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PS-30 Chromosomal studies of *Lonicera japonica* var. *miyagusukiana* (Caprifoliaceae), an endemic to the Ryukyu Archipelago of Japan: as a first step towards elucidating its origin

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Lonicera japonica var. *miyagusukiana* is a trailing or climbing vine that is distributed only on eight islands from the central to southern Ryukyus. This insular endemic taxon is clearly distinguished from the type variety *L. japonica* var. *japonica* (Japanese honeysuckle) by its smaller, thicker, and denser leaves, and smaller flowers with dense glandular hairs on the outer corolla surface. *Lonicera japonica* var. *japonica* is an extremely vigorous vine that grows in sunny forest edges and is native to temperate eastern Asia. Since it was introduced outside of Asia in the early 19th century, *L. japonica* var. *japonica* became a troublesome pest outside of its native range, with serious negative effects on native floras. In contrast to the vigorousness of the type variety, the habitat of *L. japonica* var. *miyagusukiana* is restricted to the tops of exposed windy limestone cliffs. Recent human activities threaten *L. japonica* var. *miyagusukiana* in some localities; thus, this taxon is listed in the Red Data Books for this area.

Here we report the results of the first chromosomal studies for *L. japonica* var. *miyagusukiana* as a first step towards elucidating its origin. *Lonicera japonica* var. *japonica* from Japan was also analyzed for comparison. All individuals of *L. japonica* var. *miyagusukiana* collected from three islands (Okinawa-jima, Ie-jima, and Yonaguni-jima) of the central and southern Ryukyus were tetraploid with chromosome number of $2n = 36$ [$2n = 36 = 4m + 28sm$ (2SAT) + 4st], whereas *L. japonica* var. *japonica* was diploid with $2n = 18$ [$2n = 18 = 2m + 14sm$ (2SAT) + 2st], indicating karyotype similarity. However, the karyotypes of *L. japonica* var. *miyagusukiana* and *L. japonica* var. *japonica* differed from those of previously reported diploid and tetraploid *L. japonica* from China. These results, together with the remote distribution, seem to suggest that *L. japonica* var. *miyagusukiana* is a local tetraploid derivative of the diploid *L. japonica* var. *japonica* in the Ryukyus. Because little information is available about the karyotype and phylogenetic features of *L. japonica* and its relatives, however, we cannot exclude the possibility that *L. japonica* var. *miyagusukiana* is derived from other diploid taxa found either in the Ryukyus or elsewhere.