Abstract

[Project Information]

Project Title :	Assessment of Viability Based on Conservation Genomics for Species Subject to Protection and Propagation Under the Law for the Conservation of Species
Project Number :	JPMEERF20224M02
Project Period (FY) :	2022-2024
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Keywords :	Conservation genomics, Biodiversity conservation, Endangered species, Act on Conservation of Endangered Species of Wild Fauna and Flora, Population dynamics estimation, Future projection

[Abstract]

Under the Law for the Conservation of Species, 64 species have been designated for Conservation and Propagation Programmes led by the Ministry of the Environment. Nevertheless, no species has demonstrated sufficient recovery to be removed from the list. This project applied conservation genomics to endangered species to assess genetic health and provide a scientific basis for more effective conservation strategies. The study commenced with a focus on six species: Columba janthina nitens, Melastoma tetramerum, Acheilognathus longipinnis, Parabotia curtus, Celastrina ogasawaraensis, and Melitaea protomedia. Subsequently, the scope was expanded to encompass a total of 16 species, encompassing birds, plants, fish, and insects. The construction of high-quality reference genomes was undertaken, and population genomic data were obtained using whole-genome resequencing, MIG-seq, RAD-seq, and RNA-seq. In C. janthina nitens, genomic data has revealed a long-term population decline that has been exacerbated by anthropogenic impacts since the Meiji era. Analyses of both wild and ex situ populations revealed indications of inbreeding and the accumulation of deleterious mutations, while concomitantly identifying genomic features that may have facilitated this species' rare population recovery. In M. tetramerum, the presence of extremely low genetic diversity, extensive runs of homozygosity (ROH), and a high frequency of nonsense mutations are indicative of advanced genomic

degradation, a common pattern observed in small island populations. It was a surprising finding that closely related taxa, such as Melastoma pentapetalum, exhibited even greater levels of genetic risk. In the context of freshwater fishes, the utilisation of gh-resolution genome assemblies, employing techniques such as Hi-C, has facilitated the reconstruction of historical population dynamics and the assessment of genetic structure. Captive populations were analysed for inbreeding and mutation load, providing essential data for the design of breeding programmes. In insects, C. ogasawaraensis—a species targeted under the Conservation and Propagation Programmes—was found to be undergoing long-term genetic decline, and simulations were used to estimate the minimum founding size necessary for sustainable ex situ conservation. The present study demonstrated the value of genomics in identifying hidden extinction risks, redefining conservation units and evaluating management practices. The results of the study were disseminated to the Ministry of the Environment and the relevant working groups, thereby providing a direct contribution to the formulation of national conservation policies. The integration of genomic approaches into the project established a foundation for genetic monitoring, recovery planning, and prioritization of threatened taxa.

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This research was performed by the Environment Research and Technology Development Fund (JPMEERF20224M02) of the Environmental Restoration and Conservation Agency provided by Ministry of the Environment of Japan