

学 位 論 文 要 旨	
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題 目	Study of the population genetics on the subtropical fruit viruses (亜熱帯果樹のウイルスについての集団遺伝学的研究)
<p>The genetic structure and diversity of <i>Banana bunchy top virus</i> (BBTV) and <i>East Asian Passiflora virus</i> (EAPV) were investigated using population genetics methods.</p> <p>The genetic structure and diversity of BBTV on Sumatra Island were clarified first: 61 isolates of BBTV were collected, and the sequences of DNA-R, DNA-S and DNA-U3 were determined. Although these isolates showed different sequences in the stem-loop region in DNA-U3, they were generally very similar, with little or no variation according to planting area or the varieties and genome types of the host. The genetic diversity analysis showed that the Sumatra population has very low diversity compared to other areas. The phylogenetic analysis showed that the Sumatra isolates belonged to the Asian group. A recombination analysis revealed no evidence of recombination in the Sumatra population. The selection pressure analysis indicated that all of the Sumatra isolates underwent negative selection. The selection pressure among the viruses infecting the banana varieties with the genotypes of AAB or ABB underwent weaker negative selection compared to the viruses infecting the varieties with AA or AAA genotypes. A neutrality test suggested the sudden expansion of the West Sumatra population.</p> <p>Next, a population genetics analysis of each population of BBTV from nine countries was conducted. The genetic diversity analysis showed that the China, Taiwan and Vietnam populations had higher diversity than the other populations. The selection pressure analysis showed that all nine populations underwent negative selection. The neutrality test suggested that the sizes of all of the populations were increased. The gene flow analysis suggested that gene flow occurred frequently in the Asian group and infrequently in the South Pacific group.</p> <p>The genetic structure and diversity of EAPV on Amami Oshima Island was investigated next: 15 isolates of EAPV from two different areas of Amami Oshima Island (the Yuwan area of Uke36n village, and Sumiyo town of Amami city) were collected. The sequences of polyproteins from 10 of the isolates and the N1b and CP regions of the other five isolates were determined. The nucleotide and amino acid sequence identities of polyproteins within each population were very high, and those between isolates from both areas were also high. However, five characteristic nonsynonymous substitutions were uniformly observed in the P3 and CP regions of the Sumiyo isolates. A recombination analysis revealed that there was no evidence of recombination in any of the isolates from Amami Oshima Island. The selection pressure analysis showed that as a whole, the EAPVs of both populations underwent negative selection, but the extent of the negative selection varied. These results were supported by a neutrality test. The gene differentiation and gene flow analyses suggested that the Sumiyo and Yuwan populations were clearly differentiated and that gene flow occurred only infrequently. These results were supported by a phylogenetic analysis. We concluded that the two populations evolved independently in each respective area.</p>	