A Diverse Family of Inositol 5-Phosphatases Playing a Role in Growth and Development in Dictyostelium discoideum

Received for publication, August 16, 2002, and in revised form, November 26, 2002
Published, JBC Papers in Press, December 2, 2002, DOI 10.1074/jbc.M208396200

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Inositol phosphate-containing molecules play an important role in a broad range of cellular processes. Inositol 5-phosphatases participate in the regulation of these signaling molecules. We have identified four inositol 5-phosphatases in Dictyostelium discoideum, Dd5P1–4, showing a high diversity in domain composition. Dd5P1 possesses only an inositol 5-phosphatase catalytic domain. An unique domain composition is present in Dd5P2 containing a RCC1-like domain. RCC1 has a seven-bladed propeller structure and interacts with G-proteins. Dd5P3 and Dd5P4 have a domain composition similar to human Synaptojanin with a Sac1 domain and OCRL with a RhoGAP domain, respectively. We have expressed the catalytic domains and show that these inositol 5-phosphatases have different substrate preferences. Single and double gene inactivation suggest a functional redundancy for Dd5P1, Dd5P2, and Dd5P3. Inactivation of the gene coding for Dd5P4 leads to defects in growth and development. These defects are restored by the expression of the complete protein but not by the 5-phosphatase catalytic domain.

Inositol phosphatases play a role in a variety of eukaryotic cellular processes, including chemotaxis and membrane trafficking. They are regulated by a number of enzymes. The group of phosphatidylinositol 3-kinases (PI3K) phosphorylates the lipid substrates PI, PI(4)P, and PI(4,5)P2 at the 3-position of the inositol ring (1). The lipid product PI(3,4,5)P3 has been strongly implicated to be important in chemotaxis in neutrophils and fibroblasts (2, 3). PTEN, identified as a tumor suppressor gene (4), reverses the action of PI3K by dephosphorylation of PI(3,4,5)P3 and PI(3,4)P2 at the 3-position (5). Another group of enzymes, the inositol 5-phosphatases, can remove the phosphate group at the 5-position of the inositol ring (6–8). The importance of inositol 5-phosphatase activity in PI(3,4,5)P3 regulation is demonstrated by SHIP1. In stimulated B-cells, SHIP1 accounts for the major phosphatase activity toward PI(3,4,5)P3 and inactivation of SHIP1 leads to an increased and prolonged PI(3,4,5)P3 production (9). Other inositol 5-phosphatases have been shown to play important roles in a number of cellular processes. Mutations in the inositol 5-phosphatase OCRL are responsible for Lowe syndrome in human (10), and deletion of the presynaptic inositol 5-phosphatase Synaptojanin leads to neurological abnormalities and early death of mice (11).

In the social amoeba, Dictyostelium discoideum, chemotaxis toward folic acid and cAMP is an essential strategy for survival (12). Several observations suggest that phosphatidylinositol phosphates mediate chemotaxis and, in particular, the localization of the signal inside D. discoideum cells. The PH domains of a number of proteins involved in chemotaxis, including CRAC, Akt/PKB, and PhdA, have been shown to transiently localize at the leading edge of cells moving in a chemotactic gradient (13–15). As these PH domains bind to PI(3,4,5)P3 and PI(3,4)P2, an asymmetric lipid distribution is implicated by these observations. In phosphtidylinositol 1,4,5-P3 null cells, a strain with two putative PI3Ks inactivated (16), the transient localization of PhdA can no longer be observed and cells show reduced chemotaxis (15). On the other hand, in PTEN-null cells, a strain in which a putative 3-phosphatase is inactivated, the localization of PH-domains is prolonged and broadened and chemotaxis is also reduced (17, 18). Inositol 5-phosphatases may play an important role in the regulation of the phosphoinositides. As this group of enzymes leads to the degradation of PI(3,4,5)P3 and at the same time formation of PI(3,4)P2, another PH-binding molecule, they can be central players in the metabolic route of these signaling molecules.

Phosphoinositides have also been implicated in endocytosis in D. discoideum. PI(3)k1/2-null cells are affected with respect to pinocytosis (19), suggesting a role for PI(3,4,5)P3 in this process. The inhibitors of phospholipase C, an enzyme converting PI(4,5)P2 into Ins(1,4,5)P3 and diacylglycerol, reduce the rate of phagocytosis (20, 21). Because inositol 5-phosphatases can act on PI(4,5)P2, PI(3,4,5)P3, and Ins(1,4,5)P3, they are probably important in the endocytic pathway.

To investigate the role of inositol 5-phosphatases in chemotaxis and endocytosis, we cloned and characterized four D. discoideum inositol 5-phosphatases. Catalytic activity was determined, indicating that they act as inositol 5-phosphatases. Single and double gene disruptants were obtained and growth, chemotaxis, and development were studied in these knock-out strains.

* This work was supported by The Netherlands Organization of Scientific Research. The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked "advertisement" in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

The on-line version of this article (available at http://www.jbc.org) contains appendices A–F.

The nucleotide sequence(s) reported in this paper has been submitted to the GenBank™/EBI Data Bank with accession number(s) AY184992, AY184993, AY184994, and AY184995.

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† The abbreviations used are: PI3K, phosphatidylinositol 3-kinase; PI, phosphatidylinositol; PI(3,4)P2, phosphatidylinositol 3,4-bisphosphate; PI(4,5)P2, phosphatidylinositol 4,5-bisphosphate; PI(3,4,5)P3, phosphatidylinositol 3,4,5-trisphosphate; Ins(1,4,5)P3, inositol 1,4,5-trisphosphate; Ins(1,3,4,5)P4, inositol 1,3,4,5-tetraakisphosphate; SH2, Src homology 2; SHIP, SH2 domain-containing inositol 5-phosphatase; INPP, inositol polyphosphate 5-phosphatase; PH, pleckstrin homology; GAP, GTPase-activating protein.
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EXPERIMENTAL PROCEDURES

Identification and Sequence Analysis—The first putative inositol 5-phosphatase sequence was obtained using degenerated primers complementing the conserved motifs I and II found in the inositol 5-phosphatases (see “Results”), and the PCR product was used to screen a cDNA library kindly provided by Dr. R. A. Firtel. The D. discoideum genomic (www.sdsc.edu/mpd/dicty) and cDNA databases (www.csm.biol.tsukuba.ac.jp) were screened for other putative inositol 5-phosphatases using either the conserved motif I or II. Using Sequenzer from Molecular Dynamics, contigs were formed. Additional sequences were obtained by screening a cDNA library, kindly provided by Dr. R. H. Gomer, with a PCR fragment containing part of the catalytic domain (used primers: Dd5P2: 5P2S1 + 5P2R1; Dd5P3: 5P5S1 + 5P5R1; and Dd5P4: 5P4S1 + 5P4R1, see “Appendix A”). The longest clones obtained for Dd5P3 (2122 bp) and Dd5P4 (2795 bp) encode the complete open reading frame of 1377 and 875 amino acids, respectively. For Dd5P2, the longest clone only encoded for the amino acids 1–599. In combination with data from the genomic database, a complete open reading frame of 1794 amino acids was constructed. The longest clone obtained for Dd5P1 encodes for amino acids 118–678; the missing part of the 5′-open reading frame was obtained from the database. A comparison of the sequence obtained from cDNA clones with the genomic database sequences revealed the presence of one intron in each inositol 5-phosphatase gene (Dd5P1: nucleotides 397–499; Dd5P2: nucleotides 53–187; Dd5P3: nucleotides 241–384; and Dd5P4: nucleotides 1357–1622) (GenBank accession numbers AY184992, AY184993, AY184994, and AY184995, respectively). BLAST, Smart, Pfam, and Expasy programs were used to analyze the obtained sequences. Alignments were made using ClustalW (23) and GeneDoc (24) and optimized by aligning similar domains.

Strains and Growth Conditions—The D. discoideum strains AX3 (wild type), DH1 (uracl auxotroph wild type), and the mutant strains described were grown in H5 medium supplemented with 10 μg/ml blasticidin S or G418 when necessary. Selection for presence of the pyr56 cassette was obtained using the uracil-deficient FM medium. When grown in shaking culture, the cell density was kept below 6.10^6 cells/cm^2. Chemotaxis toward cAMP was studied using the small-agar (Silica Gel 60, Merck) at three different cell densities (2.10^4, 2.10^5, and 2.10^6 cells/cm^2). Identification of Four Inositol 5-Phosphatase in D. discoideum—The first putative inositol 5-phosphatase catalytic domains were analyzed by 10% SDS-PAGE following by immunostaining with Penta-His Antibody (Qiagen) and Anti-mouse IgG peroxidase conjugate (Sigma). Bands were visualized using chemiluminescence blunting substrate POD (Roche Molecular Biochemicals) and 1-min exposure to film. Pretained Protein Marker, Broad Range (New England Biolabs) was used to determine the size.

Expression of Proteins in D. discoideum—To express proteins in D. discoideum, the desired DNA fragment was cloned into an extrachromosomal vector containing a neomycin cassette (pMB74 or pAH2). This results in expressing the protein from actin 15 promoter. To express the full-length Dd5P4 in Dd5P4-cells, the obtained full-length clone was inserted in the Bgl II site of pMB74. For Dd5P1, Dd5P2, Dd5P3, and Dd5P4, respectively.

Activity Measurements—Activity toward Ins(1,4,5)P_3 and Ins(1,3,4,5)P_4 was determined as described previously (25). 5 μl (diluted) of enzyme was added to the reaction mixture (50 m M HEPES, pH 7.4, 2 mM MgCl_2, 48 mM β-mercaptoethanol, 1 mg/ml bovine serum albumin), containing either 100 μM Ins(1,4,5)P_3 (5-P5R1), 10 μM Ins(1,3,4,5)P_4 (5-P4R1) or 10 μM [3H]Ins(1,3,4,5)P_4. After 15 min of incubation the reaction was stopped and the products were separated on Dowex columns. Activity toward PI(P_4)P and PI(3,4,5)P_3 was determined as described previously (24). 50 μg of phosphatidyl serine and 10 μg of [3H]PI(4,5)P_2 (see below for preparation method) or 20 μg of phosphatidyl serine and 10 μg of [3H]PI(4,5)P_2 (see below for preparation method) or 20 μg of phosphatidyl serine and 10 μg of [3H]PI(4,5)P_2 were resuspended in 50 μl of 50 mM Tris-HCL, pH 7.4. Vesicles were formed by sonication, and 1 μl of 1 mM MgCl_2 and 60 μl of (diluted) enzyme were added. After 30 min, the reaction was stopped and the lipids were extracted. Lipids were separated by TLC and visualized by exposure to film or PhosphorImager. In the case of the PI(P_4)P/assay, the spots were visualized using a PhosphorImager (Amersham Life Sciences) and scraped from the plates (Silica Gel 60, Merck) and radioactivity was measured.

RESULTS

Identification of Four Inositol 5-Phosphatase in D. discoideum—The first potential inositol 5-phosphatase in D. discoideum was identified by performing a PCR with degenerated primers. The obtained PCR product was used as probe for cDNA library screening. The gene found using this method was called Dd5P1 (D. discoideum 5-phosphatase 1) and codes for a protein of 678 amino acids (see “Appendix B”). To identify other putative inositol 5-phosphatases in D. discoideum, we searched the D. discoideum database for sequences showing homology to the conserved motifs I and II, WXXGDXN(Y/F/R) and PA/S/WIC(T)/DR/I/TL/ respectively, which are characteristic for inositol 5-phosphatases (6). Using the partial sequence obtained from the data base, complete sequences were obtained from cDNA library screens. Three putative inositol 5-phosphatases were identified (see “Appendix B”), coding for proteins consisting of
The other two inositol 5-phosphatase families identified in *D. discoideum* are homologous to human inositol 5-phosphatases. Dd5P3 resembles the synaptojanin-like proteins found in both human and yeast with the highest BLAST score of the catalytic domain with that of INP5Pb from fission yeast (37% identity, 59% similarity) (34). Similar to human Synaptojanin and yeast INP5P, Dd5P3 has a SacI-like domain including the conserved RAXCXDCLRNT motif (35) in front of the inositol 5-phosphatase domain (see “Appendix E”). The SacI domains of Synaptojanin and INP5Pb have been shown to remove the phosphate group of PI(4)P, PI(3)P, and at a low rate, both phosphates of PI(3,5)P₂ (36). The long C-terminal part of Dd5P3 does not have any homology with known domains and consists of poly(Q) and poly(N) repeats.

Dd5P4 is homologous to human OCRL (10) and INPP5b (37, 38), consisting of a inositol 5-phosphatase domain followed by a RhoGAP domain (see “Appendix F”). The catalytic domain has the highest BLAST score with the catalytic domain of human INP5Pb (44% identity, 60% similarity). RhoGAP domains are known to catalyze the GTPase activity of Rho proteins. The crystal structure of human RhoGAP has been solved indicating a role for two conserved amino acids, Arg-85 and Asn-194, in RhoGAP and Asn-194 in GAP-activated GTP hydrolysis (39). The role of these amino acids is supported by mutational analysis (39, 40). Mutational analysis has also shown that the conserved Arg is not predominantly involved in the binding of Rho proteins (40). In Dd5P4, the Arg and the Asn are substituted by an Ile and Gln, respectively. This observation may suggest that Dd5P4 does not exhibit high RhoGAP activity, but may still bind Rho proteins.

**Different Transcription Levels during Development**—To determine the transcription levels of the *D. discoideum* inositol 5-phosphatases, Northern blot analysis was performed. Very low transcription levels were observed for the four inositol 5-phosphatases in all stages of the *D. discoideum* life cycle (Fig. 3). *Dd5P1* and *Dd5P3* were equally transcribed in all stages with the exception of the even lower transcription of *Dd5P3* in the vegetative stage. The levels of transcription of *Dd5P2* were higher during aggregation than during growth and multicellular development. The transcription of *Dd5P4* was relatively high during growth, decreased during aggregation, and returned to almost vegetative levels in the multicellular stages. Furthermore, a smaller transcript of 2.5 kilobases was observed in the multicellular stages.

**Activity toward Soluble and Lipid Substrates of *D. discoideum* Inositol 5-Phosphatases**—To determine whether the four putative inositol 5-phosphatases identified in *D. discoideum* can function as inositol 5-phosphatases, the catalytic activity and specificity of the inositol 5-phosphatase domains were studied in vitro. The catalytic domains were expressed as His tag fusion proteins in *E. coli* and purified. The protein of the expected size could be detected by Western blot analysis for *Dd5P1–3* (Fig. 4). The Western blot analysis performed for *Dd5P4* showed a band at a higher position than expected (62 instead of 55 kDa), but the purified protein did show inositol 5-phosphatase activity. Unfortunately, because of the very low expression levels obtained for the catalytic domain of *Dd5P1*, no activity could be determined for this protein.

The purified catalytic domains of *Dd5P2*, *Dd5P3*, and *Dd5P4* were incubated with the phospholipids PI(4,5)P₂ and PI(3,4,5)P₃ and the water-soluble inositol phosphates Ino1,4,5,P₃ and Ino1,3,4,5,P₄. Substrate degradation was quantified using thin-layer chromatography for the phospholipids and ion-exchange chromatography for the water-soluble inositol phosphates. The results are summarized in Fig. 5 demonstrating good degradation of PI(4,5)P₂ by all inositol 5-phosphatases.
Inositol 5-Phosphatases in D. discoideum

FIG. 2. Amino acid sequence alignment of inositol 5-phosphatases. Amino acids conserved between the D. discoideum inositol 5-phosphatases Dd5P1, Dd5P2, Dd5P3, Dd5P4, human OCRL (AAAS59964), SHIP2 (O15357), yeast SPsynaptojanin (SPsynj, 119T_Y_A), and INP52p (NP_014293) are shown in black (100% identity) or gray (80–100% identity). Asterisks in the top row indicate amino acids interacting with a metal ion, and open circles indicate amino acids directly interacting with inositol phosphates.

whereas PI(3,4,5)P3 is degraded predominantly by Dd5P2, and also by Dd5P4 but not by Dd5P3. Good degradation of the water-soluble inositol phosphates Ins(1,4,5)P3 and Ins(1,3,4,5)P4 is observed for Dd5P2, Dd5P3, and Dd5P4, showing the best degradation of Ins(1,4,5)P3 by Dd5P3, whereas Ins(1,3,4,5)P4 is best degraded by Dd5P2 (Fig. 5C). Comparing the activity of the four enzymes for each substrate indicates the relatively preferred substrates (Table I). The protein with the highest activity toward Ins(1,4,5)P3 is the catalytic domain of Dd5P2. This protein, compared with the other proteins, is poor in dephosphorylation of lipid-soluble substrates. This substrate specificity is almost opposite to the specificity of the homologue INP51p, which degrades PI(4,5)P2 but does not hydrolyze PI(3,4,5)P3. Dd5P2, in contrast, is a very good PI(3,4,5)P3- and PI(4,5)P2-metabolizing enzyme.

Gene Inactivation Leads to Defects in Growth and Development—Upon starvation, D. discoideum wild-type cells show chemotaxis toward the cAMP secreted by other starving cells. The formed aggregate develops into a migrating slug or fruiting body. The spores of the fruiting body are resistant to severe conditions and mature into single amoeba under better conditions. To get an indication of the function of inositol 5-phosphatases in D. discoideum, the four identified inositol 5-phosphatase genes have been knocked out. The effect of gene inactivation on chemotaxis has been investigated by determining the response of cells toward different cAMP concentrations using the small-droplet chemotaxis assay. Single gene inactivation of either Dd5P3 or Dd5P4, or double gene inactivation of Dd5P2 and Dd5P3 (Dd5P2/Dd5P3) did not negatively affect chemotaxis, whereas single disruption of Dd5P1 or Dd5P2 slightly improved chemotaxis (Fig. 6). Also, the double disruption of either Dd5P1 and Dd5P2 (Dd5P1/Dd5P2) or Dd5P1 and Dd5P3 (Dd5P1/Dd5P3) resulted in slightly improved chemotaxis. Growth and development of the cells were also studied. The single gene inactivation of Dd5P1, Dd5P2, or Dd5P3 did not result in any observable difference in growth rate in axenic medium or on bacterial lawns (data not shown). The single disruptants Dd5P1-, Dd5P2-, and Dd5P3- were deposited on non-nutrient agar plates or grown on bacterial lawns to study the development of the cells. Aggregation of the cells proceeded at a rate similar to the wild type during the first 30–60 min, but after that the rate of aggregation was lower than that of wild-type cells. Therefore, the development of these strains was followed by direct microscopic observation. The wild-type cells formed tight aggregates, slugs, and culminants. Dd5P3- cells aggregated to form tight aggregates but developed into fruiting bodies in the dark. Dd5P2- cells aggregated to form tight aggregates and slugs but failed to form culminants. The Dd5P1- cells aggregated to form tight aggregates, slugs, and culminants, but the development of these cells was delayed.
**Table I**

<table>
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<th>Enzymes</th>
<th>Relative activity</th>
<th>$\text{Ins(1,4,5)P}_3$</th>
<th>$\text{Ins(1,3,4,5)P}_4$</th>
<th>$\text{PI(4,5)P}_2$</th>
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**Discussion**

The implicated role of phosphoinositide molecules in signal localization has lead to an increased interest in metabolizing enzymes such as inositol 5-phosphatases. The amount of data on mammalian inositol 5-phosphatases has expanded rapidly over the last few years, showing important functions for inositol 5-phosphatases in several processes (6).

Human inositol 5-phosphatases are divided in two groups. Type I inositol 5-phosphatases only convert the water-soluble substrates $\text{Ins(1,4,5)P}_3$ and $\text{Ins(1,3,4,5)P}_4$. They do not convert lipid substrates. Type II inositol 5-phosphatases do convert phosphoinositides (e.g. $\text{PI(4,5)P}_2$ and $\text{PI(3,4,5)P}_3$), and in most cases, they also convert water-soluble substrates. The insertions present in Type I enzymes may prevent the enzymes from binding to the membrane surface, which may explain the differences in substrate specificity between Types I and II inositol.
The four inositol 5-phosphatases in *D. discoideum* show a high diversity in domain composition compared with the evolutionary position of this organism between plants and yeast. A homologue of OCR1 (Dd5P4) and a homologue of Synaptotagmin (Dd5P3) were identified. Also, a unique combination of a RCC1-like domain in front of the inositol 5-phosphatase domain was identified (Dd5P2). This combination of domains has not been found in any other protein reported or present in the GenBank™ so far.

Knock-out strains with one or a combination of two inactive genes for Dd5P1, Dd5P2, and Dd5P3 show no defects in growth and development, suggesting a redundancy among these proteins. Chemotaxis toward cAMP is similar or slightly improved in all of the inositol 5-phosphatase knock-out cell lines compared with wild type. Recently, it has been shown that the 3-phosphatase PTEN is the major PI(3,4,5)P3/PI(3,4)P2-degrading enzyme. It has been suggested that inositol 5-phosphatases add an addition layer of regulation of these molecules, fine-tuning the chemotactic signal (42). Our results support the role of the group of inositol 5-phosphatases as a minor negative regulator of chemotaxis in *D. discoideum*. It will be interesting to study the effects of either overexpression or inactivation of the inositol 5-phosphatases in a PTEN-null background.

Inactivation of Dd5P4 resulted in defects in growth and development. The reduced growth rate, either in axenic culture or grown on bacterial plates, suggests a role for Dd5P4 in endocytosis. Development is also affected as the cells form multiple-tipped aggregates. The relative high transcription levels of Dd5P4 at vegetative and multicellular stages support the role of Dd5P4 in growth and development. Knock-out strains of PI3K1 + 2 are defective in chemotaxis, growth, and development (15, 16). The cells grow slowly on bacterial lawns and in axenic medium and form multiple-tipped aggregates resembling the phenotype of Dd5P4. No enzyme activity measurements have been reported for the PI3K in *D. discoideum*, but they have been suggested to catalyze the formation of PI(3)P, PI(3,4)P2, and PI(3,4,5)P3 on basis of sequence homology. Our results support a role for PI(3,4,5)P3 and/or PI(3,4)P2 in growth and development; Dd5P4 regulates the levels of these phospholipids by degradation of PI(3,4,5)P3 and production of PI(3,4)P2. On the other hand, the effect of inactivation of Dd5P4 could also be assigned to its action on either PI(4,5)P2 or Ins(1,4,5)P5, two signaling molecules also implicated in endocytosis (20, 21). In addition, the RhoGAP domain could be responsible for the function of Dd5P4 in endocytosis. Rho proteins have been shown to play a role in both development and growth. The defects in growth and development of Dd5P4+ cells can be rescued by overexpression of the full-length protein. These defects can not be restored by transfection of *D. discoideum* cells with an expression vector containing either the inositol 5-phosphatase catalytic domain or the RhoGAP domain. Although we can not exclude that the domains are not properly expressed or folded, the fact that the inositol 5-phosphatase catalytic domain expressed in *E. coli* is catalytically active would suggest that inositol 5-phosphatase activity is not sufficient to restore the defects of Dd5P4+ cells. It is possible that the RhoGAP and inositol 5-phosphatase catalytic domain act together to perform its function in growth. The binding of a Rho protein to the RhoGAP domain could affect the inositol 5-phosphatase activity. This would lead to a direct interaction between the Rho and phosphoinositide pathways. It would be interesting to see if and which Rho protein binds to the GAP domain of Dd5P4.

**Acknowledgments**—We are indebted to all of the teams involved in the Dictyostelium sequencing projects. We thank L. Drayer and H. Otsuka for their contribution in cloning and analyzing Dd5P1.

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**Fig. 7. Growth rate of wild type and mutant strains.** Doubling times were 15 h for wild-type AX3, 41 h for Dd5P4−, 15 h for Dd5P4−/Dd5P4, 47 h for Dd5P4−/cat5P4, and 48 h for Dd5P4−/GAP5P4.

**Fig. 8. Development of wild-type AX3, Dd5P4−, and Dd5P4−/Dd5P4 on K. aerogenes.** Pictures were taken of tipped aggregates using ×40 magnification.

5-phosphatases (28). The insertions present in Type I inositol 5-phosphatases are not present in either one of the *D. discoideum* inositol 5-phosphatases. As expected by this sequence analysis, the *D. discoideum* 5-phosphatases Dd5P2, Dd5P3, and Dd5P4 catalyze the dephosphorylation of both water-soluble and lipid substrates, which classify them as Type II inositol 5-phosphatases. The *D. discoideum* genome has been sequenced to near completion, making it unlikely that more inositol 5-phosphatases containing the motifs WXGDXNX/Y/F/R and P(A/S)/W/C/T/DR/(I/V/L) are present. Therefore, probably no Type I and only four Type II inositol 5-phosphatases are present in *D. discoideum*. Type II inositol 5-phosphatases can be divided in three subgroups on the basis of domain composition. SHIP1 represents the group of SH2 domain containing inositol 5-phosphatases Synaptotagmin, the Sac1 domain containing enzymes, and OCRL, the RhoGAP domain containing inositol 5-phosphatases (Fig. 1). Mammals contain all three groups of proteins. Six non-mammalian organisms containing putative inositol 5-phosphatases have been sequenced completely so far. The metazoa *C. elegans* and *D. melanogaster* lack inositol 5-phosphatases containing a SH2 domain, but both contain one Synaptotagmin-like protein (41) and Q9W296, respectively) and one OCRL-like protein (O17590 and O46049, respectively). The diversity in the plant *Arabidopsis thaliana*, the yeast strains *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe*, and the microsporidia *Encephalitozoon cuniculi* is even less. The inositol 5-phosphatases of *A. thaliana* contain only WD40 repeats as additional domains (e.g. Q8SKB7 and O85060), whereas in yeast only Synaptotagmin-like proteins are present (28, 34). The one inositol 5-phosphatase of *E. cuniculi* (CAD25856) only contains the inositol 5-phosphatase catalytic domain. In prokaryotes, no inositol 5-phosphatases have been identified.