The chloroplast genome sequence and characteristic analysis of *Vitex negundo* var. *heterophylla* (Franch.) Rehder

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**ABSTRACT**

*Vitex negundo* var. *heterophylla* (Franch.) Rehder is a common small shrub in northern China. In order to study the fine nectar characteristics and water and soil conservation characteristics of *V. negundo*, the analysis of chloroplast genome would provide theoretical basis for economic development and germplasm utilization of *V. negundo*. The chloroplast genome sequence (accession number MW366787) of *V. negundo* was accepted by high-throughput sequencing technology using a plant from Jiulongshan, Mentougou District, Beijing, China. The total length of the chloroplast genome is 154,438 bp, and the A, T, C and G content of the whole genome is 30.48, 31.26, 19.42, and 18.84%, respectively. The phylogenetic analysis of 16 Verbenaceae plants (including *V. negundo*) with *Arabidopsis thaliana* as the outgroup was carried out by the maximum likelihood method; and the result shows that *V. negundo* is relatively closed to *Vitex rotundifolia*.

*Vitex negundo* var. *heterophylla* (Franch.) Rehder is widely distributed in northern China and has been known as an excellent nectar plant. *Vitex negundo* var. *heterophylla* is a variant of *Vitex negundo*. The whole plant of *V. negundo* could be used medicinally to treat diseases such as asthma, stomach pain and tinea capitis (Meena et al. 2011). *V. negundo* is also widely accepted as the resource of health food due to the presence of biologically active ingredients, which could improve physical conditions in China. The seed of *V. negundo* contained a variety of phenolic compounds, which were evaluated to improve physical conditions in China. The seed of *V. negundo* is also used medicinally to treat diseases such as asthma, stomach pain and tinea capitis (Meena et al. 2011). *V. negundo* is also widely accepted as the resource of health food due to the presence of biologically active ingredients, which could improve physical conditions in China. The seed of *V. negundo* contained a variety of phenolic compounds, which were evaluated to improve physical conditions in China. The seed of *V. negundo* is also used medicinally to treat diseases such as asthma, stomach pain and tinea capitis (Meena et al. 2011).

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The assembled chloroplast genome of *V. negundo* has been submitted to the NCBI database (accession number MW366787). The *V. negundo* chloroplast genome is 154,438 bp in length, of which the GC content is 38.26%; the A, T, C and G content of the whole genome is 30.48, 31.26, 19.42 and 18.84%, respectively. The chloroplast genome distributed in a typical four-segment structure. It is found that the LSC region (large single copy region) is 85,146 bp, and the IRB region (inverted repeat B) and the other IR region IRA (inverted repeat A) is 25,686 bp, the SSC area (small single copy region) is 17,920 bp. And it is found the overall AT content is 61.7%, showing obvious AT preference. A total of 132 genes are encoded in *V. negundo* chloroplast genome, including 87 protein-coding, 37 tRNAs, and 8 rRNAs genes. The LSC region contains 62 protein-coding and 22 tRNAs genes, and the SSC region contains 14 protein-coding and 1 tRNA genes. The rRNA genes are only in the two IR regions with 4 types, respectively. Six protein-coding genes and seven tRNAs genes are only included in IR regions. Eighteen genes (including 6 tRNA genes) in the *V. negundo* chloroplast genome contains one or two introns, of which ycf3, clpP1 and rps12 contain two introns. Therefore, the position of rps12 is quite special. Its 5'-end is located in the LSC region, and the two 3'-ends are located in the IRA and IRB regions. The length of introns in the *V. negundo* chloroplast genome is different: *trnK*-UUU is with the longest intron of 2,507 bp, and *trnL*-UAA is with the shortest intron of 485 bp.

In order to confirm the phylogenetic position of *V. negundo*, another 15 complete chloroplast genome sequences from Verbenaceae plants and *Arabidopsis thaliana* (the outgroup) were downloaded from NCBI. The Maximum Likelihood method under MEGA7 (Kumar et al. 2016) in FastTree software was used to perform the phylogenetic tree. After the tree construction was completed, the reliability of the branch of the phylogenetic tree was verified (Bootstrap, 1000 replications). The result showed that *V. negundo* and *V. rotundifolia* in the genus *Vitex* were clustered together, indicating that their evolutionary relationship is closer than that of other Verbenaceae plants (Figure 1). The complete chloroplast genome of *V. negundo* is an important resource, which would help further research the population genetics, systematic geography, evolution, and conservation biology of Verbenaceae.

**Disclosure statement**

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

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**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov) under the accession no. MW366787. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA701363, SRR13684571, and SAMN17864120, respectively.

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