

Construction and Verification of Tailor-made Biological Conservation Strategy Based on Genome Information

Principal Investigator: Yuji ISAGI

Institution: Kyoto University, Kitashirakawa-Oiwake, Sakyo-ku, Kyoto, JAPAN

Tel: +81-75-753-6422 / Fax: +81-75-753-6123

E-mail: isagi.yuji.5n@kyoto-u.ac.jp

Cooperated by: Tohoku University

[Abstract]

Key Words: Biodiversity conservation, Genome analysis, Phylogenetic analysis, Conservation difficulty, Conservation value assessment, Domestic rare plant and animal species

Although the multi-level importance of biodiversity is becoming widely recognized, many species are threatened with extinction due to human impact. The limited resources available for biodiversity conservation, such as financial, time, space, and personnel resources, make it necessary to develop rational and effective methods of conserving a large number of endangered species. Until now, the conservation status of endangered species has been assessed primarily by the number of individuals surviving, but it is difficult to prioritize species for conservation based only on their population size. In this study, we evaluated the uniqueness of populations based on genetic diversity and phylogenetic perspectives through contracted genome sequencing such as RAD-seq and MIG-seq on individuals growing in Japan and overseas of rare species. Furthermore, by comprehensively analyzing the expressed genes by RNA-seq, we found genetic indicators characteristic of endangered species in terms of genetic diversity, deleterious mutation accumulation, and duplicated gene rate, thus estimating the vulnerability of species and local populations and their ability to adapt to the environment. By combining different types of genomic information (e.g., condensed genome information and transcriptome), we categorized the conservation status of endangered species and developed a tailor-made conservation strategy by which conservation resources can be allocated more effectively and rationally according to the species' unique conservation status.

[References]

- 1) T. Hamabata, G. Kinoshita, K. Kurita, P. Cao, M. Ito, J. Murata, Y. Komaki, Y. Isagi and T. Makino: *Commun. Biol.*, 2, 244 (2019) Endangered island endemic plants have vulnerable genomes (**IF: 6.268**)
- 2) Y. Isagi, T. Makino, T. Hamabata, P.-L. Cao, S. Narita, Y. Komaki, K. Kurita, A. Naiki, Y. Kameyama, T. Kondo and M. Shibabayashi: *Plant Species Biol.*, 35, 3, 166–174 (2020) Significant loss of genetic diversity and accumulation of deleterious genetic variation in a critically endangered azalea species, *Rhododendron boninense*, growing on the Bonin Islands (**IF: 2.077**)
- 3) Y. Suyama, S. Hirota, A. Matsuo, Y. Matsuo, Y. Tsunamoto, C. Mitsuyuki, A. Shimura, K. Okano: *Ecological Research*, 37: 171-181 (2022) Complementary combination of multiplex high-throughput DNA sequencing for molecular phylogeny (**IF: 1.917**)