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Plant Gene Register

An *Arabidopsis* cDNA Encoding a 33-Kilodalton Laminin Receptor Homolog[1]

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The major glycoprotein component of animal cell basement membranes, laminin, is involved in a variety of cellular activities, including cell adhesion, differentiation, and mitogenesis, that are mediated by the interaction of laminin with specific cell-surface receptors. A laminin-binding protein with an apparent molecular mass of 68 to 72 kD was first characterized in mammalian tumor cells and considered as "the laminin receptor" (Liotta et al., 1986; Wewer et al., 1986). Several putative cDNA clones encoding this protein have been isolated from mammals (Yow et al., 1988; Rao et al., 1989; Van den Ouweland et al., 1989; Grosso et al., 1991). All the clones contained an open reading frame coding for a highly conserved polypeptide with a calculated molecular mass of 33 kD. Independently, a cDNA encoding an identical polypeptide was isolated from mouse tumor cells (Makrides et al., 1988), but the expressed protein, named factor p40, was shown to be a component of the translation machinery (Auth and Brawerman, 1992). Recently, DNA-deduced amino acid sequences exhibiting homology with the previously characterized 33-kD "laminin receptor" were identified from hydra (Keppel and Schaller, 1991), *Drosophila* (M.B. Melnick, T.B. Chou, and N. Perrimon, accession No. M90422), and yeast (J. Miles and T.G. Formosa, accession No. M88277).

We have isolated a cDNA clone (*Atlrh1*) from a cDNA library of *Arabidopsis thaliana* cultured cells showing a striking homology to the laminin receptor cDNAs (Table I). Nucleotide homology of *Atlrh1* with the above-mentioned DNA sequences was restricted to the first two-thirds of the coding sequence, with highest homology to the human cDNA (66% identity). In the same way, the *Atlrh1* deduced polypeptide, 298 residues long, showed strong homology with the deduced protein sequences of other species from amino acids 12 to 222. In this region, mouse, human, and *Drosophila* polypeptides showed the highest homology to the plant sequence, corresponding to 60 to 62% identity and 78 to 79% similarity accounting for the conservative substitutions. No significant homology was found in the carboxy-terminal region from amino acids 223 to 298, apart from a relatively high conserved content in Trp. It is an intriguing feature that all deduced polypeptide sequences so far characterized are completely divergent in their carboxy-terminal part, except those belonging to the mammal class. Moreover, this region is variable in length: 76 amino acids for the *Arabidopsis* sequence, 52 for *Drosophila*, and only 34 for the yeast protein.

Evidence of a new class of laminin receptor-like proteins from *Arabidopsis* raises the question of their putative role in plants. The human and the hydra proteins have been localized in the cytoskeleton (Keppel and Schaller, 1991). On the other hand, the mouse protein was associated with polyribosomes, and it has been proposed that the protein might function in the polysome-cytoskeleton interaction required for mRNA translation (Auth and Brawerman, 1992). However, it cannot be excluded that the protein might be a

Table I. *Characteristics of the 33-kD laminin receptor homolog from Arabidopsis*

Organism:
Arabidopsis thaliana L. (Heynh.) ecotype Columbia.
Function:
Unknown in plants. Putative laminin receptor or polysome-associated translation factor in mammals.
Techniques:
Sequencing of randomly selected cDNA clones from a cDNA library in λ-ZAPII (Stratagene) prepared from cell-suspension cultures (T87 cell line). Nucleotide sequencing on double-stranded templates using the dideoxy chain termination method.
Sequence Identification:
Sequence comparison in data bases using the search programs FASTA and BLASTN. Recovery of four cDNA clones among 165 randomly selected cDNAs, showing similarity to the putative laminin receptor cDNAs from other species. One cDNA clone (*Atlrh1*), fully sequenced on both strands. Analysis of *Atlrh1* deduced amino acid sequence using program BLASTX and programs of University of Wisconsin Genetics Computer Group package.
Features of cDNA Structure:
1091-bp insert including an open reading frame of 894 nucleotides. Poly(A) tail at position 1074.
Features of Predicted Amino Acid Sequence:
Open reading frame of 298 amino acids with a calculated M_r of 32,306. Repeated motif $A_{(1-3)}P_{(1-2)}A_{(0-3)}$ present in the carboxy-terminal region.

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component involved in the cytoskeleton connection to the extracellular matrix, although laminin is not known in higher plants.

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