Characterization of Mug33 reveals complementary roles for actin cable-dependent transport and exocyst regulators in fission yeast exocytosis

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Summary
Although endocytosis and exocytosis have been extensively studied in budding yeast, there have been relatively few investigations of these complex processes in the fission yeast Schizosaccharomyces pombe. Here we identify and characterize fission yeast Mug33, a novel Tea1-interacting protein, and show that Mug33 is involved in exocytosis. Mug33 is a Sur7/PalI-family transmembrane protein that localizes to the plasma membrane at the cell tips and to cytoplasmic tubulovesicular elements (TVEs). A subset of Mug33 TVEs make long-range movements along actin cables, co-transporting with subunits of the exocyst complex. TVE movement depends on the type V myosin Myo52. Although mug33Δ mutants are viable, with only a mild cell-polarity phenotype, mug33Δ myo52Δ double mutants are synthetically lethal. Combining mug33Δ with deletion of the formin For3 (for3Δ) leads to synthetic temperature-sensitive growth and strongly reduced levels of exocytosis. Interestingly, mutants in non-essential genes involved in exocyst function behave in a manner similar to mug33Δ when combined with myo52Δ and for3Δ. By contrast, combining mug33Δ with mutants in non-essential exocyst genes has only minor effects on growth. We propose that Mug33 contributes to exocyst function and that actin cable-dependent vesicle transport and exocyst function have complementary roles in promoting efficient exocytosis in fission yeast.

Key words: Mug33, Actin filament, Schizosaccharomyces pombe, Sur7/Pall, Exocytosis, Fission yeast

Introduction
The interplay between actin filaments and subcellular vesicles is a key feature of membrane trafficking in yeast. Work in budding yeast from the 1970s onwards has identified many of the key molecules and mechanisms governing efficient endocytosis and exocytosis (Novick et al., 1980; Riezman, 1985), including several proteins regulating actin dynamics (Galletta and Cooper, 2009). During endocytosis, actin patches at the cell membrane are recruited to drive vesicle internalization (Gourlay et al., 2003; Huckaba et al., 2004; Kaksonen et al., 2003; Kubler and Riezman, 1993; Toshima et al., 2006). Once internalized, vesicles are transported on actin cables to an endosomal compartment (Huckaba et al., 2004). During exocytosis, actin cables are used for type V myosin-dependent transport of exocytic vesicles from the post-Golgi compartment to the plasma membrane (Govindan et al., 1995; Johnston et al., 1991; Pruyne et al., 1998; Schott et al., 2002; Trybus, 2008).

The exocyst, a multiprotein complex essential for polarized secretion in cell types from yeast to mammals, functions to tether exocytic vesicles at the plasma membrane before SNARE-mediated membrane fusion (He and Guo, 2009; Hsu et al., 2004; Hsu et al., 1999; Hsu et al., 2004; Kaksonen et al., 2003; Kubler and Riezman, 1993; Toshima et al., 2006). Once internalized, vesicles are transported on actin cables to an endosomal compartment (Huckaba et al., 2004). During exocytosis, actin cables are used for type V myosin-dependent transport of exocytic vesicles from the post-Golgi compartment to the plasma membrane (Govindan et al., 1995; Johnston et al., 1991; Pruyne et al., 1998; Schott et al., 2002; Trybus, 2008).

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Fission yeast Schizosaccharomyces pombe grows in a highly polarized fashion, dependent on the actin cytoskeleton (Mitchison and Nurse, 1985; Rupes et al., 1999). Cell growth and division involves the polymerization of filamentous actin in a number of highly dynamic structures: membrane-associated patches, which are nucleated by the Arp2/3 complex and localize at sites of extensive growth at cell tips (McCollum et al., 1996); cytoplasmic actin cables nucleated at cell tips by the formin For3 (Feierbach and Chang, 2001; Feierbach et al., 2004); and the cytokinetic contractile ring, in which filaments are nucleated by the formin Cdc12 (Chang et al., 1997). Fission yeast initially grows in a monopolar fashion and then switch to bipolar growth after completion of S phase, in a process requiring redistribution of polarized actin [so-called “new-end take-off” (NETO)] (Mitchison
Results

The Tea1-interacting protein Mug33 is a membrane protein associated with sites of cell growth

In a tandem-affinity purification of the cell-polarity regulator Tea1 (Mata and Nurse, 1997) we identified many known Tea1-interactors, including Tip1, Tea3, Tea4 and Mod5 (Fig. 1A) (Arellano et al., 2002; Brunner and Nurse, 2000; Martin et al., 2005; Snaith and Sawin, 2003), and several previously uncharacterized proteins, including Mug33 (SPCC1739.10; a complete list of proteins identified is presented in supplementary material Table S1). Mug33 (for meiotically-upregulated gene 33) was initially named as a result of a transcriptome analysis during meiosis (Mata et al., 2002). However, no meiotic defects have been identified in mug33 cells, which are viable (Gregan et al., 2005; Martin-Castellanos et al., 2005), and to date the function of Mug33 is unknown. We confirmed the Tea1–Mug33 interaction by co-immunoprecipitation (Fig. 1B).

Although tea1Δ mutants show a range of polarity defects, mug33Δ mutants showed minimal polarity defects. Unlike tea1Δ mutants, which grow in a monopolar fashion during exponential growth (Glynn et al., 2001; Mata and Nurse, 1997; Verde et al., 1995), mug33Δ cells grow in a bipolar fashion, like wild-type cells (supplementary material Fig. S1A, Fig. S4B), and mug33Δ cells were indistinguishable from wild-type cells by differential interference contrast (DIC) microscopy (supplementary material Fig. S4A). After stresses that transiently perturb the actin cytoskeleton, such as return-to-growth from stationary phase, up to 80–90% of tea1Δ cells form bent or branched cells (Browning et al., 2000; Sawin and Snaith, 2004; Snaith and Sawin, 2003). By contrast, in return-to-growth experiments mug33Δ cells grew as straight cells (Fig. 1C). Some mild polarity mutants in the Tea1 pathway, such as mod5Δ, grow as straight cells in conventional return-to-growth experiments but form bent or branched cells when return-to-growth experiments are performed in the presence of the microtubule-disrupting drug methyl benzimidazole-2-yl carbamate (MBC) (Snaith and Sawin, 2003). In return-to-growth experiments in the presence of MBC, mug33Δ mutants formed an intermediate number of bent or branched cells – greater than in wild-type cells but substantially less than in mod5Δ cells. (Fig. 1C). Overall, these results suggest that Mug33 plays a relatively minor role in growth–polarity regulation.

Mug33 is a 37-kDa protein that is alternatively predicted to contain either four transmembrane-spanning regions or a signal sequence and three transmembrane-spanning regions in its N-terminus; the Mug33 C-terminus (~150 amino acids) is predicted to be cytoplasmic. (Fig. 2A) (Bendtsen et al., 2004; Hofmann and Stoffel, 1993; Krogh et al., 2001). We identified obvious Mug33 primary sequence homologs in various Schizosaccharomyces species, with amino acid identity preserved along the length of the protein (supplementary material Fig. S1E). Database searching revealed that Mug33 is a member of the Sur7/Pall family (pfam 06687) of fungal transmembrane proteins, with similarity restricted to the N-terminus (Fig. 2A; supplementary material Fig. S1E). Budding yeast Sur7p, one of the more-studied members of this family, is a multicopy suppressor of mutations in the amphiphysins Rvs161p and Rvs167p,
which are involved in the scission of endocytic vesicles (Kaksonen et al., 2005; Ren et al., 2006; Sivadon et al., 1997). Sur7p and its paralogs associate with eisosomes [which are also known as MCC (for membrane compartment of Can1p)], static membrane-associated protein complexes that have been implicated in sphingolipid metabolism, membrane organization and morphogenesis (Alvarez et al., 2008; Young et al., 2002). Eiosomes/MCC have been proposed to mark sites of endocytosis in budding yeast (Malinska et al., 2004; Penalva et al., 2008). Whether the Sur7/PalI-conserved regions in these different proteins perform a specific or unique molecular function is currently unknown.

To study the dynamics of Mug33 localization, we tagged the chromosomal copy of the gene with GFP and examined its localization in wild-type cells and polarity mutants (Fig. 2B; supplementary material Fig. S2A). In wild-type interphase cells, Mug33–GFP was present in structures in the cytoplasm and on or near the plasma membrane at both cell tips. In dividing cells, Mug33–GFP was also enriched at the cell division site (supplementary material Fig. S1B). In tea1Δ cells, Mug33–GFP was also found in cytoplasmic structures and on the plasma membrane, but cell-tip localization was restricted to only one cell tip. This is probably a consequence of the monopolar growth of tea1Δ mutants rather than absence of Tea1 in itself, because we observed similar one-cell-tip localization in the monopolar-growth mutants tea3Δ, bud6Δ and pak1-34 (Arellano et al., 2002; Glynn et al., 2001; Ottilie et al., 1995; Verde et al., 1995). Mug33 localization was relatively unaffected by deletion of the gene encoding the membrane-associated Tea1-binding protein Mod5, in which most cells undergo bipolar growth (Snaith and Sawin, 2003). Co-imaging of RFP-tagged Mug33 (Mug33–mKate) (Shcherbo et al., 2007; Snaith et al., 2010) together with actin filaments labeled with a GFP-tagged calponin homology domain of the IQGAP protein Rng2 (GFP–CHD<sup>in2</sup>); (Karagiannis et al., 2005; Wachtler et al., 2003; Wang, C. H. et al., 2003) revealed that the one-cell-tip localization of Mug33 in tea1Δ cells was specific to the actin-rich growing end (Fig. 2C).

Because budding yeast Sur7 localizes to eisosomes/MCC, we examined the relationship between Mug33 and eisosomes/MCC, which has not been described in fission yeast to date. We tagged the fission yeast homolog of the budding yeast eisosome/MCC protein Pil1p with RFP (Pil1–tdTomato) and found that it localized to relatively immobile membrane-associated structures that are concentrated towards the cell middle (Fig. 2D,E) and are probably eiososome/MCC equivalents. We observed little or no overlap of Mug33–GFP with Pil1–tdTomato (Fig. 2E). To test whether the cytoplasmic C-terminal region of Mug33 was important for its localization, we generated a GFP-tagged version of Mug33 in which amino acids 181–336 are deleted but the Sur7/PalI-conserved region is left intact (Mug33ΔC–GFP). Interestingly, Mug33ΔC–GFP was no longer concentrated at cell tips but instead colocalized with Pil1–tdTomato (Fig. 2F,G). These results indicate that the Mug33 C-terminus is important for regulating Mug33 localization, perhaps overriding a PalI/Sur7 domain-driven association with an eiosome/MCC-like compartment.

**Mug33 tubulovesicular elements translocate on actin cables using the type V myosin Myo52**

Although we initially identified Mug33 as a Tea1-interacting protein, Mug33–GFP and Tea1–tdTomato showed only partial
overlapping localization at cell tips and did not colocalize in the cytoplasm (supplementary material Fig. S1C). Unlike Tea1 particles, which are dynamically transported towards cell tips by association with growing microtubule plus-ends (Behrens and Nurse, 2002; Feierbach et al., 2004; Snaith and Sawin, 2003), Mug33 cytoplasmic structures showed no colocalization with microtubules (supplementary material Fig. S1D, Movie 1).

Time-lapse imaging revealed that Mug33 cytoplasmic structures were nevertheless dynamic, showing two types of movement: oscillatory behavior over short distances, in apparently random directions; and long rapid vectorial translocation, which was much faster than Tea1 particle movement (~0.34 μm/second for Mug33 compared with ~0.04 μm/second for Tea1; Fig. 3B–D; Table 1; supplementary material Fig. S1C). In wild-type cells, 48% of Mug33 translocations terminated at cell tips, 27% started at cell tips and 25% occurred in the cytoplasm without obvious contact with cell tips (Table 1). Analysis of still and time-lapse images revealed that translocating Mug33 structures were not always discrete puncta, like Tea1 particles, but instead often showed a more extended and sometimes dynamic structure, suggesting deformation under tension (supplementary material Fig. S2, Movie 2). We will therefore refer to the Mug33-containing structures as tubulovesicular elements (TVEs).

The fast movement of Mug33 TVEs persisted after disruption of microtubules with MBC but was abolished upon disruption of filamentous actin with latrunculin B (LatB; Fig. 3A,B; Fig. 4F) suggesting that translocation involves the actin cytoskeleton. Co-imaging Mug33–mKate with actin filaments (GFP–CHDRng2) showed that Mug33 TVEs associated with and translocated along actin cables, in both wild-type and tea1Δ cells (Fig. 3C,D, Fig. 4F; supplementary material Movies 3, 4).

Mug33 TVE translocations were absent in for3Δ formin-mutant cells, which specifically lack actin cables as a result of defects in nucleation of the filaments that generate cables (Feierbach and Chang, 2001) (Fig. 4A,B,F; supplementary material Movies 5, 6). In principle, Mug33 TVE movements on actin cables could involve either polymerization-driven mechanisms or motor proteins. For example, in wild-type cells, after nucleating an actin filament, 2190

Fig. 3. Mug33 tubulovesicular elements translocate along actin cables. (A) Localization of Mug33–GFP in untreated (DMSO control), MBC-treated and LatB-treated wild-type cells. (B) Kymographs showing Mug33–mKate TVE translocations or absence of translocations in individual treated or untreated cells; images above and below kymographs show the cells at beginning and end of the kymographs. The horizontal axes of kymographs show combined projection of y- and z-information along the x-axis of images. Vertical axes of kymographs show time; the total time is 67 seconds for untreated cells, 58 seconds for MBC-treated cells and 43 seconds for LatB-treated cells (see Materials and Methods). (C,D) Time-lapse montage of Mug33–mKate (green) and GFP–CHDRng2 (actin, red) in (C) wild-type cells and (D) tea1Δ cells. Arrowheads indicate Mug33 TVEs. The elapsed time is shown in seconds. Scale bars: 5 μm.

Table 1. Analysis of Mug33 translocations

<table>
<thead>
<tr>
<th>Strain</th>
<th>Frequency (events per cell per minute)</th>
<th>Length (μm; ±s.d.)</th>
<th>Speed (μm/second; ±s.d.)</th>
<th>Towards cell tip (%)</th>
<th>Away from cell tip (%)</th>
<th>In cell interior (%)</th>
<th>Total events</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild-type</td>
<td>1.34</td>
<td>2.91±1.27</td>
<td>0.34±0.17</td>
<td>48</td>
<td>27</td>
<td>25</td>
<td>55</td>
</tr>
<tr>
<td>Wild-type, MBC-treated</td>
<td>1.39</td>
<td>3.26±0.91</td>
<td>0.34±0.13</td>
<td>56</td>
<td>25</td>
<td>19</td>
<td>77</td>
</tr>
<tr>
<td>tea1Δ</td>
<td>0.87</td>
<td>2.56±1.20</td>
<td>0.21±0.10</td>
<td>47</td>
<td>29</td>
<td>24</td>
<td>75</td>
</tr>
<tr>
<td>myo51Δ</td>
<td>0.67</td>
<td>1.85±0.72</td>
<td>0.30±0.14</td>
<td>58</td>
<td>21</td>
<td>21</td>
<td>54</td>
</tr>
<tr>
<td>Wild-type, LatB-treated</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>for3Δ</td>
<td>0.089</td>
<td>1.27±0.23</td>
<td>0.09±0.02</td>
<td>0</td>
<td>0</td>
<td>100</td>
<td>4</td>
</tr>
<tr>
<td>myo52Δ</td>
<td>0.098</td>
<td>1.56±0.46</td>
<td>0.09±0.02</td>
<td>0</td>
<td>0</td>
<td>100</td>
<td>4</td>
</tr>
</tbody>
</table>

The analysis is based on imaging three z-sections at 0.6 μm intervals (combined depth of view equal to ~35–45% of total cell height).
For3 itself is transported centripetally (inwards from the cell tips) at ~0.33 μm/second, which is comparable to the speed of Mug33 translocations, through an actin polymerization-driven mechanism (Martin and Chang, 2006). By co-imaging Mug33–mKate with For3–GFP we found that translocating For3 and Mug33 TVEs did not colocalize on actin cables (Fig. 4C,D). This, together with the fact that ~50% of Mug33 TVE translocations were unambiguously acropetal (towards cell tips), whereas For3 movement is nearly exclusively centripetal (Martin and Chang, 2006), suggested that Mug33 TVE translocations involve more than polymerization-driven movement and are likely to involve motor proteins.

We therefore investigated a role for motor proteins in Mug33 TVE translocations. Fission yeast contains two type V myosins, Myo51 and Myo52. Myo51 has no identified function in the vegetative cell cycle and instead plays a role in meiotic conjugation, cell fusion and spore formation (Doyle et al., 2009; Win et al., 2001). By contrast, Myo52 is important for growth polarity and cytokinesis (Grallert et al., 2007; Martin-Garcia and Mulvihill, 2009; Motegi et al., 2001; Mulvihill et al., 2001; Win et al., 2001). In myo51Δ cells, Mug33–GFP was localized at the cell tips and in TVEs, as in wild-type cells, and the frequency, speed and length of TVE translocations was only mildly altered (Fig. 4A,B,F; Table 1). By contrast, in myo52Δ cells, Mug33–GFP did not accumulate at the cell tips, and long-range TVE translocations were almost completely abolished, although TVE number and shape were not significantly altered (Fig. 4A,B,F; Table 1; supplementary material Fig. S2). The near-absence of TVE movement in myo52Δ was unlikely to be due to defects in actin cable organization, as the dynamics of actin cables and patches appeared relatively normal in this strain, as was also the case for mug33Δ mutants (supplementary material Movies 5, 7, 9, 10) (Motegi et al., 2001; Win et al., 2001). We further found that Myo52–GFP colocalized with Mug33–mKate in 100% of TVEs translocating more than 2 μm (n=32 translocations analyzed), whereas non-translocating TVEs did not always contain Myo52 (Fig. 4E; supplementary material Movie 11). Taken together, these data demonstrate that Mug33 TVEs translocate along actin cables using the type V myosin motor Myo52.

Mug33 cycling from cytoplasm to the plasma membrane depends on endocytosis and exocytosis

In addition to being required for translocation of Mug33 TVEs, actin filaments were also found to be important for TVE biogenesis itself, as treatment of cells with LatB for prolonged periods (>30 minutes) resulted in a reduction in the number of TVEs, in particular TVEs with extended shape, with a concomitant increase in the amount of Mug33 that was tightly associated with the plasma membrane (Fig. 3A,B; supplementary material Fig. S2). We...
hypothesized that this was due to disruption of a normal dynamic cycle in which Mug33 transits between TVEs and the plasma membrane. For an integral membrane protein such as Mug33, cycling might be expected to occur through endocytosis and exocytosis, with actin filaments (i.e. in actin patches) being required for endocytosis (Galletta and Cooper, 2009). To investigate whether Mug33 TVEs are formed by endocytosis from the plasma membrane, we examined Mug33 localization relative to that of the lipophilic dye FM4-64, which, upon uptake, inserts into the outer leaflet of the plasma membrane and is rapidly internalized by endocytosis before trafficking to vacuolar membranes (Gachet and Hyams, 2005). Mug33 was present in TVEs that were also labeled with FM4-64, and these translocated through the cytoplasm (Fig. 5A,B).

In budding yeast, Sla2p is a component of actin patches and is required for a late step of endocytosis (Aycough et al., 1997; Kaksonen et al., 2003). It has been proposed that Sla2p regulates interaction of endocytic proteins with the actin cytoskeleton, perhaps by influencing the timing of Arp2/3-mediated actin filament assembly relative to other endocytic events (Kaksonen et al., 2003). To investigate further the contribution of endocytosis to TVE formation, we examined Mug33 localization in a sla2Δ fission yeast mutant (also known as end4Δ) (Castagnetti et al., 2005; Iwaki et al., 2004). Extending previous studies of fixed cells (Castagnetti et al., 2005; Iwaki et al., 2004), we found that actin patches in live fission yeast sla2Δ cells were less dynamic than in wild-type cells and appeared as ‘comet tails’ at the plasma membrane that tapered off centripetally, similar to those seen in budding yeast sla2Δ mutants (Fig. 5C; supplementary material Movies 5, 8) (Kaksonen et al., 2003). As in LatB-treated wild-type cells, Mug33–GFP in sla2Δ cells accumulated on the plasma membrane, and the number of Mug33 cytoplasmic TVEs decreased, especially TVEs with extended shape (Fig. 5D; supplementary material Fig. S2). We also observed occasional transient colocalization of Mug33 and Sla2 (Fig. 5E; supplementary material Movie 12). These results suggest that transit of Mug33 from the plasma membrane to TVEs requires Sla2-mediated endocytosis.

If Mug33 were cycling between TVEs and the plasma membrane, one would also expect Mug33 to be present in exocytic compartments. To investigate this we co-imaged Mug33 with Syb1, the fission yeast homolog of the vesicle SNAREs mammalian synaptobrevin and budding yeast Snc1p, which regulate fusion of exocytic vesicles with the plasma membrane (Baumert et al., 1989; Edamatsu and Toyoshima, 2003; Gurunathan et al., 2000). Mug33 and Syb1 were present in the same TVEs and co-translocated together (Fig. 6A,B). We also found that Mug33 partially colocalized with exocyst subunits Sec6 and Sec8 at cell tips, and some cytoplasmic Mug33 TVEs co-translocated with these proteins (Fig. 6C,D; supplementary material Movies 13, 14). Localization of Sec6, Sec8 and Sec10 was normal in mug33Δ cells (Fig. 6E; supplementary material Fig. S3A). However, growth of temperature-sensitive sec8-1 mutant cells at the restrictive temperature led to the disappearance of Mug33–GFP from cell tips and a reduction in TVEs, despite levels of Mug33–GFP being unaltered (Fig. 6F,G). Mug33 localization was also impaired in cells lacking the exocyst-activating GTPase Rho3 (Fig. 6F). These data indicate that Mug33 colocalizes with the exocyst on exocytic vesicles and that Mug33 depends on an intact exocyst complex for proper localization on TVEs and at cell tips.

Mug33 contributes to exocytosis in a parallel pathway with actin cables

The above results demonstrate that Mug33 is present in both endocytic and exocytic compartments, but they do not indicate whether Mug33 has a role in membrane trafficking or is present only as a cargo. To investigate a functional role for Mug33 in endocytosis, we assayed uptake of FM4-64 in wild-type and mutant cells over time. In sla2Δ cells, no uptake of FM4-64 was observed, even over long time-scales (Fig. 7A,D) (Iwaki et al., 2004). By contrast, in both wild-type and mug33Δ cells, endocytic vesicles containing FM4-64 were observed as early as 45 seconds after the start of the timecourse, and these accumulated on vacuolar membranes over time (Fig. 7A,D). Similar results were obtained assaying uptake of the fluid-phase endocytic marker Lucifer Yellow (supplementary material Fig. S5) (Riezman, 1985; Takeda and Chang, 2005). We also assayed the rate of exocytosis in mug33Δ cells, measuring secretion of acid phosphatase into the culture medium, and found no difference between wild-type and mug33Δ cells.
cells (Fig. 7B). These results suggest that Mug33 is not essential either for efficient endocytosis or exocytosis. Although deletion of mug33+ alone did not produce obvious defects in either endocytosis or exocytosis, we wondered whether Mug33 might have a more subtle role in one or both of these processes. We therefore combined mug33Δ with non-lethal mutations affecting exocyst function: a temperature-sensitive allele of sec8 (sec8-1), a deletion of non-essential exocyst subunit Exo70, and a deletion of the non-essential exocyst activator Rho3 (Wang, H. et al., 2003; Wang et al., 2002). In addition, we combined all of these mutations with for3Δ and myo52Δ, as well as for3Δ with myo52Δ itself (Table 2). Strikingly, we found that a mug33Δ myo52Δ double mutant was synthetically lethal, and a mug33Δ for3Δ double mutant exhibited strong synthetic temperature sensitivity (Fig. 7C; Table 2). Moreover, a similar pattern of synthetic interactions was also observed in double mutants combining exo70Δ or rho3Δ mutations with for3Δ or myo52Δ. By contrast, mug33Δ exo70Δ and mug33Δ rho3Δ double mutants were viable, and for3Δ myo52Δ double mutants were no more impaired for growth than a myo52Δ single mutant (Table 2). Cytologically, mug33Δ for3Δ and exo70Δ for3Δ double mutants resembled for3Δ mutants, with an increased frequency of lozenge-shaped cells, whereas mug33Δ exo70Δ double mutants resembled wild-type cells (supplementary material Fig. S4).

The similar genetic interactions of mug33Δ, exo70Δ and rho3Δ mutants with for3Δ and myo52Δ mutants suggested that Mug33 has a function in exocytosis that is not essential in wild-type cells but becomes important in mutants defective in actin cable-dependent transport. Accordingly, we found that acid phosphatase secretion in mug33Δ for3Δ and rho3Δ mutants resembled for3Δ mutants, with an increased frequency of lozenge-shaped cells, whereas mug33Δ exo70Δ double mutants resembled wild-type cells (supplementary material Fig. S4).
In budding yeast, some mutations affecting endocytosis also affect exocytosis, either directly or indirectly (Goodson et al., 1996; Mulholland et al., 1997; Riezman, 1985). We found that fission yeast sla2Δ is defective not only in endocytosis, but also in exocytosis (Fig. 7B). Because mug33Δ for3Δ mutants showed an exocytosis defect, it was formally possible that the primary defect of mug33Δ for3Δ was actually in endocytosis. We therefore measured endocytic uptake of FM4-64 and Lucifer Yellow in mug33Δ for3Δ double mutants and other exocytosis mutants. Whereas sla2Δ exhibited no detectable uptake, endocytosis in mug33Δ for3Δ was comparable both to wild-type cells and to the exocytosis mutants sec8-1, exo70Δ, mug33Δ for3Δ and exo70Δ for3Δ (Fig. 7D; supplementary material Fig. S5). Taken together, these data suggest that Mug33 functions with exocyst subunits to promote efficient exocytosis.

**Discussion**

In this work, we have characterized the in vivo behavior and function of Mug33, a fission yeast transmembrane protein involved in membrane trafficking. Mug33 is a member of the Sur7/PalI family of fungal transmembrane proteins. Budding yeast Sur7p, the prototypical member of this family, localizes to eisosomes/MCC (Brach et al., 2011; Grossmann et al., 2008; Grossmann et al., 2007; Luo et al., 2008; Malinska et al., 2004; Walther et al., 2007; Walther et al., 2006). However, unlike components of eisosomes/MCC, which are static, immobile structures, Mug33 shows dynamic behavior, cycling between the plasma membrane and cytoplasmic TVEs that co-translocate with exocyst subunits along actin cables, using type V myosin Myo52. We expect that Mug33-containing TVEs correspond to endocytic and/or exocytic vesicles and/or compartments, but at present we have not distinguished among these. Mug33Δ mutants exhibit the same genetic interactions with for3Δ and myo52Δ cells as do deletion mutants of regulators of exocyst function (exo70Δ and rho3Δ), and a mug33Δ for3Δ double mutant has substantially reduced levels of exocytosis relative to wild-type cells and to either single mutant. We conclude that Mug33 contributes to exocyst-mediated exocytosis.

**Table 2. Genetic interactions of mug33Δ with mutations affecting actin cytoskeleton and exocyst function**

<table>
<thead>
<tr>
<th>Single mutant</th>
<th>With mug33Δ</th>
<th>With sec8-1</th>
<th>With rho3Δ</th>
<th>With exo70Δ</th>
<th>With for3Δ</th>
</tr>
</thead>
<tbody>
<tr>
<td>mug33Δ</td>
<td>++++</td>
<td>++</td>
<td>–</td>
<td>–</td>
<td>–/+</td>
</tr>
<tr>
<td>sec8-1</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–/+</td>
</tr>
<tr>
<td>rho3Δ</td>
<td>+++</td>
<td>+++</td>
<td>–</td>
<td>–</td>
<td>–/+</td>
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<tr>
<td>exo70Δ</td>
<td>+++</td>
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<td>–</td>
<td>–</td>
<td>–/+</td>
</tr>
<tr>
<td>for3Δ</td>
<td>+++</td>
<td>–/+</td>
<td>–</td>
<td>–</td>
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<td>myo52Δ</td>
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++++, normal growth at all temperatures; ++, normal growth at 25°C and 32°C, lethal at 36°C; +, slightly reduced growth at 25°C and 32°C, lethal at 36°C; +, more reduced growth at 25°C, limited growth at 32°C, lethal at 36°C; –/+; growth at 25°C, lethal at 32°C and 36°C; –, lethal at 25°C, 32°C, 36°C.
Our results place the main experimental evidence for this model is derived from individual pathway exocytosis is relatively unaffected, but in the absence of either exocyst regulators, including Mug33. In the absence of either individual pathway exocytosis is relatively unaffected, but in the absence of both pathways exocytosis is severely compromised. The main experimental evidence for this model is derived from genetic interactions affecting cell viability or acid phosphatase secretion. Our results place for3 and myo52 in one genetic-interaction group and mug33, exo70 and rho3 in a second group. Double mutants within a group are relatively non-additive and non-perturbing, whereas double mutants across the two groups are synthetically deleterious.

Our data showing co-translocation of Mug33 TVEs with type V myosin Myo52 and the dependency of Mug33 translocation on Myo52 strongly suggest that translocation of Mug33 TVEs on actin filaments is driven by Myo52. This is similar to post-Golgi trafficking in budding yeast, which depends on the type V myosin Myo2p (Govindan et al., 1995; Pruyne and Bretscher, 2000; Pruyne et al., 1998; Schott et al., 1999). The two types of Mug33 movements we observed – short, random movements and long, vectorial movements – are very similar to those described for GFP-tagged Myo52 itself (Grallert et al., 2007; Motegei et al., 2001). The average speed of Myo52-dependent Mug33 movements in our experiments is slightly lower than that previously described for Myo52 (0.35 μm/second compared with 0.51 μm/second) (Grallert et al., 2007). It is currently unclear whether this is due to minor differences in methodology and/or analysis or to significant differences in biology. One possibility is that Mug33 translocations represent only a subset of total Myo52 translocations and that these have reduced speed. Alternatively, although we observe both acropetal and centripetal co-translocation of Mug33 with Myo52, it is also possible that a subset of Mug33 translocations are driven by actin polymerization, in the manner of (centripetal) For3 translocations, which are generally slower than Myo52-based movement (Grallert et al., 2007; Martin and Chang, 2006); in some instances these might also oppose Myo52-dependent movement. This particular issue would be difficult to address experimentally, because a strong reduction in Myo52-dependent acropetal translocations would lead to reduced Mug33 at cell tips and thus fewer centripetal translocations, even if these did not directly involve Myo52 motor activity. The average speed and frequency of Mug33 translocations in tea1Δ cells was also slightly lower than in wild-type cells. This might be due to the fact that although tea1Δ has robust actin cables, the number of cables emanating from the non-growing cell tip is reduced (Feierbach et al., 2004); subtle alterations in cable organization in tea1Δ cells might also affect the rate of Mug33 translocations.

In principle, if Mug33 function were absolutely dependent on Myo52, one would expect myo52Δ cells (which exhibit temperature sensitivity) to be as compromised in growth as mug33Δ myo52Δ cells (which are synthetically lethal at all temperatures tested). The fact that this is not the case suggests that some Mug33 function is retained without robust acropetal transport; a similar argument applies to the exocyst complex itself, and indeed this is represented in our model (Fig. 8).

At present it is not clear how Mug33 contributes to exocyst function at a mechanistic level. Although Mug33 is present with exocyst components on TVEs and at cell tips, it is unlikely to play a role in exocyst trafficking or localization because steady-state exocyst localization at cell tips is normal in mug33ΔA cells. Related to this, in preliminary experiments we have found that the intracellular localization and movement of Myo52–GFP and GFP–Syb1 are also unperturbed in mug33Δ cells (H.A.S., unpublished data). Because Mug33 is non-essential for viability, while most fission yeast exocyst subunits are essential (Sec5, Sec6, Sec8, Sec10, Sec15, Exo84) (Kim et al., 2010; Wang, H. et al., 2003; Wang et al., 2002), we anticipate that Mug33 is not directly involved in core exocyst function but rather plays a role in regulating core exocyst function, e.g. improving its efficiency. Consistent with this view, exocyst-defective double mutants such as mug33Δ for3Δ or exo70Δ for3Δ did not show significant septation defects, unlike mutants in core exocyst components (supplementary material Fig. S4) (Wang et al., 2002). As one of the key roles of the exocyst is to activate assembly of SNARE complexes and thus membrane fusion (Grotte et al., 2000; He and Guo, 2009; Sivaram et al., 2005; Wiederkehr et al., 2004), possible roles for Mug33 could include increasing the stability of the exocyst complex, increasing its residence time on target membranes and/or otherwise enhancing its kinetic ability to activate SNARE complexes. To date we have not identified any physical interactions between Mug33 and exocyst components. Although we initially identified Mug33 as a Tea1-interacting protein, at present it is unclear how or if the interaction of Mug33 with Tea1 is important for exocyst function. In preliminary experiments we have found defects in exocytosis in tea1Δ mutants, but additional data suggest that these might not be related to Tea1 localized at cell tips (H.A.S., unpublished data). Further work will be required to clarify this issue.

As is implied in our model (Fig. 8), a better understanding of the regulation of fission yeast exocytosis will require addressing not only Mug33 functions but also how Exo70 functions alongside Mug33 as an exocyst regulator. This is of particular interest because several aspects of exocyst behavior appear to be different between budding and fission yeasts. For example, in budding yeast, the two exocyst subunits Sec3p and Exo70p localize at the plasma membrane independently of the actin cytoskeleton and are thought to provide a target for incoming secretory vesicles carrying the remaining exocyst subunits (Sec5p, Sec6p, Sec8p, Sec10p, Sec15p and Exo84p), whose plasma membrane localization requires active secretion (Boyd et al., 2004; Finger et al., 1998; He and Guo, 2009).
For 3-3xGFP Sla2-GFP
University of Kent, UK.
in YE5S in flat-bottomed 96-well plates at a starting OD 595 of 0.05. Samples were measured of cell growth rates were performed using a Sunrise microplate reader
Singapore).
variety of mechanisms that might modulate core exocyst function.
work on exocytosis in fission yeast will help to illuminate the
Mass spectrometric analysis
Digestion
A total of 60 μl of solubilized protein mixture was reduced in 5 mM TCEP at room temperature, alkylated in 10 mM iodoacetamide at room temperature in the dark, and diluted to 2 M urea in 100 mM Tris-HCl pH 8.5. CaCl2 was then added to a final concentration of 1 mM, and samples were incubated for 18 hours at 37°C in the dark with shaking in 0.015 mg/ml trypsin. Samples were neutralized with 13.5 μl 90% formic acid (final concentration 5%), and centrifuged for 30 minutes at 4°C and 21,000 g.
Multidimensional protein identification technology (MudPIT)
After digestion the proteins were pressure-loaded onto a fused silica capillary desalting column containing 3 cm of 5-µm-diameter strong cation exchange (SCX) followed by 3 cm of 5-µm-diameter C18 (reverse phase or RP material) packed into an undeactivated 250-µm internal diameter capillary. The desalting columns were washed overnight in 1.5 ml buffer A (95% water, 5% acetonitrile and 0.1% formic acid). Following desalting, a 10-µm internal diameter capillary of a 10-µm laser pulled tip packed with 10 cm of 3-µm-diameter Aqua C18 material (Phenomenex, Ventura, CA) was attached to the filter union (desalting column–filter union–analytical column) and the entire split-column (desalting column–filter union–analytical column) was placed in line with an Agilent 1100 quaternary HPLC (Palo Alto, CA) so that traces were analyzed by using low specifications of all three columns was established.

Materials and Methods
Yeast genetic methods
General yeast methods were as described previously (Moreno et al., 1991). Crosses were performed primarily by tetrad dissection, and all fluorescent-tagged proteins apart from the tubulin marker GFP–Atb2 and the actin marker GFP–CHDRng2 were expressed from endogenous promoters. Genotypes of strains used in this work are presented in supplementary material Table S2. GFP–CHDβopo, sec8-GFP, sec6-GFP, sec10-GFP, sec8-1 and rho3A strains were obtained from Mohan Balasubramanian (Tunmaek Life Sciences Laboratory, National University of Singapore). Myo2-GFP, moya1A and myo2Aa were obtained from Dan Muhllvill, University of Kent, UK. Sla2-GFP and sla2Aa were obtained from Jackie Hayles, CR-UK, London, UK. For 3-3xGFP was obtained from Sophie Martin, University of Lausanne, Switzerland; and GFP–Syb1 was obtained from Yoko Toshiyuma, University of Tokyo, Japan. The S. pombe cisisome/MIcC component Pid (SPC736.15) was identified from the fission yeast genome through homology with the S. cerevisiae protein (Walther et al., 2006; Zhang et al., 2004). Gene deletion and C-terminal epitope tagging were performed by PCR-based gene targeting, by using the kanMX6 or natMX6 selectable marker for resistance to G418 and nourseothricin, C-terminal epitope tagging was performed by PCR-based gene targeting, by using the kanMX6 or natMX6 selectable marker for resistance to G418 and nourseothricin.

Analysis of tandem mass spectra
After each step was executed, full spectra were recorded to a RAW file and converted into.mz format using RawXtract (Version 1.9). Poor quality spectra were removed from the.ms2 database using an automated spectral quality assessment algorithm (Bern et al., 2004). Remaining spectra were searched with the SEQUEST algorithm (Eng et al., 1994) against the SGD S.Pombe (October 2006) protein database concatenated to a database in which the sequence for each entry in the original database was reversed (Peng et al., 2003). All searches were parallelized and performed on a Beowulf computer cluster consisting of 100 1.2 GHz Athlon CPUs (Sadygov et al., 2003) (our unpublished data). This suggests that fission yeast homologs of Sec3p are known to exist (Wang, H. et al., 2009; He et al., 2007; Zhang et al., 2008). In budding yeast, none of an S-peptide (Kim and Raines, 1993), a TEV protease cleavage site and a ZZ tag were expressed from endogenous promoters. Genotypes of strains used in this work are presented in supplementary material Table S2. GFP–CHDβopo, sec8-GFP, sec6-GFP, sec10-GFP, sec8-1 and rho3A strains were obtained from Mohan Balasubramanian (Tunmaek Life Sciences Laboratory, National University of Singapore). Myo2-GFP, moya1A and myo2Aa were obtained from Dan Muhllvill, University of Kent, UK. Sla2-GFP and sla2Aa were obtained from Jackie Hayles, CR-UK, London, UK. For 3-3xGFP was obtained from Sophie Martin, University of Lausanne, Switzerland; and GFP–Syb1 was obtained from Yoko Toshiyuma, University of Tokyo, Japan. The S. pombe cisisome/MIcC component Pid (SPC736.15) was identified from the fission yeast genome through homology with the S. cerevisiae protein (Walther et al., 2006; Zhang et al., 2004). Gene deletion and C-terminal epitope tagging were performed by PCR-based gene targeting, by using the kanMX6 or natMX6 selectable marker for resistance to G418 and nourseothricin, C-terminal epitope tagging was performed by PCR-based gene targeting, by using the kanMX6 or natMX6 selectable marker for resistance to G418 and nourseothricin.

Immunoprecipitation
For anti-Tea1 antibody immunoprecipitations, native cell extracts were prepared from frozen powder resuspended in buffer LB. Extracts were clarified by two microfuge centrifugation steps of 900 g for 5 minutes at 4°C and the concentration adjusted to 20 mg/ml. 1 ml of extract was incubated with 10 μl of protein–G–Sepharose beads non-covalently pre-loaded with 5 μg of affinity purified anti-Tea1 antibody for 2 hours at 4°C. The beads were washed six times in 1 ml of LB and resuspended in Laemmli sample buffer for SDS-PAGE and western blotting.

Microscopy
Images were acquired at room temperature. DIC and wide-field fluorescent images (Calcofluor and Lucifer Yellow) were collected using a Nikon TE300 microscope (Nikon, Tokyo, Japan) and analyzed using a modified six-step separation, as described previously (Sadygov et al., 2003) (our unpublished data). This suggests that fission yeast homologs of Sec3p are known to exist (Wang, H. et al., 2009; He et al., 2007; Zhang et al., 2008). In budding yeast, none of an S-peptide (Kim and Raines, 1993), a TEV protease cleavage site and a ZZ tag were expressed from endogenous promoters. Genotypes of strains used in this work are presented in supplementary material Table S2. GFP–CHDβopo, sec8-GFP, sec6-GFP, sec10-GFP, sec8-1 and rho3A strains were obtained from Mohan Balasubramanian (Tunmaek Life Sciences Laboratory, National University of Singapore). Myo2-GFP, moya1A and myo2Aa were obtained from Dan Muhllvill, University of Kent, UK. Sla2-GFP and sla2Aa were obtained from Jackie Hayles, CR-UK, London, UK. For 3-3xGFP was obtained from Sophie Martin, University of Lausanne, Switzerland; and GFP–Syb1 was obtained from Yoko Toshiyuma, University of Tokyo, Japan. The S. pombe cisisome/MIcC component Pid (SPC736.15) was identified from the fission yeast genome through homology with the S. cerevisiae protein (Walther et al., 2006; Zhang et al., 2004). Gene deletion and C-terminal epitope tagging were performed by PCR-based gene targeting, by using the kanMX6 or natMX6 selectable marker for resistance to G418 and nourseothricin, C-terminal epitope tagging was performed by PCR-based gene targeting, by using the kanMX6 or natMX6 selectable marker for resistance to G418 and nourseothricin.
Acid phosphatase assays

As described previously (Wang et al., 2002). Cells were grown to mid-exponential phase in yeast extract medium (YE5S), washed twice in an equal volume of fresh medium, resuspended at a density of 5 × 10³ cells per ml, and incubated at 25°C. 500 μl samples were removed at t = 0, 1, 2, 3, and 4 hours; the cells were then pelleted and 300 μl of supernatant added to 300 μl 2 mM phenylmethylsulfonyl fluoride in 100 mM sodium acetate, pH 4.0. Assays were incubated at 30°C for 10 minutes, stopped by the addition of 300 μl 1 N NaOH, and the absorbance read at 420 nm, using the t = 0 sample for each strain as the blank. Under these conditions, secretion of acid phosphatase activity was essentially linear over time; therefore measurements for each strain were converted into a single value of secreted units per hour.

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Note added in proof

Independent of our work, two groups have very recently proposed models involving complementary roles for actin cable-dependent transport and exocyst function in fission yeast exocytosis and/or polarized growth (Bendezú and Martin, 2011; Nakano K. et al., 2011). Supplementary material available online at http://jcs.biologists.org/cgi/content/full/124/3/2187/DC1

References


