

A comparative population study of genetic diversity in *Goodyera foliosa* var. *laevis* (Orchidaceae) native to Hiroshima Prefecture, Japan*

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Abstract

Molecular analysis was carried out using random primers to infer the characteristics of RAPD generated DNA fragments and to investigate genetic diversity of six populations of *Goodyera foliosa* var. *laevis* in Hiroshima Prefecture, Japan. Using two decamer primers of OPA-01 and OPB-05, 157 reproducible DNA fragments were obtained from 30 individuals of this variety. In cluster analysis, four main clades were found in the tree. One of these clades consisted of all five individuals of Mt. Tateboshiyama population.

Introduction

Goodyera R. Br. is a member of the Orchidaceae and comprises 40 species widely distributed from the subarctic regions of the Northern Hemisphere to tropical regions in Asia (Satomi 1982). All species in this genus are terrestrial, with one exception. *Goodyera* species mainly grow in primary forests with high humidity and are often associated with dominant forest-trees. Thus, it is suggested that speciation of this group is correlated with certain associated forest-trees (Tanaka 1965).

Taxonomic treatments of *Goodyera*, however, are still imperfect, because the genus contains many rare species with not enough complete herbarium specimen masses (Schlechter 1926, Holttum 1964, Briger 1974-1975, Dressler 1981). Therefore, more examinations must be necessary to clarify these taxonomic treatments, as pointed out by some previous works (Dressler and Dodson 1960, Maekawa 1971, 1978, Seidenfaden 1978). Additionally, as same as species classification, population study to understand genetic diversity in *Goodyera* is quite important for the species conservation and its sustainable management of gene resource, since many of the species are on the decrease in the population number and size even now.

In Japan, more than ten species of *Goodyera* have been recorded (Sera 1990). Of these, *Goodyera foliosa* (Lindley) Benth. ex C. B. Clarke shows intraspecific morphological variation, and has two varieties in Japan. *Goodyera foliosa* (Lindley) Benth. var. *laevis* Finet is common type of the Japanese species, and is distributed from the north main island (Hokkaido) to the south main island (Kyushu) in the Japanese archipelago, whereas another variety, *Goodyera foliosa* (Lindley) Benth. var. *commelinoides* (Fukuyama) F. Maekawa, is native to only Kyushu island and further down south small islands belonging to Kagoshima, Okinawa Prefectures and the Tokyo metropolitan area, Japan. Moreover, in the previously investigated individuals reported by Tanaka (1965) and Sera (1990), *G. foliosa* var. *laevis* has an intraspecific polyploidy, which is generally considered to play a role to promote the geographic segregation explained by their adaptive selection to environments (Ohi *et al.* 2003). The cytotypes with different ploidy levels of *G. foliosa* var. *laevis* are commonly found in south part of the largest main island (Honshu) in Japan, especially in Hiroshima Prefecture (Sera 1990). However, even though cytological studies have been carried out to see chromosome differentiation among related taxa, there is no report of molecular investigation for estimating genetic diversity in the populations with different cytotypes of this Japanese variety.

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