Nuclear organisation of NIPP1, a regulatory subunit of protein phosphatase 1 that associates with pre-mRNA splicing factors

Laura Trinkle-Mulcahy¹,², Paul Ajuh¹, Alan Prescott¹, Felix Claverie-Martin³, Stanley Cohen³, Angus I. Lamond¹ and Philip Cohen²

¹Department of Biochemistry, The University, MSI/WTB Complex, Dow Street, Dundee DD1 5EH, Scotland, UK
²Medical Research Council Protein Phosphorylation Unit, Department of Biochemistry, The University, MSI/WTB Complex, Dow Street, Dundee DD1 5EH, Scotland, UK
³Department of Genetics, Stanford University School of Medicine, Stanford, CA 94305, USA

*Author for correspondence (e-mail: l.trinklemulcahy@dundee.ac.uk)

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SUMMARY

Protein phosphatase-1 (PP1) is complexed to many proteins that target it to particular subcellular locations and regulate its activity. Here, we show that ‘nuclear inhibitor of PP1’ (NIPP1), a major nuclear PP1-binding protein, shows a speckled nucleoplasmic distribution where it is colocalised with pre-mRNA splicing factors. One of these factors (Sm) is also shown to be complexed to NIPP1 in nuclear extracts. Immunodepletion of NIPP1 from nuclear extracts, or addition of a ‘dominant negative’ mutant lacking a functional PP1 binding site, greatly reduces pre-mRNA splicing activity in vitro. These findings implicate the NIPP1-PP1 complex in the control of pre-mRNA splicing.

Key words: Protein phosphatase, Splicing, Immunolocalisation, Targeting subunit, NIPP1

INTRODUCTION

Reversible protein phosphorylation catalysed by protein kinases and protein phosphatases regulates almost all aspects of cell life. Protein kinases and phosphatases frequently phosphorylate many proteins in vitro, raising the question of how they find their specific targets in vivo. In recent years evidence has been accumulating that these enzymes do not find their substrates by simple diffusion but are directed to them by specific ‘targeting’ subunits (Hubbard and Cohen, 1993). These accessory proteins bind to the catalytic subunit of the kinase or phosphatase, and determine its subcellular localisation and ability to be regulated by extracellular signals.

The paradigm for this phenomenon is protein phosphatase 1 (PP1), one of the major serine/threonine-specific protein phosphatases of eukaryotic cells (Hubbard and Cohen, 1993). PP1 interacts with a variety of targeting subunits, of which the best characterised are the cytosolic proteins that direct PP1 to glycogen (Stralfors et al., 1985) and to myosin (Alessi et al., 1992). Structural analysis of PP1 co-crystalized with a small PP1-binding peptide from the muscle glycogen-targeting subunit revealed that a hexapeptide sequence present in the latter (Arg-Arg-Val-Ser-Phe-Ala) interacts with a small hydrophobic channel on the surface of PP1 (Egloff et al., 1997). Similar sequences are present in many other PP1-targeting subunits, and synthetic peptides containing this motif disrupt their interaction with PP1 (Egloff et al., 1997; Kreivi et al., 1997). The same PP1-binding motif was identified independently by a different approach in which random peptide libraries were passed through PP1-affinity columns (Zhao and Lee, 1997).

Although the cytosolic forms of PP1 have been studied in greatest detail, PP1 activity is located, and even enriched, in the nucleus (Kuret et al., 1986; Jakes et al., 1986). Many nuclear events are controlled by reversible protein phosphorylation, including pre-mRNA splicing (Mermoud et al., 1992; Tazi et al., 1992; Misteli and Spector, 1996; Cao et al., 1997; Duncan et al., 1997; Xiao and Manley, 1997; Kanopka et al., 1998) and there is evidence that PP1 plays a critical role prior to the first catalytic step of splicing (Mermoud et al., 1992) and in spliceosome assembly (Mermoud et al., 1994). However, the form(s) of PP1 involved in regulating pre-mRNA splicing and the substrates that it must dephosphorylate to regulate this process are unknown. Fractionation of rat nuclear extracts by anion exchange chromatography revealed two major forms of PP1 (Jagiello et al., 1995). The species eluting at a lower concentration of NaCl comprised PP1 complexed to a 41 kDa protein termed ‘nuclear inhibitor of PP1’ (NIPP1), while the species eluting at higher NaCl comprised PP1 complexed to a much larger protein, subsequently termed p99 (Kreivi et al., 1997) or PNUTS (Allen et al., 1998).

NIPP1 was cloned (Van Eynde et al., 1995) and shown to be an RNA-binding protein (Jagiello et al., 1997). Its C-terminal 127 residues are identical to ‘activator of RNA decay’ (ARD1), the product of a mammalian gene that complements mutations in Escherichia coli caused by deleting the gene encoding E. coli ribonuclease E (Wang and Cohen, 1994). ARD1 was
subsequently reported to possess endoribonuclease activity (Claverie-Martin et al., 1997) and may be produced from the NIPP1 gene by an alternative splicing event. NIPP1 binds tightly to PP1 and prevents it from dephosphorylating a number of phosphoproteins (Van Eynde et al., 1995; Jagiello et al., 1995). This inhibition can be relieved by phosphorylation of NIPP1 in vitro with cyclic AMP-dependent protein kinase and CK2 (Nulsteka et al., 1998). p99 also suppresses the activity of PP1 towards glycogen phosphorylase (a phosphoprotein frequently used to assay PP1 activity) and contains RNA-binding motifs (Kreivi et al., 1997; Allen et al., 1998). NIPP1 and p99 both contain sequences rich in basic amino acids that may allow the import of these proteins into the nucleus.

The function of the NIPP1-PP1 complex is unknown, but in this paper we provide evidence for an important role in the control of pre-mRNA splicing. We find that NIPP1 colocalises and interacts with pre-mRNA splicing factors and that its depletion from nuclear extracts or the addition of a dominant-negative mutant to nuclear extracts greatly reduces pre-mRNA splicing activity in vitro. In addition, we show that loss of either PP1 or RNA binding has no effect on the localisation of the protein within the cell.

MATERIALS AND METHODS

Materials

Tissue culture reagents were obtained from Life Technologies Inc. (Paisley, UK), and Protein G-Sepharose, CH-Sepharose and glutathione-Sepharose from Pharmacia (Milton Keynes, UK). NIPP1 peptides corresponding to residues 175-190 (NIPP1a) and residues 127-140 (NIPP1b) were synthesised on an Applied Biosystems 430A peptide synthesizer by Mr F. B. Caudwell in the MRC Protein Phosphorylation Unit.

Antibodies

Polyclonal antibodies were raised in sheep against NIPP1 peptides NIPP1a and NIPP1b (see above) and bacterially expressed hexahistidine-tagged ARD1 (residues 225-351 of NIPP1). The antibodies were affinity purified on peptide or protein CH-Sepharose columns and used for immunoblotting and immunocytochemistry, respectively, at the following concentrations: anti-NIPP1a (0.5 µg/ml and 100 µg/ml), anti-NIPP1b (0.5 µg/ml and 100 µg/ml) and anti-ARD1 (0.1 µg/ml and 10 µg/ml). Monoclonal anti-c-myc antibodies were purified from ascites fluid from mice injected with 9E10 hybridoma cells by chromatography on Protein G-Sepharose and used for immunocytochemistry at 1 µg/ml, while goat polyclonal anti-GST antibodies (Pierce) were used at 5 µg/ml. Affinity purified sheep polyclonal antibodies against PP1 and antisera against PP2A were gifts from Dr P. T. W. Cohen and Dr G. Moorhead (MRC Protein Phosphorylation Unit, Dundee), respectively. They were used for immunoblotting at the following dilutions: anti-PP1 (0.5 µg/ml) and anti-PP2A (1:2000).

Antibodies to nuclear antigens used for immunocytochemistry included mouse monoclonal antibodies to Sm proteins (anti-Y12, dilution 1:500; Pettersson et al., 1984), U2AF65 (anti-MC3, dilution 1:10; Gama-Carvalho et al., 1997), SR proteins (anti-3CS and anti-SC53), both diluted 1:10; Turner and Franchi, 1987; Fu and Maniatis, 1990) and survival of motor neuron protein (anti-2B1, dilution 1:10; Liu and Dreyfuss, 1996), rabbit polyclonal antibodies to U1A (anti-856, dilution 1:500; Kambach and Mattaj, 1992) and p80 coilin (anti-204/10, dilution 1:500; Bohmann et al., 1995), and a human autoimmune serum that recognises the SP100 protein in PML bodies (anti-Krieb, dilution 1:10; Lamond and Carmo-Fonseca, 1993). For immunoblotting, antibodies/antisera were used at the following dilutions: anti-Y12 (1:500), anti-856 (1:2000) and anti-MC3 (1:500), HRP-conjugated (Pierce) and FITC- and Texas Red-conjugated (Jackson Laboratories) secondary antibodies were used according to the manufacturers’ recommendations.

Microinjection of FITC-coupled NIPP1 antibodies

Affinity purified antibodies to NIPP1 were directly coupled to fluorescein isothiocyanate (FITC; Molecular Probes) and dialysed into 100 mM glutamic acid, pH 7.2 (with citric acid), 140 mM KOH, 1 mM MgSO4 and 1 mM DTT prior to microinjection into living HeLa cells using an Eppendorf 5242 microinjector. The medium was changed and the cells allowed to recover before examining the staining pattern with a Bio-Rad MRC-600 Laser Scanning Confocal Imaging System.

Immunolocalisation of NIPP1

Cells were grown to near confluency on glass coverslips, washed with phosphate-buffered saline (PBS) and fixed for 5 minutes with a –20°C methanol solution (90% methanol, 10% 100 mM MES, pH 6.9, 1 mM MgCl2, 1 mM EGTA). After several washes with PBS the cells were further permeabilised for 10 minutes with PBS containing 1% (by vol) NP-40, washed several times with PBS containing 0.1% (by mass) Tween-20, and blocked for 10 minutes in the same solution containing 3% BSA. After 1 hour in primary antibody, the cells were washed extensively in PBS containing 0.1% (by mass) Tween-20 before being exposed to secondary antibody for 1 hour. In some experiments DNA was stained for 5 minutes with 0.25 µg/ml propidium iodide (Sigma). When two primary antibodies were used for double labelling experiments they were applied sequentially as described above, with extensive washes in between. After staining, cells were mounted in Mowiol/Dabco and allowed to dry before examination on either a Bio-Rad MRC-600 or a Zeiss LSM 410 Confocal Laser Scanning Microscope with excitation wavelengths of 488 nm (FITC) and 543 nm (Texas Red).

Site-directed mutagenesis of NIPP1

The Val and Phe residues of the PP1-binding motif in NIPP1 (residues 201 and 203) were changed to Ala using PCR mutagenesis of a pKS+ vector containing a cDNA encoding full length human NIPP1. This V201A/F203A double mutant was produced by two-step recombinant PCR as described (MacKintosh et al., 1995). The DNA constructs were confirmed by restriction analysis and their DNA sequences checked on an Applied Biosystems 3T3A DNA sequencer using specific oligonucleotide primers.

Expression and purification of recombinant NIPP1

For bacterial expression of the protein, the wild-type and mutant NIPP1 DNA was subcloned into the pGEX-4T3 vector using unique EcoRI and SspI sites. The truncated construct which lacked the C-terminal ARD1 domain was generated by PCR of the full-length clone from the EGFP-C1 construct with N-terminal KpnI and C-terminal BamHI restriction sites. BamHI restriction sites. BamHI digestion released nucleotides 675-1051 (amino acid residues 215-351) and the resulting fragment containing nucleotides 1-674 (residues 1-214) was subcloned into pGEX-4T3. All constructs were transformed into E. coli BL21(D3). The cells were grown to an A600 of 0.6 in 500 ml of Luria-Bertani (LB) broth containing ampicillin and chloramphenicol selection, induced for 4 hours at 37°C with 1 mM isopropylthiogalactoside, and GST-NIPP1 purified by affinity chromatography on glutathione-Sepharose as described (Helps et al., 1995).

Preparation of DIG-PF1 and Far Western analyses

Human PP1γ (Barker et al., 1993; Alessi et al., 1993) was labelled with digoxigenin (DIG-PF1) and used in Far Western assays to study the binding of the enzyme to wild-type and mutant NIPP1 (Alessi et al., 1992; Kreivi et al., 1997).

Subcloning of NIPP1 into mammalian expression vectors

Expression of wild-type and mutant NIPP1 in mammalian cells was
achieved by subcloning the DNA into a variety of vectors. pSG8M expresses the 9E10 c-myc epitope at the N terminus of the protein (Bohmann, 1996). NIPP1 was subcloned from pKS+ into pSG8M using unique EcoRI and SalI restriction sites. NIPP1 constructs were also subcloned using the same unique sites into the pEGFP-C1 and pEGFP-N3 vectors (Clontech), which express at the N terminus or C terminus of NIPP1, respectively, a fusion of the enhanced version of the green fluorescent protein from the jellyfish Aequorea victoria. ARD1 was subcloned into pEGFP-C1 using unique Asp718 and BamHI restriction sites.

GST-NIPP1 constructs were subcloned from the pGEX-4T3 bacterial vector into the mammalian pCMV5 vector using PCR to transfer the GST coding sequence in frame with the NIPP1 cDNA. To facilitate this transfer, oligonucleotides were synthesised which added a unique HindIII site upstream of the GST coding region along with a Kozak sequence, and maintained the unique SalI site at the C terminus of NIPP1 while adding a stop codon immediately upstream of this site.

Expression of wild-type and mutant NIPP1 in mammalian cells

The constructed plasmids were transiently transfected into 10 cm dishes of human embryonic kidney 293 cells using a modified calcium phosphate-mediated transfection procedure with 1 µg/ml DNA/plate (Alessi et al., 1996; Chen and Okayama, 1988). The cells were incubated for 48 hours prior to microscopic analysis or cell lysis. For preparation of total cell lysates, cells were first washed twice with ice-cold PBS and then lysed in 0.5 ml of ice-cold 50 mM Tris-HCl, pH 7.5, 0.5 M NaCl, 1% (by vol) Nonidet P-40, 1% (by mass) sodium deoxycholate, 0.1% (by mass) SDS, 2 mM EDTA plus Complete protease inhibitor cocktail (Boehringer Mannheim, one tablet per 25 ml). The lysate was repeatedly passed through a 21G hypodermic needle to break up the DNA and then cleared by centrifuging at 4°C for 15 minutes at 13,000 g.

The EGFP fusions of NIPP1 were also expressed in HeLa (human cervical carcinoma) and MCF7 (human breast carcinoma) cells. These cells were transfected using the FuGENE transfection reagent (Boehringer Mannheim) and 2 µg DNA/10 cm dish. After 48 hours the live cells were either examined by microscopy or fixed for cell staining.

Immunoprecipitation of transiently expressed c-myc-tagged NIPP1 and endogenous NIPP1 from mammalian cells

A lysate from 293 cells expressing wild-type or mutant myc-NIPP1 (0.5 ml, 6 mg/ml protein) was incubated for 1 hour on a shaking platform with 20 µl Protein G-Sepharose coupled to 5 µg anti-c-myc monoclonal antibody. 50 µl Protein G-Sepharose coupled to 100 µg anti-ARD1 antibody was then added to the supernatant to immunoprecipitate endogenous NIPP1. The beads were washed with 20 mM Tris-HCl, pH 7.5, 0.5 M NaCl, electrophoresed on a 10% SDS-polyacrylamide gel and transferred to nitrocellulose membranes for immunoblotting.

Isolation of GST-NIPP1 and associated proteins from nuclear extracts

293 cells overexpressing GST-NIPP1 were scraped into ice-cold PBS containing Complete protease inhibitors, followed by homogenisation with 10 strokes of a Dounce homogeniser and centrifugation for 5 minutes at 1,000 g to pellet the nuclei. The nuclei were resuspended in 25 mM Tris-HCl, pH 7.5, 0.14 M NaCl, 5 mM KCl, 0.5% (by mass) Triton X-100 and sonicated to release the nuclear contents. After centrifugation for 10 minutes at 13,000 g, the supernatant was decanted and incubated for 1 hour at 4°C with glutathione Sepharose on an end-over-end shaker to deplete GST-NIPP1. The resin was washed several times with 20 mM Tris-HCl, pH 7.5, 0.15 M NaCl. In some experiments the bound proteins pulled down on 50 µl of resin from 400 µg total protein were solubilised in SDS and subjected to polyacrylamide gel electrophoresis followed by staining with Coomassie blue or immunoblotting. In other experiments the bound proteins were eluted from the beads by multiple washes with Tris-HCl, 50 mM glutathione, pH 8.0. The washes were combined and dialysed overnight at 4°C against Nuclear Extract Buffer (20 mM Hepes, pH 7.9, 10% (by vol) glycerol, 0.1 M KCl, 0.2 mM EDTA, 0.5 mM phenylmethylsulphonyl fluoride and 0.5 mM dithiothreitol).

Immunodepletion of endogenous NIPP1 from nuclear extracts

HeLa nuclear extracts were prepared as described (Mermoud et al., 1992) and NIPP1 depleted using affinity purified anti-NIPP1a conjugated to Protein G-Sepharose. Depleted extracts were subjected to immunoblotting to determine the efficiency of NIPP1 depletion.

In vitro splicing assays

Splicing assays were performed using uniformly labelled, capped pre-mRNAs incubated with nuclear extracts using the in vitro splicing conditions described by Lamond et al. (1987). Adenovirus major late precursor (adeno pre-mRNA) was transcribed from Sau3A-digested plasmid pBSAd1 (Konarska and Sharp, 1987). Splicing products were separated on 10% polyacrylamide/8 M urea and denaturing gels run in Tris-borate/EDTA electrophoresis buffer. In some experiments 10 µg of recombinant GST-tagged protein or GST alone was incubated with pre-mRNA in the absence of nuclear extract (and hence splicing) for 30 minutes at 30°C. The proteins were purified on glutathione-Sepharose, washed three times with PBS, and then treated as splicing reactions and run on acrylamide gels to visualise any associated pre-mRNA.

RESULTS

Localisation of endogenous NIPP1 in mammalian cells

The localisation pattern of endogenous NIPP1 was examined in live HeLa cells by directly conjugating two separate NIPP1

![Fig. 1. Confocal images of live HeLa cells microinjected with affinity-purified FITC-conjugated NIPP1 sheep polyclonal antibodies. Nuclear speckles stained by the antibodies are indicated by arrows, and nucleoli by arrowheads. (A) Anti-ARD1 and accompanying phase image. (B) Anti-NIPP1a and accompanying phase image. Bar, 5 µm.](image-url)
Antibodies, anti-ARD1 and anti-NIPP1a, to FITC and microinjecting them individually into the cell nuclei (Fig. 1). Both antibodies showed a widespread nucleoplasmic staining pattern, with additional accumulation in 'speckled' structures (Fig. 1, arrows). NIPP1 antibodies were primarily excluded from the nucleoli, although staining within the nucleoli was observed in approximately 20% of the cells.

A similar staining pattern was observed when HeLa cells (Fig. 2), as well as MCF7, KB, 293 and GM38 cells (data not shown), were methanol-fixed and stained with the same anti-ARD1 and anti-NIPP1a antibodies, or with anti-NIPP1b (Fig. 2). Fixation of HeLa cells permitted counter-staining with antibodies to various nuclear antigens which also show punctate or speckled staining patterns. Antibodies against p80 collin (Fig. 3B), the survival of motor neuron protein and the PML body-associated protein SP100 (data not shown), each of which produce punctate nuclear staining, did not colocalise with NIPP1. However, a clear colocalisation was observed between the staining pattern for the anti-Y12 monoclonal antibody, which recognises core Sm proteins of the small nuclear ribonucleoproteins (snRNPs), and the staining pattern for anti-NIPP1a (Fig. 3A). Because these proteins are integral components of the spliceosome complex in mammalian cells, colocalisation implies that NIPP1 may be associated with splicing factors in vivo. The Sm proteins are found in both interchromatin granule clusters (speckles) and in coiled bodies (see below).

Preabsorption of the NIPP1 antibodies with their respective antigens blocked all staining (data not shown), indicating that the pattern is specific for these epitopes. Varying levels of diffuse cytoplasmic staining were observed with all three anti-NIPP1 antibodies in HeLa (Fig. 2) and other cells. However, cytoplasmic staining was not observed with any of the antibodies used to localise tagged versions of NIPP1 (see below), and NIPP1 is absent from cytosolic extracts as judged by immunoblotting (Van Eynde et al., 1995), so this cytoplasmic staining is probably not NIPP1, and likely to be artefactual.

### Localisation of EGFP-NIPP1 in mammalian cells

In order to examine further the localisation of NIPP1, we expressed it as a fusion with the enhanced green fluorescent protein (EGFP). EGFP was fused to either the N terminus or C terminus of NIPP1, and expressed in a variety of cell types by transient transfection. Fig. 4 shows the expression pattern of EGFP-NIPP1 in live HeLa cells (A) and live MCF7 cells (C and E). Both N and C terminal fusions showed identical widespread nucleoplasmic distributions with additional accumulation in speckles (compare C and E). EGFP-NIPP1 fusions were not observed in the cytoplasm. Like the endogenous protein, EGFP-NIPP1 was occasionally observed in the nucleolus. This was more prevalent in HeLa cells than in other cell types, and when cells were dividing more actively (e.g. at lower confluencies). In addition, NIPP1 fusions were more likely to accumulate in the nucleoli of cells showing the highest overexpression of this protein.

HeLa cells expressing EGFP-NIPP1 were also methanol-fixed and stained with antibodies to a variety of nuclear antigens. All three anti-NIPP1 antibodies recognised the EGFP fusions (data not shown). Much like the endogenous protein, EGFP-NIPP1 did not colocalise with p80 collin, the survival of motor neuron protein or the SP100 protein found in PML bodies (data not shown). It did, however, colocalise with antibody staining for various pre-mRNA splicing factors, including Sm proteins (Fig. 5A), U1A (Fig. 5B), U2AF65 (Fig. 5C) and SR proteins (Fig. 5D). Colocalisation was observed for U1A, U2AF65 and SR proteins in both control cells and in cells treated with actinomycin D to inhibit transcription, which induces reorganisation of the splicing factors causing them to concentrate predominantly in large speckles. However, although every EGFP-NIPP1 speckle was labelled by the anti-Sm antibody, in control cells we observed some Sm-containing speckles that did not contain EGFP-NIPP1. The reasons for this are considered further in the Discussion.

### RNA binding and localisation of NIPP1 constructs lacking the ARD1 domain

The fact that NIPP1 is known to bind RNA (Jagiello et al., 1997), and that this RNA binding is most likely mediated by the ARD1 domain which includes the C-terminal 225-351 residues of the...
NIPP1 nuclear organisation

protein (Claverie-Martin et al., 1997) led us to question whether it is this domain that is responsible for targeting NIPP1 to sites in the nucleus containing RNA splicing factors. EGFP-ARD1 shows a diffuse nuclear staining pattern in cells, however, and no accumulation in nuclear speckles (Fig. 6A). In contrast, EGFP-NIPP1 lacking this ARD1 domain shows an identical localisation to the full-length protein, accumulating in nuclear speckles (Fig. 6C) and colocalising with Sm proteins both before (Fig. 6D) and after (Fig. 6E) treatment with actinomycin D. The loss of RNA binding is demonstrated by the fact that recombinant full-length GST-tagged NIPP1 binds pre-mRNA in vitro whereas the truncated GST-NIPP1 does not (Fig. 6B).

Identification of proteins associated with expressed NIPP1

We next examined whether the colocalisation of NIPP1 with
splicing factors at the nuclear speckles may be due to the formation of a complex between NIPP1 and one or more components of the spliceosome. To assay for association of NIPP1 with splicing factors, 293 cells were transiently transfected with either plasmid pCMV5 encoding a GST-NIPP1 fusion protein or plasmid SVG8M encoding a c-myc-NIPP1 fusion protein (see Materials and Methods) and lysates prepared 36 hours following transfection. For control experiments lysates were prepared from cells expressing GST or c-myc alone. Immunofluorescence analysis indicated that the transfection efficiency was 90-100%, and the fusion proteins showed a distribution pattern similar to that of the endogenous protein (data not shown). Analysis of the total cell lysate by immunoblotting with anti-NIPP1 antibodies prior to purification revealed that the GST and c-myc fusion proteins were expressed in 10-fold and 2-fold excess, respectively, over the endogenous protein (data not shown). These expression levels facilitated the purification of NIPP1 and the detection of proteins associated with it, but contrasted with a previous report of a failure to overexpress the NIPP1 protein in COS-1 cells, despite the overexpression of its mRNA (Wera et al., 1997). GST-NIPP1 was purified from nuclear extracts by affinity chromatography on glutathione-Sepharose and the isolated proteins separated by SDS-PAGE and electrophotated on to nitrocellulose membranes. Proteins copurifying with GST-NIPP1 were detected by immunoblotting. As expected, PP1 was specifically pulled down with GST-NIPP1 (Fig. 7A) and served as a positive control for this experiment, while protein phosphatase 2A (PP2A) did not copurify with GST-NIPP1 (data not shown). Interestingly, antibody staining showed that a fraction of the Sm proteins co-purified with NIPP1 (Fig. 7B). In contrast, U1A (Fig. 7C) and U2AF65 (Fig. 7D) did not specifically associate with GST-NIPP1 under these conditions, suggesting that NIPP1 may interact with a subset of splicing components. C-myc-NIPP1 was immunoprecipitated from lysates using the 9E10 monoclonal antibody and treated as described above. Sm proteins but not U1A coprecipitated with c-myc-NIPP1 (Fig. 7E and F), supporting the results observed with the GST fusion protein.

**Loss of in vitro splicing activity following immunodepletion of NIPP1**

NIPP1 could be almost completely depleted from a nuclear extract by incubation of the extract with anti-NIPP1a antibody bound to Protein G-Sepharose (Fig. 8A, lanes 2-3). This depletion was blocked by preincubation of the antibody with a 10-fold molar excess of peptide immunogen (Fig. 8A, lanes 4-5). In comparison to a control extract (Fig. 8B, lane 2), nuclear extracts depleted of NIPP1 showed greatly decreased in vitro pre-mRNA splicing activity (Fig. 8B, lanes 3-4). The extract remained active when the depletion of NIPP1 was specifically prevented by preincubation of the antibody with its peptide immunogen (Fig. 8B, lanes 5-6). Similar results were obtained using the anti-ARD1 antibody to immunodeplete NIPP1 (data not shown).

**Inhibition of in vitro splicing activity by a dominant negative NIPP1 mutant**

All the NIPP1 in nuclear extracts copurifies with PP1 during chromatography on Mono Q (Jagiello et al., 1995) and all the PP1 in these fractions can be immunoprecipitated with an anti-NIPP1 antibody (Fig. 9), indicating that nuclear PP1

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**Fig. 5.** Confocal images of methanol-fixed HeLa cells expressing EGFP-NIPP1 counter-stained with antibodies to a variety of splicing factors. Images on the right-hand side of each panel are from cells treated for 5 hours with actinomycin D to inhibit transcription (+ Act. D). Nucleoli are indicated by arrowheads, while yellow speckles, such as those marked by arrows, represent areas within the nucleus where the EGFP proteins and antibodies colocalise. (A) EGFP-NIPP1 counter-stained with anti-Y12 (recognises the Sm family of snRNP proteins). (B) EGFP-NIPP1 counter-stained with anti-856 (recognises U1A). (C) EGFP-NIPP1 counter-stained with anti-MC3 (recognises U2AF65). (D) EGFP-NIPP1 counter-stained with anti-3C5 (recognises the SR family of non-snRNP splicing proteins). Bar, 10 µm.
In this paper we identified the subnuclear distribution of NIPP1 by studying the location of the endogenous protein and transiently overexpressed fusion proteins. A consistent localisation pattern was observed using several different approaches. We found that NIPP1 has a widespread nucleoplasmic distribution, with accumulations in snRNP speckles where it colocalises with factors involved in pre-mRNA splicing, including Sm proteins, U1A, U2AF65 and SR proteins. EGFP-NIPP1 also colocalised with these proteins after inhibition of transcription with actinomycin D, which causes the redistribution of splicing factors to larger structures (Fig. 5). In addition, Sm proteins were shown to coimmunoprecipitate with NIPP1 in nuclear extracts (Fig. 7). In contrast, p99, the other major nuclear PP1-binding protein (see Introduction), shows a quite different subnuclear localisation (C. E. Lyon and A. I. Lamond, unpublished experiments).

Splicing snRNPs associate in the nucleus in several distinct structures, including interchromatin granules and coiled bodies (for a review, see Lamond and Earnshaw, 1998). However, NIPP1 only associates with factors found in the interchromatin granules. This again indicates that NIPP1 most likely interacts with a subset of the total splicing snRNPs. The different functions of splicing factors within the interchromatin granules and coiled bodies have not yet been clearly defined. Coiled bodies have been shown to contain splicing snRNPs, but not the essential splicing factor SC35, a member of the SR protein family (Carmo-Fonseca et al., 1991, 1992; Raska et al., 1991; Spector et al., 1991; Huang and Spector, 1992). This and other evidence indicates that coiled bodies are unlikely to be major sites of pre-mRNA splicing, but may instead be involved in some aspect of snRNP maturation, transport or recycling. The interchromatin granules, on the other hand, contain the snRNPs and non-snRNP splicing factors, including the SR proteins. It associates tightly in a complex with NIPP1. The results presented above therefore indicate that the NIPP1-PP1 complex is associated with pre-mRNA splicing factors and that NIPP1 may target PP1 to a component of the spliceosome. In this case, it should be possible to displace the endogenous NIPP1-PP1 complex from spliceosomes by addition of an excess of a mutant NIPP1 that is still capable of targeting to splicing factors, but unable to bind to PP1. We therefore mutated (to alanine residues) the valine and phenylalanine of the putative PP1-binding motif (Arg-Val-Thr-Phe) located between residues 200-203 of NIPP1. In contrast to wild-type NIPP1, the V201A/F203A double mutant was unable to interact with PP1 in Far Western blotting experiments (Fig. 10A), was not associated with PP1 in nuclear extracts (Fig. 10B) and did not suppress the PP1-activity towards glycogen phosphorylase (Fig. 10C). However, the V201A/F203A mutant showed an identical localisation within the nucleus as the wild-type protein (Fig. 4B,D,F), demonstrating that the domain that targets NIPP1 to splicing factors is distinct from the PP1-binding site. In this dominant negative approach, addition of the GST-tagged V201A/F203A NIPP1 mutant to nuclear extracts partially inhibited pre-mRNA splicing, whereas GST alone had no effect (Fig. 11).

DISCUSSION

In this paper we identified the subnuclear distribution of NIPP1 by studying the location of the endogenous protein and transiently overexpressed fusion proteins. A consistent localisation pattern was observed using several different approaches. We found that NIPP1 has a widespread nucleoplasmic distribution, with accumulations in snRNP speckles where it colocalises with factors involved in pre-mRNA splicing, including Sm proteins, U1A, U2AF65 and SR proteins. EGFP-NIPP1 also colocalised with these proteins after inhibition of transcription with actinomycin D, which causes the redistribution of splicing factors to larger structures (Fig. 5). In addition, Sm proteins were shown to coimmunoprecipitate with NIPP1 in nuclear extracts (Fig. 7). In contrast, p99, the other major nuclear PP1-binding protein (see Introduction), shows a quite different subnuclear localisation (C. E. Lyon and A. I. Lamond, unpublished experiments).

Splicing snRNPs associate in the nucleus in several distinct structures, including interchromatin granules and coiled bodies (for a review, see Lamond and Earnshaw, 1998). However, NIPP1 only associates with factors found in the interchromatin granules. This again indicates that NIPP1 most likely interacts with a subset of the total splicing snRNPs. The different functions of splicing factors within the interchromatin granules and coiled bodies have not yet been clearly defined. Coiled bodies have been shown to contain splicing snRNPs, but not the essential splicing factor SC35, a member of the SR protein family (Carmo-Fonseca et al., 1991, 1992; Raska et al., 1991; Spector et al., 1991; Huang and Spector, 1992). This and other evidence indicates that coiled bodies are unlikely to be major sites of pre-mRNA splicing, but may instead be involved in some aspect of snRNP maturation, transport or recycling. The interchromatin granules, on the other hand, contain the snRNPs and non-snRNP splicing factors, including the SR proteins. It
is unlikely that the speckled pattern represents major splicing sites, however, since there is little or no transcriptional activity in these structures and splicing is likely to occur co-transcriptionally (reviewed by Lamond and Earnshaw, 1998). In addition, splicing factors are still detected in these speckles even when transcription, and hence splicing, have been blocked by treatment with actinomycin D. The speckles may instead be implicated in storage of splicing factors and/or preassembly of the splicing machinery (Misteli et al., 1997). Although NIPP1 is associated in vivo with various splicing factors, it is not detected in purified spliceosomes (Neubauer et al., 1998). This indicates a weak and/or transient interaction with these structures, like the SR proteins that also bind weakly to the spliceosome and hence are dissociated during spliceosome purification.

The second catalytic step of pre-mRNA splicing can be selectively inhibited by the addition of low levels of okadac acid to nuclear extracts, a potent inhibitor of PP2A, while the first and second catalytic steps of pre-mRNA splicing are blocked by the addition of tautomycin to the extracts, a specific inhibitor of PP1, or by microcystin, a potent inhibitor of both PP1 and PP2A (Mermoud et al., 1992). These observations indicate that pre-mRNA splicing activity is regulated by at least two different phosphorylation events. The inactivating event prior to the first catalytic step appears to be reversed by a PP1-like phosphatase activity, and the inactivating step prior to the second catalytic step by a PP2A-like activity. These regulatory steps may be more complicated, however, involving regulation of the phosphatases themselves by phosphorylation (see below). Neither tautomycin nor microcystin prevent spliceosome assembly, indicating that PP1 acts after assembly but before catalysis (Mermoud et al., 1992). However, spliceosome assembly can be inhibited by adding a large excess of the PP1 catalytic subunit to nuclear extracts (Mermoud et al., 1994), indicating that one or more phosphorylation events are essential for spliceosome assembly.

In the present study, the depletion of NIPP1 from a HeLa nuclear extract led to loss of in vitro pre-mRNA splicing activity (Fig. 8) without affecting spliceosome assembly (data not shown), but activity was retained when the depletion of NIPP1 was blocked by preabsorption of the antibody with the antigen (Fig. 8). This is similar to the effects of tautomycin and microcystin and suggests that it may be the NIPP1-PP1...
complex that reverses the inactivating phosphorylation prior to the first catalytic step of splicing. This was supported by the finding that splicing was partially inhibited by adding an excess of a NIPP1 ‘dominant negative’ mutant that does not interact with PP1 (Fig. 11) and which presumably exerts its effects by displacing the endogenous NIPP1-PP1 complex. Although both catalytic steps of splicing were inhibited by the addition of the NIPP1 mutant, the second step appeared to be more sensitive to inhibition, as demonstrated by an initial accumulation of the first intermediate at low levels of the mutant NIPP1. The reason for this is unclear, but it is possible that the effects observed with okadaic acid reflected the control of PP1, and hence the second catalytic step of splicing, by a mechanism involving PP2A, rather than a direct involvement of PP2A in the regulation of the second catalytic step of splicing. This would be consistent with the observation that the PP1-NIPP1 complex is likely to be subject to regulation by phosphorylation mechanisms (see Introduction). A clear answer to this question requires a much more detailed analysis, however, and identification of the splicing factors that are substrates for the phosphatase(s).

The NIPP1 mutant that did not bind to PP1 showed the same nuclear localisation as the wild-type protein, indicating that it is NIPP1, and not the PP1 catalytic subunit, that targets the NIPP1-PP1 complex to splicing factors. However, it was recently reported that the three different isoforms of the PP1 catalytic subunit (α, β/δ and γ) localise to distinct nuclear compartments, including nuclear speckles that may represent either interchromatin granules and/or coiled bodies (Andreassan et al., 1998). It would therefore be interesting to know whether NIPP1 is associated with a particular PP1 isoform in vivo, although in vitro it is capable of interacting with at least two isoforms (α and γ; L. Trinkle-Mulcahy, unpublished experiments).

We have been unable, so far, to restore splicing activity to nuclear extracts by the addition of bacterially expressed NIPP1 with or without bacterially expressed PP1γ, or by the addition of the native NIPP1-PP1 complex (inactive towards glycogen phosphorylase) that had been partially purified by chromatography of HeLa nuclear extracts on Mono Q (L. Trinkle-Mulcahy, unpublished experiments). The reason for this is unclear, but one possible explanation is that immunodepletion of NIPP1 removes one or more essential splicing factors in addition to PP1 and the Sm proteins (Fig. 7). It is also possible that the phosphorylation state of NIPP1 may be critical in order to restore splicing or that the bacterially expressed NIPP1 is not fully active or correctly folded.

Most of the PP1-targeting subunits described to date contain an Arg/Lys-Val/Ile-Xaa-Phe/Trp motif and small peptides containing these motifs have been shown to bind to PP1 (Johnson et al., 1996; Egloff et al., 1997; Zhao and Lee, 1997; Kreivi et al., 1997). Moreover, mutation of the Val/Ile and Phe/Trp residues in these peptides has been shown to prevent them from interacting with PP1. However, the importance of this motif for PP1-binding has not been established previously by mutagenesis of a full length targeting subunit. In this paper we have shown that the
V201A/F203A double mutant of NIPP1 is unable to interact with PP1, yet shows an identical subnuclear distribution to the wild-type protein. This demonstrates that the Arg-Val-Thr-Phe sequence located between residues 200 and 203 is indeed a PP1-binding site of NIPP1, and that the subnuclear localisation of NIPP1 is not determined by the PP1 catalytic subunit, but by a region of NIPP1 distinct from the PP1-binding site. Similar amino acid substitutions in other PP1-targeting subunits that prevent interaction with PP1 without affecting subcellular localisation may provide useful dominant negative mutants for identifying the functions of the different forms of PP1 in vivo. Such mutants may also facilitate the identification of proteins other than PP1 that interact with PP1-targeting subunits. We have also shown that deletion of the ARD1 domain of NIPP1, resulting in a loss of pre-mRNA binding, has no effect on the subcellular localisation of NIPP1 (Fig. 6). Taken together, these data suggest that targeting of NIPP1 to areas of the nucleus containing high concentrations of splicing factors is independent of both PP1 and RNA binding.

In summary, our data suggest that one or more protein factors, whose activity is required for the first catalytic step of splicing, is/are inactivated by phosphorylation and reactivated by dephosphorylation catalysed by the NIPP1-PP1 complex. NIPP1 may therefore play an important role in targeting PP1 to this protein factor(s). However, NIPP1 may not be the only protein that targets PP1 to spliceosomes, because Hirano et al. (1996) have shown that protein splicing factor (PSF) interacts with PP1 in a ‘two hybrid’ assay. This protein possesses an Arg-Val-Xaa-Phe motif close to its N terminus that is presumably critical for interaction with PP1. Future experiments will continue to address the role of NIPP1 in the splicing mechanism, including identification of the domains critical for localisation of the protein and those involved in the interaction with specific splicing factors.
NIPP1 nuclear organisation

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