

in a damaged site, imitating the way of healing works that an integral natural system carries out. Ecological restoration uses different treatments and approaches according to extents of the existing damage and to the specific goal to be achieved. An ecological diagnosis is, therefore, required prior to restoration practice. The cost and efforts to achieve a proposed goal can be significantly reduced when a restoration plan is formulated upon the results of well-conducted ecological diagnosis. Under such perspectives, restoration ecology is a practical science, which aims to solve the problems of the real world based on the existing ecological principle. Furthermore, restoration ecology offers opportunities to test the ecological concepts and theories obtained by means of the former ecological studies. Human being exploited natural environment excessively for his comfort on one hand but damaged it inevitably on the other hand. Such intensive resource utilization and continuous environmental damaging will extend into future and ultimately jeopardize the survival of humankind if no prompt action is taken. In the present situation, we must not continue on such lives without any preparation. We have to cope with the environmental crises approaching near us pursuing the ecological restoration that reduce the unnecessary use, recruit the deficient part, and strengthen the weak portion in our environment. Restoration ecology could be recognized as the ecology for the future in such viewpoints.

SL203

Molecular Phylogeny of Tribe Caucalideae (Carrot Tribe) and Its Related Plants

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Since the tribe *Caucalideae* was established for those species of *Apiaceae* (*Umbelliferae*) with spines, tubercles or bristly hairs on the primary and/or secondary ridges of the fruits, there has been considerable disagreement as to its proper circumscription, the relationships among its members, and the delimitation of certain genera. Although Heywood and Jury (Heywood, 1982) provided a checklist of *Caucalideae*, recognizing 21 genera and 68 species, no rigorously constructed estimate of phylogeny exists for these taxa. Phylogenetic relationships within *Caucalideae* were assessed using nucleotide sequence variation in the internal transcribed spacer (ITS) regions of 18S-26S nuclear ribosomal DNA, detailed restriction site mapping of the chloroplast genome, and morphological and anatomical characters. Evolutionary patterns of selected (i.e., cytological, palynological, phytochemical, and morphological) characters were interpreted by plotting their distribution on the ITS-based phylogeny, revealing that many of these characters are highly homoplastic. On the basis of these comparative data, the following results were obtained: (1) Phylogenies derived from three independent lines of evidence are largely congruent, suggesting that hybridization may not have been a factor in the evolution of this group; (2) There is little support for any existing system of classification for the tribe. *Aphanopleura*, *Psammogeton*, and *Kozlovia* are excluded from the tribe, whereas representatives from tribe *Laserpitieae* are included. The genus *Chaetosciadium* is best treated within *Torilis*; (3) Fruit primary appendage characters are more useful than those of secondary appendages for delimiting generic boundaries; (4) Tribe *Caucalideae* sensu lato is provisionally established and consists of subtribes *Daucinae* (*Daucus*,

Pseudorhiza, *Pachytenium*, *Agrocharis*, *Laserpitium*, *Orlaya*, *Ammodaucus*, *Cuminum*, *Polylophium*, and *Artemisia*) and *Caucalidinae* (*Astrodaucus*, *Turgeniopsis*, *Szovitsia*, *Torilis*, *Yabea*, *Caucalis*, *Turgenia*, and *Lisaea*).

SL204

***Medicago Truncatula*: a Model
Plant Suitable for Legume
Genomics and Symbiosis Research**

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Certain aspects of plant biology are best studied in legumes. Examples of research areas where a model legume system has unique potential to make an important contribution include human nutrition, rhizosphere interaction and nitrogen and phosphorous metabolism. *Medicago truncatula* is closely related to the important forage legume alfalfa (*Medicago sativa*), with more distant ties to pea and soybean. The annual, self-pollinating species of Mediterranean origin engages in symbiosis with nitrogen fixing soil bacterium *Rhizobium meliloti*. Several attributes of *M. truncatula* such as a small diploid genome (~400 Mbp/1C), a short life cycle, and its capacity for rapid transformation and regeneration makes it suitable as a worldwide model for legume biology and symbiosis research. Recently, pioneering multi-national research programs on *M. truncatula* are in progress both in U.S.A. and in Europe, demonstrating elevated global scientific interests in this plant species. To facilitate molecular genetic analysis of *M. truncatula*, a bacterial artificial chromosome (BAC) library was constructed. The library consists of 30,720 clones with an average insert size of 100 kb, representing approximately five

haploid genome equivalents. Molecular linkage maps generated using co-dominant DNA markers suggest conserved genome structure between *M. truncatula* and crop legumes and between *M. truncatula* and *Arabidopsis thaliana*. These observations indicate that detailed analysis of the syntenic regions enriched with symbiotic genes will aid efforts in map-based cloning of nodulation mutants, thereby accelerating the pace of characterization of agronomically important genes and traits.

SL205

Membrane Lipid Signaling in Plants

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Phospholipases were found to mediate the process of transmembrane signal transduction in animal tissues. Recently phospholipase-mediated lipid signaling has also been unraveled in plants. Several classes of phospholipases including phospholipase A₂ (PLA₂), phospholipase C (PLC) and phospholipase D (PLD) have been reported in animals and plants.

PLD has been suggested to be a key enzyme, which initiates membrane lipid degradation in senescing tissues. Disruption of membrane integrity has been suggested as a primary cause of senescence in plants. A selective degradation of membrane phospholipids has been found to be one of the early events of membrane deterioration during senescence. It has been suggested that the lipolytic cascade leading to membrane deterioration is initiated by PLD activity.

PLD expression levels are positively correlated to the rate of leaf senescence. Analysis of PLD transcript revealed an elevation of PLD during senescence of