**A216** Phylogeny of lower eudicots based on multiple genes: *atp*B, *rbc*L, 18S and 26S rDNA sequences

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Phylogenetic analyses were conducted for 60 genera of lower eudicots (Ranunculidae and lower Hamamelididae), magnoliid outgroups, and appropriate representatives for higher taxa within the higher eudicot clade based on sequences of 26S nuclear rDNA. We re-analyzed Hoots data of former three gene study (*atp*B, *rbc*L, and 18S; *Ann. Missouri Bot. Gard.* 86: 1-32, 1999) with few taxa supplement and compared 26S data with both three-gene data and combined four gene data. The following higher taxonomic groups were recognized with high bootstrap values in the four gene data (>90%): Eudicots (including Nelumbo), Ranuncluididae (including Euptilia), core eudicots (including caryophyllids, asterids, and rosids), Buxales/Didymelales, Circaeasterales, Menispermales, Berberidales, and Ranunculales. Bootstrap values of clades of Papaverales, core ranunculids, a clade consisting of lower hamamelids and core eudicots, which had high bootstrap values in the three gene data, decreased in the four gene data. *Euptilia*, a problematic taxon in the three gene data, is located at the base of the Ranunculids, which is supported with 70% of bootstrap value.

**A301** Partial Sequencing of the Intergenic Spacer Region in *Fusarium* spp.

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Based on the IGS-RFLP (Intergenic spacer - restriction fragment length polymorphism) results of 20 strains belonging to section *Elegans* and *Liseola*, we sequenced partial intergenic spacer(IGS), about 600 bp, using PCR with primer NIGS1 (5'-CTTCGCCTCGATTTCCCCAA-3') and NIGS2 (5'-TCGTCG CCGACAGTTTTCTG-3'). The strains were selected on the basis of IGS - RFLP result. The results of sequencing for 4 *Fusarium oxysporum* f. sp. showed the same phylogenetic pattern as that of IGS-RFLP. The species belonging to the section *Liseola*, *F. moniliforme 12*, *F. moniliforme* 7219, *F. proliferatum*, and *F. proliferatum* var. *minus* were not amplified with primer NIGS 1 and NIGS 2. To resolve the question that the strains in section *Liseola* didn't form PCR product, the 5 strains belonging to section *Dlaminia* which was known as intersection between section *Elegans* and *Liseola* and section *Discolor* which as remoted distance on phylogenetic relationship were tried to amplify with same primers. As the results, *F. beomiforme*, *F. napiforme*, and *F. nygamai* which belonged to section *Dlaminia* were not amplified. And *F. sambucinum* from section *Discolor* was also same to that of *Liseola*. On the other hand, *F. graminearum* belonging to *Discolor* was ,interestingly, obtained same PCR product as section *Elegans*. These results suggested possibility that the sequence included 600bp could be used the genetic marker for determining phylogenetic relationship among species.