

How Camellias evolved with the formation of the Japanese archipelago

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The Studied Camellias and Dr. Harue Abe. Credit: Niigata University

The distribution of plants has been shaped by geological and climatic

changes over time through repeated migration, extinction, and adaptation to new environments. The genus *Camellia*, comprising over 100 species mainly in East Asia, is a representative warm-temperate tree of the Sino-Japanese Floristic Region.

In Japan, four species of *Camellia* are found, with *Camellia japonica* and *Camellia rusticana* being the most well known. *C. japonica* has a broad distribution from Aomori Prefecture in the cool-temperate zone to subtropical Taiwan and the coastal regions of China, suggesting its high adaptability to different climates.

In contrast, *C. rusticana* is a Japan Sea element plant adapted to heavy snowfall areas. Plants categorized as Japan Sea elements are generally thought to have evolved from closely related species on the Pacific side, and *C. japonica* and *C. rusticana* were also believed to follow this pattern.

Following this idea, *C. rusticana* was hypothesized to have diverged from *C. japonica* as an adaptation to snow-covered environments. However, this hypothesis had not been fully tested scientifically.

A study, [appearing](#) in *Ecology and Evolution*, aimed to clarify the evolutionary history of these two species by analyzing their distributional changes using genetic analyses and ecological niche modeling.

Phylogenetic analyses revealed clear differentiation among *C. japonica*, *C. rusticana*, and *C. chekiangoleosa*, a closely related continental species. Their [common ancestor](#) is estimated to have diverged approximately 10 million years ago during the Late Miocene, coinciding with the separation of the Japanese archipelago from the continent.

This suggests that the two species diverged simultaneously due to [geographic isolation](#), contradicting the previous hypothesis that *C.*

rusticana evolved from *C. japonica* in response to Quaternary glacial cycles.

The populations of *C. japonica* are divided into three major groups: northern Japan, southern Japan (including mainland China and Korea), and the Ryukyu-Taiwan region. Among them, the northern population is particularly distinct from the others.

Tracing their evolutionary history, analyses revealed that the southern population diverged from the northern population about 3.3 million years ago, followed by the Ryukyu-Taiwan population splitting from the southern population 1.8 million years ago, and finally, the continental population (including Korea) diverging from the southern population 27,000 years ago.

These findings indicate that *C. japonica*, which originally migrated from the continent to the Japanese archipelago, later evolved and eventually recolonized the continent (reverse colonization). This provides key evidence that islands are not evolutionary dead ends but can serve as sources of genetic diversity for continental populations.

This study not only sheds light on the [evolutionary history](#) of *Camellia* but also highlights how the formation of the Japanese archipelago has influenced plant evolution.

"By unraveling the history of camellias, we may gain new insights into the evolutionary processes of other plants unique to Japan," says Dr. Harue Abe. Furthermore, the research is not just about understanding the past—it also provides clues for predicting future changes in plant distribution.

"As [global warming](#) continues, understanding how *Camellia* species will shift their ranges becomes increasingly important. Our findings will

serve as a key reference for predicting these changes," she emphasizes.

More information: Harue Abe et al, Evolutionary Histories of *Camellia japonica* and *Camellia rusticana*, *Ecology and Evolution* (2024).
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