

## 中部山岳地域における氷河遺存種 *Dryas octopetala* の遺伝的多様性の喪失 Marked loss of genetic diversity within glacial-relic populations of *Dryas octopetala* in the Japanese Alps

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For arctic-alpine species with wide-ranging distributions throughout circum-arctic regions and southward into mid-latitude mountains, range shifts in response to climatic change were both latitudinal (especially in circum-arctic areas) and altitudinal (in mountain regions). Latitudinal range shifts occurred over large areas and involved long-distance dispersal, whereas altitudinal shifts were more localized. Therefore, the genetic consequence of these types of range shift can be predicted to differ. *Dryas octopetala* L., an arctic-alpine plant, is widely distributed from the Eurasian and American arctic tundra to temperate mountains in Europe, in North America, and in Asia south to Japan, which is one of the southernmost areas for the cold-adapted species. In this study, we compared the genetic structure of *D. octopetala* populations along latitudinal transects from the High Arctic to mid-latitude mountains in the Japanese Alps. Investigation of genetic variation within *D. octopetala* populations inhabiting the Japanese Alps provides an example of how cold-adapted organisms survived at the southernmost limits of the distribution, at least since Holocene warming.

We analyzed a total of 656 individuals across 14 populations (six in the Japanese Alps, one in Hokkaido, one in China, three in North America, two in North Europe, one in the High Arctic) using nine nuclear microsatellite loci. Population genetic structure was assessed by analyzing genetic diversity indices for each population, examining clustering among populations.

The clustering analysis among the populations revealed an isolated marginal group of populations in the Japanese archipelago. The populations in the Japanese Alps exhibited low genetic diversity within populations compared with those in high latitude regions. Loss of genetic diversity was especially pronounced in the Southern Japanese Alps. High level of genetic diversity was detected in two Alaskan populations, supporting the Beringia refugium hypothesis for arctic and alpine plants. No significance of isolation-by-distance in the populations demonstrated that genetic drift was a strong force shaping the genetic structure in the Japanese Alps. The resulting stochastic reduction of genetic diversity in the cold-adapted plants at the southernmost limit of the distribution may constrain their evolutionary potential, thereby inhibiting adaptation under climate change.

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