

MITOGENOME ANNOUNCEMENT

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The complete chloroplast genome sequence of a Korean indigenous ornamental plant *Hydrangea serrata* for. *fertilis* Nakai (Hydrangeaceae)

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ABSTRACT

De novo assembly with whole genome sequencing data of *Hydrangea serrata* for. *fertilis*, a great ornamental landscape plant species worldwide, facilitated to generate the complete chloroplast genome sequence in this study. The complete sequence was a circular DNA molecule of 157 730 bp in length, containing the large single-copy (LSC) region of 86 789 bp, small single-copy (SSC) region of 18 711 bp and two inverted repeats (IRs) regions of 26 115 bp. The genome encoded 114 genes consisting of 80 protein-coding genes, 30 tRNA genes and four rRNA genes. Phylogenetic analysis with *matK* gene-coding sequences of 19 species in family Hydrangeaceae showed a close relationship of *H. serrata* for. *fertilis* Nakai with *H. macrophylla*.

ARTICLE HISTORY

Received 30 November 2015
Accepted 22 December 2015

KEYWORDS

Chloroplast; *Hydrangea serrata* for. *fertilis*; whole genome sequence

Hydrangea species are popular flowering shrubs and widely used as landscape plant with great ornamental value. The plants are famous for its inflorescences with both inconspicuous fertile and attractive neuter flowers (Reed 2002; Conolly et al. 2010; Samain et al. 2010). The increasing interests in *Hydrangea* species as decorative plants have led to increase availability of diverse *Hydrangea* species and cultivars with various coloured flowers and also to make the species one of the best-selling ornamental plants worldwide (Cerbah et al. 2001; Rinehart et al. 2006). There has been a taxonomically dispute in *Hydrangea* genus. *Hydrangea serrata* was classified as a subspecies of *H. macrophylla* by McClintock (1957), but recent publications on *Hydrangea* species have designated the two species as different species (Reed & Rinehart 2006). In this study, we generated the complete chloroplast genome sequence of *H. serrata* for. *fertilis*, called “Tamra Sansukuk” in Korea (Cho et al. 2014), to contribute to classification and authentication of *Hydrangea* species such as DNA marker application for ginseng cultivars (Kim et al. 2014).

A plant material of *H. serrata* for. *fertilis* collected from Mt. Halla, Jeju island, Korea, was provided from Hantaek Botanical Garden (<http://www.hantaek.co.kr/>), Yongin, Korea. Total genomic DNA was extracted from fresh leaves following a modified cetyltrimethylammonium bromide (CTAB) protocol (Allen et al. 2006). A pair-end (PE) library was constructed and sequenced using an Illumina MiSeq platform by Lab Genomics, Inc. (Seongnam, Korea). Raw sequence data of 1.12 Gb were filtered and *de novo* assembled by a CLC genome

assembler (v. beta 4.6, CLC Inc., Aarhus, Denmark), as described in Kim et al (2015a,b). Six representative chloroplast contigs were ordered and merged into a single draft sequence compared with the chloroplast sequence of *Zanthoxylum piperitum* (KT153018, Lee et al. 2015) as a reference. The draft sequence was validated using manual correction by PE read mapping. DOGMA software was used for annotation of protein-coding genes in the chloroplast genome (Wyman et al. 2004), and the annotation result was manually validated by BLAST searches.

The complete chloroplast genome was a circular DNA molecule of 157 730 bp in length with 37.5% of GC content, which was separated into a large single copy (LSC) region of 86 789 bp, a small single copy (SSC) region of 18 711 bp and a pair of inverted repeats (IRa and IRb) of 26 115 bp. The genome contained a total of 114 genes including 80 protein-coding genes 30 tRNA genes and four rRNA genes. The complete chloroplast genome was deposited at GenBank with accession number KU140669, which is the first complete chloroplast genome reported in family Hydrangeaceae and even in order Cornales.

The phylogenetic analysis was performed by comparison with *matK* coding sequences derived from other 19 species in family Hydrangeaceae, registered in NCBI Genbank, by a maximum likelihood analysis with 1000 bootstrap replicates using MEGA 6.0 program (Tamura et al. 2013). All tested species were clustered into their own genus groups, in which *H. serrata* for. *fertilis* was placed mostly close to *H. macrophylla* (Figure 1).

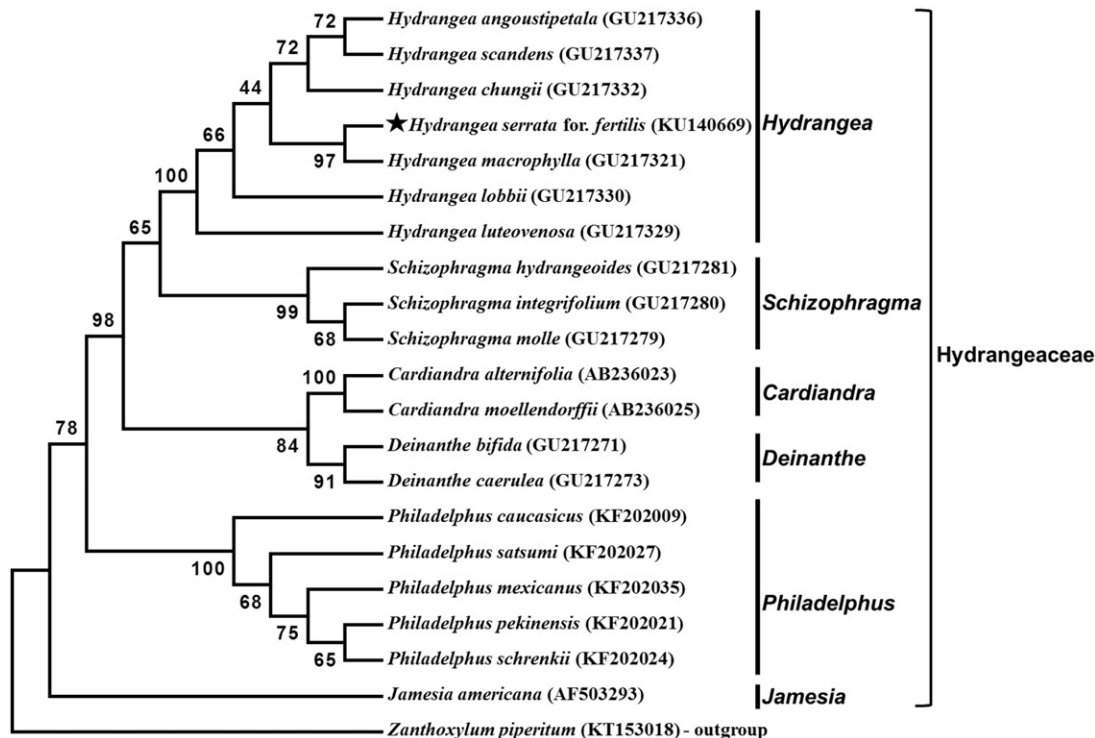


Figure 1. Maximum likelihood phylogenetic tree of *H. serrata* for. *fertilis* with other 19 species in Hydrangeaceae family based on *matK* coding sequences. Numbers in the nodes are the bootstrap values from 1000 replicates. The *matK* sequence of *Zanthoxylum piperitum* (KT153018) in family Rutaceae was set as an outgroup.

Declaration of interest

This research was supported by the Bio & Medical Technology Development Program of the NRF funded by the Korean government, MSIP (NRF-2015M3A9A5030733).

References

- Allen G, Flores-Vergara M, Krasynanski S, Kumar S, Thompson W. 2006. A modified protocol for rapid DNA isolation from plant tissues using cetyltrimethylammonium bromide. *Nat Protocols* 1:2320–2325.
- Cerbah M, Mortreau E, Brown S, Siljak-Yakovlev S, Bertrand H, Lambert C. 2001. Genome size variation and species relationships in the genus *Hydrangea*. *Theor Appl Genet*. 103:45–51
- Cho JS, Jeong JH, Kim SY, Lee JY, Lee CH. 2014. Several Factors affecting seed germination of *Hydrangea petiolaris* Siebold & Zucc. *Korean J Plant Res*. 27:534–539 (In Korean).
- Conolly NB, Bassuk NL, MacRae Jr PF. 2010. Response of five hydrangea species to foliar salt spray. *J Environ Hort*. 28:125–128.
- Kim NH, Choi HI, Kim KH, Jang W, Yang TJ. 2014. Evidence of genome duplication revealed by sequence analysis of multi-loci expressed sequence tag-simple sequence repeat bands in *Panax ginseng* Meyer. *J Ginseng Res*. 38:130–135.
- Kim K, Lee SC, Lee J, Lee HO, Joh HJ, Kim NH, Park HS, Yang TJ. 2015a. Comprehensive survey of genetic diversity in chloroplast genomes and 45S nrDNAs within *Panax ginseng* species. *PLoS One* 10:e0117159.
- Kim K, Lee SC, Lee J, Yu Y, Yang K, Choi BS, Koh HJ, Waminal NE, Choi HI, Kim NH, et al. 2015b. Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of *Oryza* AA genome species. *Sci Rep*. 5:15655.
- Lee J, Lee HJ, Kim K, Lee SC, Sung SH, Yang TJ. 2015. The Complete Chloroplast Genome Sequence of *Zanthoxylum Piperitum*. *Mitochondrial DNA*, Early Online: 1–2. DOI: 10.3109/19401736.2015.1074201.
- McClintock E. 1957. A monograph of the genus *Hydrangea*. *Proc Calif Acad Sci*. 29:147–256.
- Reed SM. 2002. Flowering performance of 21 *Hydrangea macrophylla* cultivars. *J Environ Hort*. 20:155–160.
- Reed SM, Rinehart TA. 2006. *Hydrangea macrophylla* and *serrata* – should we lump ‘em or split ‘em. In: Ranney TG, editor. Southern nursery association research conference, plant breeding & evaluation, vol. 51. Georgia: Southern Nursery Association, Inc. p. 656–659.
- Rinehart TA, Scheffler BE, Reed SM. 2006. Genetic diversity estimates for the genus *Hydrangea* and development of a molecular key based on SSR. *J Amer Soc Hort Sci*. 131:787–797.
- Samain MS, Wanke S, Goetghebeur P. 2010. Unraveling extensive paraphyly in the genus *Hydrangea* s. l. with implications for the systematics of tribe Hydrangeeae. *Syst Bot*. 35:593–600.
- Tamura K, Stecher G, Peterson D, Filipowski A, Kumar S. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. *Mol Biol Evol*. 30:2725–2729.
- Wyman SK, Jansen RK, Boore JL. 2004. Automatic annotation of organellar genomes with DOGMA. *Bioinformatics* 20:3252–3255.