

学 位 論 文 要 旨	
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題 目	A Study on Genomic Insights into the Dynamics of Amaryllidaceae Family and Their Viruses Collected from All Over Japan (日本全国から収集したヒガンバナ科植物およびそのウイルス動態に関するゲノム解析研究)
<p><i>Narcissus</i> plants and <i>Allium macrostemon</i> Bunge (wild Japanese garlic or no-biru) which belong to the family Amaryllidaceae are well known and widely distributed in Japan. Studies of the genomic of these plants and the viruses that infect them are important for understanding evolutionary analysis, virus-virus interactions, and genetic diversity.</p> <p>In particular, narcissus late season yellow virus (NLSYV) and narcissus degeneration virus (NDV), are major viruses of <i>Narcissus</i> plants and causing serious diseases outbreaks in Japan. However, details of the co-infection and distribution of narcissus viruses in Japan remain unclear. In this study, <i>Narcissus</i> plants showing mosaic or stripe leaves were collected together with asymptomatic plants in Japan and analyses evolutionary. The results showed that (1) NLSYV is widely distributed, whereas the distribution of NDV is restricted to southwest parts of Japan, (2) the genomes of NLSYV isolates share nucleotide identities of around 82%, whereas those of NDV isolates are around 94%; (3) three novel recombination type patterns were found in NLSYV; (4) NLSYV comprises at least five distinct phylogenetic groups whereas NDV has two; and (5) infection with narcissus viruses often occur as co-infection with different viruses, different isolates of the same virus, and in the presence of quasispecies (mutant clouds) of the same virus in nature.</p> <p>On the other hand, no-biru is a wild onion species that is distributed throughout Japan, and clarifying its genetic diversity and the evolutionary process is important for elucidating the historical significance of this plant. This study aimed to fill this knowledge gap by examining the genetic diversity of 47 lines of no-biru from different regions of Japan using the restriction site-associated DNA sequencing (RAD-Seq) method. The analysis identified a unique population structure, which was divided into three distinct groups (A, B and C). Notably, clear evidence of bulb propagation was found in groups A and B, but not in group C. Furthermore, Group C formed four subgroups (C1, C2, C3 and C4), and the emergence of subgroups C2, C3 and C4 through hybridization between subgroup C1 and either or both Groups A and B, which allowed us to infer that Groups A, B and C1 were the ancestral populations. Cultivation tests on the test strains also showed that the three groups had distinct morphological characteristics. These results indicated that human migrations may have affected the distribution of the plants, causing them to be actively used in the past, but then decline and are now under-utilized.</p> <p>These findings indicate that elucidating evolutionary analysis of virus and genetic diversity of plant are an important step towards strategies to control virus diseases and the effective utilization of under-utilized plant resources. Therefore, a better understanding of the evolution of these plants and their role in the ecosystem will assist in the search for sustainable conservation and utilization methods.</p>	