



Nuclear and plastid DNA data confirm that *Sedum tosaense* (Crassulaceae) has a disjunct distribution between Pacific mainland Japan and Jeju Island, Korea

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Abstract

Our molecular phylogeographic analyses based on the nrDNA ITS and cpDNA *trnLF* of *Sedum tosaense* populations in the Shikoku District, Japan and Jeju Island, Korea suggested a disjunct distribution. Plants of *S. tosaense* from the two regions comprised a well-supported clade consisted of plants from Kochi (Shikoku District) and those from Jeju Island; we estimated a divergence time of 0.61 Ma between the Kochi and Jeju populations based on the ITS and partial *trnLF*. We conclude that: 1) *S. tosaense* has a disjunct distribution between Kochi and Jeju Island, and 2) plants of this species might have dispersed between Kochi and Jeju Island over water, but not via a land bridge, which flooded before subclade divergence.

Keywords: Disjunct distribution, ITS, Japan, Jeju, Kochi, Korea, *Sedum*, *trnLF*

Introduction

The term “disjunct distribution” is applied to a distribution pattern in which a species or species lineage occurs in two or more areas, but is absent from the intermediate areas (e.g., Gray 1878; Raven 1963; Thorne 1972). Several disjunct distributions in seed plants have been confirmed by molecular evidence, such as between North and South America (e.g., Spalik *et al.* 2010; Popp *et al.* 2011), between East Asia and North America (e.g., Huang *et al.*, 2013), between Japan and Australia (e.g., Nakamura *et al.* 2012; Kokubugata *et al.* 2012), and between the Japanese Mainland and Taiwan (e.g., Mitsui *et al.* 2008).

Jeju Island is a volcanic island located off the southern coast of the Korean Peninsula. It is 73 km long (east–west), 31 km wide (north–south), and 1847 km² in area. Mount Halla is the highest mountain on the island (Woo *et al.* 2013). The coastline is bathed by the Kuroshio Current, which transports warm seawater from tropical Asia. Jeju Island is believed to have received floristic elements from mainland Korea and China and from the southern part of Japan; tropical species occur in the lowlands (e.g., Chung *et al.* 2013) and temperate species are distributed at higher elevations (e.g., Kong 2000; Dolezal *et al.* 2012).

The genus *Sedum* Linnaeus (1753: 430) (Crassulaceae) includes about 420 species that are distributed widely in both the Old and New Worlds; it is the largest and most widespread genus in the Crassulaceae (Thiede & Eggli 2007). According to Ohba (2001), there are 24 species and subspecies of *Sedum* in Japan; there are 16 in South Korea (Korea National Arboretum 2011). *Sedum tosaense* Makino (1901: 35) (Fig. 1), the target species of this study, was formally described based on a type specimen collected from Kochi Prefecture, Shikoku District, Japan; the entity had been previously reported as a *nomen nudum* (Makino 1892). The species comprises perennial rosette herbs that are diminutive in winter. Alternate leaves with retuse apices are the most distinctive features, and it occurs on rocky slopes (Ohba 2001). Given its rarity, the species is treated as critically endangered; it has been included in the Japanese Plant Red List (Japanese Ministry of the Environment, 2012). *Sedum tosaense* occurs in Kochi (Ohba 2001; Kobayashi 2009; Akiyama 2011) and Tokushima (Abe 1990) Prefectures in the southern part of Shikoku District, on the Pacific-

have migrated to ocean islands; for example, *S. boninense* Yamamoto ex Tuyama (1936: 428) occurs on the Bonin Islands, Japan (Tuyama, 1936) and *S. formosanum* N.E. Br. (1885: 134) occurs on Lanyu Island, Taiwan (Tang & Huang, 1993). Presently, no relevant morphological data on the fruits and seeds of *S. tosaense* suggests a mechanism that would allow the crossing. These data are required to test any putative mechanisms for dispersal across the strait.

Phylogenetic relationships between *Sedum tosaense* and other species

Song *et al.* (2004) determined that *S. tosaense* is morphologically related to *S. bulbiferum* Makino (1891b: 2) and *S. oryzifolium*. Mayuzumi & Ohba (2004) analyzed a part of the chloroplast DNA *trnL-trnF* region and the internal transcribed spacer region of ribosomal DNA (ITS) to determine the phylogenetic relationships of 74 taxa of East Asian *Sedum*, and concluded that *S. tosaense* falls within a single clade with *S. japonicum*, *S. oryzifolium*, and *S. zentaro-tashiroi*. Our molecular phylogenetic analyses indicate that *S. tosaense* fits best within a clade comprising *S. oryzifolium* and *S. zentaro-tashiroi*, agreeing with the findings of Mayuzumi & Ohba (2004) and some of the morphological conclusions reported by Song *et al.* (2004).

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