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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(O5-03)

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 pseudomoleclues 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, thelong-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 *Androponeae* than those of other tribes, such as *Oryzeae* and *Triticea*, 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 approximately50 million years ago (Mya).

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(O5-04)

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

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The *Brassica* and *Arabidopsis* lineages diverged ~20 MYA with comparative late and so their genome is syntenic and collinear. Based on comparative sequence analysis of 91,179 BAC end sequences (BES), we have allocated a total of 4,317 *Brassica* BAC clones (9.5%) on the counterpart region of *Arabidopsis* chromosomes that span 92 Mb of unique sequence of *Arabidopsis* chromosome. Furthermore, we selected 629 *Brassica* BAC clones that compose the minimum tiling path on *Arabidopsis* chromosome (http://www.brassica-rapa.org). The comparative tiled BACs evenly distributed in the *Brassica* genome had been sequenced in 2005. The actual location of each BAC clone of *B. rapa* can be identified by FISH or sequence based genetic mapping. Up to date, around 210 among 629 sequenced BACs have been mapped through development of SSR marker in each BAC. Totally 1500 SSRs primer pairs(1 to 3 every 629 BAC clones) were designed and among these, around 500(30%) have shown polymorphism between parental lines of two mapping populations (Jangwon $F_{2:3}$ family and Chiifu X Kenshin Double haploid). Using these SSR markers, 210(33 %) BAC clones were mapped to linkage groups of Jangwon F3 population and their actual location in *Brassica* were identified. As the same previous comparative study, BACs selected from a collinear segment on *Arabidopsis* were localized to three parts and it proves again that *Brassica* genome occurred triplication after divergence with *Arabidopsis*. Sequence based and genome widely well distributed DNA markers can be a valuable resource to provide unlimited information for breeding and genome evolution study as well as genome sequencing of the genus *Brassica*.

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In Silico identification of *Brassica rapa* BAC clones containing harboring genes related to circadian associated factors

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