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Plant Gene Register

A New Member of the Small GTP-Binding Protein Family in *Arabidopsis thaliana*[1]

Ying Yi and Mary Lou Guerinot*

Department of Biological Sciences, Dartmouth College, Hanover, New Hampshire 03755

In eukaryotes, GTP-binding proteins act as versatile molecular switches whose active or inactive state depends on the binding of GTP or GDP, respectively (Bourne et al., 1990). The rapidly growing family of small GTP-binding proteins (mol wt values between 20,000 and 36,000) is now generally subdivided into three major subfamilies: Ras-like, Rho-like, and Ypt/Rab-like proteins. Each group seems to play a distinct role in the cell: the Ras subfamily is involved mainly in cell growth and differentiation, the Rho subfamily is involved in cytoskeleton organization, and the Ypt/Rab subfamily has a role in intracellular transport and secretion. In plants, proteins have been identified that specifically bind GTP, and studies with nonhydrolyzable GTP analogs indicate a role for GTP-binding proteins in various processes, including plant hormone signal transduction and ion channel function (Terryn et al., 1993). A number of genes have now been isolated from a variety of plant species (*Zea mays, Oryza sativa, Nicotiana tabacum, Nicotiana plumbaginifolia, Arabidopsis thaliana, Pisum sativum*) by homology to members of the Ras superfamily (Nagano et al., 1993; Regad et al., 1993; Terryn et al., 1993; Bednarek et al., 1994).

Here we report on a cDNA encoding a small GTP-binding protein from *Arabidopsis thaliana* ecotype Columbia that was isolated from a root cDNA library (Peterman and Goodman, 1991). We have designated the gene *A.t.RAB11* because it belongs to the Ypt/Rab subfamily of GTP-binding proteins (Table I), showing 81% similarity to the mammalian Rab11 protein (Chavrier et al., 1990) and 80% similarity to the *Schizosaccharomyces pombe* Ypt3 protein (Miyake and Yamamoto, 1990). Chavrier et al. (1990) had previously reported that Rab11 and Ypt3 are probably homologs, with 80% similarity. Of the *Arabidopsis* small GTP-binding proteins that have been identified to date, the A.t.Rab11 protein has the highest similarity (91%) to ARA2 (Anai et al., 1991).

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* Corresponding author; fax 1–603–646–1347.

Table I. *Characteristics of a cDNA encoding a small GTP-binding protein from Arabidopsis thaliana*

Organism:
Arabidopsis thaliana, ecotype Columbia.
Gene Product:
Small GTP-binding protein.
Source:
λgt11 cDNA library constructed from *A. thaliana* root poly(A)$^+$ RNA (Peterman and Goodman, 1991), a gift from K. Peterman.
Techniques:
The cDNA library was screened with a radiolabeled genomic DNA fragment that lies upstream of a gene identified as a putative homolog of the yeast ferric reductase gene *FRE1* (our unpublished results).
Sequencing Strategy:
Double-stranded plasmid sequencing of both strands by the dideoxynucleotide chain termination method.
(G + C) Content:
44.0% overall; 47.0% in the protein-coding region.
Features of cDNA Structure:
The cDNA is 854 nucleotides in length, with a 54-nucleotide-long 5′ untranslated region, a 648-nucleotide-long open reading frame, and a 152-nucleotide-long 3′ untranslated region.
Structural Features of Protein:
The open reading frame consists of 216 amino acids. Predicted M_r 25,920. Isoelectric point 5.54.
Antibodies:
Not prepared.
Subcellular Location:
Not tested.
Method of Identification:
Sequence comparison to GenBank/EMBL data base: sequence identity/similarity to known small GTP-binding proteins.

	Amino Acid Sequence Similarity[a]					
	ARA2	Pra6	Pra7	Np-ypt3	Rab11	Ypt3
	%					
A.t.Rab11	91	96	91	91	81	80

[a] Amino acid sequences were aligned using the GAP program of the University of Wisconsin Genetic Computer Group.

A.t.Rab11 is also highly similar to Np-ypt3 from *N. plumbaginifolia* (Dallmann et al., 1992) and to Pra6 and Pra7 from *P. sativum* (Nagano et al., 1993). Whether these similarities extend to common function remains to be determined.

Using *A.t.RAB11* as a gene probe, we detect a highly expressed transcript of approximately 0.9 kb in poly(A)$^+$ RNA prepared from roots. This is interesting in light of the fact that the two pea proteins (Pra6 and Pra7) that are most similar to A.t.Rab11 are expressed abundantly in roots (Nagano et al., 1993). With nine genes encoding small GTP-binding proteins now identified in *Arabidopsis*, detailed expression studies should begin to provide clues to the function of these proteins in plant cells and may provide new insights into basic cellular processes such as transport and signal transduction cascades.

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The GenBank accession number for the sequence reported in this article is L18883.

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