Reversible protein phosphorylation plays a crucial role in the circuitry controlling diverse cellular processes, and the activities of phosphorylating and dephosphorylating enzymes must be carefully balanced in normal cells. It is well documented that many of these enzymes are constitutively expressed, but their activities are tightly regulated by a variety of post translational mechanisms. In the case of the serine/threonine-specific protein phosphatase 2A (PP2A), a catalytic subunit is bound by two regulatory subunits designated A and B. Previously, we established a functional complementation assay for PP2A-C in the yeast S. cerevisiae and used this system to isolate two dominant-defective mutants in the human PP2A-Cα gene. We generated epitope-tagged forms of the wild-type and mutant alleles and showed that the epitope-tagged alleles retain biological function in our yeast system. The mutant alleles show reduced binding of the A regulatory subunit in yeast and mammalian cells. Stable fibroblastic cell lines expressing mutant and wild-type proteins have been isolated These studies will thus increase our understanding of PP2A function in the regulation of proliferation and malignant transformation, and will yield important information about structure-function relationships in the PP2A catalytic and regulatory subunit proteins.
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TITLE: Function of Protein Phosphatase 2A in Control of Proliferation: Isolation and Analysis of Dominant-Defective Mutants

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June 12, 2000
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INTRODUCTION

Protein phosphatase 2A (PP2A) comprises catalytic (C) and regulatory (A and B) subunits, and a heterotrimeric (ABC) holoenzyme is thought to predominate in vivo, although a heterodimeric (AC) form also has been purified (reviewed in Walter and Mumba, 1993). Although the total number of PP2A substrates is not known, it is likely that regulation of PP2A activity is necessary for the correct functioning of signal transduction cascades in which PP2A participates. Essential PP2A subunit functions are strongly conserved throughout evolution, as evidenced by the ability of an Arabidopsis PP2A-A subunit gene (RCN1) to complement the temperature-sensitive phenotype of a null mutation in the yeast PP2A-A subunit gene (tpd3; Garbers et al., 1996). PP2A has not been identified as an oncogene per se, but its interactions with proteins responsible for tumorigenesis are of demonstrated functional significance. Evidence for the role of PP2A in mammalian cell proliferation has originated in studies showing that PP2A is a target for the small-T antigen of SV40 and the small- and medium-T antigens of polyoma virus. These tumor antigens bind the AC heterodimeric PP2A complex (Pallas et al., 1990; Walter et al., 1990) and exclude the B subunit. Interaction with SV40 small t antigen reduces PP2A activity toward the mitogen-activated protein kinases (MAPKs) ERK1 and MEK1, causing deregulation of the MAPK cascade and induction of cell growth (Sontag et al., 1993). Middle T antigen mutants that fail to bind PP2A also are defective in transformation (Campbell et al., 1995). Furthermore, the tumor-promoting agent okadaic acid (OKA; Suganuma et al., 1988) is a potent and specific inhibitor of PP2A and PP1, with PP2A showing approximately 100-fold higher sensitivity (Cohen et al., 1989). The targeting of PP2A by viral T antigens and the tumor-promoting effect of OKA at low concentrations both support the hypothesis that PP2A activity normally suppresses proliferation, and that antagonism of PP2A may be important in tumorigenesis.

Dominant gain-of-function alleles have revealed the identities and functions of many proteins involved in growth control. We proposed to isolate dominant-defective mutants of human PP2A as a tool for investigating potential growth control functions of PP2A in normal and breast cancer cells. Possible causes of dominance for such mutants include competition with the wild-type protein for substrates or for positive regulatory subunits. The PP2A catalytic subunit (PP2A-C) provides a good target for mutagenesis aimed at generation of dominant alleles, because putative catalytic residues have been identified and interactions with positive regulatory subunits are known to be important for normal activity.

Previously, we established a functional complementation assay for PP2A-C in the yeast S. cerevisiae and used this system to isolate two dominant-defective mutants in the human PP2A-Cα gene. We had isolated epitope-tagged forms of the wild-type and mutant alleles and tested those alleles for biological function in our yeast system. Our recent work has been focused on isolation and characterization of stably transformed cell lines expressing epitope-tagged mutant and wild-type PP2A-C alleles, and analysis of PP2A subunit interactions in yeast and mammalian cells via immunoprecipitation.

BODY

Analysis of the dominant defective phenotypes of PP2A-Cα mutants H118N and R89A

We have shown that S. cerevisiae can be used as a rapid in vivo assay system for human PP2A-C activity. Mutation of a conserved histidine residue in the Cα sequence (the Cα-H118N mutant) confers a strong dominant-defective phenotype; mutation of a conserved
arginine residue (the Cα-R89A mutant) results in a weaker dominant-defective phenotype. A detailed description of this work was published last year in *Gene*; a reprint is appended.

We have considered several alternative hypotheses that might explain the dominance of the H118N and R89A mutants in yeast cells. First the mutant enzyme might bind substrate efficiently and prevent the Pph21-ts gene product from interacting with one or more essential substrate(s). Second, the mutant enzyme might interact normally with PP2A regulatory subunits (A and/or B) that are required for normal activity of the Pph21 gene product. Third, the mutant enzyme might bind another protein (neither substrate nor classical regulatory subunit) not bound by the wild-type enzyme. We have already demonstrated that expression of the heterologous PP2A-C does not down-regulate the endogenous PP2A-C expression.

We have used immunoprecipitation to assay binding of the A regulatory subunit to mutant and wild-type Cα subunits in yeast and mammalian cells. Anti-FLAG antibody efficiently precipitates the epitope-tagged proteins from cells expressing FLAG-Cα+, FLAG-Cα-H118N, FLAG-Cα R89A and FLAG-Cα-R89A/H118N proteins. However, the endogenous yeast A regulatory subunit is co-immunoprecipitated efficiently only in extracts from cells expressing the wild-type FLAG-Cα+ protein. The H118N, R89A and double mutant R89A/H118N mutations markedly reduce the amount of co-immunoprecipitating A subunit, suggesting that these lesions weaken the association of the Cα subunit with the A regulatory subunit. To assay for a similar effect in mammalian cells, COS cells transfected with FLAG-Cα+ and FLAG-Cα-H118N expression constructs were also tested for co-immunoprecipitation of endogenous A subunit using the anti-FLAG antibody. While the A subunit was easily detected in immunoprecipitates from cells expressing the wild-type Cα+ subunit, A subunit co-immunoprecipitation was markedly reduced in extracts from cells expressing Cα-H118N. Because A subunit binding is required for formation of heterotrimeric PP2A complexes (i.e. subsequent B subunit binding; Ruediger et al., 1992), these results suggest that the protein products of the mutant alleles do not compete with endogenous C subunits for A and B subunit binding. Thus the dominant-defective phenotype is not due to competition for regulatory subunit binding. We are currently generating the R89A expression constructs required to test for co-immunoprecipitation of mammalian A subunit with the R89A mutant in COS cells. We have attempted to assay for co-immunoprecipitation of the yeast Tap42 protein (homolog of the mammalian α subunit; Di Como et al. 1996), but due to high cross-reactivity of the anti-Tap42 antibody this experiment was inconclusive. Thus our data suggest that the dominant-defective phenotype may be due to competition for substrates or for non-substrate interacting proteins.

Construction of stable cell lines expressing wild type and dominant-defective PP2A -C alleles

We have also isolated stable fibroblastic cell lines expressing FLAG-tagged mutant and wild-type Cα subunits. Interestingly, we consistently see higher expression of the epitope tagged protein in cell lines expressing the H118N mutant construct. Cell lines expressing the FLAG-Cα+ construct show lower transgene expression levels (an estimated three-fold difference on average), and several FLAG-Cα+ cell lines grow slowly. In contrast, the cell lines expressing the H118N mutant at high levels show no obvious growth phenotypes. We are currently quantitating these effects in growth curve assays.

KEY RESEARCH ACCOMPLISHMENTS

- Construction of dominant-defective alleles of human PP2A-Cα
• Development of functional epitope-tagged PP2A-Cα alleles

• Analysis of the dominant-defective phenotype in yeast cells via co-immunoprecipitation and immunoblotting

• Analysis of A regulatory subunit interaction with mutant and wild-type PP2A-Cα alleles in COS cells

• Isolation of stable cell lines expressing epitope-tagged mutant and wild-type PP2A-Cα alleles

REPORTABLE OUTCOMES


• “Using dominant defective mutants to study protein phosphatase 2A function in vivo” Donna Lizotte, Albert Siryaporn, David McManus, Kimberly Hemond and Alison DeLong; poster presentation at the Brown University MCB Graduate Program Annual Retreat, Sept. 1, 1999.

• “Using dominant defective mutants to study protein phosphatase 2A function in vivo” Donna Lizotte, Albert Siryaporn, David McManus, Kimberly Hemond and Alison DeLong; poster presentation at the Era of Hope BCRP meeting, Atlanta GA, June 8 - 11, 2000.

• Development of stable cell lines expressing native and epitope-tagged wild-type and dominant-defective PP2A-C alleles.

CONCLUSIONS

We have shown that S. cerevisiae can be used as a rapid in vivo assay system for human PP2A-C activity. Mutation of conserved histidine or arginine residues in the Cα sequence confers a strong dominant-defective phenotype. The dominant-defective phenotype does not reflect competition for A or B regulatory subunit binding, and may be due to competition for substrates or other interacting proteins. Our data indicate that even moderate over-expression of wild-type PP2A-C subunit in mammalian cells may lead to reduced growth rates, however, further experiments are required to allow accurate quantitation of this effect.
REFERENCES


Functional expression of human and Arabidopsis protein phosphatase 2A in Saccharomyces cerevisiae and isolation of dominant-defective mutants

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Functional expression of human and *Arabidopsis* protein phosphatase 2A in *Saccharomyces cerevisiae* and isolation of dominant-defective mutants


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**Abstract**

Protein phosphatase 2A (PP2A), a heterotrimeric serine/threonine-specific protein phosphatase, comprises a catalytic subunit and two distinct regulatory subunits, A and B. The primary sequence of the catalytic (C) subunit is highly conserved in evolution, and its function has been shown to be essential in yeast, *Drosophila* and mice. In many eukaryotes, the C subunit is encoded by at least two nearly identical genes, impeding conventional loss-of-function genetic analysis. We report here the development of a functional complementation assay in *S. cerevisiae* that has allowed us to isolate dominant-defective alleles of human and *Arabidopsis* C subunit genes. Wild-type human and *Arabidopsis* C subunit genes can complement the lethal phenotype of *S. cerevisiae* PP2A-C mutations. Site-directed mutagenesis was used to create two distinct, catalytically impaired C subunit mutants of the human and *Arabidopsis* genes. In both cases, expression of the mutant subunit in yeast prevented growth, even in the presence of functional C subunit proteins. This dominant growth defect is consistent with a dominant-interfering mode of action. Thus, we have shown that *S. cerevisiae* provides a rapid system for the functional analysis of heterologous PP2A genes, and that two mutations that abrogate phosphatase activity exhibit dominant-defective phenotypes in *S. cerevisiae*. © 1999 Published by Elsevier Science B.V. All rights reserved.

**Keywords:** Catalytic subunit; Dominant-negative; Functional complementation; Mutational analysis

1. Introduction

Protein phosphatase 2A (PP2A) is a member of the PPP family of protein serine/threonine phosphatases.

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(Barford, 1996). Purification of PP2A enzymatic activity from a wide variety of species typically results in the isolation of the PP2A catalytic (C) subunit in a complex with one or more regulatory subunits. A heterotrimeric holoenzyme comprising regulatory A and B subunits bound to the catalytic subunit is thought to predominate in vivo. Interactions between the catalytic and regulatory subunits have been shown to modulate PP2A activity both in vivo and in vitro [reviewed in Mumby and Walter (1993)]. Recent evidence shows that other proteins can bind to the holoenzyme or, in some cases, replace one or both regulatory subunits, resulting in altered PP2A activity [see, for example, Murata et al. (1997)]. The catalytic subunit exhibits a strong sequence similarity to protein phosphatase 1 (PP1) in regions that constitute the putative active site (Goldberg et al., 1995). Although the reaction mechanisms of PP1 and PP2A have not yet been defined, amino acid sequence conservation, crystallographic analysis of the PP1 active site (Goldberg et al., 1995) and biochemical analysis of the bacteriophage λ phosphatase (Zhuo et al., 1994) have

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identified residues required for metal ion coordination, substrate binding, and catalysis (see Fig. 1).

The amino acid sequences of C and A subunits are highly conserved in eukaryotes as distantly related as *Arabidopsis thaliana*, humans, and yeast. Conservation of the A subunit function has been demonstrated previously by complementing a *S. cerevisiae* A subunit mutant with an *Arabidopsis* A subunit gene (Garbers et al., 1996). In the animals studied to date, both the C and A subunits are expressed ubiquitously and appear to be encoded by small and fairly homogenous gene families. In plants, however, A and C subunit gene families are larger; the *Arabidopsis* genome encodes at least five C subunits and three A subunits [reviewed in Smith and Walker (1996) and Stamey and Rundle (1996)]. In both plants and animals, different B subunit isoforms are encoded by two or more unrelated gene families, some of which are expressed in a tissue-specific manner. Thus, the more variable B subunit may dictate substrate specificity (Mayer-Jaekel and Hemmings, 1994), a hypothesis supported by data showing that the tumor antigens of DNA tumor viruses replace B subunits in PP2A complexes and alter the enzyme's catalytic properties (Yang et al., 1991; Cayla et al., 1993; Sontag et al., 1993).

PP2A activity has been shown to play a negative role in growth control in systems such as *Xenopus*, *S. pombe*, and *Drosophila* (Lee et al., 1991; Kinoshita et al., 1993; Mayer-Jaekel et al., 1994). In *S. cerevisiae*, however, PP2A is required for entry into mitosis (Lin and Arndt, 1995). Two PP2A-C genes, designated *PPH21* and *PPH22*, have been identified in *S. cerevisiae*. Inactivation of both genes is detrimental but not lethal unless a gene encoding a PP2A-like phosphatase, *PPH3*, is also mutated (Sneddon et al., 1990; Ronne et al., 1991; Lin and Arndt, 1995). Cells carrying a temperature-sensitive (ts) *pph21-102* allele in a *pph21* *pph22* *pph3* null background retain viability but exhibit G2 cell-cycle arrest, reduced B-type cyclin/cyclin-dependent (Cib2-Cdc28) kinase activity and abnormal bud morphologies at the non-permissive temperature (Lin and Arndt, 1995). The PP2A-A subunit is encoded by a single gene, *TPD3*, and *tpd3* null mutants exhibit a Ts" phenotype (van Zyl et al., 1992). Two B subunits have been identified; mutants in the 55-kDa B subunit gene *CDC55* are cold-sensitive (cs), whereas mutants in the 56-kDa B' subunit gene *RT51* are ts, cs and ethanol-hypersensitive (Healy et al., 1991; Shu et al., 1997). It is unclear why the C subunit is essential, whereas the A and B regulatory subunits are only conditionally required.

The fact that each PP2A subunit is encoded by a gene family in many eukaryotes presents a significant impediment to conventional genetic analysis, and suggested to us that the isolation of dominant PP2A mutants might provide an alternative to the isolation of mutations in individual gene family members followed by the generation of multiply mutant stocks. Taking advantage of the high sequence conservation exhibited by PP2A genes and the availability of PP2A mutant strains of yeast, we have developed a functional assay for the isolation and characterization of dominant-defective alleles of PP2A catalytic subunit genes. We have demonstrated the utility of this system by the construction of dominant-defective PP2A-C mutants from *Arabidopsis thaliana* and from humans.

2. Materials and methods

2.1. Yeast strains and plasmid constructs

The yeast strains used in this work are listed in Table 1. The yeast growth media and genetic techniques were as described by Ausubel et al. (1992). After lithium acetate transformation, yeast transformants were selected at 25°C on synthetic complete glucose (SCD) medium lacking tryptophan and uracil. Segregants that had lost either the *pph21-102/YCp50* construct or the heterologous C subunit construct were isolated by growing cells non-selectively (on YPD or YPGalactose medium at 25°C), followed by replica-patching single colonies onto selective (SCD or SCGalactose) medium with or without uracil or tryptophan. Segregants were colony-purified and their phenotypes verified by restreaking on the appropriate media.

All GAL constructs used in this work are derivatives of either YCP22GAL or YEP112GAL (shown in Table 1 as pGAL/TRP/CEN and pGAL/TRP/2μ, respectively),
isogenic yeast expression vectors carrying the GAL1/GAL10 bidirectional promoter, a TRP1 selectable marker, and a CEN or 2μ circle origin of replication, respectively (Pitlik et al., 1995). Plasmid pADL302 (GAL10:ATHC1/TRP2/μ) was constructed by subcloning the AthC1 coding sequence from ppPA2-1 (a kind gift of Sabine Rundle) into the EcoRI site of YEp112GAL. Plasmids pDMC2 and pDMC16 (GAL1:HScx/TRP/CEN and GAL1:HScx/TRP2/μ) were constructed as follows: the HsC× coding sequence was amplified from plasmid pUC.HPP2AcZRM1 (a kind gift of N. Andjelkovic and B. Hemmings) and given BamHI cloning ends via polymerase chain reaction (PCR), followed by cleavage with BamHI and ligation into BamHI-cleaved YCp22GAL and YEp112GAL, respectively. The primers used were 5′ CGGGATCCTTACAGGGAAGTATGTGTTTCA 3′ and 5′ CGGGATCATGGACGAGAAGGTGTACACCAAGG 3′. Similarly, plasmid pDMC4 (GAL1:HScBT/\text{TRP/CEN}) was constructed by PCR amplification of the HscB coding sequence from plasmid pTZ18U.HFP6A2Cβ (a kind gift of N. Andjelkovic and B. Hemmings), followed by BamHI subcloning into YCp22GAL, using PCR primers 5′ CGGGATCCTTATAGGGAAGTAGTCTGTTCA 3′ and 5′ CGGGATCATGGACGAGAACAGGCGGTTCACCAAGG 3′.

To make the ADH:ATHC1 constructs, a 2-kb BamHI fragment carrying the ADH promoter and terminator was subcloned from pAAH5 (Ammerer, 1983) into pTZ19 (US Biochemical). The AthC1 coding sequence was ligated into the unique HindIII site between the ADH promoter and terminator. To make plasmids pADL316 (ADH:ATHC1/TRP/CEN) and pADL317 (ADH:ATHC1 antisense/TRP/CEN), sense and antisense ADH:ATHC1 fusions were subcloned as SpfI fragments into YCplac22 (Gietz and Sugino, 1988). To chromosomally integrate the ADH:ATHC1 construct, the pADL316 Spfl fragment was cloned into the integrating plasmid YIpplac128 (Gietz and Sugino, 1988), followed by addition of a G418 resistance cassette (Smal−SacI fragment) from pFA6-KanMX4 (Wach et al., 1994). The resulting plasmid (pADL340) was linearized with AflIII and transformed into strain CY3007, with selection for G418 resistance.

2.2. Site-directed mutagenesis

Mutants were generated using an oligonucleotide-mediated mutagenesis protocol (Deng and Nickoloff, 1992). The following mutagenic oligonucleotide primers were used. oAthCI-H115N: 5′ CGTACGCGTCTCATTATCCCTCGAGG 3′; oAthCI-R86A: 5′ CAGAATAGTATGCGCATTCGTAATCTCCATGAAAG 3′; oHsCβ-H118N: 5′ TTCTTCGAGGGAATATAATGAGACGACAGCAG 3′; oHsCβ-R89A: 5′ GGGAGATTAGTGTGACAGGATTTATATTAC 3′.

2.3. Immunoblot analysis

Standard SDS-PAGE and immunoblotting protocols were followed (Ausubel et al., 1992). The polyclonal anti-PP2A-C antibody used was raised against a conserved carboxy-terminal peptide (KVRRTPDYFL), and was a kind gift of T. Stukenberg and M. Kirchener. Peroxidase-conjugated goat anti-rabbit secondary antibody (Jackson ImmunoResearch Laboratories) was detected using a standard chemiluminescence protocol.
3. Results

3.1. Arabidopsis and human PP2A-C clones complement a yeast PP2A mutant

We established a functional complementation assay for PP2A activity in S. cerevisiae. Strain CY3007 carries null alleles in both PP2A-C genes and in the PPH3 gene, which encodes a related phosphatase; lethality of this triple mutation is rescued by a low-copy-number plasmid bearing a ts phy21 allele (phy21-102; Lin and Arndt, 1995). CY3007 cells grow at 25 or 30°C, but not at 35°C. We cloned Arabidopsis and human cDNAs encoding PP2A-C subunits into yeast expression vectors and tested their ability to complement the temperature sensitivity of strain CY3007. When expressed from the constitutive alcohol dehydrogenase (ADH) promoter and carried on a low-copy-number plasmid, the Arabidopsis AthCl cDNA (see Fig. 1; Ariño et al., 1993) complemented the Ts' phenotype of CY3007, indicating that the Arabidopsis PP2A-C subunit is functional in yeast (Fig. 2). When cloned in the antisense orientation, the AthCl cDNA failed to complement in CY3007 (Fig. 2).

To exclude the possibility that the yeast ts allele contributed to complementation, we grew cells carrying the ADH-AthCl plasmid non-selectively and screened for tryptophan or uracil auxotrophy to identify segregants that had lost either plasmid. Loss of the ADH-AthCl plasmid conferred a Trp' phenotype and restored the parental Ts' phenotype. Loss of the phy21-102 plasmid conferred a Ura' phenotype, but the resulting cells still grew at 35°C, as well as 25 and 30°C (Fig. 2). Thus, the ADH-AthCl plasmid is necessary and sufficient for complementing the Ts' phenotype, and is capable of supporting normal growth in the absence of any yeast PP2A-C protein.

Expression of either the AthCl or the human HsCα cDNA (see Fig. 1; Stone et al., 1988) under the control of a galactose-inducible GAL promoter also complemented the Ts' phenotype of CY3007. Cells expressing either the Arabidopsis or human cDNA grew at 25°C on both glucose- and galactose-containing media and at 35°C on galactose, but did not grow on glucose at 35°C (Fig. 3A and B). The sufficiency of the GAL-AthCl construct was tested by segregating either the GAL-AthCl or YCp50 phy21-102 plasmid. Again, loss of the plasmid carrying the Arabidopsis AthCl C1 gene restored the parental Ts' phenotype. Loss of the phy21-102 plasmid conferred a galactose-dependent phenotype; segregants were viable at 25, 30 and 35°C only on galactose-containing media (data not shown). Surprisingly, the human HsCβ gene (see Fig. 1; Hemmings et al., 1988) did not provide complementing PP2A activity in yeast (Fig. 3B). Failure to complement was not due to poor expression of the HsCβ protein since similar amounts of the HsCα and β subunit proteins were detected in galactose-grown cells (Fig. 4A). Thus, expression of either the AthCl or HsCα (but not HsCβ) catalytic subunit gene provides the PP2A function in yeast cells.

We predict that cells expressing a catalytically active C subunit that was unable to interact with the endogenous yeast regulatory subunits (e.g. TPD3 or RTS1) would exhibit phenotypes characteristic of loss-of-function mutations in those genes. Both tpd3 and rts1 mutations prevent growth at 37°C (van Zyl et al., 1992; Shu et al., 1997); therefore, we tested the ability of cells expressing human and Arabidopsis PP2A-C subunits to grow at 37°C. Cells carrying a GAL:HsCα or GAL:AthCl construct were viable at 37°C, suggesting that these heterologous C subunits functionally interact with the yeast A and B' regulatory subunits (Fig. 3C). Cells carrying the GAL:AthCl construct formed small colonies at this temperature. This small colony phenotype may indicate that the AthCl protein has lower affinity for Tpd3p than does HsCα, however, it is also possible that the catalytic activity of AthCl is reduced at 37°C, a temperature above the normal growth range of Arabidopsis.

High-level over-expression of PP2A-C mRNA has been shown to be toxic in S. cerevisiae, but cells expressing the PPH22 gene under control of the GALI promoter grow at a normal rate (Ronne et al., 1991). We have not observed any strong negative growth effects of GAL-driven expression of wild-type human or Arabidopsis PP2A-C genes. In fact, under permissive conditions, cells carrying a high-copy-number GAL:C construct grow slightly faster in liquid media (c. 2.5 h doubling time) than do cells carrying the vector alone (c. 3 h doubling time).
3.2. Isolation of dominant defective alleles of PP2A-C

We hypothesized that mutation of an amino acid residue involved in catalysis would produce a dominant-defective PP2A-C allele if substrate binding and/or subunit interactions were unaffected by the lesion. We chose a putative active site histidine (H115 in the Arabidopsis gene and H118 in the human sequence; see Fig. 1) and mutated this residue to asparagine using site-directed mutagenesis (see Section 2.2). Mutations at the analogous position abrogate catalytic activity but not substrate binding in calcineurin (PP2B) and λ phosphatase (Zhuo et al., 1994; Mertz et al., 1997), two enzymes that exhibit a close similarity to PP2A in putative active site sequences. To test the activity of the mutant proteins, we expressed the mutant alleles under control of GAL promoters in strain CY3007 and assayed their effects on growth (Fig. 5). Cells carrying the GAL:AtchC1-H115N construct were unable to grow on either galactose or glucose at 35°C (Fig. 5A), indicating that the mutant enzyme is defective and provides no catalytic activity at 35°C. More importantly, cells carrying this construct were unable to grow on galactose at 25°C, the permissive temperature for the pph21-102 allele (Fig. 5A) or at 30°C (data not shown). Thus, the defective phenotype of the H115N allele is dominant over the ts yeast PP2A allele and prevents growth at all temperatures tested. We have obtained the same results with the H118N mutant of the human Cα subunit (Fig. 6B and data not shown).

To test the dominance of the H115N allele with
A  

\[ \text{Glucose (pGAL off)} \]

\[ \text{Galactose (pGAL on)} \]

25°  

35°  

CY3007 transformants

B  

\[ \text{Glucose (pGAL off)} \]

\[ \text{Galactose (pGAL on)} \]

30°  

35°  

DLY6 transformants (high copy)

C  

\[ \text{Glucose (pGAL off)} \]

\[ \text{Galactose (pGAL on)} \]

30°  

35°  

DLY6 transformants (low copy)

Fig. 5. Growth of yeast cells carrying AthCl-H115N constructs, CY3007 (A) and DLY6 (B and C) transformants carrying an empty vector (–), a GAL10: AthCl construct (+) or a GAL10: AthCl-H115N construct (H115N) were streaked on duplicate plates containing selective glucose and galactose medium and incubated at the temperature indicated. Plasmid carried high-copy number (2μ circle; A and B) or low-copy-number (centromeric; C) origins of replication. Strains used: DLY11, DLY12, DLY13 (A); DLY21, DLY22, DLY23 (B); DLY24, DLY25, DLY26 (C). Similar results were obtained in streak-out tests of growth of these strains.

Fig. 6. Growth of yeast cells carrying dominant PP2A-C mutants, CY3007 transformants carrying wild-type (+), and mutant (H115N and R86A) GAL10: AthCl constructs (A: strains DLY12, DLY13 and DLY14) or wild-type and mutant (H118N) GAL1: HsCα constructs or wild-type GAL1: HsCβ (B: strains DLY17, DLY19 and DLY18) were streaked on duplicate plates containing selective galactose medium and incubated at the temperature indicated. Similar results were obtained in streak-out tests of growth of these strains.

level of the mutant protein influenced the strength of the dominant-defective phenotype, as a low-copy-number AthCl-H115N plasmid caused a weaker, but still clearly detectable, inhibition of growth (Fig. 5C). This copy number effect is consistent with the dominant-interfering activity of the mutant proteins.

To show that both the mutant and endogenous PP2A-C subunits are expressed in galactose-grown cells, we used immunoblotting to assay PP2A-C subunit levels after galactose induction of cells carrying mutant and wild-type GAL10: AthCl constructs (Fig. 4B). We have obtained the same results with wild-type and H118N mutant human HsCα (data not shown). Wild-type and mutant PP2A-C proteins accumulate to comparable levels after galactose induction, and appear equally stable over a 9-h time course (data not shown).

To determine whether other active site mutations also would confer a dominant-defective phenotype, we introduced a lesion at a position thought to be essential for binding of the phosphorylated substrate. Conversion of an active site arginine to alanine in the λ phosphatase causes a 20-fold decrease in binding of a synthetic substrate and a 500-fold catalytic defect (Zhao et al., 1994). We introduced the same mutation (R86A in the Arabidopsis protein and R89A in the human protein; see Fig. 1) into our wild-type GAL: PP2A-C constructs
and tested the activity of the mutant constructs as described above. Cells carrying AthC1-R86A failed to grow on either glucose or galactose at 35°C (Fig. 6 and data not shown), showing that, like the H115N allele, this mutant provides no complementing phosphatase activity at 35°C. Expression of the R86A allele also blocked growth of CY3007 cells at 25°C (Fig. 6A). The R86A mutant protein accumulates to levels comparable to those of the wild-type and H118N proteins after galactose induction (data not shown). These data show that the R86A mutation is also dominant-defective, and we have obtained similar results with the human HsCα-R89A mutant (data not shown). In contrast, the HsCβ provides no complementing phosphatase activity at 35°C and does not exhibit a dominant-defective phenotype (Fig. 6B).

4. Discussion

We have used yeast to screen for dominant-defective mutants of the PP2A catalytic subunit. We have shown that both Arabidopsis and human PP2A genes complement a ts mutation in a yeast PP2A-C gene. Constitutive or inducible expression of a heterologous PP2A-C subunit gene is sufficient to allow growth of yeast cells in the absence of any yeast PP2A-C protein. Site-directed mutagenesis of the Arabidopsis and human PP2A-C genes yielded catalytically inactive alleles that exhibited dominant phenotypes. Expression of the dominant-defective phenotype was influenced by copy number, consistent with a dominant-interfering effect of the mutant gene products.

The robust growth of yeast cells in which PP2A function is supplied by a heterologous C subunit protein indicates that sequences required for specific and functional interaction with essential substrates are conserved between the yeast, Arabidopsis and human PP2A-C subunits. The predicted amino acid sequences of the C subunit gene products show a very high degree of similarity, 80–90% over the length of the Arabidopsis and human sequences. Both yeast proteins carry aminoterminal extensions that are approximately 70 amino acids in length and serve unknown functions. Our work shows that the extensions are not required for essential PP2A functions in S. cerevisiae since the Arabidopsis and human clones are expressed from their native start codons. Complementation also reveals that critical recognition features of the substrate proteins are conserved. The full range of PP2A substrates required for growth of yeast cells is not known, but the available evidence suggests that essential substrates include proteins involved in bud morphogenesis, cytoskeletal organization and entry into mitosis (Ronne et al., 1991; Lin and Arndt, 1995; Evans and Stark, 1997). Finally, we tested the competence of the human and Arabidopsis C subunits to interact with the endogenous yeast regulatory subunits by assaying for growth at the restrictive temperature for the tpdβ (A subunit) and rts1 (B' subunit) mutants. Our data support the hypothesis that sequences required for interaction with regulatory subunits also are conserved in these heterologous proteins, consistent with earlier observations that an Arabidopsis A regulatory subunit complements a tpdβ null allele in cells expressing wild-type yeast C subunits (Garbers et al., 1996).

Although the human HsCα subunit supports growth of yeast, the HsCβ subunit does not provide complementing PP2A activity in S. cerevisiae. The non-complementing phenotype of the Cβ subunit construct is surprising because only eight residues differ in the predicted amino acid sequences of the Cα and Cβ subunits. Most of the substitutions are conservative changes in sequences not known to be essential for PP2A function. However, it has recently been shown that mice homozygous for a PP2A-Cα null mutation die during embryogenesis, despite significant levels of Cβ subunit expression (Götz et al., 1998). Thus, failure of the Cβ subunit to complement in yeast may reflect functional specificity in vivo.

We used site-directed mutagenesis to create two dominant-defective alleles of PP2A (H115N or H118N and R86A or R89A). Target residues for mutagenesis were chosen on the basis of putative active site function (Goldberg et al., 1995) and biochemical analysis of mutants of the bacteriophage λ phosphatase (Zhuo et al., 1994). Both mutants were inactive in our complementation assay, indicating loss of catalytic activity. The H115N/H118N mutant exhibited a strong dominant-defective phenotype, whereas the R86A/R89A mutant displayed a slightly weaker dominant-defective phenotype. Preliminary microscopic characterization of cells expressing the H115N/H118N allele reveals abnormal bud morphologies similar to those exhibited by PP2A-depleted cells (Ronne et al., 1991) or cdc55 mutant cells (Healy et al., 1991), consistent with the hypothesis that these cells undergo growth arrest due to loss of PP2A function (D. Lizotte, A. DeLong, unpublished). The H115N mutant of AthC1 was dominant in the presence of a constitutively expressed wild-type copy of AthC1, showing that the dominant-defective phenotype was not specific to the Pph21-102p protein. A partially dominant mutant of S. pombe PP2A-C has been isolated previously. A high dose of this cold-sensitive (cs) ppa2 allele was shown to arrest growth under non-permissive conditions, and to retard growth and reduce cell size under permissive conditions (Kinoshita et al., 1990). The basis of the mutant’s partial dominance is unknown. However, expression of the cs allele increased okadaic acid sensitivity mildly, suggesting a dominant-interfering mechanism (Kinoshita et al., 1993).
The severity of the dominant growth defect phenotype was clearly affected by the copy number of the mutant and wild-type genes, consistent with the hypothesis that the dominant-defective enzyme competes with the functional C subunits for substrates or regulatory subunits. Either a substrate sequestration or a regulatory subunit titration model could account for the data we have presented here. The HsCz-H118N mutant has been independently constructed and shown to be catalytically inactive despite normal substrate binding characteristics (H. Chung, D. Brautigan, pers. commun.). Equivalent mutants of λ phosphatase and calcineurin display the same biochemical characteristics, but have not been assayed for phenotypes in vivo (Zhuo et al., 1994; Mertz et al., 1997). In contrast, a λ phosphatase mutant equivalent to the R86A/R89A mutant constructed here exhibits a 20-fold decrease in substrate binding and a catalytic defect less severe than that of the histidine mutant (Zhuo et al., 1994). The weaker phenotype of the R86A/R89A mutant may indicate that substrate binding contributes to, but is not essential for, the dominant phenotype. A biochemical analysis will be required to resolve these questions. Interestingly, the HsCβ subunit does not provide complementing PP2A activity, but is not dominant-defective. This result suggests that the factors required for functional complementation also are required for the dominant-defective phenotype, and argues against the hypothesis that any non-functional C subunit may exert a dominant effect. The partially dominant mutation conferring cold sensitivity on S. pombe PP2A-C maps to a conserved region, but does not affect a residue known to play a role in substrate binding or catalysis.

An alternative hypothesis is that the expression of heterologous PP2A-C subunit proteins down-regulates synthesis of endogenous C subunit protein. Loss of Pph21p expression would be tolerated in the presence of functional heterologous C subunits, but would be lethal in the presence of catalytically inactive mutants. A post-transcriptional autoregulatory mechanism limiting PP2A-C expression in mammalian cells has been reported recently (Bahrainians and Schonthal, 1998), and it is unclear whether a similar mechanism is operative in yeast. However, we have not observed down-regulation of endogenous C subunit protein levels in cultures expressing wild-type, dominant-defective, or non-complementing C subunits under GAL promoter control (D. Lizotte, A. DeLong, unpublished). Furthermore, a significant level of PP2A-C over-expression has been achieved in S. pombe (Kinoshita et al., 1993), and induction of high levels of PP2A-C mRNA is lethal in S. cerevisiae, suggesting that the C subunit protein is indeed over-expressed (Ronne et al., 1991). Thus down-regulation of endogenous C subunit levels does not account for the dominant-defective phenotype.

We have shown that yeast provides a functional assay system for heterologous PP2A-C genes; this system is likely to be generalizable, given the high conservation of C subunit sequences. We have isolated dominant-defective mutants of PP2A genes from Arabidopsis and humans, and we plan to use these mutants to analyze PP2A functions in whole plants and in mammalian tissue culture cells. This genetic system may also prove useful for analyzing interactions between heterologous or homologous catalytic and regulatory subunits of PP2A.

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