



Letter to the Editor

## A unified nomenclature for *Arabidopsis* dynamin-related large GTPases based on homology and possible functions

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Since the cloning and characterization of ADL1 (Dombrowski and Raikhel, 1995) and phragmoplastin in plants (Gu and Verma, 1996), there has been significant progress in research on this group of large GTPases which share sequence homology with the animal dynamins (Hinshaw, 2000). As compared to small GTP-binding proteins, such as Rab, Rop and Ran, which have molecular mass of 18–24 kDa and act as signaling GTPase, dynamin-related proteins are larger (60–110 kDa) and function in part by wrapping around pinching off membranes, though there is evidence that they also have a signaling role. However, besides binding to GTP, they share little homology with other large GTP-binding proteins such as trimeric G protein  $\alpha$ -subunit (96 kDa) and elongation factor Tu (EF-Tu, 52 kDa). Plant dynamin-like proteins have been shown to be present in different subcellular locations including the cell plate, plasma membrane, Golgi apparatus, vesicles, mitochondria and chloroplasts. They have also been implicated in diverse subcellular processes such as cell plate formation, endocytosis, exocytosis, protein sorting to the vacuole and plasma membrane, and division of mitochondria and chloroplasts. Different acronyms (ADL for *Arabidopsis* dynamin-like, DLP for dynamin-like proteins) have been used to describe this group of proteins. The initial

naming system for dynamin-like proteins in *Arabidopsis* also inaccurately reflects the relationship among members of this family and has caused certain confusion in the literature. The diversity of this group of proteins has led to difficulties in naming new members of this family. As more such proteins (16 in *Arabidopsis*, for example) are identified, there is a need for systematic classification and nomenclature to emphasize their functional relevance. This has become more necessary in light of the fact that this group of proteins, like tubulins and actins, participate in diverse cellular processes.

Proteins containing the dynamin signature (Figure 1A) are designated dynamin-related proteins, with *DRP* representing the gene acronym (Table 1). The 16 *Arabidopsis* DRPs are grouped into 6 functional subfamilies (DRP1–6) on the basis of their phylogeny (Figure 1B) and the presence of functional motifs in the proteins (Figure 2). An individual member of a subfamily is specified by a letter. Thus, ADL1 is designated as DRP1A and the rest of the DRP1 proteins are designated as DRP1B–E. When necessary, species of origin may be specified by abbreviations for genus and species (e.g. AtDRP1A for *Arabidopsis thaliana* DRP1A).

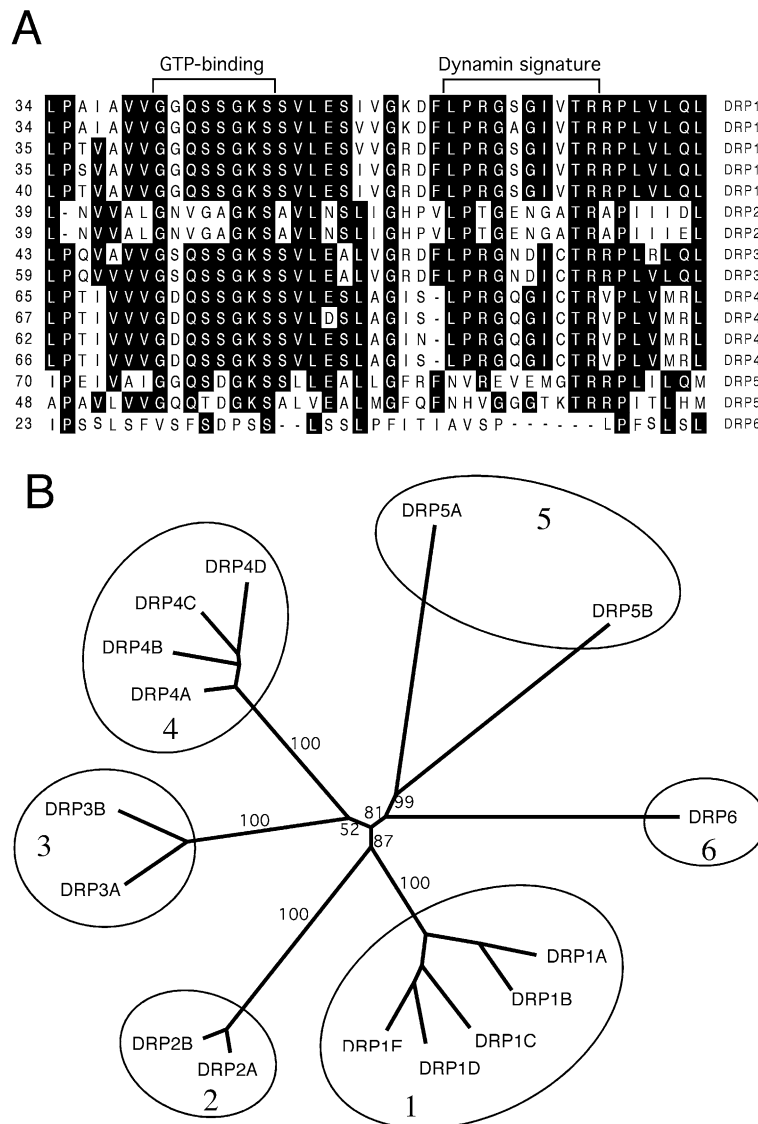
Table 1. Dynamin-related proteins in *Arabidopsis*.

Name	Name used	Gene locus	Exon numbers	Amino acid residues*	cDNA	T-DNA lines	Reference
<b>1. Phragmoplastin-like DRPs</b>							
DRP1A	ADL1A/ADL1/a68	At5g42080	16	610	yes	yes	Dombrowski and Raikhel, 1995; Park <i>et al.</i> , 1998; Kang <i>et al.</i> , 2001, 2003a
DRP1B	ADL1B	At3g61760	14	610	yes	yes	Kang <i>et al.</i> , 2003a, b
DRP1C	ADL1C/ADL5/DLP1	At1g14830	16	614	yes	yes	Kang <i>et al.</i> , 2003b
DRP1D	ADL1D/DLP3a/DLP3b	At2g44590	15	612	yes	yes	Kang <i>et al.</i> , 2003b
DRP1E	ADL1E/ADL4/DLP2	At3g60190	15	621	yes	yes	Kang <i>et al.</i> , 2003a
<b>2. Plant dynamins</b>							
DRP2A	ADL6	At1g10290	22	914	yes	yes	Jin <i>et al.</i> , 2001; Lam <i>et al.</i> , 2002; Lee <i>et al.</i> , 2002
DRP2B	CF1/ADL3	At1g59610	22	920	yes	yes	Mikami <i>et al.</i> , 2000
<b>3. Mitochondria (chloroplast)-associated DRPs</b>							
DRP3A	ADL2; ADL2a	AT4g33650	20	809	yes	yes	Kang <i>et al.</i> , 1998; Kim <i>et al.</i> , 2001
DRP3B	ADL2b	At2g14120	20	782	yes	yes	Arimura and Tsutsumi, 2002; Nishida <i>et al.</i> , 2003
<b>4. Mx-like DRPs</b>							
DRP4A		At1g60530	2	301	no	yes	
DRP4B		At1g60540	1	648	no	yes	
DRP4C		At1g60500	2	669	yes	no	
DRP4D		At1g60510	6	676	no	yes	
<b>5. Chloroplast-associated DRPs</b>							
DRP5A		At1g53140	11	841	yes	yes	
DRP5B	ARC5	At3g19730	17	777	Yes	Yes	Gao <i>et al.</i> , 2003; Miyagishima <i>et al.</i> , 2003
<b>6. Unknown DRP</b>							
DRP6		At5g28410	8	251	no	yes	

\*When differentially spliced variants are found, the cDNA with longer coding region is presented.

The *Arabidopsis* DRP1 subfamily contains five members and is closest to soybean phragmoplastin (Gu and Verma, 1996). Members of this subfamily are similar in molecular size, ranging from 610 to 621 amino acids (Table 1) and do not contain a pleckstrin homology (PH) domain or a proline-rich (PR) motif (Figure 2). DRP1A, DRP1C and DRP1E are localized to the forming cell plate in cytokinetic cells (Gu and Verma, 1996, 1997; Lauber *et al.*, 1997; Kang *et al.*, 2001, 2003a, b; Hong *et al.*, 2003) and may also play specific roles in the plasma membrane (Kang *et al.*, 2003a, 2003b) and cytoskeleton (Hong *et al.*, 2003).

The DRP2 subfamily represents the *bona fide* plant dynamins as it is characterized by the presence of a PH domain in the middle of the molecule and a PR motif (RXPXXP) near the C-terminus (Figure 2). The PH domain is believed to bind to phosphoinositides with a broad range of specificity and affinity, whereas the PR motif may interact with the SH3 domains of proteins like amphiphysins and endophilins in mammalian cells. DRP2A (also known as ADL6) has recently been shown to bind to phosphatidylinositol 3-phosphate (PI-3-P) and PI-4-P (Lee *et al.*, 2002; Lam *et al.*, 2002) and interacts with  $\gamma$ -adaptin and an

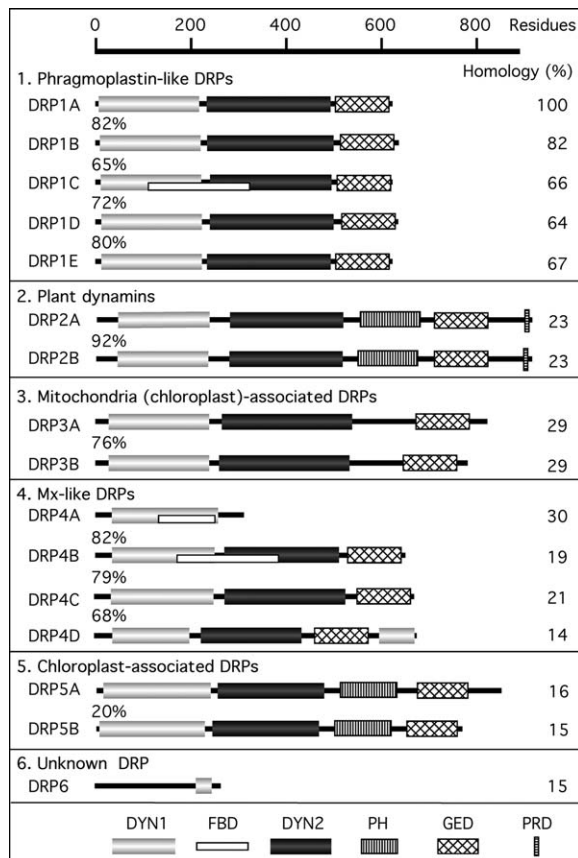


**Figure 1.** Homology and classification of DRPs in *Arabidopsis*. **A.** Amino acid sequence alignment of *Arabidopsis* DRPs in the dynamain GTPase region. Protein sequences (see Table 1 for accession numbers) were compiled using CLUSTAL X. The GTP-binding motif (GXXXSGKS/T) and dynamain signature (L-P-[PK]-G-[STN]-[GN]-[LIVM]-V-T-R) are marked on the top of the alignment. Amino acid residue number of each peptide is indicated on the left. **B.** Phylogenetic tree of dynamain-like proteins in *Arabidopsis*. Phylogenetic tree was generated using CLUSTAL X and viewed with the TreeView software. Bootstrap values, produced from the analysis of the neighbor-joining trees using PAUP 4.0 software, are shown at nodes.

SH3 domain-containing protein in *Arabidopsis* (Lam *et al.*, 2002). In general, DRP2 proteins may be involved in clathrin-coated vesicle trafficking between Golgi, plasma membrane including cell plate, and vacuoles (Jin *et al.*, 2001; Lam *et al.*, 2002; Hong *et al.*, 2003).

Two members are present in DRP3 subfamily. They share only 29% homology with DRP1A (Figure 2) and do not contain PH or PR motifs. DRP3B

(ADL2b) and its orthologue from *Cyanidioschyzon merolae*, CMDnm1, have been localized to the division site of mitochondria and may participate in mitochondrial division (Arimura and Tsutsumi, 2002; Nishida *et al.*, 2003). It is uncertain whether or not DRP3A (ADL2) contains a plastid-targeting signal sequence at the N-terminal region as reported earlier (Kang *et al.*, 1998). Given the high sequence similarity between DRP3A and DRP3B (76%, Figure 2), it is



**Figure 2.** Functional domains of DRPs in *Arabidopsis*. The percentage of amino acid identity with DRP1A is shown after each peptide. The identity (%) between the two adjacent peptides is shown at the left. DYN1, dynamin 1 (pfam00350) which, also referred as dynamin GTPase domain, includes a GTP-binding motif (GXXXSGKS/T) and a dynamin signature (see Figure 1A). FBD, FeoB domain (pfam02421) which is found in the ferrous iron transport protein B. DYN2, dynamin 2 (dynamin central region; pfam01031). PH, pleckstrin homology (pfam00169) domain which binds to membrane phospholipids such as PI-3-P and PI-4-P. GED, dynamin GTPase effector domain. PRD, proline-rich domain which interacts with SH3-domain proteins.

possible that both members are part of the mitochondrial division machinery.

The DRP4 subfamily contains orthologues of the animal antiviral Mx proteins. They contain a GTPase domain in the N-terminal region and a GTPase-effector domain in the C-terminus. Both domains have been shown to be essential for the anti-viral activity in animals. The four Mx-like genes of *Arabidopsis* are located next to each other in the same orientation on chromosome 1. *DRP4A*, *DRP4B* and *DRP4D* appear to be pseudogenes, and may have arisen recently during evolution and have yet to gain any function.

*DRP4C* is transcribed in *Arabidopsis* but its function has not been established.

The DRP5 subfamily has two members which share only 15–16% homology with DRP1A (Figure 2). They contain a GTPase domain, a dynamin middle domain and a GTPase effector, an arrangement of functional motifs similar to that in DRP2 proteins. Unlike plant dynamins (subfamily 2), they do not contain a PR motif at the C-terminus. It is uncertain if DRP5 proteins contain a PH domain for lipid binding. *Arabidopsis* DRP5B (also known as ARC5) and its orthologue from *Cyanidioschyzon merolae* (Cm-Dnm2) have recently been localized to the chloroplast division ring (Gao *et al.*, 2003; Miyagishima *et al.*, 2003). DRP5 proteins do not contain an N-terminal signal peptide for plastid targeting. Instead, they are recruited to the cytosolic side of the chloroplast division site to form a ring in the late stage of chloroplast division. DRP5A shares only 20% sequence identity with DRP5B (ARC5) and it is unknown if DRP5A also plays a role in chloroplast division.

Finally, one gene (DRP6) is classified in the subfamily of unknown dynamin-related genes. It encodes a polypeptide of 251 amino acids which is much smaller than other DRPs. It is not known if *DRP6* gene is transcribed, and if its encoded protein is a GTPase.

We hope that these changes will make it easier to follow the exciting research on DRPs in plants. Unlike actins and tubulins that polymerize into linear structures, DRPs perform functions by creating polymeric structures that wrap around the membrane and thus facilitate membrane tubularization and vesicle pinching (see Verma, 2001). Many such steps are required in vesicle trafficking and membrane compartmentation in eukaryotic cells. In addition, dynamins have been proposed to function as a signaling GTPase (Sever, 2002). Therefore, new functions for DRP proteins are likely to be discovered in future studies.

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