

Low-molecular-weight rRNAs sequences and plant phylogeny reconstruction: Nucleotide sequences of chloroplast 4.5 S rRNAs from *Acorus calamus* (Araceae) and *Ligularia calthifolia* (Asteraceae)*

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Abstract: Chloroplast 4.5 S rRNAs of the monocot *Acorus calamus* and the dicot *Ligularia calthifolia* have been sequenced. Phylogenetic trees for the chloroplast 4.5 S and 5 S rRNAs and also for cytosol 5 S rRNAs have been constructed by several methods. They are compared with previous studies. Evidently, it is necessary to consider the inequality of nucleotide substitution rates in different lines for adequate phylogenetic reconstructions. Some relevant conclusions are presented. The possibilities and prospects for using data on low-molecular-weight rRNAs from cytosol and organelles for deducing phylogenetic relationships in plants are discussed.

Although many different taxonomic systems and phylograms for plants have been suggested, no consensus on this item has been reached yet. True, according to TAKHTADJAN (1980), modern macrosystems of the flowering plants have more common than divergent features. Yet he makes this reservation: “Nevertheless in very many cases we are limited by lack of data and there is still quite a number of the taxa of obscure affinities, even among the families and the orders. In spite of the great success of systematic and evolutionary botany, only comparatively few groups of the flowering plants have been studied thoroughly enough to draw reliable phylogenetic conclusions from the available data”. This admission from one of the authorities in the field is an eloquent testimony that phylogenetic studies still remain an open field of research.

* Dedicated to the memory of S. V. MEYEN, Vice-president of the International Organization of Palaeobotany (Dec. 17, 1935–March 30, 1987).