

更新世におけるキンロバイの繰り返された移入 - 日本とチベット高原の集団の分子系統学的比較から
Repeated migration of *Dasiphora fruticosa* during the Pleistocene revealed by comparison between Japan and Tibetan

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Alpine plants would experience several cycles of range contractions and expansions in response to the Pleistocene climate fluctuations. Such range and demographic changes affects the geographical patterns of genetic variation within and among populations. Such genetic variation indicates where species survived and how species colonized their present-day distribution using the molecular approaches

Dasiphora fruticosa L. (Rosaceae), an alpine shrub, is widely distributed in Northern hemisphere. In this study, phylogeographic analysis was conducted using samples from Qinghai-Tibetan Plateau and Japanese archipelago to reveal that the Japanese populations have been migrated to Japan in several times.

Leaf materials of *D. fruticosa* were collected from 23 populations from inner to northeast across the Qinghai-Tibetan Plateau and five populations from Japan. The sequence variation and geographical distribution of the chloroplast *matK* region were analyzed. 33 and 23 haplotypes were detected from the Qinghai-Tibetan plateau and Japan, respectively.

Two Japanese haplotypes were closely related to haplotypes detected in the inner plateau. These were belonging to different clades. One clade indicated deep divergence and included relatively ancestral haplotypes. The other clade included relatively derived haplotypes. These results suggested that *D. fruticosa* has been migrated to Japanese Archipelago at least two times. Although just one of the two clades was detected in central Japan, two clades were detected in Northern Japan.

The population of Hokkaido mountain showed high levels of genetic diversity and had unique haplotypes that were restricted to this area. The Hokkaido mountain maintains longer history of *D. fruticosa* and/or enough population size avoiding bottleneck from past to present than other regions.

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