The complete chloroplast genome of cold hardiness individual of Coffea arabica L. (Rubiaceae)

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ABSTRACT

Coffea arabica is major cultivated species of coffee. We selected cold hardiness of C. arabica (named as CH3) based on selection of coffee seeds in Jeju Island, Korea. Here, we presented complete chloroplast genome of cold resistance C. arabica which is 155,192 bp long and has four subregions: 85,163 bp of large single copy (LSC) and 18,137 bp of small single copy (SSC) regions are separated by 25,946 bp of inverted repeat (IR) regions including 131 genes (86 protein-coding genes, eight rRNAs, and 37 tRNAs). The overall GC content of the chloroplast genome is 37.4% and those in the LSC, SSC, and IR regions are 35.3%, 31.3%, and 43.0%, respectively. Three non-synonymous single nucleotide polymorphisms and three insertions and deletions are found, indicating that further analysis will be required to understand genetic elements of cold hardiness of CH3.

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one of parental species of *C. arabica* (Figure 1; Lashermes et al. 1999). Without CH3-specific sequence variations, genetic elements linked to cold hardiness will be identified through further analyses of its mitochondrial or whole genomes.

**Disclosure statement**

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**References**

Barre P, Layssac M, D’Hont A, Louarn J, Charrier A, Hamon S, Noirot M. 1998. Relationship between parental chromosomal contribution and nuclear DNA content in the coffee interspecific hybrid *C. pseudozanguebariae* × *C. liberica* var ‘dewevrei’. Theoretical and Applied Genetics. 96:301–305.

Bentley JW, Baker PS. 2000. The Colombian Coffee Growers’ Federation: organised, successful smallholder farmers for 70 years. Bogotá (Colombia): ODI.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30:772–780.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2013. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol. 35:1547–1549.

Lashermes P, Combes M-C, Robert J, Trouslot P, D’Hont A, Anthony F, Charrier A. 1999. Molecular characterisation and origin of the *Coffea arabica* L. genome. Mol General Genet MGG. 261:259–266.

Li H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv preprint arXiv:1303.3997.

Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R. 2009. The sequence alignment/map format and SAMtools. Bioinformatics. 25:2078–2079.

O’Brien TG, Kinnaird MF. 2003. Caffeine and conservation. Am Assoc Adv Sci. 300:587.

Samson N, Bausher MG, Lee SB, Jansen RK, Daniell H. 2007. The complete nucleotide sequence of the coffee (*Coffea arabica* L.) chloroplast genome: organization and implications for biotechnology and phylogenetic relationships amongst angiosperms. Plant Biotechnol J. 5:339–353.

Willson K. 1999. Coffee, cocoa and tea. Wallingford: CAB International.

Wu D, Bi C, Wang X, Xu Y, Ye Q, Ye N. 2017. The complete chloroplast genome sequence of an economic plant *Coffea canephora*. Mitochondr DNA B. 2:483–485.

Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. Genome Res. 18:821–829.

Zhao Q-Y, Wang Y, Kong Y-M, Luo D, Li X, Hao P. 2011. Optimizing *de novo* transcriptome assembly from short-read RNA-Seq data: a comparative study. BMC Bioinform. 12:52.