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学位論文題名	Population genetic study of *Morus australis* Poir. in the Ogasawara and other islands of Japan 小笠原諸島および日本の他の諸島におけるシマグワの集団遺伝学的研究（英文）
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【論文の内容の要旨】

Invasive species are serious threat to biota in the Ogasawara Islands, which are oceanic islands harboring many endemic species. The islands are now invaded by *Morus australis* that was artificially introduced from the Ryukyu and Izu Islands. Hybridization was reported to take place between this species and an endemic species *M. boninensis*.

To clarify the invasion routes and the genetic composition of founding populations, plant samples of *M. australis* were collected from 32 populations across Japan, including 12 from the Ogasawara Islands and population genetic analyses were conducted using 14 microsatellite markers. In addition, to elucidate extent of hybridization between invasive *M. australis* and native *M. boninensis*, plant sampling was performed from two wild seedling populations, two populations of *M. boninensis* and another population of *M. australis* in the Ogasawara Islands. Then, the same population genetic analyses were conducted also for the additional samples.

The UPGMA dendrogram based on Nei's genetic distance, the Principal Coordinate Analysis based on pairwise F_{ST} values, and the Bayesian Clustering using STRUCTURE software indicated that the populations of *M. australis* in the Ogasawara Islands are genetically similar to those in the Ryukyu Islands, while they are clearly

differentiated from those in the Izu Islands and mainland of Japan. The level of genetic diversity in the Ogasawara Islands ($A_R = 4.24$; $H_E = 0.60$) was similar to that of the Ryukyu Islands ($A_R = 4.70$; $H_E = 0.66$), higher than the Izu Islands ($A_R = 3.70$; $H_E = 0.51$) and lower than mainland of Japan ($A_R = 5.80$; $H_E = 0.73$).

The obtained results in this study showed that the *M. australis* plants now growing in the Ogasawara Islands are descendants of those introduced from the Ryukyu Islands. The individuals from the Izu Islands might not be able to successfully expand their distribution in the Ogasawara Islands. It was also suggested that numbers of transplanted individuals from the Ryukyu Islands to the Ogasawara Islands were large because similar amount of genetic variation was observed in the two island groups. Such high genetic diversity might have enhanced invasiveness of *M. australis* in the Ogasawara Islands.

This study also revealed that *M. boninensis* is genetically differentiated from *M. australis*, and hybrids between the two species are very rare, maybe due to the difference in ploidy levels between them. Thus, a limited bad effect of *M. australis* to the endemic *M. boninensis* through hybridization was detected. However, all the seedling individuals were those of *M. australis,* suggesting regeneration of *M. boninensis* rarely occurs in the Ogasawara Islands. Meanwhile, the amount of genetic diversity within *M. boninensis* was similar to that within *M. australis*. The endangered *M. boninensis* still maintains high genetic diversity and may be able to survive if we increase the number of its individuals.

The results obtained in this study provide us basic information to prevent disturbance of the invasive *M. australis* in the Ogasawara Islands since knowing the origin of the invasive species may help to understand its ecological features.