

Cytological Analyses of *Iris ruthenica* K. Gawl. (Iridaceae), an Endangered Species in Korea

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Iris L. is a perennial genus comprising approximately 300 species worldwide, with the greatest number of endemic species occurring in Asia. *Iris* is one of the largest genera in the family Iridaceae and includes ca. 15 species native to Korea. Although chromosome number change, karyotype restructuring, and genome size variation play an important role in plant genome diversification, understanding the karyotype variation in Korean *Iris* species has been hampered by the wide range of base chromosome number ($x = 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 22$) reported to date. This study documents the chromosome numbers, karyotype structure and genome size variation in *Iris ruthenica* K. Gawl., an endangered species in Korea obtained using classic Feulgen staining and flow cytometry. The chromosome number of all investigated plants from the nine populations was $2n = 42$. All individuals studied possessed metacentric and submetacentric chromosomes. The genome size of the *I. ruthenica* in eight wild populations ranged from 2.39 pg/1C to 2.45 pg/1C (2.42 ± 0.02 pg/1C: mean \pm SD). This study provides the first report of genome size variation in *Iris ruthenica* in Korea. This study lays foundation for cytogenetic further analyses employing by fluorescence *in situ* hybridization (FISH) to better understand the chromosomal evolution in this species and in the whole genus.

Key words: Chromosome number, Genome size, *Iris ruthenica* K. Gawl., Karyotype

[This work was supported by grants from the National Research Foundation of Korea (NRF) funded by the Korea government (grant numbers NRF-2018R1C1B6003170) to T.-S. Jang.]

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