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著者	FUSHIMI Manato, MATSUKI Yu, KAWAHARA Takayuki, TAKAHASHI Hideki, IZAWA Takeshi, SUYAMA Yoshihisa
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**Local Genetic Differentiation within Rebun Island in  
*Cypripedium macranthos* var. *rebunense* Revealed by  
Genome-wide SNP Analysis Using MIG-seq**

**Manato FUSHIMI<sup>1</sup>, Yu MATSUKI<sup>1</sup>, Takayuki KAWAHARA<sup>2</sup>,  
Hideki TAKAHASHI<sup>3</sup>, Takeshi IZAWA<sup>4</sup> and Yoshihisa SUYAMA<sup>1</sup>**

<sup>1</sup>Field Science Center, Graduate School of Agricultural Science, Tohoku University, Japan

<sup>2</sup>Forestry and Forest Product Research Institute, Japan

<sup>3</sup>The Hokkaido University Museum, Hokkaido University, Japan

<sup>4</sup>Systematic Botany, Graduate school of agriculture, Hokkaido University, Japan

*Cypripedium macranthos* var. *rebunense* is an endangered orchid endemic to Rebun Island, Hokkaido, Japan. The natural habitats of the species are geographically separated into northern and southern regions of the island. It has been reported that the southern population showed relatively low genetic diversity by the bottleneck effect due to illegal collecting since the 1950's. Here we performed population genetic study for the species using MIG-seq analysis, PCR-based method for genome-wide SNP genotyping using the next-generation sequencing platform, to obtain more accurate population genetic data than previous one. Our study revealed that the genetic diversity within populations was not significantly different between northern and southern populations. However, northern and southern populations showed high level of genetic differentiation ( $F_{ST}$ : 0.140). Moreover, we estimated the demographic history of the populations by using approximate Bayesian computation (ABC)-based analysis. The ABC analysis suggested that (i) the divergence of northern and southern populations occurred *ca.* 7,000 years ago, (ii) population size of the southern population is much larger than previously estimated (effective population size; 1,000–2,000), (iii) the population sizes have not fluctuated since the population divergence. Thus, it is suggested that the northern and the southern populations experienced independent long-term history. Based on these results, we recommend that the both populations should be treated as independent conservation units. That is, “artificial gene flow” such as transplantation and artificial crossing between the two populations should not be conducted for conservation activities.