

## Tailor-made Biological Conservation of Endangered Plant Species with Genomic Information

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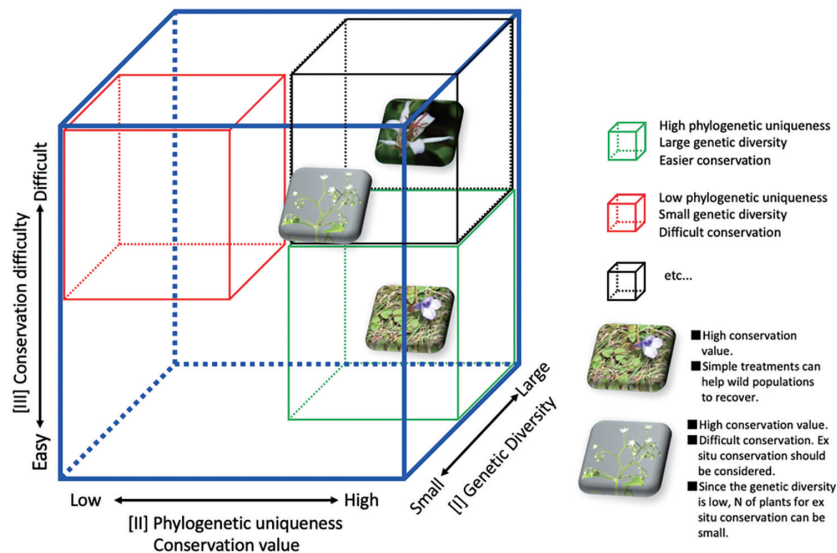
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The multifaceted importance of biodiversity is increasingly recognized, but the situation in various ecosystems is crucial and many endangered species are recognized. Based on the “Conservation of Species Act”, the Japanese government has designated the species with the highest conservation priority as Domestic Rare Wild Fauna and Flora and is trying to conserve them, and the number of the designated species is scheduled to be as many as 700 in the near future. However, limited resources available for the conservation of biodiversity require the development of rational and effective methods for the conservation of many endangered species. How can we appropriately preserve such a large number of endangered species with limited conservation resources? 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. We explored ways to appropriately conserve a large number of endangered species with three criteria: (I) genetic diversity of remnant populations, the most common value for assessing the status of endangered species, (II) conservation value based on the phylogenetic uniqueness of the taxon, and (III) conservation difficulty estimated from the status of the genome. We evaluated the uniqueness of populations based on genetic diversity and phylogenetic perspectives through contracted genome sequencing 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.

As a result of detailed genome-level analysis of endangered plant species growing in the Ogasawara and Ryukyu islands, which are designated World Natural Heritage sites, we found significant differences between species in phylogenetic uniqueness, amount of deleterious mutation, and ability to adapt to a variety of environments. By combining these evaluation axes I, II and III described above based on the different types of genomic information, 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 (**Figure**).



**Figure.** Categorization of critically endangered species based on [I] genetic diversity, [II] phylogenetic uniqueness and [III] conservation difficulty