

HYVV-[UK2]. Grafting studies with a HYVV infected plant with a healthy *L. japonica* showed that virus was transmitted to virus infected *L. japonica* to healthy *L. japonica* and produced typical disease symptoms. Electron microscopy of thin sections of infected *L. japonica* leaves revealed the presence of crystalline inclusion showing a granular structure in some of the nuclei in phloem cells. Based on sequence comparisons and phylogenetic analysis, this virus studied was identified as Korean strain of HYVV and named HYVV-K

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**Evolution of genes encoding non-specific lipid transfer proteins  
in the *Poaceae* family**

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The genes encoding non-specific lipid transfer proteins (nsLTPs), which are members of a small multigene family, show a complex pattern of expression regulation suggesting some diversification caused by the partitioning of their expression after duplication. In this study, the evolution of nsLTP genes in the *Poaceae* family was examined by surveying the pseudogenes and unigenes encoding the nsLTP from rice pseudomolecules and the NCBI unigene database, respectively. Interestingly, there were nsLTP-rich regions on the distal parts of rice chromosomes 11 and 12, which resulted from the most recent large duplication in the rice genome. Two independent tandem duplications are expected to occur in the nsLTP-rich regions of rice. However, both groups of duplicate genes might have undergone different patterns: one is subfunctionalization and the other is mainly silencing (pseudogenization). Compared with the genomic distribution of wheat nsLTP genes, the nsLTP-rich regions do not appear to exist in other cereals, which is probably due to chromosome rearrangements or gene amplifications followed by differential gene losses after the divergence of the major cereals. The pattern of the genomic distribution of nsLTP genes in the *Poaceae* family show some differences between the cereal nsLTP genes that diverged from an ancient gene. In particular, the long-term conservation of certain features, e.g. expression frequency and partition, tends to be continued throughout their evolution. There are somewhat fewer nsLTP unigenes in *Andropogoneae* than those of other tribes, such as *Oryzaceae* and *Triticeae*, which suggest that the differential loss of nsLTP genes occurred in the *Poaceae* family. These results might provide some clue as to the evolution process of nsLTP genes after the divergence of the *Poaceae* family approximately 50 million years ago (Mya).

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**Sequence based genetic mapping of *Brassica rapa* BAC clones which  
compose comparatively tiled path on the *Arabidopsis* chromosomes**

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