

## Mitochondrial DNA

The Journal of DNA Mapping, Sequencing, and Analysis

ISSN: 1940-1736 (Print) 1940-1744 (Online) Journal homepage: <http://www.tandfonline.com/loi/imdn20>

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To cite this article: Yoonjee Kang, Hyoungseok Lee, Mi-kyeong Kim, Seung Chul Shin, Hyun Park & Jungeun Lee (2015): The complete chloroplast genome of Antarctic pearlwort, *Colobanthus quitensis* (Kunth) Bartl. (Caryophyllaceae), *Mitochondrial DNA*, DOI: [10.3109/19401736.2015.1106498](https://doi.org/10.3109/19401736.2015.1106498)

To link to this article: <http://dx.doi.org/10.3109/19401736.2015.1106498>



Published online: 25 Nov 2015.



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## MITOGENOME ANNOUNCEMENT

**The complete chloroplast genome of Antarctic pearlwort, *Colobanthus quitensis* (Kunth) Bartl. (Caryophyllaceae)**Yoonjee Kang<sup>1</sup>, Hyoungseok Lee<sup>1</sup>, Mi-kyeong Kim<sup>1</sup>, Seung Chul Shin<sup>1</sup>, Hyun Park<sup>1,2</sup>, and Jungeun Lee<sup>1</sup><sup>1</sup>Division of Life Sciences, Korea Polar Research Institute, Incheon, South Korea and <sup>2</sup>Department of Polar Sciences, University of Science and Technology, Incheon, South Korea**Abstract**

We determined the complete chloroplast DNA sequence of an extremophile plant, *Colobanthus quitensis* (Antarctic pearlwort), by *de novo* assembly based on the sequencing results from Illumina MiSeq platform (Illumina Inc., San Diego, CA). The chloroplast genome of *C. quitensis* (NCBI accession no. KT737383) is a sequence of 151 276 bp long with a typical quadripartite structure composed of a large single copy region, a small single copy region and a pair of inverted repeats. The overall GC content of *C. quitensis* genome is 36.7% and it has 66 simple sequence repeats. It contains a total 112 genes including 78 protein coding genes, 30 tRNA genes, and four rRNA genes.

**Keywords**

Chloroplast genome sequence, *Colobanthus quitensis*, extremophile plant

**History**

Received 16 September 2015  
Revised 30 September 2015  
Accepted 7 October 2015  
Published online 17 November 2015

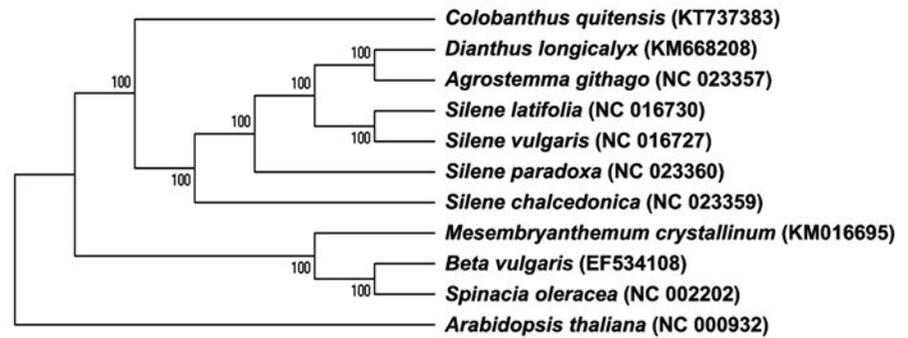
The Caryophyllaceae (Caryophyllales) is a family with 86 genera of 2200 species of herbaceous annuals and perennials. Although the distribution of the family is mainly north temperate, there are genera endemic to North America, South America, Africa, and Asia, and some species have settled in dry and exposed habitats in the high latitude regions (Bittrich, 1993). *Colobanthus quitensis* (caryophyllaceae) is one of the two native Antarctic plants with specific traits to adapt the extreme environment (Bascunan-Godoy et al., 2012; Day et al., 1999; Xiong et al., 2000). The previous phylogenetic studies with sequences of the nuclear ribosomal ITS region and five chloroplast genes and intergenic spacers support that it is included in Sagineae (Greenberg & Donoghue, 2011). However, the phylogenomic data is still limited for the species within Caryophyllaceae family. In this study, we generated the complete chloroplast genome sequence of *C. quitensis* to provide the genetic resources for better understanding of phylogenetic relationships between the Caryophyllaceae species.

*Colobanthus quitensis* plants growing under natural conditions were collected in the vicinity of the Korean King Sejong Antarctic Station (62°14'29"S, 58°44'18"W) on the Barton Peninsula of King George Island. The samples were transferred to the

laboratory in KOPRI and grown at 16 °C. Total genomic DNA was isolated from leaves of *C. quitensis* plants grown in the growth chamber. An illumina paired end library was constructed and sequenced using an Illumina MiSeq platform with the paired-end (300 × 2) mode. Total 4.2 G of nucleotides and 15 722 932 sequences in pairs were obtained and assembled using a CLC Genomics Workbench 7.5 (CLC Bio Aarhus, Denmark). The assembled contigs were aligned to the reference genomes of two Caryophyllaceae species, *Agrostemma githago* (NC\_023357) and *Silene paradoxa* (NC\_023360), because these species were identified as the top-hit species when the input reads were blasted against the nr database. The draft sequence was manually revised through a series of reads mappings. The genes in the chloroplast genome were annotated using the DOGMA program (Wyman et al., 2004) and blast searches.

The complete chloroplast genome of *C. quitensis* (GenBank accession KT737383) was 151 276 bp long. It is composed of a large single copy (LSC) of 83 462 bp and small single copy (SSC) of 17 208 bp, separated by a pair of completely identical inverted repeats (IRA and IRB, 25 303 bp for each). The overall GC content of the *C. quitensis* is 36.7% and 66 simple sequence repeats (SSRs) were detected. The chloroplast genome had a total 112 genes including 78 coding genes, 30 tRNA genes and four rRNA genes. Phylogenetic analysis was performed using complete chloroplast genome sequence of *C. quitensis* with publicly available chloroplast genomes of 9 species belong to Caryophyllales, by MAFFT alignment (Katoh & Standley, 2013) and a maximum likelihood analysis of MEGA 6.0 (Tamura et al., 2013) (Figure 1). The phylogenetic analysis placed *C. quitensis* most closely to *Dianthus longicalyx* and *Agrostemma githago* within the Caryophyllaceae family, as expected.

Figure 1. Molecular phylogenetic analysis of *C. quitensis* with species in the Caryophyllales order by maximum likelihood method. The chloroplast sequence of *Arabidopsis* was used as the outgroup.



## Declaration of interest

The authors report that they have no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This work was funded by Korea Polar Research Institute (PE15070).

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