

J. Plant Res. **113**: 259-269, 2000 Journal of Plant Research
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A Comparison of ITS Nuclear rDNA Sequence Data and AFLP Markers for Phylogenetic Studies in Phyllostachys (Bambusoideae, Poaceae)

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Two contrasting molecular techniques, namely DNA sequences and amplified fragment length polymorphisms (AFLP) were used to investigate phylogenetic relationships of *Phyllostachys*, a large, economically important genus of woody bamboos. DNA sequences of the internal transcribed spacer (ITS) region of nuclear ribosomal DNA (nrDNA) were used in a parsimony analysis. *Phyllostachys* was well supported as monophyletic with *Chimonobambusa* as its closest allied genus. The 5S spacer region of nrDNA was investigated but found unsuitable for this purpose. The AFLP analysis showed much higher discriminating power between species and was more useful for phylogenetic reconstruction at this taxonomic level. The combined data were used to review the previous infra-generic classifications. *Section Heteroclada* Wang & Ye is strongly supported and can be further divided into sub-groups. A group within section *Phyllostachys* is strongly supported, but a further group of taxa previously included in this section is difficult to place. The ability of the methods to help separate species such as *P. sulphurea* and investigate genetic diversity at the infra-specific level was also assessed. It is argued that AFLPs could often be the method of choice for phylogenetic studies of closely related taxa for which DNA sequence data provide insufficient resolution.

Key words: AFLP — Bambusoideae — ITS — Molecular — Phylogeny — *Phyllostachys* — Poaceae