



Title	Incongruence between cpDNA- and nrDNA-based phylogenies suggests the allopolyploid origin of tetraploid <i>Hydrangea liukuensis</i> (Saxifragaceae), an endemic shrub distributed on Okinawajima Island in the central Ryukyus.
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PS-22 Incongruence between cpDNA- and nrDNA-based phylogenies suggests the allopolyploid origin of tetraploid *Hydrangea liukiensis* (Saxifragaceae), an endemic shrub distributed on Okinawajima Island in the central Ryukyus.

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Hydrangea liukiensis is an endemic shrub only distributed on central to northern part of Okinawajima Island in the central Ryukyus of Japan. Despite narrow distribution, intraspecific polyploidy (diploid and tetraploid) has been reported in this species. To elucidate the origin of tetraploid *H. liukiensis*, chromosome and molecular phylogenetic analyses were conducted.

Tetraploids were found at three of the 17 localities investigated, while only diploids were found in the remaining 14 localities. Intra-population variation in the ploidy level was only observed in one locality (Taiho River), where diploids constituted a large majority of the population and only four tetraploids occurred contiguously.

Six diploids and six tetraploids of *H. liukiensis*, together with four closely related species (*H. chinensis*, *H. grosseserrata*, *H. kawagoeana*, *H. yayeyamensis*) and an outgroup species (*Cardiandra alternifolia*) were used for molecular analyses. Maximum parsimony (MP) and maximum likelihood (ML) trees based on the *trnS-G* region of chloroplast DNA (cpDNA) showed that diploid and tetraploid *H. liukiensis* were monophyletic and sister to the clade of the remaining four *Hydrangea* species. In contrast, in MP and ML trees based on the ITS region of nuclear ribosomal DNA (nrDNA), tetraploid *H. liukiensis* nested with *H. chinensis* and formed a monophyletic clade together with *H. grosseserrata*, *H. kawagoeana*, and *H. yayeyamensis*. This clade was sister to a monophyletic clade comprised of only diploid *H. liukiensis*.

The incongruence between cpDNA- and nrDNA-based phylogeny of *H. liukiensis* seems to suggest an allopolyploid origin of tetraploid *H. liukiensis*. Although no other *Hydrangea* species except *H. liukiensis* are distributed on Okinawajima Island in the current Ryukyus, past interspecific hybridization event(s) between diploid *H. liukiensis* and an extinct parent may have led to the origin of tetraploid *H. liukiensis*.