



Fine-scale spatial genetic structure of an endangered marsh herb, *Caldesia grandis* (Alismataceae)

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ABSTRACT. The endangered marsh herb, *Caldesia grandis*, is native to China. We investigated the spatial structure of the genetic variation of three populations of *C. grandis* using RAPD markers and spatial autocorrelation analysis, based on the method of equal distance interval. A total of 157 individuals were sampled from four patches collected from the region of Hunan and Yunnan Provinces, China. Among the polymorphic bands generated by seven selective primers, polymorphic bands with frequencies ranging from 20 to 80% were used to calculate Moran's *I* spatial autocorrelation coefficient for each patch. We found significant spatial structure of genetic variation in the three patches in Bei Hai (BH) (patches BH-1 and BH-2) and Guai Hu (GH) (patch GH-1) populations of *C. grandis* (with significant positive autocorrelation within the short distance class). In contrast, the genetic variation in

the Lang Pan Hu (LPH) population (patch LPH-1) was found to be randomly distributed. The different spatial distribution patterns may be attributed to environment differences. These results have implications for the conservation and management of this species, especially for sampling strategies for *ex situ* conservation.

Key words: *Caldesia grandis*; Conservation genetics; Endangered species; Spatial genetic structure