



Population Genetic Analysis for Identifying Hybrid Origin of a Dwarf Bamboo Species in Sasaella

著者	KANNO Takamasa, SUYAMA Yoshihisa
journal or	Journal of Integrated Field Science
publication title	
volume	13
page range	53-53
year	2016-03
URL	http://hdl.handle.net/10097/64091

Population Genetic Analysis for Identifying Hybrid Origin of a Dwarf Bamboo Species in *Sasaella*

Takamasa KANNO and Yoshihisa SUYAMA

Field Science Center, Graduate School of Agricultural Science, Tohoku University, Japan

Phylogenetic systematics of bamboo species is rather complicated possibly due to the existence of not only interspecific but also intergeneric hybrids. Therefore, studies of the genetic origin of such hybrids are required to clarify their systematic relationships. It has been pointed out that, as an example of putative hybrids, the species in the genus *Sasaella* are intergeneric hybrids between the genera *Pleioblastus* and *Sasa*, based on their morphological characteristics. Here, we conducted population genetic analysis for identifying the parental species of a putative hybrid species of *Sasaella*.

DNA samples were collected from five bamboo species; *Sasaella masamuneana* f. *hashimotoi* as a putative hybrid, *P. chino* and *Sasa palmata* as its putative parents, *Sasa spiculosa* and *Sasamorpha borealis* as sympatric species in Kawatabi Field Science Center, Tohoku University. These samples were analyzed using simple sequence repeat (SSR) markers and single nucleotide polymorphisms obtained by next-generation sequencer (NGS-SNP). (i) Genetic diversity, (ii) structure, (iii) parentage assignment analysis, and (iv) approximate Bayesian computation analysis for demographic history of the populations were conducted using the population genetic data. In addition, (v) chloroplast DNA nucleotide sequences were investigated for the putative hybrid and parent species.

(i) Based on seven SSRs and 36 NGS-SNPs, the highest value of observed heterozygosity was detected in the putative hybrid. (ii) Both of the genetic structure analysis estimated by seven SSRs and 94 NGS-SNPs showed that the putative hybrid has intermediate genetic composition between the putative parents. (iii) Parentage assignment analysis detected offspring-parents groups in the populations of putative hybrid and parents. (iv) Demographic history of the populations supported the putative hybrid originated from hybridization between populations of two putative parents of the hybrid population. (v) Chloroplast DNA haplotypes of the putative hybrid were shared by the putative parents.

These results strongly suggested that the putative hybrid of *Sasaella* is intergeneric hybrid origin between *Pleioblastus* and *Sasa*. Our study approach can be applied to investigating a wide range of hybrid species, and will be able to contribute to systematic studies of many species.