

## 学 位 論 文 要 旨

氏 名	Huy Duc Nguyen
題 目	Studies on the spatial and temporal evolution of <i>Turnip mosaic virus</i> (カブモザイクウイルスの空間的・時間的進化に関する研究)

Studies on the spatial and temporal evolution have been reported for animal and plant viruses, however little information was known for those of potyviruses. *Turnip mosaic virus* (TuMV) is a species of the genus *Potyvirus* in the family *Potyviridae*. TuMV is probably the most widespread and damaging virus that infects cultivated brassicas worldwide. This study focused on the spatial and temporal evolution of TuMV populations.

Spatial evolution was analysed using 30 Vietnamese and 105 worldwide isolates of TuMV. The Vietnamese isolates were collected from *Brassica* and *Raphanus* plants during 2006-2008. Sequence-based phylogenetic and population genetic analyses were made of the complete polyprotein coding sequences, and of four non-recombinogenic regions of those sequences [the helper component-proteinase protein (HC-Pro), protein 3 (P3), nuclear inclusion b protein (NIb) and coat protein (CP)]. These were used to assess the subpopulation differentiation and divergence between Vietnamese TuMV populations and those of China and Japan. Nine inter- and intralineage recombination type patterns were identified in the genomes of the Vietnamese isolates, of which seven were novel. All the Vietnamese non-recombinant isolates fell into the world-B group and clustered with Chinese isolates. The estimates of genetic differentiation and gene flow revealed that the TuMV populations of Vietnam, China and Japan were genetically linked but have clear local founder effects. These results show for the first population genetic study of TuMV in Southeast Asia.

Temporal evolution was analysed using 155 isolates of TuMV collected mostly from Brassicaceae during 1968-2007 from worldwide. A sister lineage from European wild orchids (TuMV-OM) to the brassica-infecting TuMVs (TuMV-BIs) was identified. Extensive host-range tests showed that all of the TuMV-OMs were biologically similar, but distinct from TuMV-BIs and did not readily infect brassicas. Bayesian coalescent analyses were applied for analyses of temporal evolution using a combination of novel and published sequences data from three TuMV protein coding regions; HC-Pro, P3 and NIb. The dating analyses of those coding regions indicated that the TuMV-BI viruses diverged from TuMV-OMs around 1000 years ago. Only 150 years later, the four lineages (basal-B, basal-BR, Asian-BR and world-B groups) of the present global population of TuMV-BIs diverged from one another. These dates are congruent with historical records of the spread of agriculture in West Europe.