

# 琉球大学学術リポジトリ

## Genetic Structure of an Insular Plant in the Northwestern Pacific and its Implication for Conservation

|       |  |
|-------|--|
| メタデータ | 言語:<br>出版者: 琉球大学21世紀COEプログラム<br>公開日: 2008-10-07<br>キーワード (Ja):<br>キーワード (En):<br>作成者:<br>メールアドレス:<br>所属: |
| URL   | <a href="http://hdl.handle.net/20.500.12000/7376">http://hdl.handle.net/20.500.12000/7376</a>            |

S2-F

## Genetic Structure of an Insular Plant in the Northwestern Pacific and its Implication for Conservation

Shun'ichi Matsumura

Faculty of Education, University of the Ryukyus, Senbaru, Nishihara, Okinawa 903-0213, Japan

Insular organisms have been focused because they have played an important role in the development of evolutionary biology. In general, islands more or less vary in size, degree of spatiotemporal isolation, geology, climate, and biotic environmental factors. In northwestern Pacific, subtropical archipelagoes located in Japanese territory include both continental and oceanic islands. In the Ryukyu Archipelago, many continental islands are arranged in a line between Taiwan and Japanese mainland and are also situated close to several oceanic islands, such as those belonging to the Daito and Izu-Ogasawara Islands. Despite the geographical proximity, the dates and processes of formations of these subtropical islands are quite different. In this context, the island biota in northwestern Pacific provides us a good opportunity to investigate what factors affect evolution of insular organisms.

So far, I have examined genetic variation in a coastal sea lavender, *Limonium wrightii* (Hance) Kuntze (Plumbaginaceae) on the basis of sequences in chloroplast DNA and nuclear ribosomal DNA (hereafter cpDNA and nrDNA, respectively). This species is distributed over almost whole of the northwestern Pacific islands. This study revealed characteristic genetic structure, which had not been predicted in previous morphological studies. In this presentation, I first report two issues inferred from the characteristic genetic structure in *L. wrightii*; namely, 1) high rate of nucleotide substitutions in the Daito Islands populations, and 2) past hybridization between *L. wrightii* and its closely related species on the Amami-Oshima Island and adjacent islets of the central Ryukyus. The Daito populations and Amami populations obviously represent separate lineages, seemingly deserving recognition as distinct evolutionary significant units (ESUs). Next, I evaluate genetic diversity and genetic differentiation within *L. wrightii* on the basis of allozyme data, and compare the results with those of some previous studies on other insular plants.

The nrDNA sequences of the Daito populations were different from other conspecific populations in nine apomorphic substitutions. However, I could not detect any consistent nucleotide differences for subdivision of the Ryukyu and Izu-Ogasawara assemblage. This result indicates a distance-independent geographical genetic structure in this species.

I estimated the average rate of nucleotide substitutions in the Daito populations as  $1.41 \times 10^{-8}$  substitutions per site per year. To the best of my knowledge, this substitution rate in nrDNAs is the highest among those in all flowering plants so far studied, and thus represents a quite idiosyncratic case.

Accelerated evolution in insular organisms is generally attributed to their small population sizes, or strong mutagenic effects from high metabolic activity at low latitude environments, or both. There seem to be no significant differences in their metabolic activities throughout the geographical range of *L. wrightii*, because in both mean annual temperature and solar radiation, the Daito Islands is similar to Okinawa Island of the central Ryukyus. Therefore, the observed high substitution rate in

the Daito populations might reflect a strong effect of genetic drift due to their small population sizes. This phenomenon was predicted by the nearly neutral theory in population genetics.

Second, the results showed an incongruence of sequences between cpDNA and nrDNA in three populations on Amami-Oshima Island and its adjacent islets. The cpDNA sequences of these populations accorded with those of two closely related species, *L. tetragonum* and *L. sinense*. By contrast, the nrDNA sequences of these populations were identical to those of other conspecific populations. This suggests a past hybridization or incomplete lineage sorting between *L. wrightii* and those two closely related species. On Amami-Oshima Island, although there is no living individual of *L. tetragonum* at all, broad occurrence of this species in the past was confirmed by examination of herbarium specimens. Hence, despite the current absence of *L. tetragonum* there, I suspect an occurrence of hybridization between *L. wrightii* and *L. tetragonum*.

Allozyme diversity in *L. wrightii* was relatively high in both total genetic diversity and genetic differentiation among populations. Total genetic diversity of *L. wrightii* in the Ryukyu Archipelago showed a relatively high value ( $H_T = 0.238$ ) among those of flowering plants reported there ( $H_T = 0.142-0.312$ ). The average  $H_T$  of six plant species in the Ryukyu Archipelago (0.206) is higher than those of oceanic islands (average  $H_T$  in representative plants were 0.186 in the Canary Islands, 0.039 in the Ogasawara Islands, and 0.064 in other oceanic islands in the Pacific). It is generally assumed that long isolation in small islands reduces genetic diversity of an organismal population through the genetic drift, although in some Canary Islands plants high genetic diversity is also attributed to their long isolation there.

The coefficient of gene differentiation ( $G_{ST}$ ) for the whole *L. wrightii* was 0.705. This value indicates that approximately 70% of the total genetic variation within *L. wrightii* is derived from variation among populations, and that the remaining 30% resides within each population. The average  $G_{ST}$  of six plant species including *L. wrightii* in the Ryukyu Archipelago (0.579) was higher than those of some oceanic islands plants, e.g., 0.286 in the Canary Islands plants and 0.338 in Juan Fernández Island plants. Thus, it should be safe to say that the degree of genetic differentiation among populations is extraordinarily high. The sizes of organismal populations on continental islands are also sometimes restricted and may repeat expansion and contraction. These properties will produce forces leading to their local genetic differentiations. *Limonium wrightii* should have a high risk of outbreeding depression because of such high genetic differentiation as mentioned above. For the purpose of conservation, therefore, a primary requirement may be maintenance of a number of populations in their original habitats.

In the Ryukyu Archipelago, most of plants so far analyzed for genetic diversity are endemic or semi-endemic perennial herbs. For the better understanding of genetic diversity in insular plants, we need to examine plant species having large geographic ranges or various states in life-history traits, such as life form and breeding systems.

Negative impacts by invasive species on native insular organisms and ecosystems have been argued repeatedly. However, the types and degrees of such influences by invasive plants on continental islands are still unclear. Toward a better understanding of insular organisms and the progress of evolutionary and conservation biology, we need to integrate relevant ecological and genetic information appropriately.