Kohlrabi (*Brassica oleracea* var. *gongylodes* L.) is an important dietary rhizome vegetable in the Brassicaceae family. However, to date, few mitochondrial genomic resources have been reported for kohlrabi. In this study, we obtained the complete mitochondrial DNA sequence of 219,964 bp from an individual green kohlrabi. A total of 61 genes were annotated, including 33 protein-coding genes, 23 transfer RNA genes, three ribosomal RNA genes, and two pseudo genes. In addition, 1,001 open reading frames and five RNA editing sites were annotated. Relative synonymous codon usage analysis revealed significant difference in usage frequency of synonymous codon. Phylogenetic inference showed that kohlrabi is closely related to *B. oleracea* var. *botrytis*. This study provides a good foundation for further understanding the relationship and evolutionary origins among Brassicaceae crops.
great preference choices in its usage. Scattered repeats analysis identified 245 repeats, including 128 forward repeats and 117 palindromic repeats. The phylogenetic relationships among 13 species and kohlrabi based on coding sequences was determined using RAxML v8.2.10 (https://cme.h-its.org/exelixis/software.html) with the maximum-likelihood method and 1000 bootstrap replicates. *Oryza sativa* (NC 031333.1) was used as the outgroup. The results showed that kohlrabi (MW900252) is more closely related to *B. oleracea* var. *botrytis* (KJ820683.1) than to var. *capitata* (KU831325.1) (Figure 1), indicating similar evolution between kohlrabi and cauliflower. This study lays a good foundation for further understanding the relationships and evolutionary origins among Brassicaceae crops.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

**Funding**

This research was financially supported by the Key Research and Transformation Plan of Qinghai Provincial Science and Technology Department [2021-NK-124], Qinghai Natural Science Foundation [2020-ZJ-766], The Project of Qinghai Key Laboratory of Vegetable Genetics and Physiology [2020-ZJ-Y02].

**Data availability statement**

The data that support the findings of this study are openly available in NCBI at (https://www.ncbi.nlm.nih.gov/nuccore/MW900252) under the accession no. MW900252. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA721268, SRR14211765 and SAMN18713453.

**References**

Chan PP, Lowe TM. 2019. tRNAscan-SE: Searching for tRNA Genes in Genomic Sequences. Methods Mol Biol. 1962:1–14.

Han R, Tian M, Zhang G, Shao D, Ren Y. 2020. Complete chloroplast genome sequence of turnip (*Brassica rapa* ssp. *rapa*): genome structure and phylogenetic analysis. Mitochondrial Dna Part B. 5(3):3573–3575.
Hatono S, Nishimura K, Murakami Y, Tsujimura M, Yamagishi H. 2017. Complete mitochondrial genome sequences of Brassica rapa (Chinese cabbage and mizuna), and intraspecific differentiation of cytoplasm in B. rapa and Brassica juncea. Breed Sci. 67(4):357–362.

Jahangir M, Kim HK, Choi YH, Verpoorte R. 2009. Health-affecting compounds in Brassicaceae. Compr Rev Food Sci Food Saf. 8(2):31–43.

Liao X, Zhao Y, Kong X, Khan A, Zhou B, Liu D, Kashif MH, Chen P, Wang H, Zhou R. 2018. Complete sequence of kenaf (Hibiscus cannabinus) mitochondrial genome and comparative analysis with the mitochondrial genomes of other plants. Sci Rep. 8(1):12714.

Lim T. 2015. Brassica oleracea (Gongylodes group). In: Edible medicinal and non medicinal plants. Dordrecht: Springer; p. 768–776.

Palmer J, Herbon L. 1988. Plant mitochondrial DNA evolved rapidly in structure, but slowly in sequence. J Mol Evol. 28(1–2):87–97.

Palmer JD, Herbon LA. 1987. Unicircular structure of the Brassica hirta mitochondrial genome. Curr Genet. 11(6–7):565–570.

Park WT, Kim JK, Park S, Lee SW, Li X, Kim YB, Uddin MR, Park NI, Kim SJ, Park SU. 2012. Metabolic profiling of glucosinolates, anthocyanins, carotenoids, and other secondary metabolites in kohlrabi (Brassica oleracea var. gongylodes). J Agric Food Chem. 60(33):8111–8116.

Porebski S, Bailey LG, Baum BR. 1997. Modification of a CTAB DNA extraction protocol for plants containing high polysaccharide and polyphenol components. Plant Mol Biol Rep. 15(1):8–15.

Rahim MA, Robin AHK, Sathishkumar N, Jung HJ, Lee J, Kim H, Kim HT, Park JI, Nou IS. 2017. Identification and characterization of anthocyanin biosynthesis-related genes in Kohlrabi. Appl Biochem Biotechnol. 184:1120–1141.

Shen J, Zhang Y, Havey MJ, Shou W. 2019. Copy numbers of mitochondrial genes change during melon leaf development and are lower than the numbers of mitochondria. Hortic Res. 6:95.

Sloan DB, Alverson AJ, Chuckalovcak JP, Wu M, McCauley DE, Palmer JD, Taylor DR. 2012. Rapid evolution of enormous, multichromosomal genomes in flowering plant mitochondria with exceptionally high mutation rates. PLoS Biol. 10(1):e1001241.

Wang P, Lu Q, Ai Y, Wang Y, Li T, Wu L, Liu J, Cheng Q, Sun L, Shen H. 2019. Candidate gene selection for cytoplasmic male sterility in pepper (Capsicum annuum L.) through whole mitochondrial genome sequencing. Int J Mol Sci. 20:578.

Wyman SK, Jansen RK, Boone JL. 2004. Automatic annotation of organelar genomes with DOGMA. Bioinformatics. 20(17):3252–3255.

Yang K, Nath UK, Biswas MK, Kayum MA, Yi GE, Lee J, Yang TJ, Nou IS. 2018. Whole-genome sequencing of Brassica oleracea var. capitata reveals new diversity of the mitogenome. Plos One. 13(3):e0194356.

Zhang Y, Hu Z, Zhu M, Zhu Z, Wang Z, Tian S, Chen G. 2015. Anthocyanin accumulation and molecular analysis of correlated genes in purple kohlrabi (Brassica oleracea var. gongylodes L.). J Agric Food Chem. 63(16):4160–4169.