


Elucidation of the Formation Process of Forest Ecosystems in the Japanese Archipelago

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Purpose and Background of the Research

● Outline of the Research

The benefits from nature, known as ecosystem services, are significant, amounting to about US\$125 trillion annually for the entire planet, including air, water, food, energy, and medicines, and the value of agricultural products produced by insects and other pollinators is estimated to be about US\$6 trillion annually for the entire world. In particular, forests are home to more than 70% of terrestrial species, and this diversity provides human with many resources. Forest biodiversity is also considered to play a role in controlling pests and diseases and pollinators in the production of nearby agricultural products. However, human activities have caused global climate change, which has led to the destruction of forest ecosystems, and this has had a significant impact on biodiversity. Although forest ecosystem protection areas have been designated among forest protected areas, little is known about which forests are genetically important. These forests have been strongly influenced by distributional shifts associated with past global-level climate changes, which have continued to the present (Fig. 1). We will conduct a large scale population genetic study of many trees and insect species using the same genetic and model-based statistical methods to elucidate the origins and formation process of Japan's forest ecosystems (Fig. 2). The results will also help to identify hotspots of high genetic diversity and endemism in Japan's forest ecosystems, and can be used to formulate conservation guidelines.

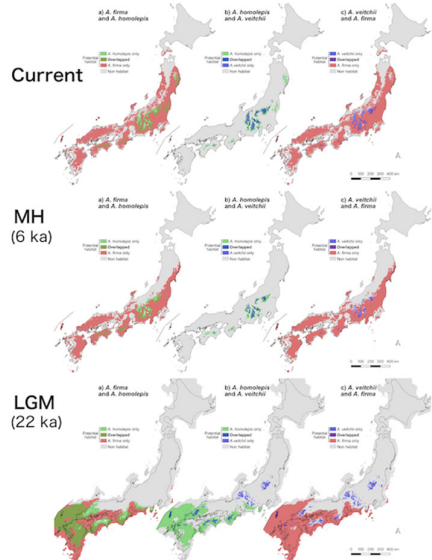


Fig.1 Distribution change of three *Abies* species from LGM to current

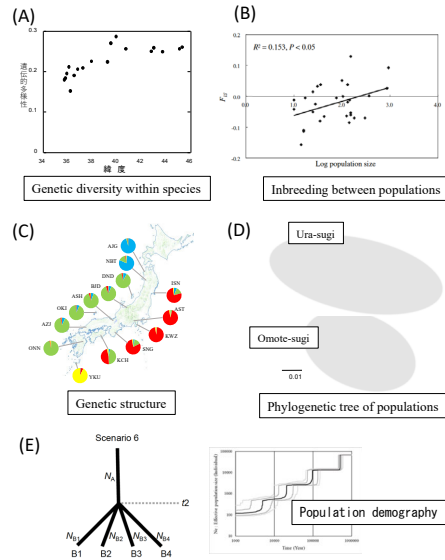


Fig.2 Examples of intraspecific genetic analysis

Expected Research Achievements

To elucidate the establishment process of forest ecosystems in Japan, we will collect research materials on many tree species and forest insects representing the subarctic, cool temperate, warm temperate, and subtropical zones in Japan. Using these materials, we will conduct MIG-seq analysis to clarify the genetic diversity, genetic structure, estimated divergence age of genetic groups, and population dynamics. We will also typify the genetic results of all analyzed species. The divergent time between species and within-species populations will be verified and corrected using species distribution models (SDMs) and fossil data to accurately estimate branching ages. Using the genetic diversity and genetic structure information obtained in this study and the results of SDM, we will conduct an integrated analysis using an integrated model to clarify the details of patterning and interspecific relationships, such as genetic regionality. We will also search for genes involved in speciation and genetic differentiation by utilizing common garden forests. Through these studies, we will clarify the formation process of Japan's forest ecosystems and predict the future state of forest ecosystems due to global warming and other factors.

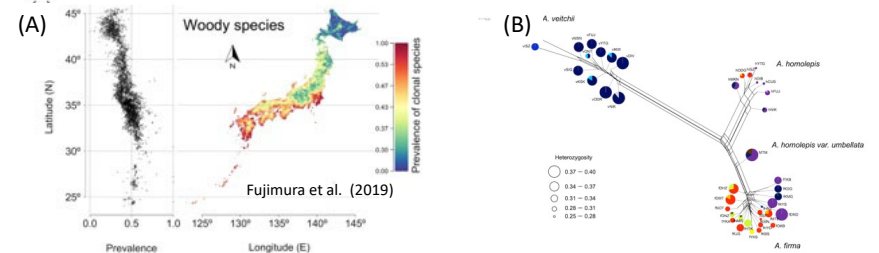
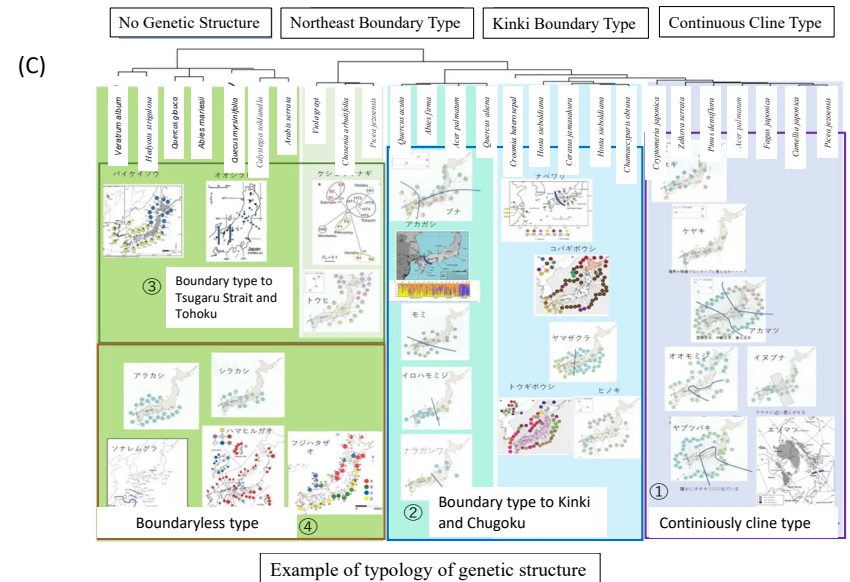


Diagram of the genetic diversity of the entire target species

Phylogenetic relationships and genetic diversity among species



Example of typology of genetic structure