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Phylogeny of the genus *Hypericum* (Hypericaceae) based on nuclear ribosomal DNA (ITS) sequence data

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Hypericum is the largest genus in the family Hypericaceae. The species numbers are estimated approximately 350-400 species, and are distributed worldwide. Several species are widely cultivated in all over the world. We have constructed molecular phylogenetic analysis of the nuclear ribosomal DNA internal transcribed spacer (ITS) sequences from 36 Korean and Japanese *Hypericum* species and six other outgroup species (*Triadenum tuberulosum*, *Triadenum virginicum*, *Triadenum walferi*, *Triadenum japonicum*, *Thorea calcicola*, and *Thorea matudae*). The sampling included most of previously described species both from Korea and Japan. Trees from these markers are largely congruent and provide several insights. The ITS phylogeny suggests that *Hypericum* species from Korea and Japan grouped into two monophyletic sections (*Roscyna* and *Trigynobrathys*). But sect. *Hypericum* is not monophyletic group. *H. sampsonii* was aligned to sect. *Hypericum* or to sect. *Drosocarpium* by previous morphological studies, but the ITS tree suggest that the species should be a member of sect. *Roscyna* or of the distinct fourth sect. rather than section *Hypericum*. The taxonomically problematic *H. kamtschaticum* was a sister species of *H. erectum* and *H. attenuatum* within the section *Hypericum*. Although can not reason correct evolutionary trend untreating all taxons of three sections in this research, we could have evolutionary trend conclusion of *Hypericum* from *Roscyna*. This result is in agreement with recent suggestions based on morphological and cytological studies. Phylogenetic relationships among species from Korea and Japan are mostly resolved on the ITS tree. To clear system of whole Genus *Hypericum* need additions of more taxon and various maker's choice.

Keywords: *Hypericum*, Internal transcribed spacer (ITS), monophyletic group