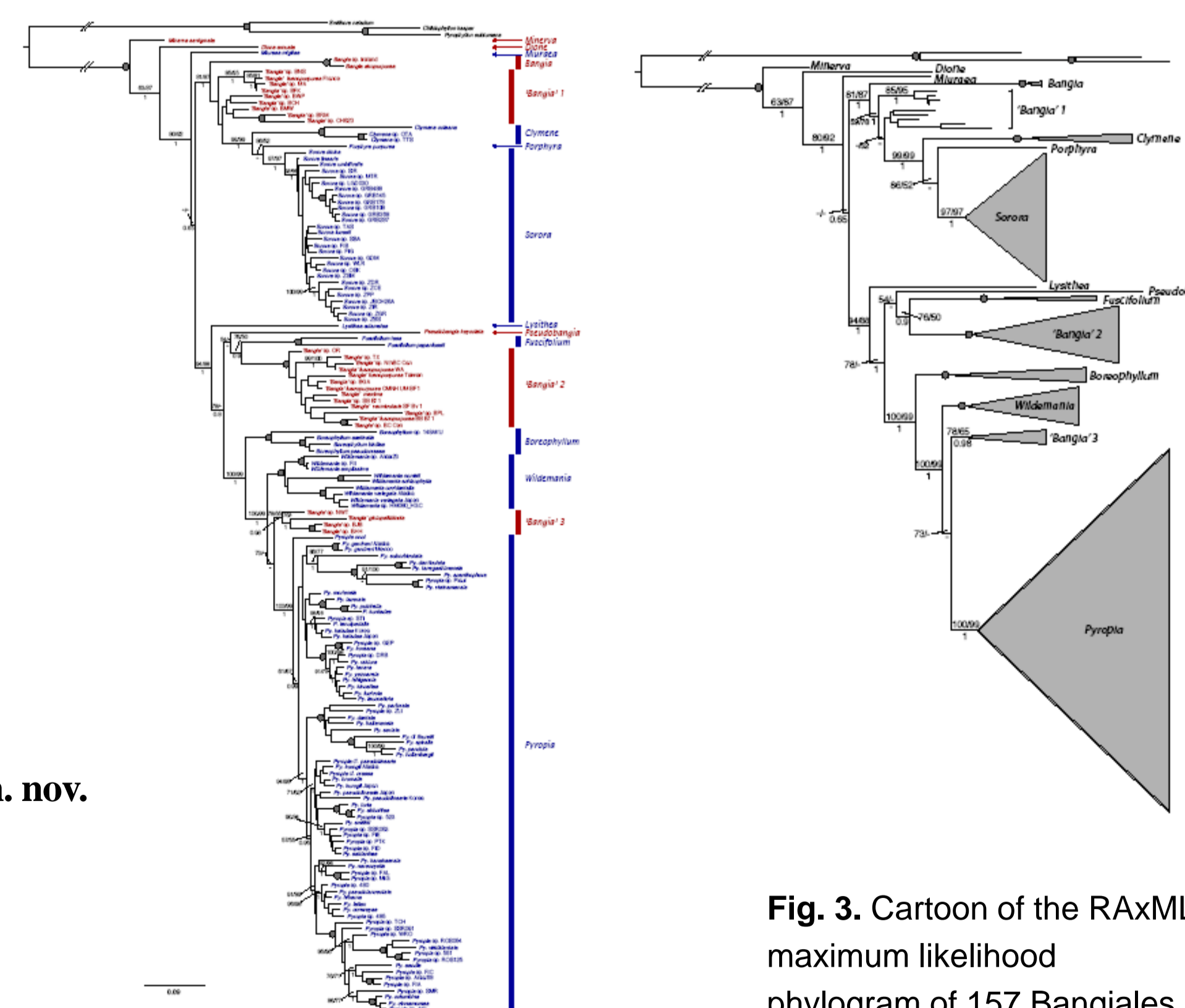
Wildemania De Toni 1890

Pyropia J. Agardh 1899

Fig. 2. Maximum likelihood phylogram of 157 Bangiales taxa calculated from the concatenated dataset under RAxML. Bootstrap values for RAxML and GARLI are shown above and Bayesian PP values below the nodes. Some internal support values are omitted for clarity. Gray circles indicate nodes supported at 100/100/1 (Sutherland et al. 2011).

Fig. 3. Cartoon of the RAxML maximum likelihood phylogram of 157 Bangiales taxa calculated from the concatenated dataset showing existing and proposed new genera with support for nodes along the backbone of the tree. Gray circles indicate nodes supported at 100/100/1 (Sutherland et al. 2011).

RESULTS AND DISCUSSION

1. Phylogenetic relationships of Antarctic Bangiales

Pyropia endiviifolia from the Antarctica was different from the material of Pyropia sp. from Chile by 2 bp in SSU, 18-19 bp in rbcL and 28 bp in cox1 gene sequences, showing that two materials would be the different species. This species grouped into a clade with Py. aeodis from South Africa, Py. viridiidentata and Py. cinnamomea from New Zealand and Pyropia sp. from Chile and Falkland Island based on combined SSU rDNA and rbcL data.

Wildemania plocamiestris from the Antarctica and Chile which has one cell layer of blade grouped into a clade with P. miniata and P. amplissima from north Atlantic having two cell layer in SSU rDNA, and with five species from north Pacific and north Atlantic having two cell layer based on combined data.

Porphyra woolhousiae from Chile grouped into a clade with P. dioica, P. lucasii, P. purpurea and P. umbilicalis based on combined data.

Bangia sp. from the Antarctica showed the same sequence with B. fuscopurpurea from north Pacific and north Atlantic in SSU rDNA, whereas it was different from B. fuscopurpurea by 1-2 bp in rbcL and from B. fuscopurpurea from north Pacific (Korea and Japan) by 11-12 bp in cox1 gene sequence. These results imply that this species would be a different one from B. fuscopurpurea.

2. Cox1 barcoding

Cox1 barcoding would be a powerful method in the identification of the members of the Bangiales such as in cases of other red algal groups (Saunders 2005). In all cases of this study intraspecific divergence values ranged from 0 to 5 bp, whereas interspecific divergences were more than 12 bp.

3. Taxonomic issues

Important taxonomic characters such as cell layer, sexuality (monoecious or dioecious), arrangement of reproductive cells (mixed or sectored vertically) do not reflect the molecular phylogeny.
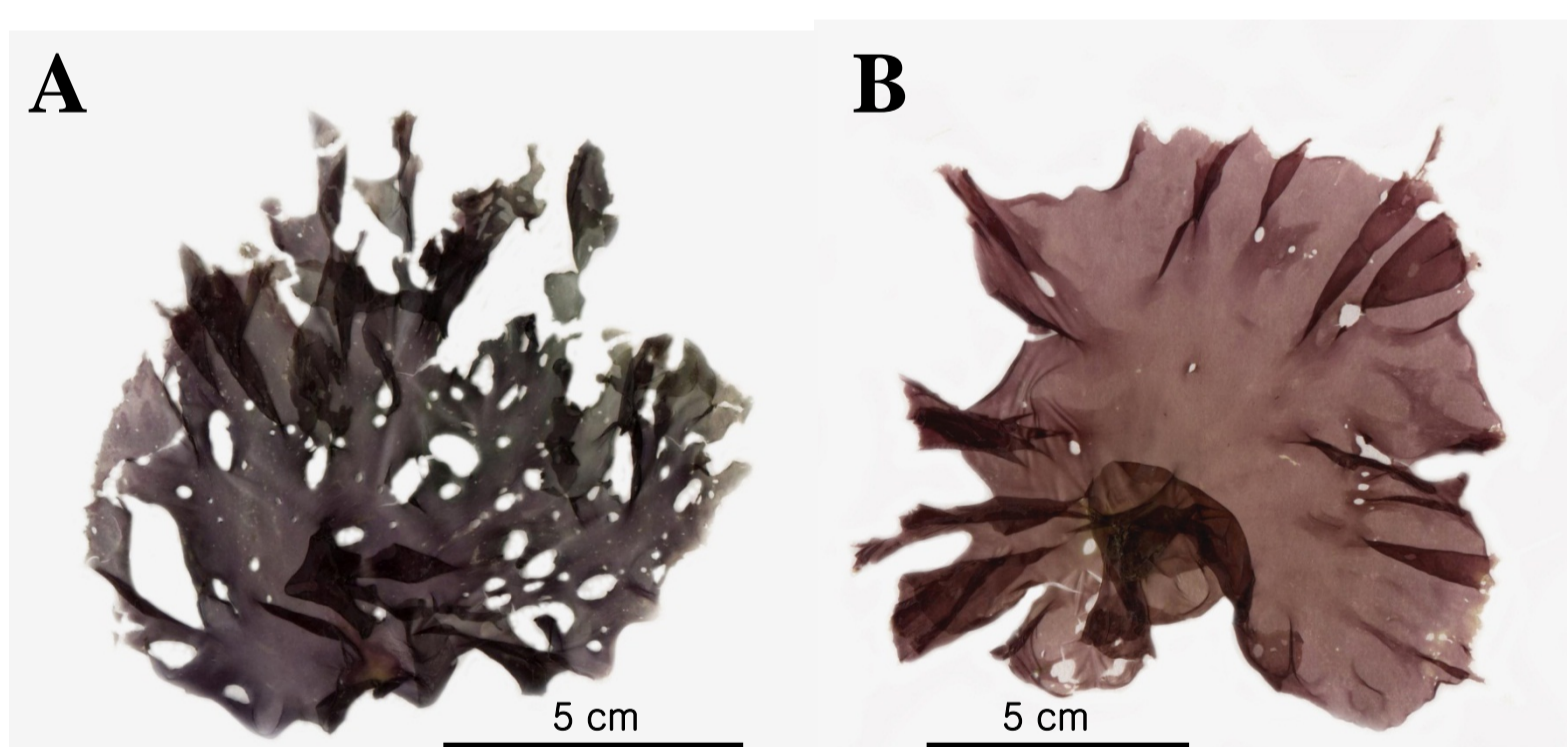
Morphology

Fig. 4. Pyropia endiviifolia and P. sp. A: A plant from King George Island, Antarctica. B: A plant from Punta Arenas, Chile.
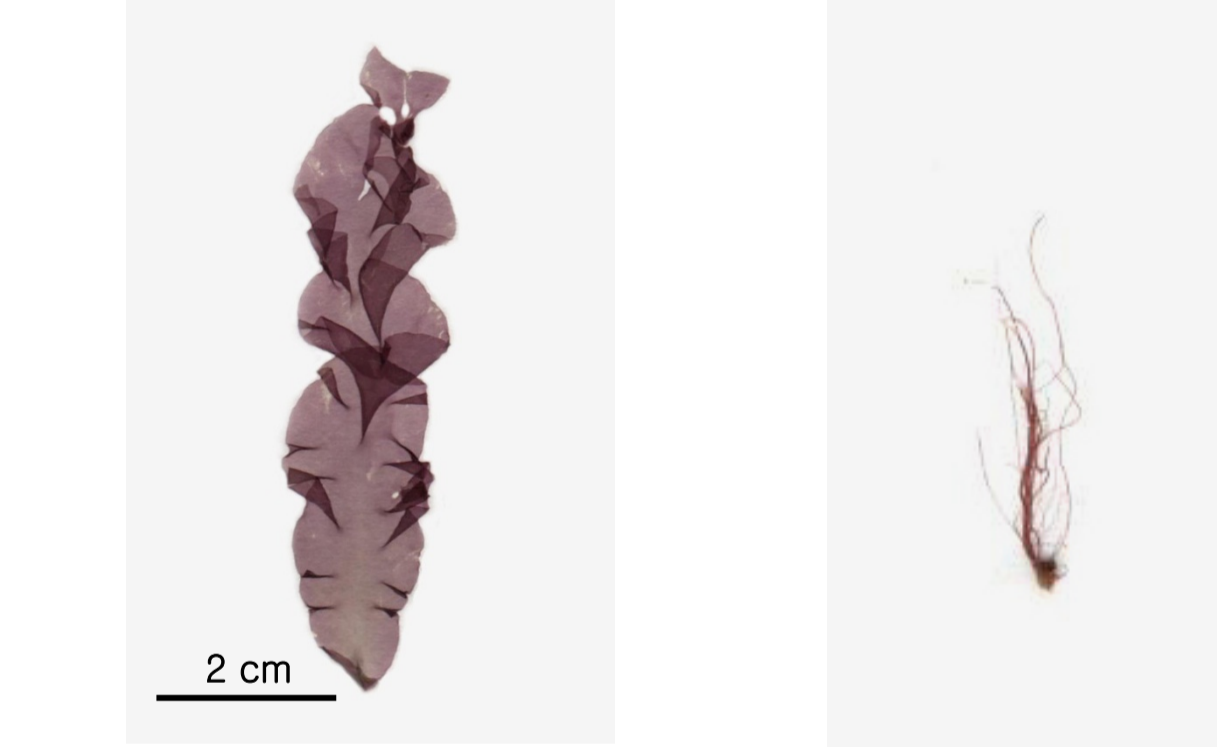

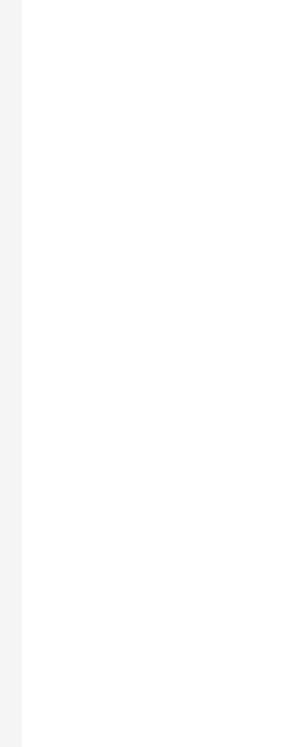**Fig. 5.** Porphyra woolhousiae from Punta Arenas, Chile.

Fig. 6. Bangia sp. from King George Island, Antarctica.

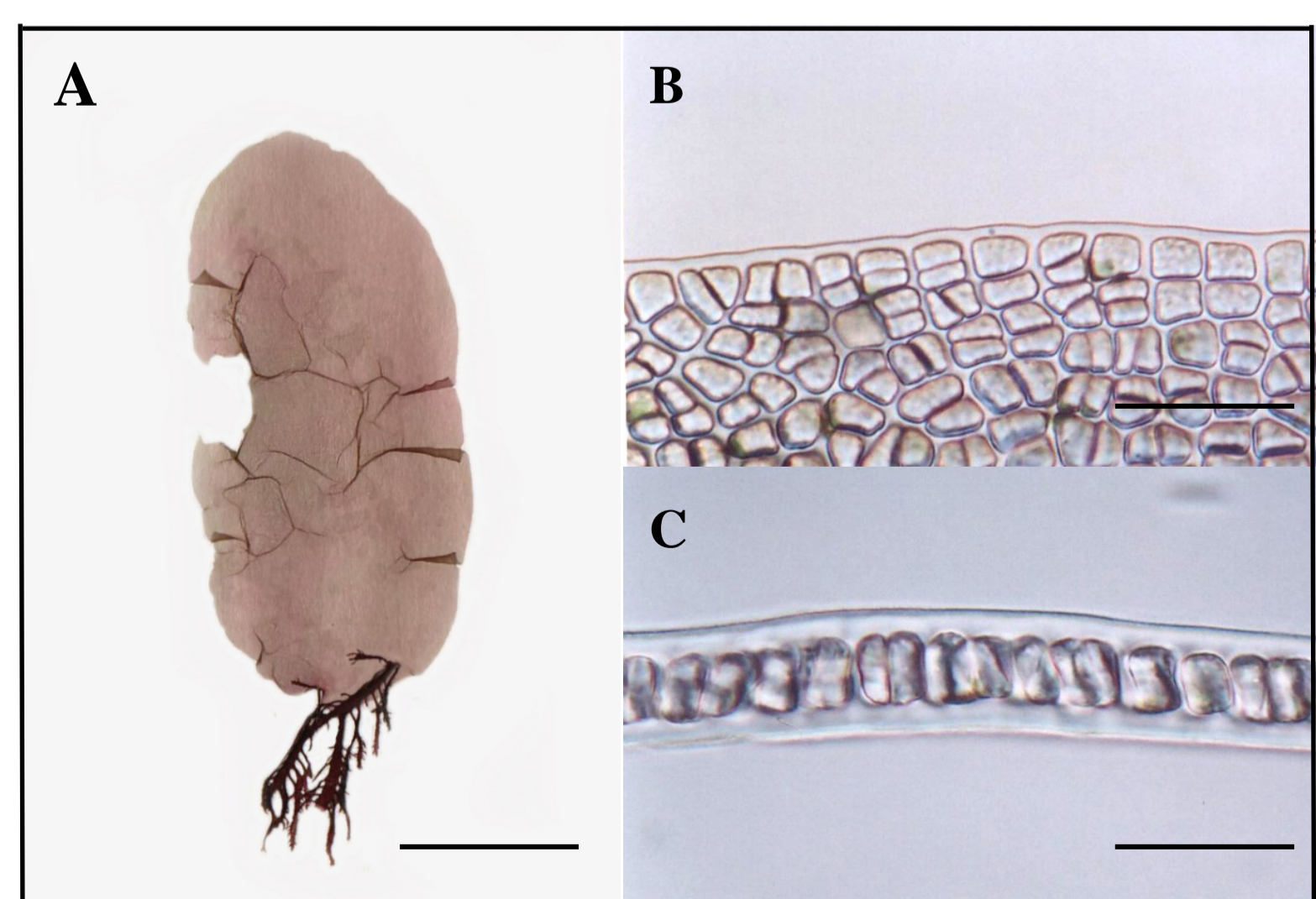**Fig. 7.** Wildemania plocamiestris from King George Island, Antarctica. A: Habit, B: Surface view of vegetative cells and margin of blade, C: Cross-sectional view of vegetative cells. Scale bars: 2 cm (A), 40 μm (B-C).
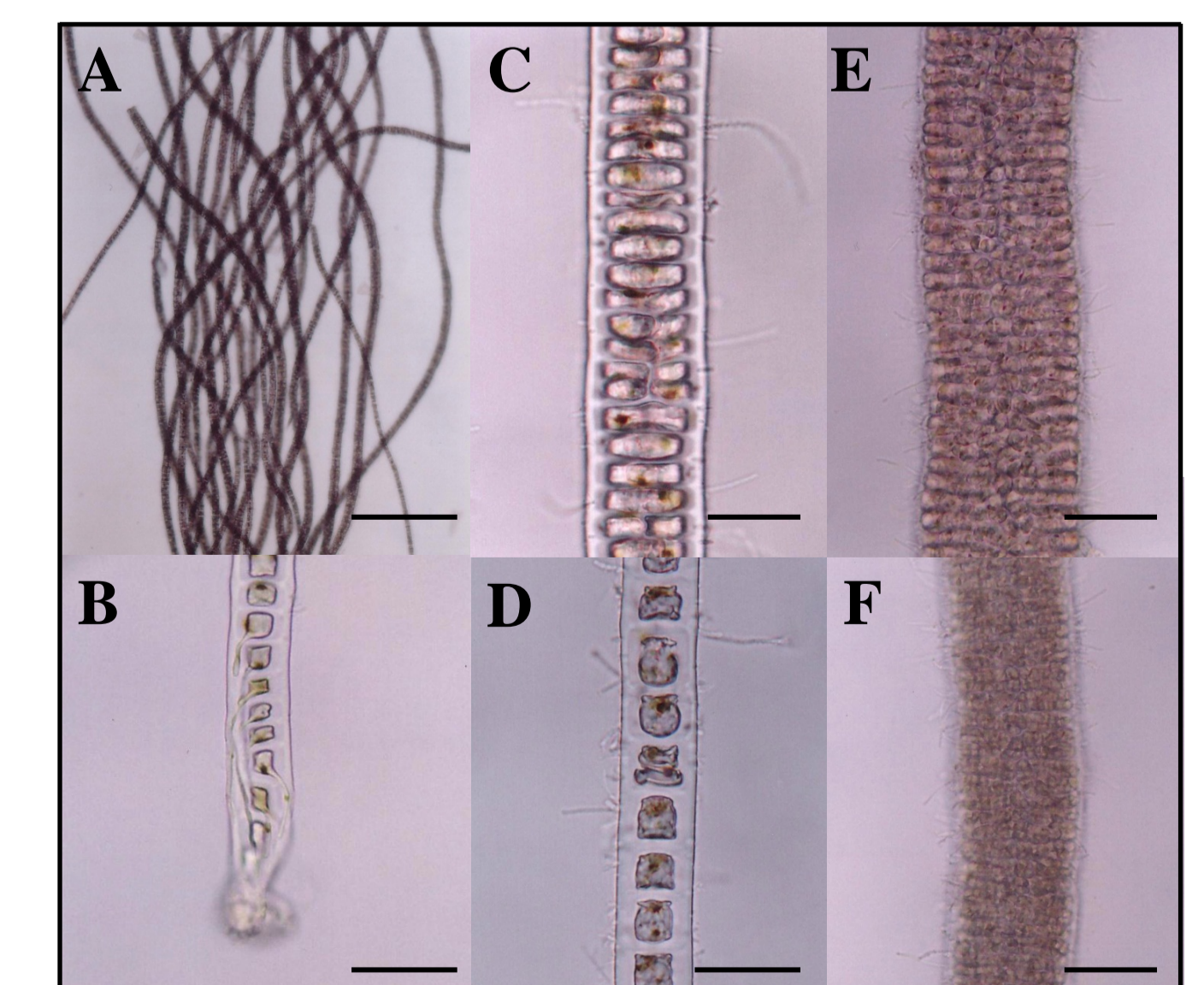

Fig. 8. Bangia sp. from King George Island, Antarctica. A: Habit, B: Rhizoidal cells, C: Cells of middle parts, D: Cells of lower part, E: Zygotosporangia, F: Spermatangia. Scale bars = 200 μm (A), 50 μm (B-D), 100 μm (E-F).
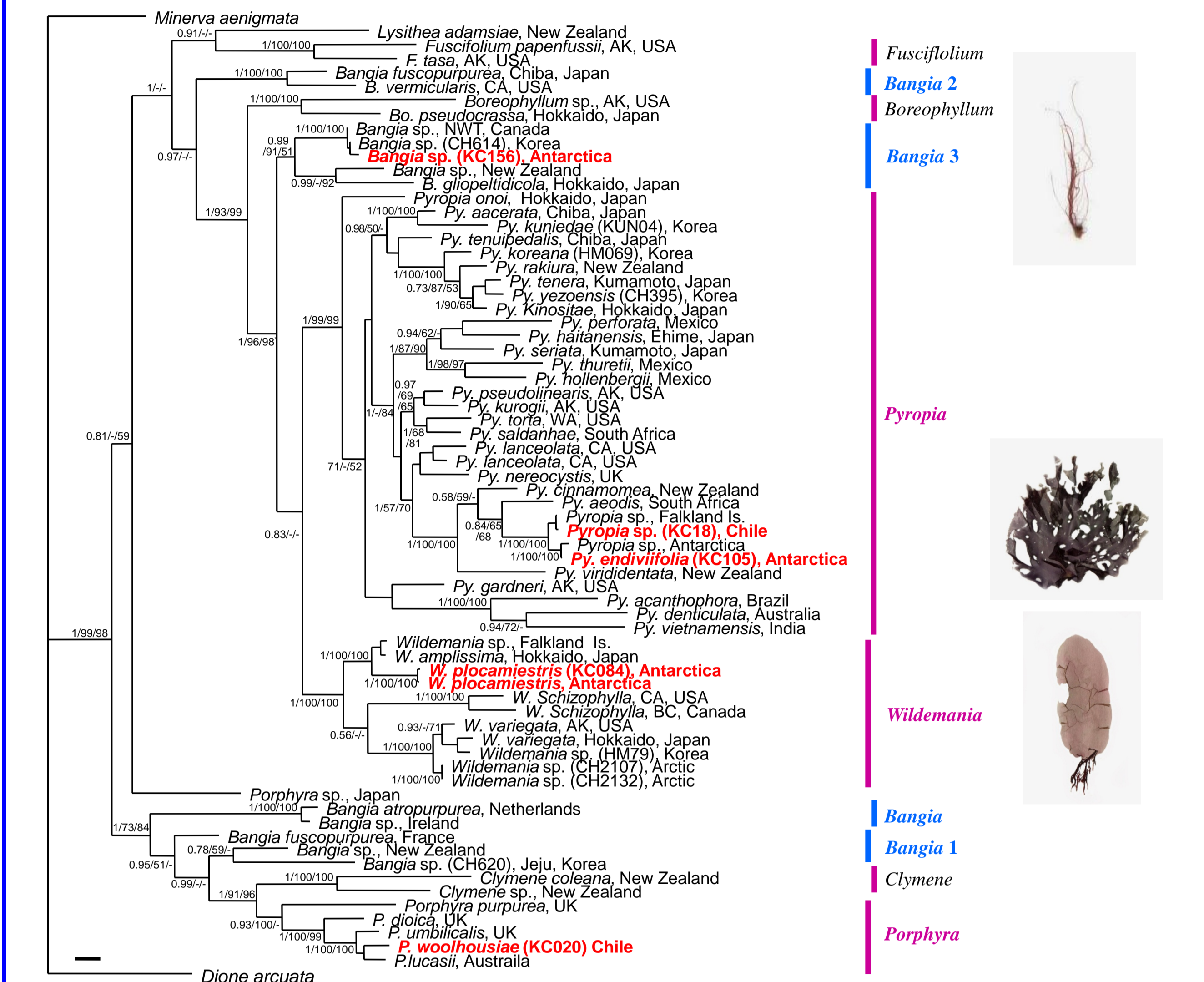
Molecular Phylogeny

Fig. 9. Tree constructed with Bayesian inference for the concatenated nuclear SSU rDNA and plastid rbcL data set (GTR+I+G model). Values at branches represent Bayesian posterior probabilities (left value), 2000 and 1000 bootstrap replicates each for distance and maximum parsimony (center and right values, respectively) analyses. Branches lacking values received less than 50% support. Scale bar = 0.01 substitutions/site.
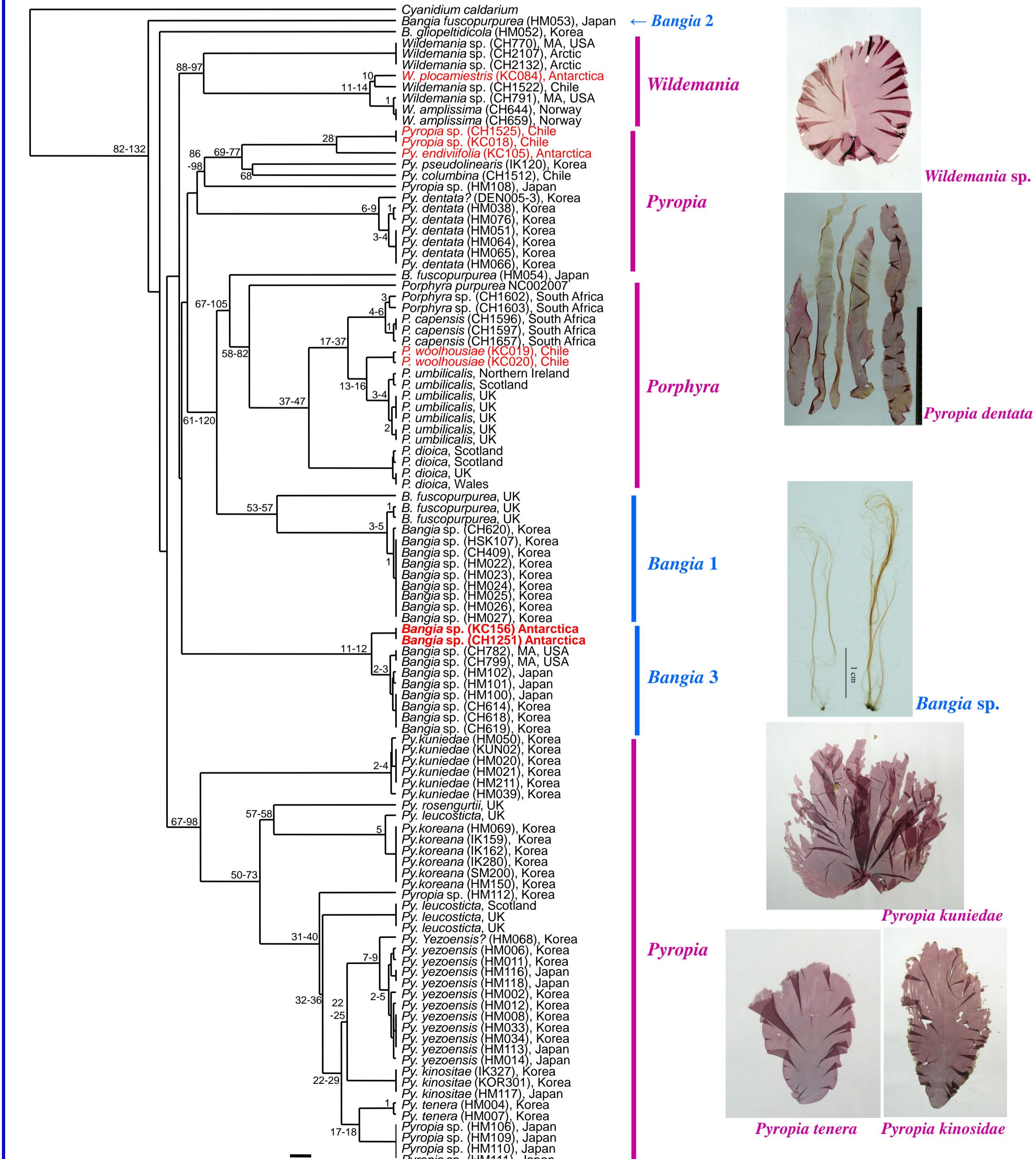

Fig. 10. Phylogram (UPGMA) displaying clustering of the included species for DNA barcoding by cox1 data in this study. Numbers in the right side of each node indicate numbers of nucleotide changes between related taxa. Scale bar = 5 changes.

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