Identification and Characterization of Genes Required for Hyphal Morphogenesis in the Filamentous Fungus Aspergillus nidulans

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Identification and Characterization of Genes Required for Hyphal Morphogenesis in the Filamentous Fungus Aspergillus nidulans

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ABSTRACT

In the filamentous fungus Aspergillus nidulans, germination of an asexual conidiospore results in the formation of a hyphal cell. A key feature of spore germination is the switch from isotropic spore expansion to polarized apical growth. Here, temperature-sensitive mutations are used to characterize the roles of five genes (sepA, hypA, podB-podD) in the establishment and maintenance of hyphal polarity. Evidence that suggests that the hypA, podB, and sepA genes are required for multiple aspects of hyphal morphogenesis is presented. Notably, podB and sepA are needed for organization of the cytoskeleton at sites of polarized growth. In contrast, podC and podD encode proteins that appear to be specifically required for the establishment of hyphal polarity during spor germination. The role of sepA and the pod genes in controlling the spatial pattern of polarized morphogenesis in germinating spores is also described. Results obtained from these experiments indicate that the normal pattern of germ-tube emergence is dependent upon the integrity of the actin cytoskeleton.

A characteristic feature of fungal morphogenesis is its highly polarized nature. Fungal cells grow by inserting new membrane and cell wall at localized sites on the cell surface. Vesicles laden with components required for cell-surface expansion are thought to be transported to these sites along a polarized cytoskeletal network (reviewed by Gow 1995). Different types of fungal cells acquire their unique morphologies by employing distinctive patterns of polarized morphogenesis (reviewed by Mata and Nurse 1998). For example, budding yeast cells attain their ellipsoidal shape by undergoing alternating periods of apical and isotropic growth (Lew and Reed 1993), whereas fission yeast cells become rod shaped by restricting growth to the cell poles (Mitchison and Nurse 1985). Notably, both yeasts cease polarized growth during mitosis and relocalize the morphogenetic machinery to the incipient division site to allow septum formation and cytokinesis. In contrast to yeast cells, the distinct tubular shape of hyphal cells is achieved by confining growth to the apical pole. Furthermore, hyphal cells do not depolarize during mitosis and instead assemble an apparently distinct morphogenetic complex at cell division sites (reviewed by Harris 1997).

Budding yeast cells are capable of initiating polarized growth in response to either internal or external spatial cues (reviewed by Roemer et al. 1996). Internal cues (i.e., Bud3p, Bud4p) direct bud site selection during the cell cycle (Chant et al. 1995; Sanders and Herskowitz 1996; Zahner et al. 1996), whereas external cues (i.e., bound pheromone receptor) dictate the site at which mating projections form prior to conjugation (Jackson et al. 1991; Valtz et al. 1995). In both cases, spatial information is relayed to the morphogenetic complex by a series of GTPase signaling modules (reviewed by Pringle et al. 1995). Ultimately, polarized growth requires numerous gene products involved in cytoskeletal and secretory functions (reviewed by Govindan and Novick 1995). Notably, many of the gene products that control polarized growth in yeast were initially identified by mutations that alter normal cellular morphology (Sloat and Pringle 1978; Adams et al. 1990; Mondonest et al. 1997).

Many approaches have been employed to experimentally investigate polarized morphogenesis in hyphal cells. Detailed physiological studies have established that Ca2+ flux plays an important role in regulating the establishment and maintenance of hyphal polarity in filamentous fungi (Jackson and Heath 1993; Grinberg and Heath 1997). Molecular and genetic studies have demonstrated that the maintenance of hyphal polarity in Neurospora crassa requires both the cAMP-dependent protein kinase (PKA) and the COT1 kinase (Yarden et al. 1992; Bruno et al. 1996). The relevant targets of these kinases remain unknown. Furthermore, the establishment and maintenance of hyphal polarity depends upon both actin-based (McGoldrick et al. 1995) and microtubule-based (Lehmler et al. 1997; Seiler et al. 1997; Wu et al. 1998) motor proteins. Although the role of GTPase signaling modules in controlling polarized morphogenesis in hyphal cells has not been fully addressed, the analysis of a Ras homologue in A. nidu-
lans suggests that it regulates the establishment of hyphal polarity (Som and Kolaparthi 1994). Despite these insights, a coherent picture of the molecular mechanisms underlying polarized morphogenesis in hyphal cells has yet to emerge.

A. nidulans forms dormant asexual conidiospores that germinate to form hyphal cells. Spore germination occurs in three sequential stages: (i) activation of the dormant spore, (ii) isotropic expansion driven by hydration and wall growth, and (iii) initiation of polarized growth at the site of germ-tube emergence (d’Enfert 1997). Concomitant with these events, the uninucleate spore reenters the cell cycle and undergoes nuclear division. As a result, A. nidulans hyphal cells are multinucleate (Fiddy and Trinci 1976; Harris 1997). In mature hyphae that have formed septa, the tip cell continues to grow at the apical pole, whereas subapical cells establish new axes of polarized growth and form lateral branches (Fiddy and Trinci 1976; Harris 1997). In this report, we present the identification and phenotypic characterization of temperature-sensitive (ts) mutations that define four genes required for normal hyphal morphogenesis (hypA, podB–podD) in A. nidulans. We demonstrate that two of these genes, hypA and podB, are needed for both the establishment and the maintenance of hyphal polarity. Results obtained from microscopic analyses suggest that the podB gene is required for cytoskeletal organization in the hyphal tip. In contrast, we show that the podC and podD genes are required only for the establishment of hyphal polarity. We also characterize the polarity defects caused by mutations in the previously described sepA gene (Harris et al. 1997). Analysis of double mutants suggests that the function of the PODD protein depends upon the SEPA formin. Finally, we show that mutations in sepA, and to a lesser extent podB and podD, alter the spatial pattern of polarized morphogenesis in germinating A. nidulans spores.

**MATERIALS AND METHODS**

**Strains, media, and growth conditions:** The genotypes of all strains used in this study are presented in Table 1. Media used [complete medium (CM) and minimal medium (MN)] were as described previously (Harris et al. 1994). YGV (0.5% yeast extract, 2% glucose, and 0.1% vitamins; Kafer 1977) was also used.

A. nidulans was grown on glass coverslips in liquid media as described previously (Harris et al. 1994). For all experiments, permissive temperature was 28°, semipermissive temperatures ranged from 35.5° to 37°, and restrictive temperature was 42°. Temperature shift experiments were initiated by inoculating conidiospores into YGV and allowing them to germinate into hyphal cells at 28° for 12 hr. Coverslips with adherent germings were removed for staining and microscopy just prior to the temperature shift. Cultures were then shifted to 42°, and additional coverslips were removed at 3 and 6 hr postshift. The polarity index was calculated as the length of a hypha (measured from the spore/hypha junction to the hyphal tip) divided by its width (measured at the approximate midpoint of the hypha).

**TABLE 1**

**A. nidulans strains**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Relevant genotype</th>
<th>Source</th>
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</thead>
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<tr>
<td>A28</td>
<td>pabaA6 biA1</td>
<td>FGSC*</td>
</tr>
<tr>
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<td>G. May</td>
</tr>
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<td>argB2; wa2; chaA1</td>
<td>Lab stock</td>
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<tr>
<td>ASH 5*</td>
<td>sepA1; wa2</td>
<td>Lab stock</td>
</tr>
<tr>
<td>ASH 35</td>
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<td>Lab stock</td>
</tr>
<tr>
<td>ALH 1*</td>
<td>sepA4Δ8m</td>
<td>L. Hamer</td>
</tr>
<tr>
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<td>hypA6 pabaA6</td>
<td>This study</td>
</tr>
<tr>
<td>ASH 83</td>
<td>podB1; pabaA6; pyrA4</td>
<td>This study</td>
</tr>
<tr>
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<td>podC1; pabaA6</td>
<td>This study</td>
</tr>
<tr>
<td>ASH 134</td>
<td>podD1; pabaA6; wa3</td>
<td>This study</td>
</tr>
<tr>
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<td>podC1 wa2; argB2</td>
<td>This study</td>
</tr>
<tr>
<td>ASH 311</td>
<td>podD1; pabaA6; argB2; wa3</td>
<td>This study</td>
</tr>
<tr>
<td>ASH 334</td>
<td>podB1; argB2; chaA1</td>
<td>This study</td>
</tr>
<tr>
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<td>sepA1 ya2; podD1; argB2</td>
<td>This study</td>
</tr>
<tr>
<td>AAS202</td>
<td>sepA3 pyrG89; podD1; wa3</td>
<td>This study</td>
</tr>
</tbody>
</table>

*1 Fungal Genetics Stock Center, Department of Microbiology, University of Kansas Medical Center (Kansas City, KS 66160-7420).
*2 The sepA4Δ8m allele was created by replacing an internal 2.2-kb BamHI fragment with the argB gene. Phenotypic analyses suggest that this is a null allele (Harris et al. 1997), and preliminary Western analyses with anti-SEPA sera detected only degradation products (K. Sharpless and S. Harris, unpublished results).
*3 Based on phenotypic analyses (Harris et al. 1997), the sepA1 and sepA3 alleles are presumed to be hypomorphic. Preliminary Western analyses with anti-SEPA sera detected full-length protein in these mutants (K. Sharpless, S. Avatapalli and S. Harris, unpublished results).

To monitor polarization kinetics in sepA and pod mutants, conidiospores were inoculated into YGV and incubated at 42°. Samples were collected at regular intervals, and the percentage of spores with a visible germ tube was determined (n = 200). The first sample in which 10–20% of the spores had germinated was chosen for further analysis, as we reasoned that most of the spores at this timepoint were on the verge of forming a germ tube. Samples were stained, and both nuclear number and cell volume were determined for 25 randomly selected swollen, ungerminated spores. The nonparametric Mann-Whitney test (Zar 1984) was used to determine if values obtained for a given mutant were significantly different from those of wild-type strains.

To determine the effects of cytochalasin A (CA) or nocodazole on the spatial pattern of germ-tube emergence, wild-type conidiospores were inoculated into YGV and incubated at 37° for 6 hr. Germinated spores were subsequently treated for 3 hr with either 5μg/ml CA or 2μg/ml nocodazole or were left untreated. They were then released into fresh YGV at 37° for an additional hour. Coverslips were then removed and processed for staining and microscopy.

**Genetic manipulations:** Methods used for the genetic analysis of A. nidulans were as described previously (Kafer 1977; Harris et al. 1994). Putative double mutants were backcrossed to a wild-type strain to confirm the presence of the parental mutations. Candidate pod mutants were identified by screening a previously described collection of 1156 ts mutants that were generated using 4-nitroquinoline 1-oxide (4NQO) as mutagen (Harris et al. 1994). For each mutant, the original isolate was patched onto a CM plate and examined under a...
dissecting microscope following 48 hr incubation at 42°. Mutants displaying morphologies consistent with defects in polarized morphogenesis were subjected to a secondary screen by growing them on coverslips at 42° in liquid YGV, followed by staining and microscopy. Mutants unable to establish hyphal polarity were selected and backcrossed to a wild-type strain at least two times prior to subsequent genetic and phenotypic analyses.

**Staining and microscopy:** Coverslips with adherent cells were processed for microscopy and stained with Calcofluor (to visualize cell walls and septa) and Hoechst 33258 (to visualize nuclei) as described previously (Harris et al. 1994). For labeling cell walls, coverslips with adherent cells were stained with 1 mg/ml FITC-conjugated wheat germ agglutinin (FITC-WGA; Sigma, St. Louis). Immunofluorescence microscopy for the detection of the actin and tubulin cytoskeletons was performed using standard protocols (Oakley and O smani 1993; Harris et al. 1994). The protocol for detecting the actin cytoskeleton was modified by substituting PEM (50 mM Pipes, pH 6.7; 25 mM EGTA, pH 7.0; 5 mM MgSO4) + 3% BSA for the PBS (phosphate-buffered saline) + BSA washes (Oakley and O smani 1993; Harris et al. 1994). Primary antibodies used were the mouse anti-actin C4 monoclonal (ICN Biomedicals, Inc.) at 1:400 and the mouse anti-α-tubulin DM1A monoclonal (Sigma Immunochromicals) at 1:200. The secondary antibody was FITC-conjugated sheep anti-mouse (Sigma Immunochromicals) at 1:200.

**RESULTS**

**Identification and phenotypic characterization of the pod mutants:** To systematically identify gene products required for polarized morphogenesis in A. nidulans, we screened for mutants defective in the establishment of hyphal polarity. Because we sought mutations that cause specific defects in morphogenesis without adversely affecting cellular growth and/or nuclear division, we screened for mutants displaying the following phenotypes: (i) failure of germinating spores to produce a germ tube, (ii) continued growth and enlargement of spores in a depolarized manner, and (iii) accumulation of multiple nuclei. A collection of 1156 ts mutants was screened as described in materials and methods. Five mutants displaying defects in the establishment of hyphal polarity were recovered following the secondary screen. Several backcrosses to a wild-type strain demonstrated that the morphogenetic defect co segregated with temperature sensitivity in four of these mutants, and, in each case, both phenotypes were caused by a recessive mutation in a single gene. Complementation and linkage analyses revealed that these four mutations define four distinct genes, which were named podA–D for polarity defective (Figure 1).

Analysis of multiple segregants from each backcross showed that the podB1, podC1, and podD1 mutations prevent the establishment of hyphal polarity at restrictive temperature. These mutations lead to the accumulation of swollen round spores possessing 4–8 (podC1), ≥8 (podB1), or ≥16 (podD1) nuclei (Figure 1, C–E). Under the same conditions, the podA1 mutation causes a severe delay in the establishment of hyphal polarity.

Germ-tube emergence occurs when podA1 spores typically possess 4 nuclei and have swollen to an average volume of 141.4 ± 52.1 μm³ (vs. 81.2 ± 28.7 μm³ for wild-type spores). Upon germination, podA1 mutants form multinucleate hyphae that are abnormally wide (Figure 1, A and B). The podA1 morphotypes are not ts lethal, because, to varying extents, they were able to grow at permissive temperature following an extended incubation (i.e., ~12 hr) at 42° (S. Harris, unpublished data). Furthermore, in no case were the phenotypes caused by these mutations osmotically remedial.

Linkage analyses revealed that the podA1 mutation maps to chromosome I and displays tight linkage to the sepA locus (3/100 recombinant segregants). Another mutation that causes morphogenetic defects, hypA1, also maps to this region of chromosome I (Kaminskyj and Hamer 1998). Complementation tests demonstrated that the podA1 and hypA1 mutations are allelic (S. Kaminskyj, personal communication; see discussion); hence the podA1 mutation has been renamed hypA6/podA1. The podB1 mutation maps to chromosome II and displays linkage to the wa locus (75/800 recombinant segregants). The podC1 mutation also maps to this region of chromosome II (43/395 recombinants with respect to wa), but the observation that ts1 recombinants can be readily obtained (33/100) from a podC1 × podB1 cross shows that podC1 defines a locus distinct from podB1. The podD1 mutation has not yet been unambiguously assigned to a chromosome.
The germination site. Elongation within 3 hr (Figure 4A). The polarity index of two nuclei and have swollen to an average volume of 81.2 ± 28.7 μm³. However, in a sepA4 mutant, germ-tube emergence does not occur until spores possess at least four nuclei and have attained an average volume of 198.1 ± 87.3 μm³. The difference in cell volume at the time of germination in the sepA4 mutant is statistically significant when compared to the wild-type strain (α = 0.05, Z = 5.50). Furthermore, the large swollen spores formed by the sepA4 mutant possess an actin cytoskeleton that has not become polarized (Figure 2). These observations demonstrate that the establishment of hyphal polarity is severely delayed in the absence of sepA function. In addition, they suggest that SEPA may be needed to properly organize the actin cytoskeleton at the germination site.

Characterization of sepA pod double mutants: The characterization of SEPA as a member of the formins suggests that it may be required for organization of the actin cytoskeleton at sites of localized cell-wall deposition (Harris et al. 1997). According to this model, the localization and/or activity of gene products involved in polarized morphogenesis may be dependent upon SEPA function. In such a scenario, mutations in the sepA gene may exacerbate the phenotypes caused by inactivation of these gene products. This notion was investigated by constructing sepA pod double mutants and testing for synthetic phenotypes (i.e., defects that exceed those caused by either parent).

The analysis of sepA1, hypA6/podA1, sepA1;podB1, and sepA1;podC1 double mutants failed to reveal detectable synthetic growth defects at permissive or semipermissive temperatures. In contrast, unlike the parent single mutants, sepA1;podD1 double mutants failed to form colonies at 37°C (Figure 3A). Whereas sepA1 or podD1 mutants can establish hyphal polarity at this temperature, double mutants underwent considerable swelling, accumulated ≥16 nuclei, and failed to produce germ tubes (Figure 3B–D). Moreover, the ability of podD1 mutants to form colonies on agar-solidified media at 42°C was abolished by the sepA1 mutation (Figure 3A). These synthetic defects were not allele-specific, as sepA3;podD1 double mutants displayed an identical spectrum of phenotypes (sepA4;podD1 double mutants could not be constructed). These observations suggest that the activity and/or localization of PODD may depend upon SEPA function.

The podC and podD genes are required only for the establishment of hyphal polarity: Phenotypic characterization of the pod mutants has demonstrated that the podB, podC, and podD genes are required for the establishment of hyphal polarity. To determine if these genes are also needed for the maintenance of polarity, mutant spores were allowed to form germ tubes at permissive temperature and were then shifted to 42°C. The polarity index (hyphal length/hyal width; see material and methods) was determined for samples taken prior to the shift and during the subsequent period of incubation at 42°C. Under these conditions, mutants able to maintain hyphal polarity will continue to elongate and will possess a polarity index that increases with time. In contrast, the polarity index will remain unchanged or will decrease in mutants that cease hyphal elongation due to a failure to maintain polarity.

Following growth at 28°C, hyphae formed by hypA6/podA1 and podC1 mutants displayed a polarity index that was noticeably lower than that of wild type or any of the other pod mutants (Figure 4A). This observation indicates that the hypA6/podA1 and podC1 mutations caused mild defects in polarized growth even at permissive temperature. When shifted to restrictive temperature, hypA6/podA1 and podB1 mutants ceased hyphal elongation within 3 hr (Figure 4A). The polarity index for podB1 mutants subsequently declined due to exten-
Figure 3.—Growth phenotype and cellular morphology of sepA1 podD1 double mutants. (A) Growth phenotype. Conidiospores were streaked onto triplicate CM plates. Plates were incubated at 28° for 3 days, 37° for 2 days, or 42° for 2 days. The following strains were used: (1) ASH35 (sepA1); (2) ASH134 (podD1); (3) AAS100 (sepA1;podD1). Note that podD1 mutants are able to grow on agar-solidified media at restrictive temperature. Under these conditions, mutant hyphae are swollen and display considerable lysis. They do not undergo asexual development. (B–D) Cellular morphology. Conidiospores were germinated on coverslips for 12 hr at 37°. Cells were stained with Calcofluor and Hoechst 33258 to visualize cell walls and nuclei, respectively. (B) ASH134 (podD1), (C) ASH35 (sepA1), (D) AAS100 (sepA1;podD1). Bar, 5 μm.
The normal pattern of cell-wall deposition in *A. nidulans* requires a functional *podB* gene. The altered pattern of cell-wall deposition in *podB1* mutants could be attributed to an underlying defect in cytoskeletal organization. This possibility was investigated by using indirect immunofluorescence with monoclonal anti-actin and anti-tubulin antibodies to examine cytoskeletal organization in upshifted *podB1* mutants. The organization of the actin and microtubule cytoskeleton in wild-type hyphae subjected to a temperature shift are shown in Figure 5. The pattern of actin localization displays two features (Figure 5A, left): (i) a dense patch at the immediate hyphal tip and (ii) cortical spots extending in a basal direction from the tip. Wild-type hyphae also form actin rings at septation sites (not shown; Harris et al. 1994). Cytoplasmic microtubules are found as longitudinal arrays that parallel the axis of hyphal growth and extend into the region subtending the tip (Figure 5A, right).

Following the shift to 42°C, *podB1* mutants displayed apparent defects in actin cytoskeletal organization in hyphal tips (Figure 5). In particular, swollen hyphal tips did not contain a dense patch of actin staining (Figure 5, B and C). Instead, actin spots were distributed in a somewhat irregular fashion throughout the cortical region of the hyphal tip. Furthermore, atypical clusters of actin spots were observed in basal regions of swollen hyphae (Figure 5D). These clusters may correspond to the subapical sites of cell-wall deposition noted in the WGA-labeling experiment. Note that septation-associated actin rings were observed in upshifted *podB1* hyphae (Figure 5E), which suggests that the mutation does not affect the organization of all actin-based structures. In contrast to the actin cytoskeleton, microtubule organization did not appear to be dramatically affected by the *podB1* mutation (Figure 5E). However, it was noted that cytoplasmic microtubules did not form organized arrays in the vicinity of swollen tips. Collectively, these observations suggest that the *podB* gene is needed for proper organization of the cytoskeleton at the hyphal tip.

**Patterns of polarized morphogenesis in *sepA* and *pod* mutants**: Germinating *A. nidulans* conidiospores typically produce two or three germ tubes in a sequential manner; following the formation of the first germ tube, the spore establishes a second axis of polarity upon which the next germ tube emerges. To determine if the first axis of polarity exerts any influence over the selection of the second axis, the pattern of germ-tube emergence was examined in wild-type spores possessing two germ tubes. Three patterns were observed (Table 2): (i) bipolar, whereby the second germ tube emerges from the opposite hemisphere (≈180°) relative to the first, (ii) quarterpolar, whereby the second germ tube emerges at a ≈90° angle relative to the first, and (iii) random, whereby the second germ tube emerges at a
random site within the same hemisphere as the first. At all temperatures tested, the majority of wild-type conidia (>80%) displayed the bipolar pattern of germination (Table 2). Notably, <3% of wild-type spores exhibited the random pattern of germination. These results define the normal spatial pattern of germ-tube emergence in germinating A. nidulans conidia.

During routine observations, it was noted that the normal pattern of germ-tube emergence appeared to be altered in sepA mutants. Indeed, when examined at restrictive temperature, two different alleles of sepA dramatically perturb this pattern (Table 2; Figure 6). The bias toward the bipolar pattern is abolished by the sepA1 and sepA4 mutations, and both mutations also lead to an increase in the percentage of spores displaying the random pattern of germ-tube emergence (Table 2; Figure 6). Similar, but less severe, disruption of the normal pattern of polarized morphogenesis was observed when podB1 and podD1 mutants were incubated at the maximum permissive temperature that allowed formation of two germ tubes (Table 2). In contrast, hypA6/podA1 and podC1 mutations had no effect. These results suggest that SEPA and, to a lesser extent, PODB and PODD are needed for the spatial control of polarized morphogenesis in germinating A. nidulans conidia.

Two possible explanations could account for the ability of sepA mutations to disrupt the normal pattern of germ-tube emergence. First, the absence of a septum could permit the use of inappropriate germination sites. However, the failure of the sepD5 mutation, which also prevents septum formation (Harris et al. 1994), to perturb the normal pattern of germ-tube emergence suggests that this possibility is unlikely (Table 2). Alternatively, the failure of sepA mutants to properly organize the actin cytoskeleton at presumptive germination sites could affect the pattern of germ-tube emergence. If so, other perturbations of the actin cytoskeleton should have a similar effect. To test this notion, wild-type spores were treated with CA following the formation of the first germ tube. In A. nidulans, CA treatment causes loss of normal actin cytoskeletal organization and blocks actin-dependent processes such as polarized growth, secretion, and septation (Harris et al. 1994; Torralba et al. 1998). Following CA treatment, spores were released into fresh medium and the site at which the second germ tube emerged was determined. As was observed in sepA mutants, the bias toward the 180° bipolar pattern was reduced by CA treatment (Table 2). Furthermore, the fraction of CA-treated spores displaying the random pattern was much larger than that of untreated controls. Because disruption of the microtubule cytoskeleton with nocodazole does not dramatically alter the pattern of

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Figure 5—podB mutants display defects in cytoskeleton organization. (A) Wild type and (B–E) podB1 conidiospores germinated on coverslips for 12 hr at 28° were shifted to restrictive temperature. Samples were removed at 3 hr postshift, stained with mouse anti-actin or anti-α-tubulin monoclonal antibodies, and examined by indirect immunofluorescence microscopy. (A) Left, actin localization in wild-type hyphae. The accumulation of actin at the hyphal tip is depicted by the arrowhead. Right, tubulin localization in wild-type hyphae. (B–D) Left, nuclei (stained with Hoechst 33258) and septa (stained with Calcofluor) in podB1 mutants. Right, actin localization in podB1 mutants. The arrowhead in B indicates random arrays of cortical patches in the tips of swollen podB1 hyphae. The arrowhead in D depicts a subapical region where aggregates of actin patches have formed. (E) Left, nuclei (stained with Hoechst 33258) and septa (stained with Calcofluor) in podB1 mutants. The arrowhead points to a cluster of nuclei in a swollen hyphal tip. Right, tubulin localization in podB1 mutants. Bar, 5 μm.
TABLE 2
Spatial patterns of polarized morphogenesis

<table>
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<tr>
<th>Genotype</th>
<th>Temperature</th>
<th>180° biopolar</th>
<th>90° quarterpolar</th>
<th>random</th>
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<tr>
<td>1 wt</td>
<td>42°C</td>
<td>84</td>
<td>16</td>
<td>0</td>
</tr>
<tr>
<td>2 wt</td>
<td>37°C</td>
<td>83.5</td>
<td>15</td>
<td>1.5</td>
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<td>3 sepA1</td>
<td>42°C</td>
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<td>40</td>
<td>16</td>
</tr>
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<td>42°C</td>
<td>34</td>
<td>40</td>
<td>26</td>
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<td>1</td>
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<td>67</td>
<td>31</td>
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Conidiospores were germinated on coverslips for 9–12 hr at the indicated temperature. Coverslips were stained with Calcofluor and Hoechst 33258. For each strain, the pattern of germ-tube emergence was scored only in those conidia that possessed two germ tubes (n = 100). wt, wild type.

In this pattern, the second germ tube emerges from the opposite hemisphere (z=180°) of the spore relative to the first.

In this pattern, the second germ tube emerges at z=90° relative to the first.

In this pattern, the second germ tube emerges from a random site within the same hemisphere as the first.

For these experiments, conidia were germinated on coverslips for 6 hr at 37°C. Germinated conidia were subsequently treated for 3 hr with either 5 μg/ml CA or 2 μg/ml nocodazole (Noc) or were left untreated. They were then released into fresh media at 37°C for an additional hour.

germ-tube emergence (other than causing increased use of the quarterpole; Table 2), these observations suggest that the spatial control of polarized morphogenesis in germinating A. nidulans spores primarily depends upon the integrity of the actin cytoskeleton.

DISCUSSION

During the process of germination, A. nidulans spores undergo a morphogenetic switch from isotropic expansion to polarized apical growth. Thereafter, cell-surface expansion is confined to the hyphal tip. Here, we report a first systematic attempt to identify and characterize genes that are required for the establishment and/or maintenance of hyphal polarity in A. nidulans. In particular, we show that: (i) the sepA, hypA, and podB genes are required for multiple aspects of polarized morphogenesis, (ii) the podC and podD genes are specifically needed for the establishment of hyphal polarity, and (iii) polarized morphogenesis relies upon spatial controls that are dependent upon the integrity of the actin cytoskeleton.

Genes required for the establishment and maintenance of hyphal polarity: Mutations in the sepA, hypA, and podB genes cause pronounced defects in multiple aspects of polarized morphogenesis in A. nidulans hyphae. In podB1 mutants, spores and hyphal cells undergo isotropic expansion without defining polarized axes of growth. In contrast, spores possessing sepA or hypA6/podA1 mutations are able to switch from isotropic expansion to polarized apical growth, but only after a severe delay. In addition, they form hyphal cells that...
are abnormally wide and have a tendency to undergo apical branching (Harris et al. 1994; Kaminsky and Hamer 1998). These observations imply that the sepA, hypA, and podB genes encode products that are involved in both the establishment and the maintenance of hyphal polarity in A. nidulans.

Previous molecular analyses demonstrated that SEPA is a member of an expanding family of proteins known as the formins (Frazier and Field 1997; Harris et al. 1997; Wasserman 1998). It has already been shown that SEPA is required for the formation of actin rings during septation in A. nidulans (Harris et al. 1997). Here, we provide evidence that SEPA is also needed to efficiently organize the actin cytoskeleton at the site of germ-tube emergence. As with other formins, the morphogenetic functions performed by SEPA are likely to be mediated by actin-associated proteins such as profilin and Bud6p (Manseau et al. 1996; Chang et al. 1997; Evangelista et al. 1997). In addition, spatial regulation of SEPA function presumably requires interactions with Rho-related GTPases (Evangelista et al. 1997; I mamura et al. 1997; Watanabe et al. 1997). However, it remains unclear how these interactions control the apparently distinct functions of SEPA during septation (i.e., formation of an actin ring) vs. germination (i.e., formation of a dense patch of cortical actin). Perhaps interactions between SEPA and different Rho-related GTPases permit spatial discrimination of its function. Alternatively, particular SEPA function may be mediated by specific interactions with other proteins (such as PODD).

Complementation and linkage analyses have revealed that the podA1 mutation resides in the recently characterized hypA gene (S. Kaminsky, personal communication). Mutations in hypA cause two distinct phenotypes: (i) delocalized cell-wall deposition in tip hyphal cells and (ii) failure to arrest growth and nuclear division in normally quiescent subapical hyphal cells (Kaminsky and Hamer 1998). Molecular characterization of the hypA gene has failed to provide any clues to its function. In particular, hypA encodes a 5.3-kb open reading frame that does not show significant similarity to any sequence in current databases, nor does it possess informative motifs (Kaminsky and Hamer 1998). Thus, hypA encodes a novel gene that is required for localized cell-surface expansion and cell-pattern formation in fungal hyphae. Because it is not known if hypA1 and hypA6/ podA1 are null alleles, further functional characterization of hypA will require the construction and phenotypic analysis of a null mutant.

Although the molecular nature of PODD has yet to be determined, two observations suggest that it is required for the proper localization and/ or function of the morphogenetic machinery at the hyphal tip. First, temperature shift and cell-wall labeling experiments show that the podB1 mutations leads to isotropic cell-surface expansion. Second, results from indirect immunofluorescence microscopy demonstrate that the organization of the actin and microtubule cytoskeletons in the hyphal tip is disrupted by the podB1 mutation. These phenotypes suggest that PODD may function in a manner analogous to the Saccharomyces cerevisiae polarity establishment proteins (i.e., Cdc24p, Cdc42p, and Cdc43p; Pringle et al. 1995). For example, it could be a component of a signal transduction pathway (i.e., a GTPase cascade; Chant and Stowers 1995) that orchestrates multiple events at sites of polarized morphogenesis. In this context, it should be noted that expression of the A. nidulans homologue of the Rho-related GTPase Cdc42p does not alter the morphogenetic defects caused by the podB1 mutation (M. Lee, A. Hofmann and S. Harris, unpublished results).

**Genes specifically required for the establishment of hyphal polarity:** Temperature shift experiments show that the podC and podD genes are needed only for the establishment of hyphal polarity. If spores possessing a mutation in either of these genes are allowed to form a germ tube prior to imposition of restrictive conditions, hyphal elongation continues despite the apparent absence of PODC or PODD. Preliminary results obtained from indirect immunofluorescence experiments indicate that actin localizes normally in hyphal tips of upshifted podD1 mutants, but is arranged in an apparently random array of cortical spots in the extremely swollen subtending spore (S. Harris, unpublished results). These observations suggest that the podC and podD genes encode functions specifically required for the switch from isotropic expansion to polarized apical growth that precedes spor germination. It should be noted that other aspects of the germination program (i.e., breaking of spore dormancy, isotropic expansion, reentry into the cell cycle; d'Enfert 1997) occur normally in podC1 and podD1 mutants. This is the first evidence that spor germination in A. nidulans depends upon specific morphogenesis-related functions beyond those involved in general polarized growth.

Although the specific function of PODD remains to be determined, the observation that sepA mutations exacerbate the phenotypes caused by the podD1 mutation implies that its localization and/ or activity is dependent upon the presence of functional SEPA. In this context, the delayed switch to polarized apical growth caused by sepA mutations may in part be due to their effects on PODD.

**Spatial control of polarized morphogenesis:** A. nidulans conidiospores show a consistent spatial pattern of polarized morphogenesis, which was quantified in spores by scoring sites of germ-tube emergence. Because of the absence of morphological markers in ungerminated spores, the possibility that specific rules govern the emergence of the first germ tube could not be addressed. However, by using the first germ tube as a marker, it was possible to define the pattern in which the second germ tube emerged. Our experiments revealed the existence of a pronounced bias toward the
use of the opposite pole when the second germ tube is emerging from a spore.

To explore potential mechanisms that may be involved in specifying the site of germ-tube emergence, the spatial orientation of the second germ tube was scored in mutants that are defective in polarized morphogenesis. Notably, mutations in the sepA gene, and to a lesser extent in the podB and podD genes, reduce the bias toward bipolar germination. More strikingly, the use of random sites increased significantly in the bias toward bipolar germination. More strikingly, position morphological landmarks at specific cortical podB and sepA genes, reduce the normal pattern of polarized morphogenesis suggests an underlying role for the actin cytoskeleton. Consistent with this notion, treatment of wild-type spores with CA, which prevents kinetochore and cdc12p, a protein required for cytokinesis in yeast, is a component of the cell division ring and interacts with profilin in A. nidulans (Torralba et al. 1998), the actin cytoskeleton also plays a role in the spatial control of hyphal morphogenesis. Although the function of cytoplasmic microtubules in the spatial control of hyphal morphogenesis in A. nidulans is less obvious, two observations do suggest a possible role. First, depolymerization of microtubules causes increased use of the quarterpole when the second germ tube is emerging from a spore. Second, loss of microtubules affects the maintenance of polarized axes of morphogenesis (Jochova et al. 1993). The unicellular yeasts each display a bipolar pattern of polarized morphogenesis during vegetative growth (reviewed by Mata and Nurse 1998). The bipolar pattern of germ-tube emergence exhibited by A. nidulans shares a number of similarities with bipolar budding in S. cerevisiae. In both conidiospores and yeast cells, opposite poles are used for successive polarization events. Furthermore, in both organisms, the site selection process depends upon the integrity of the actin cytoskeleton (Yang et al. 1997) and is compromised by mutations in related proteins (i.e., SEPA in A. nidulans, Bni1p in S. cerevisiae; Zahner et al. 1996). In contrast, cytoplasmic microtubules play a predominant role in establishing the bipolar mode of growth in S. pombe (Mata and Nurse 1997). Despite these differences, both yeasts use the appropriate cytoskeletal network to position morphological landmarks at specific cortical sites (Chant et al. 1995; Sanders and Herskowitz 1996; Mata and Nurse 1997; Yang et al. 1997). Thus, it is tempting to speculate that a functionally analogous cortical marking system may exist in A. nidulans conidiospores.

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LITERATURE CITED


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