Fission Yeast Myosin-I, Myo1p, Stimulates Actin Assembly by Arp2/3 Complex and Shares Functions with WASp

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Abstract. Fission yeast myo1+ encodes a myosin-I with all three tail homology domains (TH1, 2, 3) found in typical long-tailed myosin-Is. Myo1p tail also contains a COOH-terminal acidic region similar to the A-domain of WASp/Scar proteins and other fungal myosin-Is. Our analysis shows that Myo1p and Wsp1p, the fission yeast WASp-like protein, share functions and cooperate in controlling actin assembly. First, Myo1p localizes to cortical patches enriched at tips of growing cells and at sites of cell division. Myo1p patches partially colocalize with actin patches and are dependent on an intact actin cytoskeleton. Second, although deletion of myo1+ is not lethal, Δmyo1 cells have actin cytoskeletal defects, including loss of polarized cell growth, delocalized actin patches, and mating defects. Third, additional disruption of wsp1+ is synthetically lethal, suggesting that these genes may share functions. In mapping the domains of Myo1p tail that share function with Wsp1p, we discovered that a Myo1p construct with just the head and TH1 domains is sufficient for cortical localization and to rescue all Δmyo1 defects. However, it fails to rescue the Δmyo1 Δwsp1 lethality. Additional tail domains, TH2 and TH3, are required to complement the double mutant. Fourth, we show that a recombinant Myo1p tail binds to Arp2/3 complex and activates its actin nucleation activity.

Key words: fission yeast • myosin-I • WASp • Arp2/3 complex • actin assembly

Introduction

Myosin-I is an actin-dependent membrane-based molecular motor. Many organisms express multiple myosin-Is with similar catalytic domains but different tails containing binding sites for membrane lipids and a variety of proteins. These tail-ligand interactions are postulated to target myo1+ isoforms to various intracellular locations and/or to adapt them to different actin-dependent processes such as motility, endocytosis, phagocytosis and polarized cell growth (Doberstein et al., 1993; Baines et al., 1995; McGoldrick et al., 1995; Goodson et al., 1996). Identifying the tail ligands and understanding the significance of the tail-ligand interactions have been the object of much study in several different organisms.

The catalytic domain of all myosin-Is is followed by a tail homology domain (TH1) that binds acidic phospholipids (Doberstein and Pollard, 1992) and actin filaments (Lee et al., 1999). In addition to TH1, long-tailed myosin-Is contain a Gly/Pro/Ala-rich TH2 domain and an Src homology 3 domain called TH3. TH2 also binds actin filaments (Jung and Hammer, 1994; Rosenfeld and Rener, 1994) and TH3 mediates interactions with adaptor proteins.

The COOH terminus of WASp/Scar proteins, containing an acidic A-domain, stimulates actin assembly by interacting with Arp2/3 complex. In animal cells, WASp/Scar proteins provide a link to signaling molecules affecting the actin cytoskeleton (reviewed by Higgs and Pollard, 1999). Interestingly, budding yeast myosin-I tails also bind Arp2/3 complex via a WASp-like A-domain at their COOH termini (Evangelista et al., 2000; Lechler et al., 2000). Deletions of A-domains from the yeast WASp/Scar homologue, Bee1p/Las17p, and myosin-Is led to drastic growth and actin organization defects (Evangelista et al., 2000; Lechler et al., 2000). Although data was not presented showing activation of Arp2/3 complex, these results implicated budding yeast myosin-Is in Bee1p-stimulated and Arp2/3 complex-mediated actin assembly.

Before any knowledge of this work on budding yeast myosin-Is, we identified a WASp-like acidic A-domain at the COOH terminus of Myo1p, a myosin-I from Schizosac-
Materials and Methods

Strains, Media, and Transformation

Table I lists the S. pombe strains used in this study. Fission yeast culture and genetic manipulations were carried out by standard methods. Transformation of S. pombe was achieved by electroporation (Moreno et al., 1991).

Identification and Cloning of myo1+ and wsp1+

Three uncharacterized myosin heavy chain genes in the Sanger database were identified by blasting (Altschul et al., 1990) with the catalytic domain sequence of Acanthamoeba myosin-IA. Phylogenetic analyses (Lee et al., 1999) of these new myosin sequences established the one in cosmid SPBC146 as a type-I myosin gene, and the two in SPBC2D10 and SPCC1919 are type-V myosin genes, so we named them myo1+, myo5+, and myo5-.

We cloned a 5-kb EcoRI fragment containing the myo1+ locus from SPBC146 into pHbluecs. This construct is pBSmyo1. Total RNA from mid-log wild-type cells was amplified by 5'-RACE PCR (Life Technologies) and the products were subcloned and sequenced.

We identified a WASP-like gene in cosmid SPAC4F10. This wsp1+ gene was previously submitted to Genbank (GenBank/EMBL/DBJ accession number AAB92587). We identified exons in wsp1+ by comparing its sequence with other WASP sequences and searching for the usually conserved 5' (GTAC) and 3' (CCAG) splice sites. We amplified a 3-kb fragment containing the entire wsp1+ locus from genomic DNA, cloned it into pHbluecs, and sequenced it. This construct is pBSwsp1.

Table I. Strains Used in this Study

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
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<tbody>
<tr>
<td>FY527</td>
<td>h·his3-D1 leu3-32 ura4-D18 ade6-M216</td>
</tr>
<tr>
<td>FY528</td>
<td>h·his3-D1 leu3-32 ura4-D18 ade6-M210</td>
</tr>
<tr>
<td>FY436</td>
<td>h·his7-366 ura4-D18 leu3-32 ade6-M216</td>
</tr>
<tr>
<td>TP135</td>
<td>h·Δmyo1·his3-Δ48 his3-D1 leu3-32 ura4-D18 ade6-M216</td>
</tr>
<tr>
<td>TP137</td>
<td>h·Δmyo1·his3-Δ48 puc1-1::(gfp-urn4) his3-D1 leu3-32 ura4-D18 ade6-M216</td>
</tr>
<tr>
<td>TP138</td>
<td>h·Δmyo1·his3-Δ48 puc1-1::(gfp-urn4) his3-D1 leu3-32 ura4-D18 ade6-M216</td>
</tr>
<tr>
<td>TP139</td>
<td>h·Δmyo1·his3-Δ48 puc1-1::(gfp-urn4) ΔJ2/D4 ura4-D18 his3-D1 leu3-32 ura4-D18 ade6-M216</td>
</tr>
<tr>
<td>TP140</td>
<td>h·Δmyo1·his3-Δ48 puc1-1::(gfp-urn4) ΔJ2/D4 ura4-D18 his3-D1 leu3-32 ura4-D18 ade6-M216</td>
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<tr>
<td>TP141</td>
<td>h·Δmyo1·his3-Δ48 puc1-1::(gfp-urn4) ΔJ2/D4 ura4-D18 his3-D1 leu3-32 ura4-D18 ade6-M216</td>
</tr>
<tr>
<td>TP142</td>
<td>h·Δmyo1·his3-Δ48 puc1-1::(gfp-urn4) ΔJ2/D4 ura4-D18 his3-D1 leu3-32 ura4-D18 ade6-M216</td>
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<tr>
<td>TP145</td>
<td>h·Δwsp1·leu1-32 his3-D1 leu3-32 ura4-D18 ade6-M210</td>
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Construction of myo1+ or wsp1+ Disruption Strains

Integration of linear myo1+ and wsp1+ disruption constructs (see Figs. 1 A and 6 A) into his3-D1 or leu3-32 wild-type diploid cells was screened by PCR. Stable transformed diploids were sporulated on malt extract and individual spores were dissected from tetrad and germinated on Yeast Extract Supplemented (YES). In either disruption, four viable spores were obtained, of which two were His+ or Leu+ containing the disrupted allele. We verified disruptions in viable haploids by PCR and Southern blot. Disruption of wsp1+ allows expression of only the NH2-terminal 346 residues, since an in-frame stop codon was created at the 5' ligation site of the leu+ insert.

The myo1+ locus is flanked 5' by a coatomer beta subunit gene and 3' closely by a ubiquinone biosynthesis monooxygenase gene. The coatomer beta subunit gene has the same transcriptional orientation as myo1+, but the ubiquinone monooxygenase gene is in opposite orientation. Disruption of myo1+ by removing an NdeI-Sall fragment was lethal and could not be rescued by transforming plasmids carrying full-length myo1+ gene (pUR-myol or pSGP-myo1). This NdeI-Sall fragment includes sequences coding for residues 249–1217 and 179 bp of 3' untranslated region of myo1+ gene, leaving the open reading frame of the downstream ubiquinone monooxygenase gene intact. Since we were unable to rescue this myo1+ disruption with complementing plasmids, we concluded that the function of the downstream ubiquinone monooxygenase gene was most likely affected, perhaps at the level of transcript stability.

Construction of Expression and Complementation Constructs

We used sequences of other myosin-Is for which tail domains have been defined protoclyotically (Lynch et al., 1986; Lee et al., 1999) to determine the boundaries between TH1, 2, 3, and A-domains of Myo1p: head consisted of residues 1–771; TH1, 772–966; TH2, 967–1112; TH3, 1113–1163; A, 1164–1217. To express full-length Myo1p with green fluorescent protein (GFP) fused to its NH2 terminus, GFP-H/1/2/3/A, an engineered NotI-Sall fragment containing myo1+ without the ATG and intron was cloned into NotI- and Sall-digested pSGP573, a GFP-tagging vector that carries the thiamine-repressible nmt1+ promoter and the ura4+ marker (Pasion and Forsburg, 1999). GFP-1, GFP-2/3/A, and GFP-1/2/3/A were made similarly in pSGP573 using primer sets that annealed to corresponding domains. We replaced a BamHI-Sall fragment coding the whole tail in GFP-H/1/2/3/A with one containing just TH1 for GFP-H/1. We removed this BamHI-Sall fragment for GFP-H, but this construction resulted in 62 non-Myo1p residues COOH-terminal to GFP-H. To test for complementation and overexpression, Ura+ transformants were selected and streaked to permissive and nonpermissive conditions ±15 μM thiamine.

We made constructs expressing mutant Myo1p with COOH-terminal deletions designed to integrate at the puc1+ locus. We cloned a NotI fragment containing S. pombe puc1+ (Forsburg and Nurse, 1991) into NotI-digested pkJ210 (Keeney and Boeke, 1994), a pbLuBluescript plasmid containing only the ura4+ marker. The resulting vector is pJK-puc1. We then subcloned myo1+ into pJK-puc1 at a unique EcoRI site for H/1/2/3/A. We replaced a BamHI-Sall fragment coding the whole tail in GFP-H/1/2/3/A with TH1, TH1/2, and TH1/2/3 fragments amplified using appropriate primer sets for H/1 (residues 1–966), H/1/2 (residues 1–1112), and H/1/2/3 (residues 1–1163). We made H (residues 1–786) by removing a ubiquinone monooxygenase gene intact. The coatomer ubiquinone monooxygenase gene was in opposite orientation. Disruption of the COOH terminus of Wsp1p, a fission yeast WASp homologue, results in synthetic lethality. The Journal of Cell Biology, Volume 151, 2000
by XhoI in the middle of the *Ura*+ transformants were selected and streaked to permissive and nonpermissive conditions.

pUR19-wsp1 was made by subcloning *wsp1* from pBSwsp1 into a unique EcoRI site in pUR19, an ars1-containing fission yeast vector that carries the *ura4* marker (Barbet et al., 1992). To identify strains carrying *ura4*+-marked *wsp1* in the background of *ura4*+-marked Myo1p mutants, we made pUR-wsp1/Kan by subcloning a SalI-SacI fragment containing the kanamycin resistance gene from pFA6a (Wach et al., 1994) into SalI- and SacI-digested pUR19-wsp1. All constructs above were verified by sequencing.

**Microscopy**

Cells were stained with calcofluor (Balasubramanian et al., 1997) and with rhodamine-phalloidin by modification of a published procedure (Balasubramanian et al., 1997). Incubation with rhodamine-phalloidin for 30 min at 24°C and washing with 1 ml PBS improved staining. For actin disruption experiments, cells were treated with 100 μM latrunculin-A dissolved in DMSO or with the same volume of DMSO. After a 20-min incubation at 32°C, cells were fixed and stained for actin as

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**Figure 1.** Targeted disruption of *myo1*+. (A) Scale drawing of the *myo1*+ locus. Sequences coding the domains of Myo1p are filled with different patterns. Dashed lines indicate sequences outside the disruption construct, which is shown below the locus. *myo1*+ was disrupted in a *his3*+ diploid strain by replacing an NdeI–BglII fragment with the *his3*+ gene. The gel shows PCR amplification of the genomic locus from His+ diploids disrupted in one of the two *myo1* loci. Primers used for amplification are indicated as small arrows, and are indicated above each lane of the agarose gel. (B–C) Wild-type and Δ*myo1* cells grown to log phase in EMM-His at 25°C were shifted to 36°C for 5 h. Cells were stained before and after shifting with calcofluor (B) or rhodamine-phalloidin (C). Arrows indicate examples of aberrant cell morphology, mistargeting of cell-wall material, and actin abnormalities. Scale bar, 10 μm.
above. For localization studies, mid-log cells grown in 0.05 μM thiamine (Javerzat et al., 1996) were visualized directly or fixed in −80°C methanol. Cells were observed with a 100× objective on an IX70 microscope (Olympus) and images were collected on a digital CCD camera (Hamamatsu). Deconvolution microscopy was performed as described (Bezanilla et al., 2000).

**Actin Polymerization and Binding Assays**

Actin was purified from rabbit skeletal muscle (Spudich and Watt, 1971). Purified Arp2/3 complex was from *Acanthamoeba* and bovine thymus (Blanchoin et al., 2000). We subcloned TH2/3/A insert into the BamHI and EcoRI sites of pGex2T vector for bacterial expression. GST-2/3/A was purified on a glutathione-Sepharose column (Amersham Pharmacia Biotech), and dialyzed versus 10 mM Tris, pH 7, 65 mM NaCl, and 1 mM DTT. Actin polymerization (Higgs et al., 1999), glutathione bead copelleting, and actin filament copelleting assays (Lee et al., 1999) were as described. We measured actin polymerization lag and concentration of barbed ends as described (Pollard, 1986).

**Table II. Fractions of Δmyo1, Δwsp1, and Wild-Type Cells with Normal or Abnormal Shape, with no Septum, One Septum, or Abnormal Septal Material**

<table>
<thead>
<tr>
<th>Morphology</th>
<th>Cell wall by calcofluor staining</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>Normal rod</td>
</tr>
<tr>
<td>25°C</td>
<td>%</td>
</tr>
<tr>
<td>wild-type</td>
<td>99.8</td>
</tr>
<tr>
<td>Δmyo1</td>
<td>84.0</td>
</tr>
<tr>
<td>36°C, 5 h</td>
<td></td>
</tr>
<tr>
<td>wild-type</td>
<td>99.7</td>
</tr>
<tr>
<td>Δmyo1</td>
<td>48.0</td>
</tr>
<tr>
<td>32°C</td>
<td></td>
</tr>
<tr>
<td>wild-type</td>
<td>99.7</td>
</tr>
<tr>
<td>Δwsp1</td>
<td>66.8</td>
</tr>
</tbody>
</table>

*n* ≥ 250 cells in every case.

**Figure 2.** Complementation of temperature and salt sensitivities of Δmyo1. (A) Δmyo1 cells transformed with integrated constructs: H/1/2/3/A, H/1/2, H/1, H, or pJK-puc1 (vector control). (B) Δmyo1 cells transformed with GFP-H/1/2/3/A, GFP-2/3/A, or pSGP573 (vector control). All strains in A and B were streaked to EMM-Ura at 25°C, 36°C, or 25°C + 1 M KCl. (C) Schematic diagrams of constructs, the promoters controlling their expression, and their ability to rescue the temperature or salt sensitivity or mating defects of Δmyo1, and the lethality of Δmyo1 Δwsp1.
Online Supplemental Material

The online version of this article includes detailed methods used in constructing myo1+ and wsp1+ strains and two additional figures showing phylogenetic analysis of myosins, alignment of IQ motifs, 59 RACE PCR of myo1+ and latrunculin-A disruption of GFP-Myo1p patches. Available at http://www.jcb.org/cgi/content/full/151/4/789/DC1

Results

Identification of the myo1+ Gene

As of August 2000, the S. pombe genome contained five genes with significant homology to Acanthamoeba myosin-I A catalytic domain. Of these five, two were previously characterized myosin-IIs called myo2+ and myp2+ (Bezanilla et al., 1997; Kitayama et al., 1997). We named the other myosin heavy chain genes myo1+ (1,217 residues), myo5+ (1,471 residues), and myp5+ (1,516 residues). A phylogenetic tree built from sequence alignments of catalytic domains grouped S. pombe Myo1p with Saccharomyces cerevisiae myosin-Is (Myo3p and Myo5p) and Aspergillus nidulans MYOA with a bootstrapping value of 100% within the large myosin-I cluster (1,000 trials; see Figure S1 at http://www.jcb.org/cgi/content/full/151/4/789/DC1). In the same tree, S. pombe Myo5p and Myp5p joined S. cerevisiae (Myo2p and Myo4p), fly, chicken, and mouse myosin-Vs with a bootstrapping value of 100%. We conclude that S. pombe Myo1p is a myosin-I, and S. pombe Myo5p and Myp5p are myosin-Vs.

Myo1p and other known fungal myosin-Is have two similar IQ motifs, especially the first (Figure S1). Beyond the IQ motifs, Myo1p is a typical long-tailed myosin-I with the addition of a COOH-terminal A-domain. The basic TH1 domain has a calculated pI of 10. The TH2 domain is rich in Pro (20%), Ala (18%), Ser (12%), and Thr (11%). Abundant Ser and Thr in TH2 are unusual, found only in S. cerevisiae Myo3p and Myo5p, but not in other long-tailed myosin-Is. The A-domain is found on all fungal myosin-Is reported so far, but not on animal or protozoa myosin-Is. Two independent 59-RACE products obtained from total S. pombe RNA using different sets of antisense and nested primers (Fig. 1 A, primers 7–9) established the presence of a 44-bp intron separating the ATG codon from the remaining coding sequence. myo1+ transcript begins 43 bp upstream of the ATG.

Targeted Disruption of myo1+

We disrupted myo1+ by replacing >50% of the catalytic domain and the first IQ motif with the his3+ gene (Fig. 1 A). This disruption allowed expression of only the NH2-terminal 248 residues. Amplification with primers inside the his3+ gene and primers outside the disruption construct verified that myo1+ was disrupted in a His+ diploid (Fig. 1 A, primers 1+3, 2+3, 4+6, and 4+5). All four progeny of this diploid were viable in YES at 25°C. Of these four colonies, two were His+ (Δmyo1::his3+) and always smaller in size. In liquid Edinburgh minimal media (EMM) at 25°C, Δmyo1 cells grew with a doubling time of 12.5 h (n = 2) compared with 6.1 h (n = 4) for wild-type. These mid-log Δmyo1 cells had aberrant morphology: 16% were round, slightly swollen, or irregularly shaped (Table II; Fig. 1 C); 13.7% had abnormal septal material.

Figure 3. Localization of GFP-Myo1p in mid-log wild-type haploid cells. (A) Differential interference contrast and GFP-Myo1p fluorescence in live cells at three different focal planes. (B–C) Stereo pairs of three-dimensional reconstructions of live cells expressing GFP-Myo1p showing localization of Myo1p patches at cell periphery. (D–E) Colocalization of GFP-Myo1p and actin in fixed cells stained with rhodamine-phalloidin shown as full thickness stack of images from three-dimensional reconstructions (D) and as stereo pair (E). Images were obtained by a conventional fluorescence microscope (A) or a deconvolution Deltavision microscope (B–E).
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H/1/2, H/1, and H) under control of the native myo1 promoter into Dmyo1 cells. All constructs, except H, restored growth at 17°C (not shown), 36°C, and 25°C with 1 M KCl (Fig. 2 A). Dmyo1 cells transformed with construct H were indistinguishable from cells transformed with empty vector. Similarly, all constructs, except H, rescued Dmyo1 mating defects assessed by iodine vapor staining. Thus, the head plus TH1 are the minimum domains needed to complement the absence of functional myo1+.

GFP-Myo1p and GFP-H/1 restored wild-type growth to Dmyo1 cells at 36°C or 25°C with 1 M KCl (Fig. 2, B and C), showing that the GFP tag did not interfere with function. In the presence of thiamine, where they were expressed at a low level, as verified by microscopy, transformants had near wild-type morphology and colony size. In contrast, GFP fusions of head or tail alone (GFP-H, GFP-1, GFP-1/2/3/A, and GFP-2/3/A) failed to complement Dmyo1 defects.

Full-length GFP-Myo1p localized to patches in wild-type as well as Dmyo1 cells. Three-dimensional reconstructions made by deconvolution microscopy showed that all GFP-Myo1p patches were located at the periphery of living cells (Fig. 3, B and C), so they appeared in different focal planes by conventional fluorescence microscopy (Fig. 3 A). Like actin patches, these Myo1p patches usually concentrated at both growing ends or in the middle of dividing cells, and were dynamic, since we observed them moving along the cell cortex. We found that GFP-Myo1p patches partially colocalized with actin patches (Fig. 3, D and E). Staining of GFP-Myo1p–expressing cells with rhodamine-phalloidin revealed that ~25% of patches contained only GFP-Myo1p (green patches) and ~15% contained only actin (red patches). Approximately 60% of patches contained a variable ratio of actin and GFP-Myo1p, since these patches ranged in color from yellow to orange (350 patches counted). Latrunculin-A reversibly dispersed GFP-Myo1p from patches to a diffuse cytoplasmic fluorescence, indicating that cortical localization of...
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Myo1p depended on intact actin filaments. Expression levels from the nmt1 promoter varied from cell to cell, producing patches of different intensities but otherwise indistinguishable. Overexpression of GFP-Myo1p, while not toxic, produced uniform fluorescence throughout the cell periphery and large fluorescent aggregates in the cytoplasm. We conclude that expression of GFP-Myo1p at low levels mimics endogenous Myo1p localization.

GFP-H/1, a construct that rescued Δmyo1 defects, localized to discrete patches similar to GFP-Myo1p in Δmyo1 (Fig. 4) and wild-type cells. However, the level of expression was more variable from cell to cell and cytoplasmic fluorescence was greater for GFP-H/1 than for GFP-Myo1p. GFP fusions that failed to complement Δmyo1 were either mislocalized to the nucleus (Fig. 4, GFP-1 and GFP-1/2/3/A), aggregated (GFP-H), or diffuse in the cytoplasm (GFP-2/3/A). Nuclear localization of GFP-1 and GFP-1/2/3/A were confirmed by staining with DAPI.

Myo1p Tail Binds and Activates Arp2/3 Complex

The sequence of Myo1p A-domain is similar to A-domains of WASp/Scar proteins that bind Arp2/3 complex (Fig. 5 A). Among known myosin tails, only fungal myosin-Is have A-domains. Two assays established that Myo1p tail interacts with Arp2/3 complex. In a supernatant depletion assay, purified amoeba Arp2/3 complex bound a fusion protein GST-2/3/A (GST fused to the NH2 terminus of TH2/3/A-domains of Myo1p) immobilized on beads with a Kd of ~5 μM (Fig. 5 B). Control glutathione beads did not deplete Arp2/3 complex from the supernatant.

Purified GST-2/3/A stimulated actin filament nucleation by amoeba (Fig. 5 C) and bovine Arp2/3 complex (not shown). GST alone did not promote actin polymerization by Arp2/3 complex. Separately, neither GST-2/3/A nor the Arp2/3 complex had an appreciable effect on the time course of spontaneous polymerization, but together they reduced the lag at the outset of polymerization up to threefold (not shown) and generated ninefold more filament ends (Fig. 5 D). These effects plateaued at concentrations of GST-2/3/A > 1 μM. GST-2/3/A had lower affinity and activity than the GST-WA-domain of WASp (Higgs et al., 1999), perhaps due to using proteins from different species.

GST-2/3/A did not pellet with muscle actin filaments in actin polymerization buffer (not shown). Based on the concentrations used, the minimum value of the Kd for GST-2/3/A binding muscle actin filaments is 20 μM.

Figure 5. Activation of actin nucleation by Arp2/3 complex by Myo1p TH2/3/A. (A) Alignments of A-domains with WASp/Scar A-domains. Numbers in parentheses represent the starting residue in the alignment. Invariant and conserved residues are shaded black and gray. (B) Supernatant depletion assay for GST-2/3/A binding amoeba Arp2/3 complex. Conditions: GST-2/3/A immobilized on beads (●) was titrated into 0.3 μM amoeba Arp2/3 complex in 65 mM NaCl, 10 mM Tris, pH 7, 1 mM DTT.

The same volumes of beads were the control (○). Beads were pelleted at 16,000 g and supernatant proteins were separated by SDS-PAGE, stained with Coomassie, and scanned to measure the fraction bound. The binding isotherm gives a Kd of ~5 μM. (Inset) Coomassie-stained gel of the supernatants showing Arp2/3 complex depletion. Numbers above each lane indicate total GST-2/3/A concentration on beads in micromolar. (C) Time course of polymerization of 4 μM monomeric Mg-ATP-actin (5% pyrene labeled). Conditions: 10 mM Tris, pH 7, 50 mM KCl, 1 mM MgCl2, 1 mM EGTA, and 0.2 mM ATP. (●) Actin alone, (△) actin with 50 nM amoeba Arp2/3 complex, (○) actin with 500 nM GST-2/3/A. Actin with 50 nM amoeba Arp2/3 complex and GST-2/3/A at concentrations of (nM): 63 (●), 125 (△), 375 (○), 500 (■), and 5,000 (●). (Inset) SDS-PAGE of purified GST-2/3/A. (D) The concentration of filament ends produced by 50 nM amoeba Arp2/3 complex as a function of GST-2/3/A.
Targeted Disruption of wsp1 and Its Genetic Interaction with myo1

We identified a WASp-like gene, wsp1\(^1\), in the Sanger database as a potential activator of Arp2/3 complex. The genomic sequence of wsp1\(^1\) has four exons encoding domains similar to WASp proteins: WH1 domain, a polyproline region, WH2 domain, and an acidic A-domain, but no GBD/CRIB sequence that might bind Cdc42p.

We made a wsp1\(^1\) disruption strain (\(D_{wsp1}\)), which would produce a COOH-terminally truncated Wsp1p protein (Fig. 6 A). Tetrad dissection of individual asci and random spore analysis of a \(\Delta wsp1\)/\(wsp1\) diploid revealed that COOH-terminal truncation of Wsp1p is not lethal. Amplification with specific primers from the genomic locus verified that wsp1\(^1\) was disrupted in Leu\(^1\) haploids (Fig. 6 A). \(\Delta wsp1\) cells formed smaller colonies than wild-type in selective EMM, were sensitive to 1 M KCl (Fig. 6 B) and mated inefficiently. A genomic clone of wsp1\(^1\) ([pUR19-wsp1]) fully complemented the salt phenotype and mating defects. Like \(\Delta myo1\) cells, \(\Delta wsp1\) cells had depolarized actin patches and morphological defects (Fig. 6 C). Disruption of wsp1\(^1\) did not cause faulty targeting of septal material, but mid-log \(\Delta wsp1\) cells grown at 32°C did have more uniseptated cells than wild-type (Table II; Fig. 6 C). The lack of aberrant septal targeting suggests that, unlike Myo1p, Wsp1p is not involved in proper septal deposition.

To test for genetic interactions between wsp1\(^1\) and myo1\(^1\), we crossed \(\Delta wsp1\) with \(\Delta myo1\) cells, by transforming each strain first with a complementing plasmid before mating ([pUR-wsp1 for \(D_{wsp1}\), pSGP573-myo1 for \(D_{myo1}\)]. The progeny from the cross were examined by random spore analysis after germination at 25°C. Marker analysis of 657 progeny indicated that wild-type (250, His\(^2\), and Leu\(^2\), \(D_{myo1}\) (192 His\(^1\)), and \(D_{wsp1}\) (215 Leu\(^1\)) spores could be recovered. No spores carrying disruption of myo1\(^1\) and wsp1\(^1\) (0 His\(^1\) and Leu\(^1\)) were recovered, so at the permissive temperature for both disruptions, \(\Delta wsp1\) is synthetically lethal with \(\Delta myo1\).

To test for functional redundancy between the tail of Myo1p and Wsp1p, we crossed \(\Delta myo1\) cells containing integrated Myo1p mutants (H/1/2/3/A, H/1/2/3, H/1/2, H/1, and H) with \(\Delta wsp1\) cells carrying a modified pUR-wsp1. We
added the kanamycin resistance gene to pUR-wsp1 (= pUR-wsp1/KanR) to identify progeny carrying ura4<sup>+</sup>-marked wsp1<sup>+</sup> in the presence of ura4<sup>+</sup>-marked Myo1p mutants. The progeny from these crosses were examined by random spore analysis after germination at 25°C in YES. We analyzed >400 progeny for each cross. Progeny carrying disruption of myo1<sup>+</sup> and wsp1<sup>+</sup> in the presence of integrated H/1/2/3/A or H/1/2/3 were recovered with expected mendelian segregation and independent of pUR-wsp1/KanR. H/1/2, H/1, or H progeny carrying both disruptions were always kanamycin resistant, indicating the presence of wsp1<sup>+</sup>, and were recovered with significantly lower than expected frequency. We conclude that H/1/2/3/A and H/1/2/3, but not H/1/2, H/1 or H, rescue the lethality of Δmyo1 Δwsp1.

Discussion

Judging from the available sequence information (~95%) at the Sanger Genome Center, fission yeast potentially contains only one type-I myosin gene, making it attractive for detailed analysis of myosin-I functions. Multiple myosin-I genes in other organisms are interesting in terms of their specialized functions, but have been a burden experimentally in studies of basic functions.

Functions of Myo1p

Deletion of myo1<sup>+</sup> causes defects in cell morphology and actin organization. Nonpermissive conditions greatly enhance these defects, leading to branched and rounded cells and eventually to cell death. Fission yeast cells grow in a polarized fashion, using the actin cytoskeleton to deliver essential materials to the growing ends of cells. The morphology of Δmyo1 cells suggests that Myo1p has a role in regulating the sites of polarized growth, like the S. pombe tea and orb gene products (Verde et al., 1998). Interestingly, one of the round orb mutants, orb2, is the pak1<sup>+/shk1</sup> gene (Verde et al., 1998), a member of the Ste20p/PAK family of kinases. As demonstrated in other organisms (Wu et al., 1997; Brzeska et al., 1989), Ste20p/PAK kinases activate myosin-I motor activity by phosphorylating a serine or threonine residue (TEDS rule site) in the catalytic domain. The TEDS rule site of Myo1p, Ser-361, may be a target of Pak1p/Shk1p, since disruption of myo1<sup>+</sup> mimics the actin patch delocalization and rounded shape found in orb2 mutant cells.

Consistent with a role in regulating polarized growth, Myo1p and Pak1p/Shk1p localize to growing ends. Localization of Myo1p depends on an intact actin cytoskeleton. However, not all Myo1p-containing patches are actin patches and not all actin patches contain Myo1p (Fig. 3, D and E). This intriguing observation indicates that there are distinct populations of patches that vary in molecular composition. If Myo1p is a target of Pak1p/Shk1p, it would be interesting to investigate whether these Myo1p-containing actin-deficient patches also contain Pak1p/Shk1p. Genetic interactions between pak1<sup>+/shk1</sup> and myo1<sup>+</sup>, phosphorylation of Myo1p by Pak1p/Shk1p, and localization of both proteins will be the subject of future work. We expect that Myo1p is part of a complicated and redundant system of proteins establishing polarity, since mutation in a variety of genes (for example, tea, orb, and now wsp1<sup>+</sup>) clearly exhibit similar phenotypes.

Like Pak1p/Shk1p (Marcus et al., 1995; Ottilie et al., 1995), Myo1p is required for mating. Although the role of Myo1p in mating is not yet clear, it may again function downstream of Pak1p/Shk1p. In S. cerevisiae, a key regulator of PAK kinases, Cdc42p, localizes to the tip of α-factor–induced mating projections (Ziman et al., 1993). Given the conservation between budding and fission yeast Cdc42p (Miller and Johnson, 1994), we expect fission yeast Cdc42p to regulate Pak1p/Shk1p and thus Myo1p functions during conjugation.

Cells lacking Myo1p accumulate septal components abnormally, especially at high temperature (Fig. 1 B) and in high salt. Even under permissive conditions, most Δmyo1 cells have a thick septum, and twice the number of Δmyo1 cells have septa compared with wild-type. This function of Myo1p may be distinct from its role in maintaining cell shape, as many Δmyo1 cells with normal rod morphology deposit cell wall abnormally. Thus, Myo1p may contribute to proper septation, perhaps transporting vesicles containing septal material to the division site.

Contribution of Myo1p Domains to Function

All known defects of Δmyo1 cells are corrected by a construct with just the head and TH1 domains, a protein similar to a short-tailed myosin-I–like brush border myosin-I. This is surprising since important functions have been attributed to conserved parts of myosin-I tails that are missing in this construct: TH2 binds actin filaments (Jung and Hammer, 1994; Rosenfeld and Rener, 1994; Lee et al., 1999), TH3 binds adaptor proteins (Xu et al., 1995; Anderson et al., 1998), and A-domain interacts with Arp2/3 complex (Evangelista et al., 2000; Lechler et al., 2000). TH1 is essential for myosin-I function in fission yeast, since the H construct (with only the motor domain and IQ motifs) corrects no known defects of Δmyo1 cells. The rest of the tail is not only unnecessary for function, but the tail does not even localize properly without the head.

Head and TH1 sequences are required and sufficient for proper localization of Myo1p. GFP-H/I localizes like full-length Myo1p to cortical patches, but when expressed alone as a GFP-fusion protein, TH1 mislocalizes to the nucleus. TH1 contains many potential nuclear localization sequences, clusters of arginines and lysines, such as KKKRRR in the first 10 residues of this domain. Artificial nuclear localization shows that associations of TH1 with acidic phospholipids and actin filaments are insufficient to prevent transport of a GFP-1 construct into the nucleus. The head, but not TH2/3/A, overrides this nuclear targeting. This intriguing observation indicates that the motor domain of a myosin-I participates in targeting the protein in the cell. Similar work on mammalian myosin-Is (Ruppert et al., 1995; Durbach et al., 1996) demonstrated that motor domain also contributes to localization in actin-rich cell surface structures like lamellipodia and membrane ruffles.

Role of Myo1p in Actin Assembly

The COOH-terminal A-domain of Myo1p is similar to the COOH-terminal A-domains of WASp/Scar proteins. Similar motifs on budding yeast myosin-Is and Bee1p/Las17p as well as other WASp proteins mediate physical interactions with Arp2/3 complex. In budding and fission yeasts,
ablation of Arp2/3 complex subunits is lethal or severely debilitating (Balasubramanian et al., 1996; Moreau et al., 1997). Purified Arp2/3 complex is intrinsically inactive in nucleating actin assembly, so it requires activation in the cell. We show here that a GST fusion protein containing the A-domain of Myo1p binds to and stimulates the nucleation activity of Arp2/3 complex. Our genetic results, however, show that this A-domain is not required for viability and Myo1p function, suggesting that myosin-I is not the only activator of Arp2/3 complex. Our findings provide evidence that Wsp1p is another essential activator of Arp2/3 complex. A wsp1Δ disruption that would produce a COOH-terminally truncated Wsp1 protein is not lethal, but this disruption leads to phenotypes similar to ∆wsp1 and is synthetically lethal with ∆myo1, indicating that these genes may share functions in regulating actin dynamics.

Interestingly, the minimal Myo1p construct for myosin-I function and localization, H/1, fails to rescue the ∆myo1 ∆wsp1 double-mutant lethality. Additional TH2 and TH3 domains are required to rescue the double-mutant, and rescued cells grow normally at 25°C in YES (data not shown). This differs from budding yeast, where deletion of A-domains from WASp and myosin-I result in severe growth defects. Our findings implicate TH3 domain in myosin-I–mediated activation of Arp2/3 complex in fission yeast, perhaps by recruiting an additional A-domain containing protein.

Function and Evolution of Myosin-I Tails

Work on other organisms has shown that tail domains are important for myosin-I function and localization, but the domains required appear to differ from organism to organism. In S. cerevisiae, a point mutation in TH3 or deletion of TH2 and TH3 domains disperses myosin-I–containing patches into diffuse cytoplasmic staining or alters the asymmetric distribution of patches to buds. These myosin-I mutants fail to complement defects of null cells (Anderson et al., 1998; Evangelista et al., 2000). In Dictyostelium, myoB lacking TH3 fails to rescue null phenotypes, but appears to localize properly (Novak and Titus, 1998). Aspergillus nidulans MYOA, on the other hand, does not require the TH3 domain, but deletion of TH1 or 30 residues rich in proline immediately COOH-terminal to TH3 results in a nonfunctional protein that does not localize properly (Yamashita et al., 2000). We find that TH1 is the crucial part of the tail in fission yeast Myo1p.

These functional differences in myosin-I tails may reflect a loss or gain of particular tail-ligand interactions subsequent to the divergence of these organisms during evolution. Phylogenetic analysis revealed that all myosin-I genes had a common ancestor in an early eukaryote more than one billion years ago. The sequences of their head domains distinguish them from other classes of myosin. On the other hand, analysis of their tail sequences suggested that myosin-I genes acquired their TH3 domains relatively late, in more than one independent event after the separation of contemporary organisms from their common ancestors (Lee et al., 1999). Thus, TH3 domains from various organisms would likely bind different ligands. This may explain why fission and budding yeast do not have a gene corresponding to Acanthamoeba Acn125 or Dictyostelium p116, proteins that bind the TH3 domains of amoeboid myosin-I tails. Also, acquisition of TH2 may also have been a relatively late and independent event, as suggested by the lack of alignment among TH2 sequences.

Addition of a COOH-terminal A-domain on fungal myosin-Is appears to have occurred once, soon after fungi diverged from animals and plants, ~800 million years ago. No known animal, plant, or protozoan myosin-Is has an A-domain. The A-domain on fungal myosin-Is was in place 550 million years ago when S. pombe diverged from the lineage giving rise to S. cerevisiae and A. nidulans. In fact, the four fungal myosin-Is are closely related throughout: the head sequences form a tight phylogenetically related cluster, the IQ motifs are similar, TH2 is abundant in serine and threonine (except MYOA), and all have an A-domain at their COOH-termini (Figs. 5 A and S1, see supplemental material).

Since acquisition of the A-domain by fungal myosin-Is was a recent event, we hypothesize that other proteins may have also acquired A-domains late in their evolution. Similar acidic A-domain sequences are observed in various proteins not related to the WASp/Scar family or myosin-I, such as S. cerevisiae Abp1p and the intracellular domain of Toxoplasma gondii thrombospondin-related anonymous proteins (TRAP-related proteins). It would be interesting to investigate whether any of these A-domain–containing proteins may link nonfungal myosin-Is to Arp2/3 complex.

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