Pseudorlaya, Pachyctenium, Agrocharis, Laserpitium, Orlaya, Ammodaucus, Cuminum, Polylophium, and *Artedia*) 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 A_2 (PLA_2), 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

castor bean leaf discs, suggesting that gene activation and protein synthesis are involved in regulating the increased PLD activity in senescing tissues (Ryu and Wang 1995).

Products of PLA_2 activity, lysophospholipids, are novel bioactive lipid molecules which retard plant senescence and stimulate cell growth. PLA_2 mediates numerous signal transduction pathways in animal systems. It was found that PLA_2-generated lysophospholipids act as novel lipid-derived growth regulators by retarding senescence of leaf, flower, and fruits as well as by stimulating plant cell growth.

PLA_2-generated lysophospholipids is specific inhibitors of PLD activity. Interestingly, lysophospholipids including LPE inhibited PLD activity *in vitro* in a highly specific manner (Ryu et al. 1997). LPE inhibition of purified cabbage PLD was dependent on the fatty acid chain length and the degree of unsaturation of LPE. LPE with longer and more unsaturated acyl chain was found to be more effective.

It is proposed that the interaction between PLD and PLA_2 may regulate plant growth and senescence. Since there is evidence for the inhibition of PLD by lysophospholipids, it is proposed that the lysophospholipids may play a role as cellular regulators of PLD *in vivo*. The further elucidation of cross-talk mechanisms between PLA_2 and PLD may provide better understanding on plant senescence process.

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SL206

Chracterization of Protein Complexes Containing NDPK with Characteristics of Light Signal Transduction in Plant and Fungi

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Light signals constitute major factors in regulating gene expression and morphogenesis in plants and fungi. Phytochrome A and B were well characterized red and far-red light receptors in plants. Red light signals increased the phosphorylation of 18 KDa protein, which was identified to be nucleoside diphosphate (NDP) kinase. The NDP kinase catalyzed auto-phosphorylation and had a protein kinase activity phosphorylating myelin basic protein. As candidates for blue light photoreceptors, cDNAs for CRY 1 and CRY2 were isolated by the group of *A. cashmore*. The N-terminal regions of these proteins showed a high homology to DNA photolyase. The 120 KDa protein first detected in *Pisum sativum*, which showed blue light induced phosphorylation was also detected in *Arabidopsis thaliana* by the group of W. R. Briggs. The 120 KDa protein designated as phototropin was encoded by the nph 1 gene, which regulated positive phototropism of the plant. In *Neurospora crassa*, blue light irradiation of the membrane fraction prepared from mycelia stimulated the phosphorylation of the 15KDa protein, which was also identified to be an NDP kinase. Recent progress in understanding early events in light signal transduction mainly in *Pisum sativum* ALASKA, *Arabidopsis thaliana* and *Neurospora crassa* were summarized.