

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>

The complete chloroplast genome of two Brassica species, *Brassica nigra* and *B. Oleracea*

Young-Joo Seol, Kyunghee Kim, Sang-Ho Kang, Sampath Perumal, Jonghoon Lee & Chang-Kug Kim

To cite this article: Young-Joo Seol, Kyunghee Kim, Sang-Ho Kang, Sampath Perumal, Jonghoon Lee & Chang-Kug Kim (2015): The complete chloroplast genome of two Brassica species, *Brassica nigra* and *B. Oleracea*, *Mitochondrial DNA*, DOI: [10.3109/19401736.2015.1115493](https://doi.org/10.3109/19401736.2015.1115493)

To link to this article: <http://dx.doi.org/10.3109/19401736.2015.1115493>



Published online: 28 Dec 2015.



Submit your article to this journal [↗](#)



Article views: 8



View related articles [↗](#)



View Crossmark data [↗](#)

MITOGENOME ANNOUNCEMENT

The complete chloroplast genome of two *Brassica* species, *Brassica nigra* and *B. Oleracea*

Young-Joo Seol^{a,*}, Kyunghye Kim^{b,c,*}, Sang-Ho Kang^a, Sampath Perumal^b, Jonghoon Lee^b and Chang-Kug Kim^a

^aGenomics Division, National Academy of Agricultural Science (NAAS), Rural Development Administration (RDA), Jeonju, Republic of Korea;

^bDepartment of Plant Science, Plant Genomics and Breeding Institute, and Research Institute of Agriculture and Life Sciences, College of Agriculture and Life Sciences, Seoul National University, Seoul, Republic of Korea; ^cPhyzen Genomics Institute, Gwanak-Gu, Seoul, Republic of Korea

ABSTRACT

The two *Brassica* species, *Brassica nigra* and *Brassica oleracea*, are important agronomic crops. The chloroplast genome sequences were generated by *de novo* assembly using whole genome next-generation sequences. The chloroplast genomes of *B. nigra* and *B. oleracea* were 153 633 bp and 153 366 bp in size, respectively, and showed conserved typical chloroplast structure. The both chloroplast genomes contained a total of 114 genes including 80 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Phylogenetic analysis revealed that *B. oleracea* is closely related to *B. rapa* and *B. napus* but *B. nigra* is more diverse than the neighbor species *Raphanus sativus*.

ARTICLE HISTORY

Received 13 October 2015
Revised 19 October 2015
Accepted 29 October 2015
Published online
22 December 2015

KEYWORDS

B. nigra, *B. oleracea*, chloroplast, genome sequence

The genus *Brassica* belonged to the family Brassicaceae is an annual herbaceous plant and known to be native to the middle and central Asia and Europe. *Brassica nigra* and *B. oleracea* are widely cultivated for supplement of vitamin C, dietary fiber, ingredients, and vegetable for cuisine in the world. Three *Brassica* species, *B. rapa* ($2n = 20$, AA genome), *B. nigra* ($2n = 16$, BB genome), and *B. oleracea* ($2n = 18$, CC genome), represent basal *Brassica* species and the natural allotetraploid between the three species were also reported (UN, 1935). Many research for *Brassica* genome evolution have been reported (Cheng et al., 2014; Palmer et al., 1983; Park et al., 2005; Yang et al., 2006). Recently, chloroplast genome sequences of *B. rapa* (DQ231548) and *B. napus* (NC016734) were reported (Hu et al., 2011). However, there is no information for the complete chloroplast genome sequences of *B. nigra* and *B. oleracea*. In this study, we generated the complete chloroplast genome sequences of *B. nigra* and *B. oleracea* to provide the genome information in the genus *Brassica*.

Total genomic DNAs of *B. nigra* (IT119326) and *B. oleracea* (accession no. C1176) were extracted from young leaves provided from the RDA-Genebank (<http://www.genebank.go.kr/>) and Joeun Seeds Co. (Chungcheongbuk-Do), Korea. An Illumina paired-end (PE) genomic library with 300-bp insert was constructed and sequenced using an Illumina HiSeq platform (Illumina Inc., San Diego, CA) by Labgenomics (<http://Labgenomics.com>), Seongnam, Korea. PE reads of 2 Gb and 1.5 Gb were obtained for *B. nigra* and *B. oleracea*, respectively, and assembled by a CLC genome assembler (ver. 4.06 beta, CLC Inc, Rarhus, Denmark), as mentioned in Kim et al (2015). The representative chloroplast contigs were extracted,

ordered, and joined into a single draft sequence, by comparison with the chloroplast sequence of *B. rapa* (DQ231548) as a reference. The draft sequence was confirmed and manually corrected by PE read mapping. The genes in the chloroplast genome were predicted using the DOGMA program (Wyman et al., 2004) and BLAST searches.

The chloroplast genomes of *B. nigra* (GenBank accession no. KT878383) and *B. oleracea* (GenBank accession no. KR233156) were a circular form of 153 633 bp and 153 366 bp in length, respectively. The chloroplast genomes showed conserved typical structure such as large single copy (LSC) regions of 83 552 bp and 83 137 bp, small single copy (SSC) regions of 17 695 bp and 17 835 bp, and a pair of inverted repeat regions of 26 193 bp and 26 197 bp in *B. nigra* and *B. oleracea*, respectively. The both chloroplast genomes contained 114 genes including 80 protein-coding genes, 30 tRNA genes, and 4 rRNA genes. Sequence homology of whole chloroplast genome between *B. nigra* and *B. oleracea* was 96.8%.

Phylogenetic relationship was revealed using total chloroplast protein-coding sequences of *B. nigra* and *B. oleracea* with those of 10 reported species in the order Brassicales by a maximum likelihood (ML) analysis of MEGA 6.0 (Tamura et al., 2013). The phylogenetic analysis revealed that *B. oleracea* (CC genome) is closely related to *B. rapa* (AA genome) and *B. napus* (AACC genome) but *B. nigra* (BB genome) is more diverse than the neighbor species *Raphanus sativus* (Figure 1), which is coincident with the genome study (Jeong et al., 2014; Yang et al., 2002)

*These authors contributed equally to this work.

CONTACT Chang-Kug Kim ✉ chang@korea.kr Genomics Division, National Academy of Agricultural Science (NAAS), Rural Development Administration (RDA), Jeonju 54874, Republic of Korea

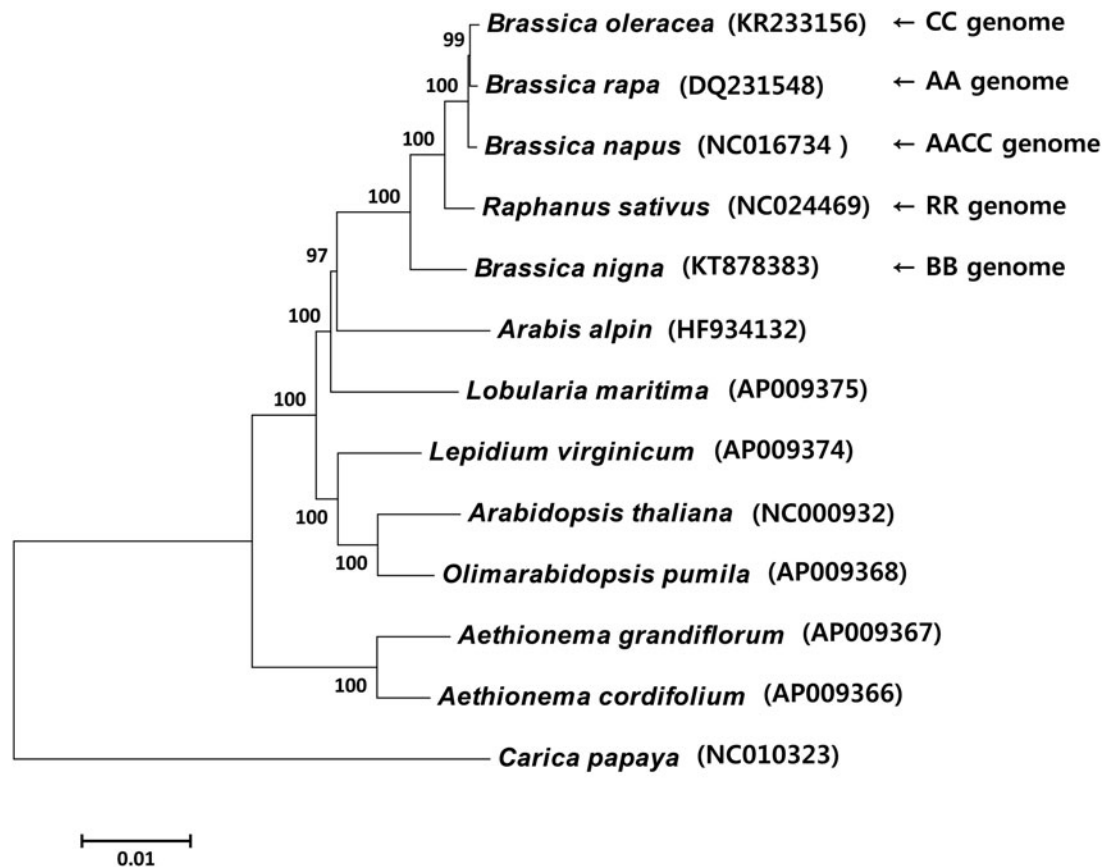


Figure 1. ML phylogenetic tree of *B. nigra* and *B. oleracea* with 10 species in the order Brassicales based on chloroplast protein-coding sequences. Numbers in the nodes are bootstrap values from 1000 replicates. The chloroplast sequence of *Carica papaya*, a species of the family Caricaceae, was set as the outgroup.

Declaration of interest

This study was conducted with supports from the research program for agricultural science and technology development (Project no. PJ010112) of the NAAS and from "Cooperative Research Program for Agriculture Science & Technology Development (SSAC, Grant no. PJ011650)", RDA, Republic of Korea.

References

Cheng F, Wu J, Wang X. (2014). Genome triplication drove the diversification of *Brassica* plants. *Horticult Res* 1. Article no: 14024 (2014). doi:10.1038/hortres.2014.24.

Hu ZY, Hua W, Huang SM, Wang HZ. (2011). Complete chloroplast genome sequence of rapeseed (*Brassica napus* L.) and its evolutionary implications. *Genet Resour Crop E* 58:875–87.

Jeong YM, Chung WH, Mun JH, Kim N, Yu HJ. (2014). De novo assembly and characterization of the complete chloroplast genome of radish (*Raphanus sativus* L.). *Gene* 551:39–48.

Kim K, Lee SC, Lee J, Lee HO, Joh HJ, Kim NH, Park HS, Yang TJ. (2015). Comprehensive survey of genetic diversity in chloroplast genomes and 45S rDNAs within *Panax ginseng* species. *PLoS One* 10:e0117159

Palmer JD, Shields CR, Cohen DB, Orton TJ. (1983). Chloroplast DNA evolution and the origin of amphidiploid *Brassica* species. *Theor Appl Genet* 65:181–9.

Park JY, Koo DH, Hong CP, Lee SJ, Jeon JW, Lee SH, Yun PY, et al. (2005). Physical mapping and microsynteny of *Brassica rapa* ssp. *pekinensis* genome corresponding to a 222 kbp gene-rich region of *Arabidopsis* chromosome 4 and partially duplicated on chromosome 5. *Mol Genet Genomics* 274:579–588.

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. (2013). MEGA6: Molecular evolutionary genetics analysis version 6.0. *Mol Biol Evol* 30:2725–9.

UN (1935). Genome analysis in *Brassica* with special reference to the experimental formation of *B. napus* and peculiar mode of fertilization. *Jap J Bot* 7:389–452.

Wyman SK, Jansen RK, Boore JL. (2004). Automatic annotation of organellar genomes with DOGMA. *Bioinformatics* 20:3252–5.

Yang TJ, Kim JS, Kwon SJ, Lim KB, Choi BS, Kim JA, Jin M, et al. (2006). Sequence-level analysis of the diploidization process in the triplicated *FLOWERING LOCUS C* region of *Brassica rapa*. *Plant Cell* 18:1339–1347.

Yang YW, Tai PY, Chen Y, Li WH. (2002). A study of the phylogeny of *Brassica rapa*, *B. nigra*, *Raphanus sativus*, and their related genera using noncoding regions of chloroplast DNA. *Mol Phylogenet Evol* 23:268–75.