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Molecular Cloning of a Mouse Epithelial Protein-Tyrosine Phosphatase With Similarities to Submembranous Proteins

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Abstract Protein-tyrosine phosphatases (PTPases) form an important class of cell regulatory proteins. We have isolated overlapping cDNA clones that together comprise an 8 kb transcript encoding a novel murine PTPase which is expressed in various organs. Sequence analysis revealed an open reading frame of 2,460 amino acid residues. The predicted protein, PTP-BL, is a large non-transmembrane PTPase that exhibits 80% homology with PTP-BAS, a recently described human PTPase. PTP-BL shares some intriguing sequence homologies with submembranous proteins. It contains a band 4.1-like motif also present in the tumor suppressors neurofibromatosis 2 and expanded, five 80 amino acid repeats also present in the discs-large tumor suppressor, and a single catalytic phosphatase domain. No obvious homologies to other proteins were found for the N-terminal region of the protein other than human PTP-BAS. RNA in situ hybridization experiments show that the PTP-BL gene is expressed in epithelial cells, predominantly in kidney, lung, and skin. These data suggest a cell cortical localization for PTP-BL in epithelial cells and a possible role in the morphology and motility of epithelial tissues. © 1995 Wiley-Liss, Inc.

Key words: gene expression, mouse embryo, signal transduction, band 4.1, discs-large homologous region, membrane skeleton, cytoskeleton

Cells of multicellular organisms have the ability to respond to external stimuli, and such responses can lead to apoptosis, quiescence, differentiation, mitosis, or cell movement. Transmission of signals triggered by hormones or growth factors, or by cell-cell or cell-matrix contacts, is commonly mediated by transmembrane molecules. Failure in these processes can lead to improper cell growth or differentiation and tumor formation. Indeed, defects in components of growth factor signalling pathways have been demonstrated for many cancer types, and the importance of cell contact-signalling molecules in the process of tumor metastasis is well established [van Roy and Mareel, 1992]. In addition, evidence is accumulating that defects in cell-cell and cell-matrix contact signalling can be involved in tumor initiation [Hedrick et al., 1993]. That cell adhesion molecules as well as the corresponding peripheral membrane proteins have a regulatory role in growth control is also demonstrated by studies on tumor suppressor genes in Drosophila [Bryant et al., 1993]. The discs large (dlg) gene, for example, is needed to enable Drosophila imaginal disc cells to leave the cell cycle and differentiate into polarized cells [Woods and Bryant, 1991]. Absence of the protein in dlg mutants therefore leads to uncontrolled proliferation. The DlgA protein is localized in the undercoat of the septate junctions, which are the counterpart of the vertebrate tight junctions. Other cell cortical proteins that exert growth control include the Drosophila expanded (ex) tumor suppressor [Boedigheimer and Laughon, 1993] and the human neurofibromatosis type 2 tumor suppressor, otherwise known...
as merlin (Trofatter et al., 1993) or schwannomin (Rouleau et al., 1993). Both proteins were found to be members of the family of band-4.1-like proteins (Boedigheimer et al., 1993), which mediate the contact of integral membrane proteins with the actin cytoskeleton [Luna and Hitt, 1992]. It has been postulated, therefore, that merlin/schwannomin and ex may be involved in membrane-cytoskeletal organization and the control of cell shape, locomotion, and, perhaps, responses to external stimuli [Boedigheimer et al., 1993; Algrain et al., 1993; Tsukita et al., 1993]. Finally, recent observations have implicated cadherin-catenin complexes in neoplasia. Loss of cadherin function results in increased metastatic potential of certain tumors [van Roy and Mareel, 1992]. It has been postulated, therefore, that merlin/schwannomin and ex may be involved in membrane-cytoskeletal interactions, by binding and/or dephosphorylating specific submembranous proteins.

MATERIALS AND METHODS

Isolation of mPTP14 cDNAs

The mPTP14 PCR fragment (Hendriks et al., 1995) was isolated, labelled radioactively by random priming [Feinberg and Vogelstein, 1983], and used to screen a mouse brain λ-ZAPII cDNA phage library (Stratagene, La Jolla, CA). To obtain larger clones, a 5' fragment of clone mPTP14-5 was used to screen a mouse skin λ-ZAPII cDNA phage library (Stratagene). Hybridization conditions were those of Church and Gilbert [1984]. Washing at high stringency (0.1% SDS, 0.04 M sodium phosphate buffer/pH = 7.4, 1 mM EDTA) was performed three times at 65°C for 20 min. Autoradiography was on Kodak X-omat S1 films at -70°C for 1–2 days using Dupont Cronex (Dupont, Wilmington, DE) intensifying screens. Positive phages were plaque-purified and inserts were rescued as pBluescript SK plasmids according to the manufacturer's protocols.

Clone mPTP14-1.3 was generated by RTPCR. The sense primer (5'-GGCTT CATTCTCTCCATG-3'), corresponding to position 149–168 of the PTP-BL cDNA sequence, was designed on the basis of the human [Maekawa et al., 1994] and bovine (Walton et al., personal communication) homologous sequence. The antisense primer (5'-CCCTGATTGATCAAGTTGCC-3') was chosen close to the 5' end of clone mPTP14-2 (position 1,390–1,409 of the PTP-BL cDNA sequence). Mouse keratinocyte RNA (2 μg) was isolated and used for cDNA synthesis in a reverse transcription reaction employing random hexamers as described previously [Hendriks et al., 1994]. Following a 5 min incubation at 90°C, 5 μl of the single-stranded cDNA preparation was used as template for PCR. Primers (final concentration 1 ng/μl) were added to a 50 μl reaction mixture containing 20 mM Tris-HCl (pH = 8.4), 50 mM KCl, 2.5 mM MgCl₂, 0.01% BSA, all four dNTPs (each at 250 μM), 1 U Tag DNA Polymerase (Perkin-Elmer Cetus, Norwalk, CT), and template material. Thirty-five cycles were performed on a Perkin-Elmer thermal cycler; each cycle involved incubation at 94°C for 45 s, at 50°C for 45 s, and at 72°C for 1.5 min.

Clone mPTP14-R5 was produced by an anchored PCR method described previously [Deen et al., 1992]. An antisense oligonucleotide (5'-GGCTGCTTGGGAGTACT-3'; pos. 352–369 in the PTP-BL cDNA sequence) served as primer during reverse transcription of mouse keratinocyte mRNA. A nested antisense oligonucleotide (5'-GGATCTTCTCTCAGATCGG-3'; pos. 286–305) and an oligo(dC) primer were used during amplification as described [Deen et al., 1992]. PCR products were cloned into the Smal site of plasmid pBluescript as described in Hendriks et al. [1995].

Sequence Analysis

Nucleotide sequences were determined using the DNase shotgun strategy [Lin et al., 1985] in combination with the double-stranded DNA dideoxy sequencing method [Hattori and Sakaki, 1986]. DNA sequence gel readings were recorded, compared, edited, and assembled using the IG-SUITE 5.35 package (Intelligenetics, Inc., Mountain View, CA). Deduced protein sequences were analysed using the GCG package (Devereux et al., 1984) provided by the Dutch CAOS/CAMM Center. Databases (EMBL release 40, GenBank rel. 83, PIR-protein rel. 41.1, and
Hendriks et al.

SWISS-PROT rel. 30) were searched for homologous sequences using the BLAST program [Altschul et al., 1990] and DHR-containing proteins were identified using the pattern (K,R)X[2,4]GL(G,R)X[1,5]GGX [8,20]GXXAX[6,9] (G,N)DXXX(V,I)N allowing 2 mismatches, and subsequent manual screening. Homologies of sequences aligned with PILEUP and LINEUP were determined using DISTANCES with thresholds of 1.5 and 0.6 for identity and similarity values, respectively [Devereux et al., 1984].

Assay of Phosphatase Activity

pGEX-BL was constructed by ligating the 1.2 kb DNA polymerase-treated (blunt) HindIII fragment of mPTP14-2, encoding the last 360 amino acids of PTP-BL, into the SmaI site of pGEX-3X [Smith and Johnson, 1988]. Escherichia coli DH-5a (Gibco-BRL, Gaithersburg, MD) transformed with pGEX-BL or the empty vector pGEX-3X were grown in 100 ml of Luria broth containing 100 µg/ml ampicillin until A650 reached 0.7, and induced with 0.1 mM IPTG for 4 h at 37°C. GST-containing proteins were isolated according to Frangioni and Neel [1993]. Briefly, 1.5 ml of the bacterial culture was pelleted, washed once with 200 µl of cold STE (10 mM Tris, pH 8.0, 150 mM NaCl, 1 mM EDTA), resuspended in 135 µl of STE containing 100 µg/ml of lysozyme, and incubated on ice for 15 min. Then 1.5 µl 0.5 M DTT and 1 µl PMSF (100 mM) were added, and bacteria were lysed by the addition of 24 µl of 10% N-laurylsarcosine in STE. After brief vortexing and 1 min sonication on ice, the lysate was clarified by centrifugation at 10,000g for 5 min, at 4°C. The supernatant was transferred to a new tube, and 40 µl of 10% Triton X-100 in STE was added. From the 200 µl lysate, the GST fusion protein was purified over glutathione agarose beads (Sigma, St. Louis, MO) exactly as described [Frangioni and Neel, 1993]. Purified GST or GST-BL protein was then used for tyrosine phosphatase assay as described by the manufacturer (Boehringer Mannheim, Indianapolis, IN).

RNA In Situ Hybridization

Embryos were isolated from pregnant NMRI mice at developmental stages indicated in the text. The day of plug detection was considered to be day 0.5 post conception (p.c.). Embryos and tissue samples were fixed overnight with 4% paraformaldehyde in PBS at 4°C. Cryosections (10 µm) were mounted on 3-aminopropyltriethoxy-silane-coated slides and RNA in situ hybridization was performed as described previously [Bächner et al., 1993]. To generate “sense” and “antisense” RNA probes, the mouse mPTP14-2 cDNA clone in pBlueScript-SK was linearized with XhoI or NotI and used for in vitro transcription by T3 or T7 RNA Polymerase, respectively. Both probes were labelled with α32P-UTP to a specific activity of >10⁶ dpm/µg. Probe length was reduced to 150–200 nucleotides by alkaline hydrolysis. The slides were prehybridized at 54°C in a solution containing 50% formamide, 10% dextran sulphate, 0.3 M NaCl, 10 mM Tris, 10 mM sodium phosphate (pH 6.8), 20 mM DTT, 0.2 × Denhardt’s reagent, 0.1% Triton X-100, 0.1 mg/ml E. coli RNA, and “cold” 0.1 mM α32P-UTP. For hybridization, 80,000 dpm/µl α32P-UTP labelled RNA probe was added to the hybridization mix and the hybridization was continued at 54°C for 16 h in a humid chamber. Subsequently, the slides were washed in hybridization salt solution to which 20 mM dithiothreitol was added. After RNase A digestion, slides were washed for 30 min at 37°C with 2 × SSC, 0.1% SDS, and 30 min with 0.1 × SSC, 0.1% SDS, and dehydrated by increasing concentrations of ethanol. The slides were coated with Ilford K5 photoemulsion for autoradiography. After 14–21 days of exposure at 4°C, the slides were developed in Kodak D19b and stained with Giemsa. The sections were analyzed with bright- and dark-field illumination using a Zeiss (Thornwood, NY) SV8 stereo-microscope and an Axiosphot microscope and photographed using Agfa Ortho black-and-white film.
RESULTS
Cloning of mPTP14 cDNAs

We recently isolated murine PTPase cDNA fragments [Hendriks et al., 1995] using degenerate primers based on conserved regions in the rapidly expanding PTPase gene family [Walton and Dixon, 1993]. One of these fragments, mPTP14, showed the highest homology with the PTPases MEG [Gu et al., 1991] and PTPH1 [Yang and Tonks, 1991] (29 and 31% identity at the amino acid level, respectively). MEG and PTPH1 contain one catalytic phosphatase domain and an amino-terminal stretch with significant similarity to the band 4.1-type protein family. However, the length of the mPTP14 transcript (8 kb) that was detectable in various murine tissues [Hendriks et al., 1995] was significantly larger than those reported for MEG and PTPH1 (around 4 kb), and was therefore expected to encode a much larger protein product. To determine the nature of the additional sequence motifs present in the large mPTP14 transcript, we set out to clone the corresponding cDNA.

Screening of a mouse brain cDNA library yielded several positive clones, among which mPTP14-5 was the largest with an insert length of 4.5 kbp. A murine skin cDNA library was screened to obtain longer clones, since strong signals were detected by the mPTP14 probe on Northern blots containing keratinocyte RNA [Hendriks et al., 1995]. The longest cDNA identified, mPTP14-2, spanned 6.5 kbp and its DNA sequence was determined. As expected from the length of the corresponding transcript, mPTP14-2 does not represent a full-length clone. While this work was nearing completion, the sequence of human PTP-BAS [Maekawa et al., 1994] was published that exhibited high homology with our clones. A bovine homolog has also been reported [Mauro and Dixon, 1994]. By comparing the human and bovine (kindly provided by Drs. K. Walton, Q. Vega, and J. Dixon) nucleotide sequences, we were able to design an oligonucleotide primer close to the 5' end of the open reading frame. Using this primer in combination with an antisense primer from the 5' region of clone mPTP14-2, a 1.3 kbp cDNA fragment (mPTP14-1.3) was amplified by RT-PCR from mouse keratinocyte RNA. Subsequently, using the mPTP14-1.3 sequence data, antisense oligonucleotide primers were designed to clone additional 5' sequences by anchored PCR. In this way, a nearly full-length cDNA sequence for the mPTP14 transcript was assembled from mPTP14-2, mPTP14-1.3, and mPTP14-R5 (Fig. 1A). The 7,922 bp sequence spans 7 nucleotides of the putative 5' untranslated region, the complete open reading frame and the poly-(A) addition signal-containing 3' untranslated region (acc. no. Z32740).

Analysis of the Encoded PTP-BL Protein

The 2,460 amino acid protein that is predicted by the mPTP14 open reading frame (Fig. 1B) displays 80% identity and 86% similarity to the human PTP-BAS type 1 sequence [Maekawa et al., 1994], and we therefore propose the name PTP-BL (BAS-like) for the mPTP14-encoded protein. Recent reports have also described the cloning of PTPL1 [Saras et al., 1994] and hPTP1E [Banville et al., 1994], which are actually splice variants of PTP-BAS. Like its human homologs, PTP-BL exhibits intriguing sequence features (Fig. 1). As was anticipated from its homology to PTPH1 and MEG, PTP-BL contains a tyrosine phosphatase domain (residues 2,181–2,431) and a band 4.1-like sequence (aa 577–872), which is regarded as being a plasma membrane binding sequence that serves as a molecular link between integral membrane proteins and the cytoskeleton [Luna and Hitt, 1992]. In between the band 4.1-like sequence and the
catalytic phosphatase domain, five 80-amino acid repeat regions were found that are known as GLGF motifs [Cho et al., 1992] or discs-large homologous regions (DHR) [Bryant et al., 1993; Woods and Bryant, 1993] (Fig. 1). The DHR motif was first detected in a family of membrane-associated guanylate kinases that are localized at specialized junctional structures or junction-like areas [Bryant et al., 1993; Woods and Bryant, 1993]. It has been speculated that the DHR motif mediates coiled-coil interactions with the actin cytoskeleton [Woods and Bryant, 1991] or that it is capable of regulating guanylate kinase enzyme activity [Cho et al., 1992]. Over the past year several other proteins have been reported to contain DHR motifs, including the PTPases PTP-BAS/PTPL1/hPTP IE, MEG, and PTPH1 [Maekawa et al., 1994; Saras et al., 1994; Banville et al., 1994; Theisen et al., 1994; Prasad et al., 1993; Lue et al., 1994]. Experiments to establish a possible function for the DHR motif have been limited to the observation that protein 4.1 can bind to the DHR-containing region of the human homolog of DlgA in vitro [Lue et al., 1994]. No homologies other than to the human PTP-BAS isoforms were found for the N-terminal segment of PTP-BL in the databases.

**Comparison of PTP-BL to Its Human Homolog**

The availability of both human and murine sequences for this unusually large non-receptor-type PTPase has allowed an interspecies comparison (Fig. 1; Table I). As outlined above, the PTP-BL sequence can be divided into several domains. The evolutionary conservation of these domains has been determined and amino acid identities and similarities for the different segments are listed in Table I. For the band 4.1-like sequence, the five DHR motifs and the single phosphatase domain, 90% or more identity (94–96% similarity) is observed between the human and mouse sequences. The spacer regions surrounding the DHR motifs are only 64% identical (73% similar), indicating reduced structural or functional constraints within these segments. The N-terminal segment, which lacks obvious homologies to other proteins in the databases, displays higher values, of 86% identity and 92% similarity, respectively (Table I). A more careful scrutiny of the murine and human N-terminal sequences (Fig. 1B) shows them to comprise three regions. Regions 1 and 3 yield similarity scores as high as those of the other conserved protein domains described above. In contrast, region 2 (corresponding to residues 213–393 of PTP-BL) is less well conserved and is spliced out in some hPTP1E variants. Interestingly, this region contains two conserved potential tyrosine kinase phosphorylation sites at residues 255 and 339, which suggests a regulatory role for this module in the stability, activity, or subcellular localization of the protein. A putative leucine zipper motif has been identified within the third part of the N-terminal domain [Saras et al., 1994] which may explain the high degree of similarity between the mouse and human sequences in this region of PTP-BL. However, the third leucine residue present in the human zipper motif has been replaced by a methionine in the mouse sequence (residue 478). Nevertheless, a significant potential to form coiled coil structures can be predicted for the third...
Fig. 2. Expression pattern of PTP-BL during mouse embryogenesis. Bright (a,c) and dark field (b,d) recordings of parasaggital sections hybridized with the antisense PTP-BL riboprobe are shown. A sense control hybridization did not result in a specific signal (data not shown). a,b: High expression of PTP-BL in all cells of a 9.5-day-old embryo is shown. No specific expression is found in the placenta. c,d: The restriction of the PTP-BL expression to epithelial cells of a 16.5-day-old embryo is visible. e, embryo; ki, kidney; lu, lung; me, metencephalon; mm, mesometrium; nc, nasal cavity; pi, placenta; to, tongue; ur, ureter. The bar represents 1 mm.
We have isolated cDNAs encoding a novel murine cytoplasmic-type protein-tyrosine phosphatase activity for PTP-BL. Preliminary Northern blot analyses had shown PTP-BL to be expressed at low levels in many different tissues [Hendriks et al., 1995]. In addition, RT-PCR experiments had revealed the expression of PTP-BL mRNA in murine embryonic stem cells derived from the blastocyst inner cell mass [Hendriks et al., 1994]. Therefore, we performed RNA in situ hybridization experiments on fetal and postnatal murine tissue sections to determine the expression patterns during development and in adult tissues more precisely. As demonstrated in Figures 2 and 3, hybridization with the PTP14-2 antisense riboprobe reveals distinct spatial and temporal expression patterns. In the early development PTP-BL is expressed at high levels throughout the embryo (Fig. 2a,b). During subsequent development, expression becomes restricted to epithelial cell lineages, e.g., epithelia of the skin and the oesophagus, the epithelia surrounding the vesicles of the brain, the epithelia of the nasal cavity, the lung, the kidney, the ureter, and the bladder (Fig. 2c,d). In late development high expression is found, e.g., in the ependymal cell layer, which forms the epithelia surrounding the ventricles in brain (Fig. 3a,b), the epithelia of bronchioli in the lung (Fig. 3c,d), and the epithelia of the stomach (Fig. 3e,f). High expression is also evident in cells of the Bowman’s capsules of the kidney (Fig. 3g,h) and the seminiferous epithelia of the testis (Fig. 3i,k). There is only low expression in epithelial cells of the gut. Expression was also detected in some non-epithelial cells, such as the connective tissue surrounding the vertebrae in day 14.5 p.c. embryos (data not shown). No expression was observed in neuronal cells, muscle, or liver.

**DISCUSSION**

We have isolated cDNAs encoding a novel murine cytoplasmic-type protein-tyrosine phos-
phatase, PTP-BL, from brain and skin cDNA libraries. Using RNA in situ hybridization, PTP-BL expression was studied in a developmental perspective. PTP-BL mRNA expression is already detectable at very early stages of development, e.g., in embryonic stem cells [Hendriks et al., 1994] and in all cells of a 9.5-day-old embryo (Fig. 2). In late stages of development PTP-BL expression could be demonstrated in epithelial cell layers, most notably in the skin, nasal cavity, oesophagus, stomach, kidney, and brain. This in keeping with the expression pattern for the human gene as judged from Northern analysis. PTP-BAS expression was found in a wide variety of human tissues and a comparison of fetal and adult expression patterns points to a higher expression level in fetal brain for the PTP-BAS transcript [Maekawa et al., 1994]. This observation may be due to the relative prominence of the brain cavities, and thus ependymal cell layers, during the early embryonic stages compared to adult brain.

The deduced protein sequence for PTP-BL displays an 80% sequence homology with the recently published human PTPases PTP-BAS/PTPL1/hPTP1E [Maekawa et al., 1994; Saras et al., 1994; Banville et al., 1994]. The N-terminal segment of PTP-BL exhibits no apparent homology to other known proteins, but does contain two putative tyrosine kinase phosphorylation sites and a leucine zipper motif with coiled coil-forming potential. PTP-BL also contains a band 4.1-like domain, five DHR motifs, and a single protein-tyrosine phosphatase catalytic domain (Fig. 1) suggesting a membrane/cytoskeletal localization for this PTPase. Five possible PEST domains surrounding the fourth and fifth DHR motif have been reported [Banville et al., 1994], suggesting that PTP-BAS might be rapidly degraded within the cell. In general, however, cell cortical and cytoskeletal proteins are rather stable. In line with this view, preliminary pulse-chase experiments on cells transfected with expression constructs containing the BglII/Smal fragment spanning the PTP-BL DHR region (Fig. 1B) point to a half-life of more than 16 h for this segment (Hendriks et al., unpublished data). This period is much longer than that observed for genuine PEST-containing proteins [Rechsteiner et al., 1987].

Over the past year several proteins other than protein-tyrosine phosphatases and membrane-associated gyanylate kinase homologues have been found to contain DHR motifs [Banville et al., 1994; Maekawa et al., 1994; Lue et al., 1994; Prasad et al., 1993; Saras et al., 1994; Theisen et al., 1994]. Most of these proteins contain a single DHR motif, such as LCF [Cruikshank et al., 1994], syntrophins [Adams et al., 1993b; AF-6 [Prasad et al., 1993], dishelled [Theisen et al., 1994], X11 [Duclos et al., 1993], and the product from an altered ros1 transcript [Sharma et al., 1989]. Interestingly, lymphocyte chemottractant factor (LCF) is a novel type of interleukin that consists almost entirely of a single DHR motif and whose biological activity depends on autoaggregation [Cruikshank et al., 1994], suggesting that DHR motifs mediate homophilic interactions. As mentioned previously, the DHR region of hdig can bind to protein 4.1 in vitro [Lue et al., 1994], implying that heterophilic DHR-mediated interactions can occur as well. Association to band 4.1 has also been observed for the DHR-containing protein p55 [Marfatia et al., 1994]. Syntrophins are dystrophin-associated proteins located at the cell cortex [Adams et al., 1993b] but it is not known whether their DHR motifs mediate this interaction. Genetic evidence suggests that the Drosophila protein dishelved participates in signalling events downstream of wingless that occur close to the membrane [Theisen et al., 1994]. Like DlgA, dishelved is required to establish cell polarity and it is tempting to speculate that the DHR motif determines the cell cortical localization required for its function. The human X11 protein contains two DHR motifs at its C-terminus. This protein is a candidate for Friedreich Ataxia (FRDA), an autosomal recessive degenerative disorder affecting both central and peripheral nervous systems [Duclos et al., 1993]. A crucial role for X11 as part of the membrane skeleton in establishing polarity of neuronal cells would be in line with the observed FRDA phenotype.

To obtain more clues about potential roles for DHR motifs we performed homology and pattern searches using the latest database releases, and five additional sequences were found to contain a DHR motif (Fig. 4). Surprisingly, one of these proteins, X104, is the product of an other gene which resides within the FRDA gene region, but which has been excluded as a candidate for the disease [Duclos et al., 1994]. X104 is in fact the human homolog of canine ZO-2 [Jesaitis and Goodenough, 1994], a ubiquitous component of the epithelial tight junction complex, and was found to contain three DHR motifs (Fig. 4). Two expressed sequence tags, T06631
Fig. 4. Multiple sequence alignment of DHR motifs from various proteins. Black dots indicate gap positions and a deduced consensus sequence is shown at the bottom. Protein segments that were used are flanking the motif sequences. Motifs are numbered starting from the N-terminus of the corresponding motif.

The following sequences were used: mouse PTP-BL (acc. no. Z32740); human PTPH1 (P26045) and MEG (P29074), Drosophila DilgA (P31007), rat PDP-95 (P31016), and T08317 [Adams et al., 1993a], also harboured DHR-like sequences in their open reading frames. In addition, the N-terminal tail of the small leucine zipper-containing protein B3-1 [Dixon et al., 1993] is comprised of a DHR motif. Finally, and most interestingly, we identified a single DHR motif in the testis-specific serine/threonine kinase MAST205 [Walden and Cowan, 1993]. MAST205 can associate to MAP-coated microtubules and this binding is displayed by a small protein segment just downstream of the kinase domain. This downstream segment displays 20–23% sequence identity to the DHR motif prototypes of DilgA (Fig. 4). Since the segment does not bind to MAP-free tubulin, these data suggest that DHR motifs may enable interactions with proteins that decorate tubulin filaments. Indeed immunoprecipitation of MAST205 coprecipitates a 75 kDa protein [Walden and Cowan, 1993]. It is noteworthy to mention that a 78 kDa component was also detected in precipitates of the human homolog of PTP-BL, PTP11 [Saras et al., 1994]. In conclusion, evidence is accumulating that the DHR motif is a protein-binding interface that can mediate assembly into submembranous and cytoskeletal protein complexes.

The mRNA expression pattern and the sequence homologies in PTP-BL imply that its substrates will be found among the proteins located at the cell cortex of epithelial cells. Many submembranous proteins contain phosphotyrosine residues and protein phosphorylation has indeed been implicated in the regulation of structural changes in the membrane skeleton and cytoskeleton [Luna and Hitt, 1992]. The cloning of the neurofibromatosis type 2, dlg, and ex tumor suppressor genes has demonstrated the tremendous impact of peripheral membrane proteins on cell growth and differentiation [Algrain et al., 1993; Boedighheimer et al., 1993; Bryant et al., 1993; Tsukita et al., 1993]. Further investigations of the biochemical properties of PTP-BL are therefore expected to yield more information on the interplay of membrane-cytoskeletal protein complexes, both in normal and malignant cells.

NOTE ADDED IN PROOF

After submission of this manuscript an almost identical PTPase sequence was described:

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