

Phosphatidylinositol transfer proteins: sequence motifs in structural and evolutionary analyses

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ABSTRACT

Phosphatidylinositol transfer proteins (PITP) are a family of monomeric proteins that bind and transfer phosphatidylinositol and phosphatidylcholine between membrane compartments. They are required for production of inositol and diacylglycerol second messengers, and are found in most metazoan organisms. While PITPs are known to carry out crucial cell-signaling roles in many organisms, the structure, function and evolution of the majority of family members remains unexplored; primarily because the ubiquity and diversity of the family thwarts traditional methods of global alignment. To surmount this obstacle, we instead took a novel approach, using MEME and a parsimony-based analysis to create a cladogram of conserved sequence motifs in 56 PITP family proteins from 26 species. In keeping with previous functional annotations, three clades were supported within our evolutionary analysis; two classes of soluble proteins and a class of membrane-associated proteins. By focusing on conserved regions, the analysis allowed for in depth queries regarding possible functional roles of PITP proteins in both intra- and extra- cellular signaling.

Keywords: Protein Evolution; Structural Domain; Phylogenetics; Sequence Motif

1. INTRODUCTION

Phosphatidylinositol transfer proteins (PITP) are monomeric, lipid-binding proteins that bind and transfer phosphatidylinositol (PtdIns) and phosphatidylcholine (PtdCho) between membrane compartments (see reviews by: [1,2,3,4,5,6]). Inositol lipids have specialized functions in the regulation of eukaryotic cells, providing a source of second messengers and acting as signaling molecules. Monomeric phospholipids have extremely

low solubilities and negligible spontaneous transfer rates between membranes, necessitating protein factors to shield them in the aqueous environment of the cell. Almost all phospholipid exchange activity within the eukaryotic cytosol is accomplished by three groups of proteins: PITP, phosphatidylcholine transfer protein (PCTP), or sterol carrier protein 2. PITP-domain proteins, which are the focus of this study, are found in five classes of proteins: three are soluble and cytosolic, and two are membrane-associated proteins [1,2] (**Figure 1**).

Soluble PITPs are found in virtually all metazoan organisms. These are approximately 77% identical at the amino-acid level. Two isoforms, PITP α and PITP β , exist in mammals; they are highly conserved with about 98% sequence identity at the amino acid level. The proteins bind one molecule of PtdIns or PtdCho and are typically about 32 kDa in mass.

PITP-like domains are also detected in the retinal degeneration B (rdgB) class of proteins (see reviews [6,7]). These 160-170 kDa proteins are membrane-associated proteins first identified in *Drosophila melanogaster*, as mutations in these genes lead to retinal degeneration. The rdgBs contain an

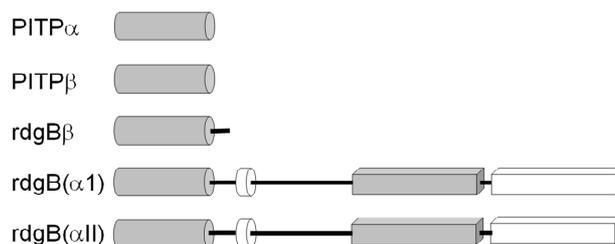


Figure 1. Gene structure of PITP-domain proteins. Grey cylinder is PITP-like domain, white cylinder is the FFAT region of ER binding, the grey box is the DDHD region, and the white box is the LSN2 region. The the human pitpnm1 protein, the FFAT region is residues 360-365, the DDHD region is 686-879, and the LSN2 domain is residues 1022-1152 [6].

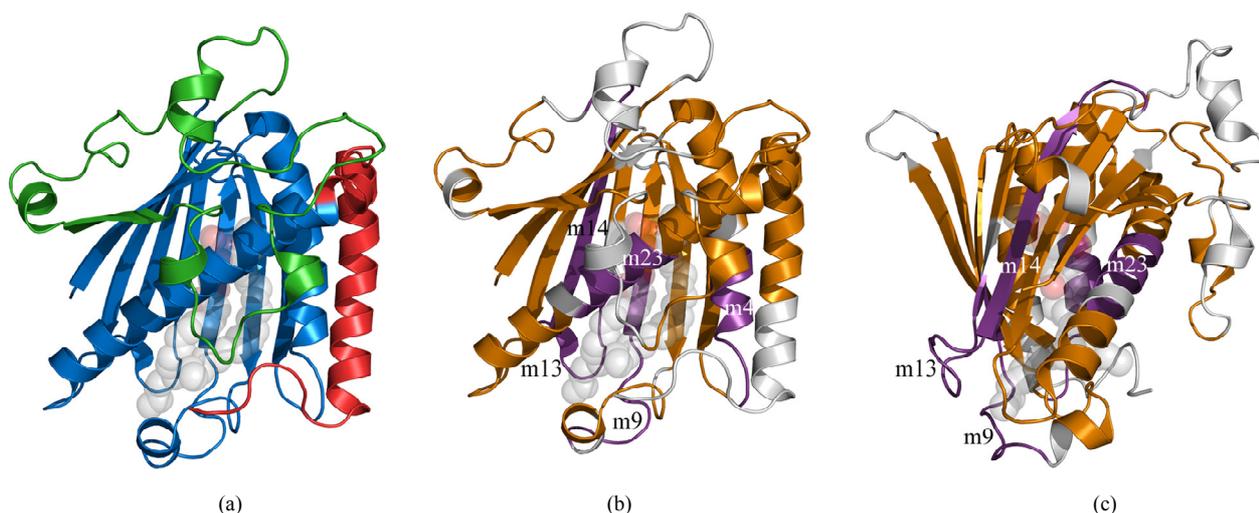


Figure 2. Cartoon representation of rat PITP α complexed to PtdCho. (a). Structural domains of the class I PITPs displayed on a representative PITP (PDB:1T27). The lipid binding core is shown in blue, the regulatory loop in green, and the C-terminal region in red. The PtdCho molecule is in transparent spheres with standard CPK coloring; (b) Conserved sequence motifs mapped onto the same structure. The four conserved sequence motifs; m4, m9, m13, m14, and m23, representing branch points in the cladogram shown in **Figure 3** are in purple and are annotated. The remaining sequence motifs are in gold, regions not present in conserved sequence motifs are colored grey; (c) Image B is rotated 90° counterclockwise around a vertical axis.

N-terminal PITP-like domain (42% sequence identity to PITP isoforms), a FFAT sequence motif [2,8], a DDHD metal binding domain (which has calcium-binding capabilities in the human proteins [9]), and a LNS2 domain. The FFAT motif is a short sequence containing two phenylalanines in an acidic tract that targets the protein to the endoplasmic reticulum [8]. The DDHD domain of 180 residues may be involved in metal binding, but the function of this domain is unknown [6]. The LNS2 domain is believed to be involved in protein: protein interactions, and in the human homologues is a protein tyrosine kinase 2 (PYK2) binding domain [9]. Two homologues of *rdgB* are found in most mammalian genomes studied to date and are usually called 1) *rdgB*(I), *rdgB* α I, or PITPnm1 and 2) *rdgB*(II), *rdgB* α II, or PITPnm2. In *Drosophila*, *rdgB* is believed to function in the termination of phototransduction and in the establishment and maintenance of rhodopsin levels in photoreceptor cells [10,11]. In humans, PITPnm1 has widespread tissue distribution and can rescue fly *rdgB* mutant phenotypes [1]; whereas PITPnm2 has a neuronal-specific expression pattern and is unable to functionally rescue fly *rdgB* mutants [12]. Although *Drosophila* *rdgB* possesses the capability to transfer PtdCho and PtdIns *in vitro* [10,11], the PITP-domains of *rdgB* and PITP α are not functionally interchangeable [10].

An additional class of PITP-like proteins, *rdgB* β , has been identified in mice, humans, and *Drosophila*. These are 38 kDa, soluble proteins that have sequence similarity most comparable to the N-terminal region of *rdgB*-class proteins. It shares approximately 40% sequence

identity with PITP α . The purified protein has been shown to possess *in vitro* PtdIns transfer capabilities [13,14].

Plants and fungi generally do not contain a sequence homologue to PITP, but do possess a functional analog referred to as Sec14p in yeast systems. Sec14p is approximately the same size as PITP, and although there is no detectable amino acid similarity between the two proteins, temperature-sensitive mutants of yeast Sec14p are rescued by rat PITP α and PITP [15,16]. Likewise, Sec14p can successfully substitute for PITP in the PITP-dependent reconstitutions studied to date [17,18,19,20]. Interestingly, the slime mold *Dicystostelium discoideum* has been shown to contain not only homologues to PITP, called DdPITP1 and DdPITP2, but also a Sec14p relative, called DdSec14 [21].

The experimentally determined three-dimensional structures of rat PITP α -PtdCho [22] and PITP-PtdCho [23], human PITP α -PtdIns [24], and the apo form of mouse PITP α [25] have been reported. The PITP structures share little resemblance to the crystal structure of yeast Sec14p [26]. The PITP structure is composed of three regions (**Figure 2(a)**): a lipid-binding core, a regulatory loop, and the C-terminal region. The lipid-binding core of PITP α -PtdCho shares a fold with the steroidogenic acute regulatory protein-related transfer (START) domain [22] first observed in human MLN64 [27]. It has been proposed that the START domain may be a common fold adapted for binding lipid molecules. PCTP is a START-domain protein based on structure and sequence

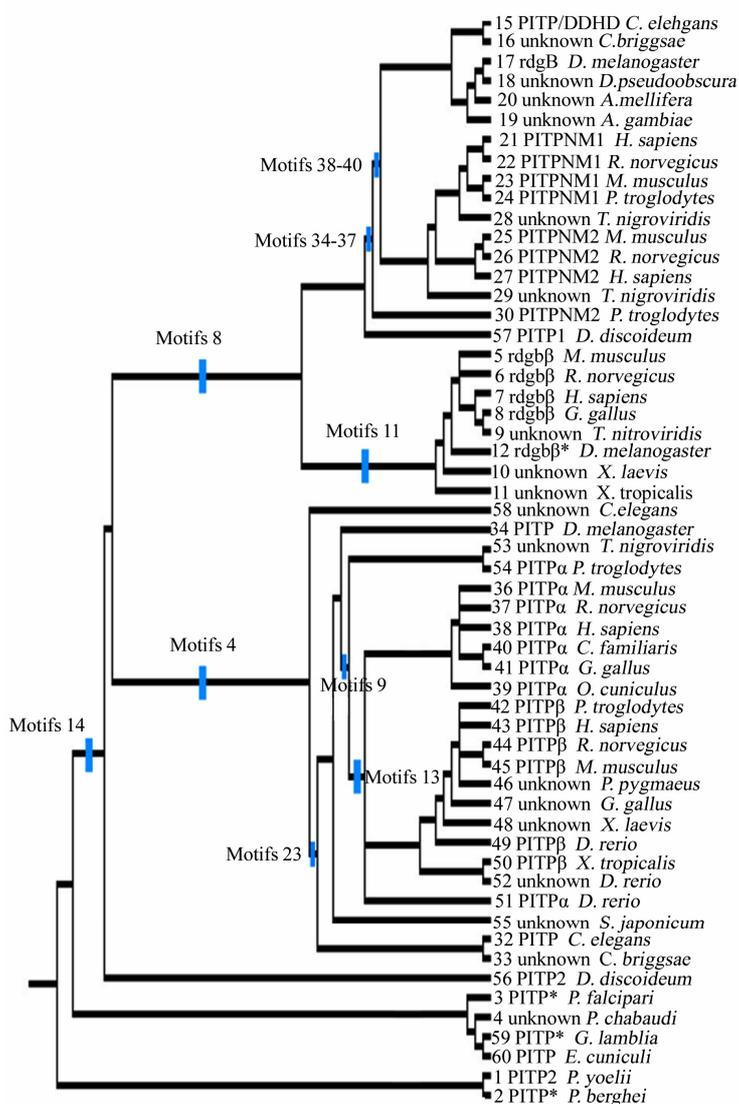


Figure 3. Phylogenetic tree for 56 PITP family proteins. A strict consensus tree was derived from the presence/absence of sequence motifs as well as the motif sequence, analyzed via parsimony as described in the text. The blue lines show which sequence motifs are uniformly gained within each clade on the tree.

identity, whereas PITP is not considered to be a START-domain protein due to a lack of sequence identity.

Mutations and gene-knockout studies provide insight into the functions of PITP. In mice, a mutation in the PITP α gene causes the *vibrator* phenotype, which is characterized by a progressive-action tremor, degeneration of brain stem and spinal cord neurons, and juvenile death. PITP β does not compensate for loss of PITP α [40]. Furthermore, in mice, embryonic stem cells deficient in PITP α or PITP β reveal differences in physiological function between the two isoforms. PITP β deficiency leads to catastrophic failure early in embryonic

development, and the protein is therefore posited to have an essential housekeeping role in the cell [29]. In contrast, PITP α -deficient embryonic stem cells are not compromised in growth or in bulk phospholipid metabolism; however, PITP α is required for neonatal survival. PITP α deficiency affects regulation of phospholipid transport in the ER, endocrine pancreas function, and glycogen metabolism, due to compromised lipid absorption, homeostatic problems, and severe hypoglycemia [30].

Protein similarity is usually detected by conservation of function as revealed by biochemical analysis, sequence

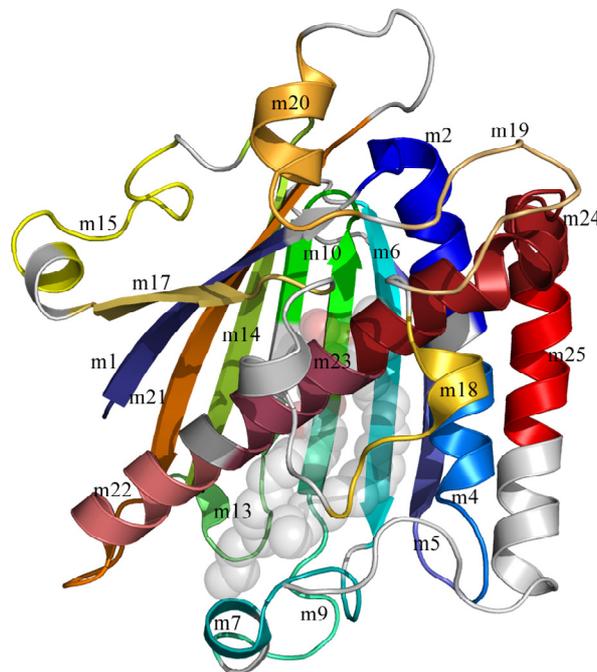


Figure 4. Sequence motifs mapped to the structure of rat PITP α :PtdCho. The sequence motifs present in class I PITPs are shown in a rainbow spectrum of colors from blue to red and from the *N*- to the *C*-terminus. Sequence motifs are annotated ‘m1’ to m25’, the PtdCho molecule is in transparent spheres with standard CPK coloring. The lipid binding core contains sequence motifs 1-2, 4-7, 9-10, 13-15, and 17-25. The regulatory loop contains sequence motifs 15, 17, and 18-20. The C-terminal region contains part of sequence motif 24 and all of motif 25.

similarity as detected by amino acid pattern recognition, or by structural similarity as detected by X-ray crystallography or NMR spectroscopy. The PITP/rdgB proteins possess intriguing patterns of similarity. PITP has functional similarity to Sec14p, but lacks sequence or structure similarity. PITPs have sequence similarity to rdgB and both possess the hallmark ability to transfer phospholipids between the protein and membranes. PITP has been shown to have structural similarity to the START domains, even though it does not share amino acid sequence similarity. Here, we have used a comprehensive evolutionary analysis to synthesize information from sequence analysis and structural comparisons. This approach leads to a cohesive understanding of evolutionary, structural, and functional relationships of the PITP/rdgB protein families, and may suggest that a re-analysis of PITP protein naming conventions is overdue.

2. MATERIALS AND METHODS

2.1. Identification of Sequences

Rat PITP α (gi:8393962) was used as a query sequence in a BLASTp (version 2.2.11, database versions as of May 8, 2005) [31] search. The 134 returned sequences

were manually culled to remove duplicated or significantly fragmented sequences, reducing the number to 60 sequences in 26 species (Table 5). The final data set contained both cytosolic PITP and rdgBs of approximately 270-330 residues each, as well as the membrane-associated rdgB/PITPnm proteins, of approximately 1250 residues. Several proteins were determined to be splice variants of existing proteins in the tree; they are annotated in all figures and tables.

2.2. Phylogenetic Analysis

Unaligned proteins were processed using the MEME program [32] (implemented in the Wisconsin Package, version 10.4) [33], using the “zero or more” setting, which permits anywhere from zero instances of a block to extreme repetition of blocks, thereby permitting the generation of the most robust matrix of sequence motifs possible. The phylogenetic parsimony tree for the sequence motifs was made by PAUP* (version 4.0b) [34]. The consensus tree was imported into MacClade (v 4.08) [35] for further character-state analysis. Character-state changes were traced along tree clades and unambiguous changes were examined. A database of sequence motifs and proteins was created to facilitate this study and the

Table 1. Conserved sequence motif matrix of PITP and rdgB proteins, PITP domain only.

Track- ing #	Sequence motif identifier																								
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
1	1	1	0	0	1	1	1	0	0	1	0	0	0	0	0	0	1	0	1	0	1	0	0	1	0
2	1	1	0	0	1	1	1	0	0	1	0	0	0	0	0	0	1	1	1	0	1	1	0	1	0
3	1	1	0	0	1	1	1	0	0	1	0	0	0	0	0	0	1	1	1	0	0	0	0	1	0
4	1	1	0	0	1	1	0	0	0	1	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0
59	0	1	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
60	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
56	1	1	0	1	1	1	0	0	1	1	0	0	0	1	1	0	1	0	1	0	1	0	0	1	0
15-16	1	1	1	0	1	1	0	1	0	1	0	0	0	1	0	1	0	1	1	0	1	0	0	1	0
17-19, 25, 28-29	1	1	1	0	1	1	1	1	0	1	0	1	0	1	0	1	0	1	1	0	1	0	0	1	0
20	0	0	1	0	1	1	1	1	0	1	0	1	0	1	0	1	0	1	1	0	1	0	0	1	0
21-24	1	1	1	0	1	1	1	1	0	1	0	1	0	1	0	1	0	1	1	0	1	0	0	1	1
26	0	0	0	0	1	1	1	1	0	1	0	1	0	1	0	1	0	1	1	0	1	0	0	1	0
27	1	1	1	0	1	1	1	1	0	1	0	1	0	1	0	0	1	1	1	0	1	0	0	1	0
30	1	1	1	0	1	1	1	1	0	1	0	1	0	1	0	0	1	1	1	0	1	0	0	0	0
57	1	1	0	0	1	1	1	1	0	1	0	0	0	1	1	0	0	1	1	0	1	0	0	1	0
5-7	1	1	1	0	1	1	1	1	0	1	1	0	0	1	0	0	1	1	1	0	1	0	0	1	0
8	0	1	1	0	1	1	1	1	0	1	1	0	0	1	0	0	1	1	1	0	1	0	0	1	0
9	0	1	1	0	1	1	1	1	0	1	1	0	0	1	0	0	1	0	1	0	1	0	0	1	0
10	1	1	1	0	1	1	1	1	0	1	1	0	0	1	0	0	1	1	1	0	1	0	0	0	0
11	1	1	1	0	1	1	1	1	0	1	1	0	0	1	0	0	1	0	1	0	1	0	0	1	0
12	1	1	1	0	1	1	1	1	0	1	1	0	0	0	0	0	1	1	1	0	1	0	0	1	0
58	1	1	0	1	1	1	0	0	0	1	0	0	0	1	0	0	1	0	1	0	1	0	0	1	0
34	1	1	0	1	1	1	1	0	1	1	0	0	0	1	1	0	1	1	1	0	1	1	1	1	0
53	1	1	0	1	1	1	1	0	1	1	0	0	1	1	1	0	1	1	1	0	0	0	1	1	1
54	0	1	0	1	1	1	0	0	1	1	0	0	1	1	1	0	1	1	1	0	0	0	1	1	1
36-39, 42-51	1	1	0	1	1	1	1	0	1	1	0	0	1	1	1	0	1	1	1	1	1	1	1	1	1
40-41, 52	0	1	0	1	1	1	1	0	1	1	0	0	1	1	1	0	1	1	1	1	1	1	1	1	1
55	1	1	1	0	1	1	1	0	0	1	0	0	0	1	0	0	1	1	1	0	1	0	0	1	1
32	0	1	0	1	1	1	0	0	1	1	0	0	0	1	0	0	1	0	1	0	1	0	0	1	0
33	1	1	0	1	1	1	0	0	1	1	0	0	0	1	0	0	1	0	1	0	1	0	0	1	0

tables from it are available upon request.

In this phylogenetic analysis, the tree root was designated by the branch that incorporated the most sequence motif additions and that led to the most consistent character-state changes along the tree. That is, the basal proteins that rooted the tree had the fewest sequence motifs character-state changes within the tree with this root

present. This rooting was borne out by the consistency and was utilized. This rooting suggested the fewest character state changes and least amount of homoplasy within the tree. The tree root consisted of small PITP proteins from *Plasmodium*, *Giardia*, and *Encephalitozoon*. Sequence motif 14 defined this branch point, proteins from these species lacked the motif, and all other proteins possessed

Table 2. Conserved sequence motif matrix of rdgB proteins, C-terminal of the PITP-domain.

Tracking #	Sequence motif identifier																				
	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46
15	0	0	0	0	1	1	0	0	1	1	1	1	1	1	1	0	1	0	0	0	0
16	0	0	0	0	1	1	0	0	1	1	1	1	1	1	1	0	1	0	0	0	1
17,21-22, 26, 28	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0
18	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	0	0	0
20	0	1	1	0	1	1	0	0	1	1	1	1	1	1	1	1	1	1	0	0	0
19	1	0	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0
23	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
24	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0
25	1	1	1	1	0	1	0	0	1	1	1	1	1	1	1	1	1	1	0	0	0
27	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0
29	1	1	1	0	0	0	0	0	1	1	1	1	1	1	1	1	0	0	0	0	0
30	1	0	1	1	1	1	1	0	1	1	1	1	0	0	0	0	0	0	0	0	0

Table 3. Gene and protein nomenclature for proteins utilized in this study.

	PITP α	PITP	rdgB β	rdgB(1)	rdgB(2)
Gene name	Pitpna (mouse) Pitpn (rat) Pitpna (human)	Pitpnb (mouse) Pitpnb (rat) Pitpnb (human)	pitpnc1 (human)	pitpnm1 (mouse) NIR2 rdgB α 1 (fly) DRES9	pitpnm2 (mouse) NIR3 rdgB α 2 (fly)
Gene symbols	Pitpna (mouse) Pitpn (rat) Pitpna (human)	Pitpnb (mouse) Pitpnb (rat) Pitpnb (human)	pitpnc1 (human)	pitpnm1 (mouse)	pitpnm2 (mouse)
Gene aliases	Pitpn, vib1A	Vib1B		Rd9; RdgB; DRES9; mpt-1; Pitpnm	NIR3; rdgB2; rdgB 2; mKIAA1457
Protein name	PITP α	PITP	rdgB β ; rdgB 1; PITP, cyto- plasmic 1*	PITP mem- brane-associated 1	PITP mem- brane-associated 2
Approved gene symbol	PITPNA	PITPNB	PITPNC1	PITPNM1	PITPNM2

the conserved sequence motif.

3. RESULTS

3.1. Characterization of PITP-Like Proteins

An initial approach to characterizing the PITP family was relatively standard. Rat PITP α was used as the seed for a BLAST search targeting relatively distant protein relatives. BLAST results were imported to Pileup [33] to generate a “first pass” global alignment. Under a variety of different conditions, including weighting end gaps, not weighting end gaps, utilizing low gap opening and extension penalties, high-road and low-road alignment options, alignments were very weak, with notable cases where locally homologous segments identified by BLAST were not aligned in the global matrix. The derived nature

of many of the proteins in the PITP family was already apparent; sequence motifs appeared in some classes but not others, rendering standard alignment and analysis methods ineffective. A novel approach was required to identify and analyze the large, divergent PITP family.

3.2. Identification of Conserved Sequence Motifs

When a high-confidence global alignment in Pileup proved impossible, unaligned proteins were processed using MEME [32] which identifies conserved sequence motifs in proteins. The program makes identifications based on prior probabilities of amino acid occurrence. Because it performs ungapped determinations, no preceding global alignment of sequence motifs was necessary, families with highly derived members. Of the 46 conserved sequence motifs detected by MEME, 25 fell

Table 4. Conserved sequence motifs in the P1TP-domain.

Motif Identifier	secondary structure element, P1TP α^a	Sequence range ^b :	
		P1TP α P1TPnm1 P1TPNC1	Motif sequence ^b : P1TP α P1TPnm1 P1TPNC1
1	sheet 1 (3-11)	2-9	2-VLLKEYRV-9
1		1-8	1-MLIKEYHI-8
1		1-8	1-MLLKEYRI-8
2	helix A (14-33)	12-24	PVSVDEYQVGQLY
2		11-23	PMSLDEYQVAQLY
2		11-23	PLTVDEYKIGQLY
3		-	-----
3		24-31	MIQKKSRE
3		24-31	MISKHSHE
4	helix A (14-33)	26-36	VAEASKNETGG
4		-	-----
4		-	-----
5	sheet 2 (39-49)	37-48	GEGVEVLVNEPY
5		37-48	GSGVEILANRPY
5		36-47	GEGVEVVQNEPF
6	sheet 3 (55-64)	55-64	GQYTHKIYHL
6		56-65	GQYTHKVYHV
6		55-64	GQFTEKRVYL
7	helix B (70-75)	66-73	SKVPTFVR
7		204-211	AKIEQFIH
7		198-205	TRVEQFVH
8		-	-----
8		69-79	IPGWFRALLPK
8		68-78	LPSWARAVVPK
9		76-86	APEGALNIHEK
9		-	-----
9		-	-----
10	sheet 4 (84-91)	87-96	AWNAYPYCRT
10		88-97	SWNAYPYTRT
10		86-95	AWNYYPYTIT
11		-	-----
11		-	-----
11		97-104	YTCSFLPK
12		-	-----
12		98-105	RYTCPFVE
12		-	-----
13	sheet 5 (94-100)	99-106	TNEYMKED
13		-	-----
13		-	-----
14	sheet 6 (108-117)	107-120	FLIKIETWHKPDLG
14		107-120	FSIEIETYYLPDGG
14		105-118	FSIHIEKTYEDNKG
15	helix C (132-137)	123-134	ENVHKLPEAWK
15		-	-----
15		-	-----
16		-	-----
16		124-146	NVFNLSGAERRQRILDTIDIVRD
16		-	-----
17	sheet 7 (138-142)	137-144	EAVYIDIA
17		-	-----
17		134-141	EVCFIDIA
18		153-160	DYKAEEDP
18		152-159	EYKAEEDP
18		149-156	YYKESEDP
19		163-173	FKSIKTGRGPL
19		162-172	YHSVKTGRGPL
19		159-169	FKSEKTGRGQL
20	helix E (177-183)	175-183	PNWKQELVN
20		-	-----
20		-	-----
21	sheet 8 (191-201)	190-206	MCAYKLVTVKFKWWGLQ
21		187-203	MCAYKLCKVEFRYWGMLQ
21		181-197	MCSYKLVTVKFEVWGLQ

22	helix F (206-232)	207-214	NKVENFIH
22		-	-----
22		-	-----
23	helix F (206-232)	217-224	ERRLFTNF
23		-	-----
23		-	-----
24	helix F (206-232)	225-244	HRQLFCWLDKVVDLTMDDIR
24		223-242	HRQAWCWQDEWTELSMADIR
24		216-235	HRQAFWVDEWYDMTMDEV
25	helix G (240-261)	245-253	RMEEEKRQL
25		243-252	ALEETARML
25		-	-----
26		-	-----
26		294-301	PPGPDASP
26		269-276	RSAPSSAP

^aSecondary structure nomenclature for rat PITP as defined in [22], parenthesis indicate the complete range of the secondary structure element.

^bSequences and residue numbering refer to human proteins, PITP α is gi:5453908, tracking #38; PITPnm1 is gi:18490106, tracking #21; PITPNC1 is gi:32307140, tracking #7. PITPNC1 is also called rdgB β .

within PITP-like domains.

3.3. Phylogenetic Analysis

With sequence motifs identified, two character-state matrices were created. One contained character-state information on the presence or absence of detected motifs, and one contained aligned amino acid data (Tables 1 and 2). These matrices were utilized for the creation of a character state phylogenetic tree via maximum parsimony. The overall shape of the tree was determined by the presence/absence matrix, with the amino acid alignment data utilized to determine internal clade structures. Gaps, i.e., missing sequence motifs were considered a new state, and thus, the difference between having a specific set of amino acids and not having an amino acid could served as an informative character state.

Twelve most parsimonious trees of differing structures were identified by PAUP, but the strict consensus tree structure suggests the likely evolutionary history of this intriguing family of proteins (Figure 3). The tree revealed that membrane-associated proteins are derivatives of a group of PITP-like genes, and that many genes previously thought to be related to PITP α and PITP via sequence homology fell outside of clades that contain exclusively PITP α or PITP genes.

3.4. Identification of Clades Within the Phylogenetic Tree

In order to be cladistically sound, nomenclature must be hierarchical; all proteins in the tree were "PITP-like." The tree lends itself to consideration of the PITP-like family consisting of three large divisions (the classification nomenclature proposed by Allen-Baume [1] is adapted here): Class I comprised the soluble PITPs, Class IIA were the membrane-associated rdgB proteins (which contain additional domains C-terminal to the PITP-like domain), and Class IIB were the soluble

rdgB β proteins. Further subdivisions along cladistic lines allowed for the naming of the Alpha clade and the Beta clade within Class I, and an ancestral group of PITP-like proteins, predominantly from protista, that occurred in several clades rooting the tree. Table 3 lists the nomenclature commonly utilized for the genes and proteins in this study, as well as the HUGO-approved nomenclature.

3.5. Examination of Conserved Sequence Motifs

To understand the functional shifts that have occurred, examination of some of the sequence motifs in each proposed class was necessary. The amino acid sequence of each motif in the human proteins PITP α (Class I), PITPNM1 (Class IIA), and PITPNC1, also called rdgB β (Class IIB) are given in Table 4.

Class I: These proteins are cytosolic and contain sequence motifs 1-2, 4-7, 9-10, 13-15, and 17-25 (Figure 4). This class was distinguished from the Class II divisions by sequence motif 8, which was unique to the Class IIA and IIB clades, and sequence motif 4, which was unique to the non-protista Class I PITPs. A striking observation about sequence motif 8 was that it appears to be an amino acid sequence overlap with sequence motif 9, which defines subnodes within Class I. In the structure of rat PITP α , the residues defined by sequence motif 9 incorporate helix B, which is a putative membrane insertion helix [25]. There was no unique conserved sequence motif that distinguishes the functionally divergent alpha and the beta clades.

Class IIA: These proteins are membrane-associated and typically are 160 kDa. In this analysis they were distinguished by the unique presence of sequence motifs 34-40, which consisted of amino acids residues 831-844, 856-866, 899-920, 937-951, 993-1015, 1022-1038, and 1040-1086 in the human PITPnm1 protein. The division had two major subnodes, one consisting of non-mamma-

Table 5. Proteins used in phylogenetic analysis.

gi #	Tracking #	Species	common	Protein designations
55243798	19	<i>Anopheles gambiae</i>	mosquito	
48135931	20	<i>Apis mellifera</i>	honeybee	
39590557	16	<i>Caenorhabditis briggsae</i>	nematode	
39590636	33	<i>Caenorhabditis briggsae</i>	nematode	CB09751 ^b (NCBI-COG: PITP)
17556182	32	<i>Caenorhabditis elegans</i>		
17554244	15	<i>Caenorhabditis elegans</i>	nematode	PITP DDHD (NCBI-COG: PITP)
48059855	58	<i>Caenorhabditis elegans</i>	nematode	Y71G12B.17 ^b (NCBI-COG: PITP)
57091327	40	<i>Canis familiaris</i>	dog	similar to PITP α ^a
41055500	49	<i>Danio rerio</i>	zebrafish	PITP
41055576	51	<i>Danio rerio</i>	zebrafish	similar to PITP
28422482	52	<i>Danio rerio</i>	zebrafish	
8307957	56	<i>Dictyostelium discoideum</i>	slime mold	PITP 2
8307955	57	<i>Dictyostelium discoideum</i>	slime mold	PITP 1
24641869	17	<i>Drosophila melanogaster</i>	fruit fly	CG11111-PB, isoform B, rdgB
62484257	12	<i>Drosophila melanogaster</i>	fruit fly	CG17818-PA, rdgB β
7300495	35	<i>Drosophila melanogaster</i>	fruit fly	CG5269-PA PITP, vib
20151901	34	<i>Drosophila melanogaster</i>	fruit fly	SD01527p, vib
54642914	18	<i>D.pseudoobscura</i>	fly	GA10766-PA, <i>Dpse</i> /GA10766
19170839	60	<i>Encephalitozoon cuniculi</i>		PITP
50758480	41	<i>Gallus gallus</i>	chicken	similar to PITP α ^a
50756343	31	<i>Gallus gallus</i>	chicken	similar to PITP, membrane-associated 2 ^a
50755397	13	<i>Gallus gallus</i>	chicken	similar to rdgB β ^a
53134209	47	<i>Gallus gallus</i>	chicken	
50757849	8	<i>Gallus gallus</i>	chicken	similar splicing variant rdgB β ^a
29250063	59	<i>Giardia lamblia</i>		similar to <i>D. discoideum</i> PITP1
18490106	21	<i>Homo sapiens</i>	human	PITPNM1
24308237	27	<i>Homo sapiens</i>	human	PITPNM2
5453908	38	<i>Homo sapiens</i>	human	PITP α
6912594	43	<i>Homo sapiens</i>	human	PITP β
32307140	7	<i>Homo sapiens</i>	human	PITP, rdgB β 1
6679337	36	<i>Mus musculus</i>	mouse	PITP α
9790159	45	<i>Mus musculus</i>	mouse	PITP β
22003862	5	<i>Mus musculus</i>	mouse	rdgB
6679339	23	<i>Mus musculus</i>	mouse	PITPNM1
47124324	25	<i>Mus musculus</i>	mouse	PITPNM2
2137007	39	<i>Oryctolagus cuniculus</i>	rabbit	PITP α
55660937	42	<i>Pan troglodytes</i>	chimp	PITP ^a
55644759	54	<i>Pan troglodytes</i>	chimp	similar to PITP α ^a
55639157	30	<i>Pan troglodytes</i>	chimp	similar to PITP membrane-associated 2 ^a
55636463	24	<i>Pan troglodytes</i>	chimp	similar to PITP membrane-associated 1 ^a
56493706	2	<i>Plasmodium berghei</i>		PITP ^b
56509884	4	<i>Plasmodium chabaudi</i>		protein ^b
23619433	3	<i>Plasmodium falciparum</i>		PITP ^b
23485539	1	<i>Plasmodium yoelii yoelii</i>		PITP 2
55731914	46	<i>Pongo pygmaeus</i>	orangutan	protein ^b
56605814	22	<i>Rattus norvegicus</i>	rat	PITPnm, PI membrane-associated ^a
62658898	26	<i>Rattus norvegicus</i>	rat	similar KIAA1457, PITPnm2 ^a
8393962	37	<i>Rattus norvegicus</i>	rat	PITP, PITPn
16758568	44	<i>Rattus norvegicus</i>	rat	PITP
62657241	6	<i>Rattus norvegicus</i>	rat	rdgB
56756428	55	<i>Schistosoma japonicum</i>		Unknown, similar to <i>vib</i> (fly)
47228496	53	<i>Tetraodon nigroviridis</i>	pufferfish	
47228470	28	<i>Tetraodon nigroviridis</i>	pufferfish	
47223953	9	<i>Tetraodon nigroviridis</i>	pufferfish	
47206861	14	<i>Tetraodon nigroviridis</i>	pufferfish	
47226436	29	<i>Tetraodon nigroviridis</i>	pufferfish	
47937798	48	<i>Xenopus laevis</i>	frog	MGC84500 protein ^b
49256286	10	<i>Xenopus laevis</i>	frog	MGC84224 protein
62860160	11	<i>Xenopus tropicalis</i>	frog	protein LOC549393 ^b
38512077	50	<i>Xenopus tropicalis</i>	frog	PITP β

^aindicated as a predicted protein, ^bindicated as a hypothetical or a putative protein

lian proteins and containing the canonical rdgB protein from *D. melanogaster*, and the other subnode containing

the mammalian sequences PITPNM1 and PITPNM2. There were 21 conserved sequence motifs outside the

PITP domain, with sequence motifs 34-37 observed in all analyzed proteins in this class. In human *pitpnm1*, the FFAT domain was found at the end of sequence motif 27, with a derived motif sequence of EFFDCLD. The DDHD region contained sequence motifs 30-35, which comprises 35% of the defined DDHD range, and the LSN2 region contained sequence motifs 39 and the N-terminal portion of sequence motif 40, which is 23% of this region. Lev, *et al.* defined six, short hydrophobic regions based on hydrophathy plots that were originally postulated to be transmembrane domains [9] then later to mediate membrane association [7]. None of the six regions fell in a conserved sequence motif identified in this study. On the other hand, sequence motif 26 appeared in multiple repeats throughout the non-PITP domain in sequence motifs 29, 32-33, and 44-45. This is a Ser rich motif of eight amino acids, the significance of this observation is currently unclear.

Class IIB: The proteins in this class are historically referred to as *rdgB*βs and are monomeric, cytosolic proteins of ~330 amino acids. They were distinguished by the unique presence of sequence motif 11, which consists of residues 97-104 in the human PITPNC1 sequence. Sequence motif 11 is interesting; although it was only present in proteins in this division, it overlapped in sequence with motif 12 and motif 13. Sequence motif 12 was only observed in class IIA, whereas sequence motif 13 was unique to Class I, alpha and beta clades. Another notable feature of this division was PITP1 from *D. discoideum*. It grouped outside the other *rdgB* proteins and rooted the class IIA clade.

4. DISCUSSION

4.1. Phylogenetics

Ocaka *et al* [36] provide an extensive analysis of the chromosomal location of the PITPN genes in humans with a phylogenetic tree rooted with *C. elegans* PITP as the chosen outgroup. The analysis presented here differs in two respects. First, the original gene-duplication event leading to the evolution of soluble and membrane-associated PITP proteins likely occurred not early in animal evolution, but instead was initiated in some protists. *D. discoideum* has been shown to have two genes, *pitA* and *pitB*, and expression has been demonstrated for both proteins, PITP1 and PITP2 [21]. The phylogeny shown here indicates that PITP1 is a class IIB protein, perhaps representative of an ancestral precursor to class IIA proteins. Second, data presented here indicate that the Class IIB proteins are derived from Class I proteins, and the membrane-associated Class IIA proteins are derived from the class IIB proteins. Previous cladograms and dendrograms have indicated different derivization patterns. Ocaka *et al* [36] indicate that mammalian PITPNC1 (Class IIB in the present analysis) shares a most recent common ancestor (MRCA) with

PITPNA and PITPNB; more so than with any of the PITPNMs. Fullwood *et al.* present a dendrogram in which the membrane-associated PITPs and the soluble PITPs split from a shared derivation from Class IIB proteins (*rdgB*β). An increased sample size, an unbiased tree root, and the use of conserved sequence motifs for global alignment in the present study lead to a different interpretation of the evolution of this protein family.

The phylogenetic tree produced here is indicative of the evolutionary history of these sequence motifs, and not of the proteins as a whole. This is important, because in some proteins, large sequences with no known sequence motif patterns are observed (such as in the *Plasmodium yoelli* "PITP1" protein) that may be the result of gene conversion, unequal crossing-over, or repeat expansion during the evolution of specific proteins. Such large insertions and deletions in protein sequence are difficult to utilize in any phylogenetic analysis; they are purely derived characters that are phylogenetically uninformative. However, the existence of these derived sequences suggests that either the function or regulation of proteins in this family has changed dramatically, indicative of the type of specific adaptation often seen within protein families.

4.2. Functional Shifts in PITP Proteins

Alignment and subsequent phylogenetic analysis of divergent members of protein families is a problem compounded by shifts in primary, secondary, and tertiary structure that occur during protein evolution and functional diversification. Global alignments of complete protein coding regions often fail when functional units (such as regulatory regions, transmembrane domains, DNA-binding domains, protein-protein interaction domains, etc.) are gained or lost over evolutionary time. This issue complicates the otherwise straightforward phylogenetic analysis of related proteins. Additional complications arise in organismal surveys in which entire genomes are sequenced and annotated by automated algorithms based on homology. BLAST and FASTA searches find protein regions with high local identity, which can suggest functional similarity. However, outside of these identified regions, major changes can occur in protein function that obscure identity and make global protein alignment difficult or impossible. Without corresponding functional data, these genes are often named inconsistently. For example, a gene found in one species with locally high homology to a protein region in another species is often named "Similar to..." or "Species X homologue of Species Y protein". Because BLAST is a local homology search tool, it is inadequate for identification and annotation of species orthologs. For this reason, many of the genes identified in species genome projects are insufficiently annotated; phylogenetic analysis of all proteins labeled as "Phosphatidylinositol transfer proteins, Beta" for example will yield a spurious

alignment and therefore a misleading tree. As demonstrated in this study, analysis of the PITP/rdgB family was complicated by both issues. It should be noted that full-length sequences produce similar phylogenetic trees for alignments of many related sets of proteins (all Class I or Class II proteins, for example).

The resultant phylogenetic tree reveals that the general naming convention for the PITP family needs to be critically examined. Many of the proteins in this family cannot be named exclusively by local sequence identity, as their functions appear to be significantly altered from previously studied proteins. Many annotated genes are named in a way that might not be truly indicative of their function. In other words, sequence homology in local segments has obscured the greater functional diversification within this family. For example, although the membrane-associated proteins (Class IIB) are shown to be derived and monochadistic, the tree root appears to be within the PITP family, suggesting that many other functions are derived characteristics from this single-domain protein. At best, this tree demonstrates the need for better functional and structural classification of PITP-like proteins before final assignment of their names.

An additional feature of the strict consensus tree is the hypothesis it suggests about the evolution of PITP protein family members. First, no PITP proteins are found within prokaryotes or within yeast. Yeast have an analogous enzyme, Sec14p, but it appears to have an independent evolutionary origin. The slime-mold and *Plasmodium* sequences represent the most primitive species in this PITP family tree. In contrast, the multiplication of forms within mammals is impressive. Humans, mice, and rats have well-characterized genomes and each have a variety of PITP family-member proteins.

4.3. Conserved Sequence Motifs

The use of conserved sequence motifs in a cladistic analysis of the PITP family highlights several regions for consideration. Two regions are of particular interest: one containing sequence motifs 7, 8, and/or 9, and the other containing sequence motifs 11, 12, or 13. These two regions form loops at the surface of the protein near the ends of the acyl chains of the bound phospholipid (**Figure 2(b)** and **2(c)**). Sequence motif 7 is the only motif present that is not found in the same primary sequence space in the three main protein classes. In human PITP α , the amino acid sequence is at residues 66-73, while it occurs at residues 204-211 and 198-205 in human PITPNM1 and PITPNC1, respectively. Sequence motif 8 is not present in class I PITPs, and partially overlaps with sequence motif 9, which is exclusive to the alpha/beta clades of class I. Sequence motif 7 in the class I PITP's partially overlaps with sequence motif 8 of class IIA and IIB. Sequence motif 7 contains the putative helix insertion loop proposed to anchor PITP α to the mem-

brane during lipid exchange [25]. It is tempting to speculate that this helix has adapted a different conformation or perhaps has migrated across the lipid-binding cavity to near residues 200-208 relative to the PITP α structures.

The second region of interest contains sequence motifs 11, 12, or 13. These three motifs are present in approximately the same space in primary sequence, but each is unique to the three family classes. Sequence motif 11 is unique to class IIB, whereas Sequence motif 12 is unique to class IIA, and sequence motif 13 is unique to class I. The role of this loop in the structure or the function of any class of PITP is currently unexplored.

A concern with the novel phylogenetic analysis technique used in this study is the proportion of the sequence data actually used in the evolutionary analysis and whether amino acids that have been structurally and functionally shown to affect phospholipid transfer and signal transduction capabilities are included in the alignment matrices. In human PITP α , 214 of the 270 amino acids (79.3%) are included in the conserved sequence motifs. Most site-directed mutagenic analysis of the role of specific residues in the phospholipid transfer, specificity, and PLC reconstitution capabilities have been done on human or rat PITP α and PITP β . Residues in rat PITP α that have been studied and shown to play a functional role in PITPs include Thr59, Lys61, Glu86, Asn90, Tyr103, and the double Trp pair at 203-204 [37,38]. These residues are all in conserved sequence motifs. Thr59 and Lys 61 map to sequence motif 6, which is the only sequence motif present in all sequences in this study. Interestingly, sequence motif 9, containing Glu 86, is present only in Class I proteins. Tyr103 has been shown to diminish PLC reconstitution without affecting phospholipid transfer. This residue is a Tyr only in the Class I proteins, and is a conservative substitution to a Phe in the class IIA and class IIB proteins. Examination of these amino acids and sequence motifs from an evolutionary perspective enables a more thorough understanding of their importance in shaping PITP function and structure.

4.4. Functional Specialization across Evolution

Functional shifts within the PITP family are difficult to assess in light of the relative paucity of experimental analysis of different family members. In rat, PITPs are broadly expressed and have been detected in at least 20 tissues [39]. Unigene expression profiles (<http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene>) for mammalian species indicate a slightly more general and ubiquitous expression for the alpha isoform than the beta isoform. Mouse PITP β *-/-* embryonic stem cells are embryonically lethal, indicating essential functions in cell viability [29]. In contrast, mice deficient in PITP α develop normally to term, but fail to thrive neonatally [30].

These observations and the EST expression profiles support the argument that PITP isoforms are not redundant, and have different functions [29]. One implication of the consensus tree is that, given that the ancestral proteins have putative roles in cellular function, e.g., PITP2 in *Dictyostelium*, they may be more widely expressed than the more derived family members, which appear to have roles only in specific tissues or at specific developmental times. PITPnm1 in mice, for example, is highly expressed primarily in the retina, with weaker expression in the brain and some suggestion (from rat data) of central nervous system expression. Other studies in humans showed PITPnm2 and PITPnm3 expression in brain and retina.

The phylogenetic analysis described here has demonstrated the utility of the use of conserved sequence motifs in detecting evolutionary relationships among proteins in large and/or diverse functions. This method uses short conserved sequence motifs instead of single character amino acids. The presence and absence of motifs becomes an important data point. The use of sequence motifs in phylogenetic analysis as described here should be applicable to the analysis of a wide range of protein families, particularly large, diverse families where re-shuffling of domains occurred over evolutionary time.

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