Lipid droplet dynamics during Schizosaccharomyces pombe sporulation and their role in spore survival

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ABSTRACT
Upon nitrogen starvation, the fission yeast Schizosaccharomyces pombe forms dormant spores; however, the mechanisms by which a spore sustains life without access to exogenous nutrients remain unclear. Lipid droplets (LDs) are impregnated in sporulation (Fan et al., 2015; Lin et al., 2013; Ren et al., 2014); however, the precise role of LDs in spor development remains elusive. An LD is a membrane monolayer organellae that is primarily comprised of the neutral lipids triacylglycerols (TAGs) and sterol esters (Thiam et al., 2013). LDs play a role in diverse biological pathways involved in the supply of lipids for membrane synthesis, energy production, and formation of lipophilic molecules (Blom et al., 2011; Diclbberger et al., 2013; Pol et al., 2014; Rambold et al., 2015; Shpilka et al., 2015), and interact with various other organelles to exert specific functions (Gao and Goodman, 2014). To elucidate the role of LDs in spore development, an understanding of the dynamic movements of these organelles during sporulation is required.

The fission yeast Schizosaccharomyces pombe undergoes sporulation when deprived of nitrogen sources. Upon induction of sporulation, the yeast enters meiosis to generate four haploid nuclei. These haploid nuclei are packaged into four ascospores (FSM), which will subsequently be utilized as the spore plasma membrane, and is assembled via fusion of the membrane vesicles at the spindle pole body (SPB) during meiosis II (Ikemoto et al., 2000; Nakase et al., 2008). A proportion of the membrane vesicles arise from robust endocytosis of the ascus plasma membrane (Kashiwazaki et al., 2011). The endocytic membrane vesicles transport cargo, including the SNARE proteinPsi1, to the meiotic SPB (Nakamura et al., 2008, 2001). Vesicle tethering at the SPB is facilitated by the Rab GDP/GTP exchange factor Spo13 localized at the cytoplasmic plaque of the meiotic SPB (Yang and Neiman, 2010), and these vesicles subsequently fuse with each other to form the FSM through SNARE complex formation (Maeda et al., 2009; Nakamura et al., 2005; Neiman, 1998; Yang et al., 2008).

The opening of a growing FSM is decorated with the leading edge proteins (LEPs), which assemble into ring structures at the leading edge and guide the FSM along the nuclear envelope (Moreno-Borchart et al., 2001; Neiman, 2011). In S. pombe, the LEP rings are comprised of Mei14, actin, and Mcp4 (Ohtaka et al., 2007; Okuzaki et al., 2003; Yan and Balasubramanian, 2012). Following capture of the nucleus by the FSM, constriction of the LEP rings facilitates FSM closure (Diamond et al., 2008; Yan and Balasubramanian, 2012).

FSM closure is a process equivalent to cytokinesis, separating the ascus cytoplasm from the spore cytoplasm. The septation initiation network (SIN), which regulates cytokinesis, modulates sporulation in S. pombe (Goyal et al., 2011; Krapp et al., 2006), and a kinase cascade that occurs during SIN signaling ultimately activates the nuclear Dbf2-related (NDR) kinases (Rhind and Russell, 2012). Notably, a strain harboring a deletion of the gene encoding the meiosis-specific NDR kinase Mug27 (mug27Δ) produced FSMs that were small in size and frequently failed to enclose the nucleus during spor formation (Ohtaka et al., 2008; Perez-Hidalgo et al., 2008; Yan et al., 2008). Moreover, meiotic actin ring constriction in NDR-kinase mutants show slow kinetics (Yan and Balasubramanian, 2012), indicating that SIN signaling regulates FSM closure.

In this study, we examined the dynamics of LDs in sporulating cells of S. pombe. LDs were actively transported to forespores, and most LD-depleted spores were incapable of germination.

RESULTS AND DISCUSSION
LDs form clusters during meiosis II and partition into forespores
To elucidate the mechanism by which spores acquire LDs, we observed living sporulating cells expressing Ptl2-GFP. Ptl2, a TAG lipase of S. pombe (Yazawa et al., 2012), localizes to the LDs (Fig. S1); the average number of LDs labeled by Ptl2-GFP in a sporulating cell was 25. LDs showed dynamic movements during sporulation, scattering in the cytoplasm during meiosis I (Fig. S2, 0–18 min), but clustering around the two divided nuclei just before the onset of meiosis II (Fig. S2, 36–42 min). Clustering of LDs occurred in proximity to the site of initiation of FSM assembly in meiosis II
(Fig. 1A, arrows). However, in the spo13Δ mutant, LDs clustered efficiently at the nucleus without FSM assembly (Fig. S3), indicating that LD clustering occurs independent of FSM assembly. As the FSM grew into a crescent-shaped structure in anaphase II, the LD clusters further partitioned into each of the four FSMs (Fig. 1A, 12–24 min, arrowheads). Continuous extension of the FSM eventually enclosed the LDs within the forespore (Fig. 1A, 24–60 min).

LDs were found in close proximity to the leading edges of the FSM during FSM extension (Fig. 1A, 12 min, arrowheads). Consistently, when the cell undergoing FSM extension was further subjected to electron microscopy (EM) (Fig. 1B,C), LDs were often observed near the leading edge of each FSM (Fig. 1D, arrows). FSM leading edges are decorated by the three LEP rings: the Meu14 ring located at the ascus cytoplasmic side of the FSM leading edge; the Mcp4 ring at the future spore cytoplasmic side; and the meiotic actin ring situated between the Meu14 ring and the Mcp4 ring (Fig. 1E) (Ohtaka et al., 2007). Co-localization analysis revealed that LDs closely associate with the Mcp4 ring, but localize behind the meiotic actin ring and the Meu14 ring (Fig. 1F–H), indicating that the LDs were located at the future spore cytoplasm.

**LEPs facilitate efficient inclusion of LDs by the FSM**

We next examined whether the LEPs play a role in LD movement. The meiotic actin ring was dispersed by treating the sporulating cells with the actin polymerization inhibitor Latrunculin A. While most LDs clustered at the FSM initiation sites in the control cells (Fig. 2A, 0 min), the LDs in the Latrunculin A-treated cells remained scattered upon initiation of FSM assembly (Fig. 2B, 0 min), suggesting that actin polymerization is required for LD clustering at the FSM assembly site. Furthermore, the FSM leading edge in the Latrunculin A-treated cells was associated with few or no LDs (Fig. 2B, 24 min, arrowheads), resulting in inefficient inclusion of LDs by FSMs in these cells (Fig. 2B, 48 min, arrows). As in the Latrunculin A-treated cells, LDs failed to cluster well at the FSM initiation site, and numerous LDs were excluded from the spore cytoplasm in the mcp4Δ mutant (Fig. 2C, 48 min, arrows). The similarity in the phenotype of Latrunculin A-treated cells and mcp4Δ cells is consistent with a previous study reporting that Mcp4 is involved in F-actin positioning (Ohtaka et al., 2007).

Meanwhile, depletion of the Meu14 ring had little effect on initial clustering of LDs (Fig. 3A, 0 min). In contrast with the wild-type cells (Fig. 1A, 12 min, arrowheads), the meu14Δ mutant exhibited poor association of LD clusters with the FSM leading edges (Fig. 3A, 12 min, arrowheads). As a result, LDs were not enclosed by the FSM, instead remaining in the ascus cytoplasm in the meu14Δ mutant (Fig. 3A, 48 min, arrows).

We propose that LD transport into spores involves two steps: first, actin polymerization is required for LD clustering at the FSM assembly site; second, the LEP rings facilitate efficient inclusion of LDs by the FSM. A previous study demonstrated that Mug27 regulates constriction of the meiotic actin rings without affecting their assembly (Yan and Balasubramanian, 2012). Accordingly, we examined LD movements in the mug27Δ mutant. In agreement with our hypothesis, initial clustering of LDs was normal in the mug27Δ mutant (Fig. 3B, 0 min); however, most of the LDs were still excluded from the forespores (Fig. 3B, 48 min, arrows). Therefore, fewer LDs were enclosed by FSMs in the LEP-disruption mutants than in the wild-type cells (Fig. 3C), indicating that LEP rings mediate LD transport to the forespores.

**LDs are required for spore germination and spore wall integrity**

In addition to enclosing LDs with low efficiency relative to the wild type, the FSMs of meu14Δ and mug27Δ mutants exhibit abnormal formation and frequently fail to engulf the spore nucleus (Ohtaka et al., 2008; Okuzaki et al., 2003), making it complex to verify the requirement of LDs for spore survival. By contrast, in the present study, the mcp4Δ mutant formed four spores per ascus (tetrads) as frequently as wild-type cells (Fig. 4A). We assayed spore survival...
by analysis of spore germination rate. Fewer than 50% of the LDs were transported into the forespores (Fig. 3C); despite this, the mcp4Δ spores germinated well (Fig. 4A). This might be attributable to the incomplete depletion of LDs within the mutant. We therefore deleted the genes required for TAG synthesis. The enzymes Dga1 and Phl1, which convert lipids such as free fatty acids and phospholipids into TAG, are responsible for LD formation in S. pombe (Meyers et al., 2016). The characteristic BODIPY-stained punctate structures were largely lost in the sporulating cells of the dga1Δphl1Δ mutant, indicating diminishment of the LDs (Fig. 4B).

Noticeably, while the dga1Δphl1Δ mutant produced a comparable amount of tetrads to the wild-type cells (Fig. 4A), most of the spores (83%) failed to form colonies owing to germination defects (Fig. 4A,C). Those dga1Δphl1Δ spores that failed to form colonies showed no sign of germination (Fig. 4D), whereas the wild-type spores exhibited expansion growth, and emergence of germ tubes within 5 to 10 h after transfer to the growth medium, as previously reported (Hatanaka and Shimoda, 2001). The frequency...
of spore germination was only 17% (Fig. 4A); intriguingly, however, the frequency of tetrads containing four viable spores was strikingly higher (5%; 2 out of 42 asci) than that predicted by random distribution of viable spores in an ascus (0.08%; 0.17^4=0.0008). This result of non-random distribution indicates that spores in each ascus share the same fate. Thus, it is likely that the viability of spores in the absence of TAG synthesis is metabolically determined during meiosis and sporulation. Although the viability of spores produced by the dga1Δplh1Δ mutant largely decreased during sporulation, it further decreased gradually when maintained in the absence of TAG synthesis (Fig. 4E). In contrast, the spores of wild-type cells retained high
viability in sporulation medium for 16 days (Fig. 4E). These results indicate that TAG plays a necessary role in spore survival under starvation conditions.

The LD-deficient mutant not only exhibits defects in spore germination but also in spore wall integrity (Fig. 4F). Spore wall deposition after FSM assembly confers resistance to spores against various stresses (Coluccio et al., 2008; Fukunishi et al., 2014). The outermost layer of the S. pombe spore wall comprises a protein layer composed of Isp3, which is highly palmitoylated (Fukunishi et al., 2014; Zhang et al., 2013). This Isp3 coating was defective in the spores of the dga1Δplh1Δ strain (Fig. 4F), raising the possibility that TAGs mediate the characterized lipid-modification of Isp3. These results indicate that LDs are important for spore germination and spore wall integrity.

LDs are crucial for the survival of starved cells (Rambold et al., 2015; Shiplka et al., 2015). Our study revealed that LDs are actively transported to nascent spores, and that dga1Δplh1Δ spores, bearing few LDs, barely germinate. These data indicate that LDs represent an important cellular energy source for spores under starvation conditions. Alternatively, apoptosis may be induced in dga1Δplh1Δ spores as a result of their failure to transform diacylglycerol into TAG (Zhang et al., 2003). Further studies will clarify the mechanisms by which LDs support spore survival.

MATERIALS AND METHODS

Yeast strains and culture

The S. pombe strains used in this study are listed in Table S1. All strains were grown on yeast extract with supplements (YES) plates at 30°C, as described by Moreno et al. (1991). To induce sporulation, freshly cultured cells were collected in nitrogen-free Edinburgh minimal medium (Moreno et al., 1991) supplemented with adenine, uracil, histidine, lysine, and uracil (EMM-N+5S) at a density of 10⁷ cells/ml. Cells were then transferred to malt extract (ME) plates to allow sporulation at 26°C.

Gene disruption was performed using a polymerase chain reaction (PCR)-based strategy (Bähler et al., 1998). The PCR primers used in these analyses are listed in Table S2. For deletion of the meu14+ gene, DNA fragments with homology to the target gene locus were amplified using the primers HJO423, HJO424, HJO425, and HJO426, whereas DNA fragments for the deletion of the dga1+ gene were amplified using the primers HJO684, HJO685, HJO686, and HJO687. The plh1+ gene was replaced with the drug resistance gene module kanMX6 using the plasmid pFA6a-kanMX6 and primers HJO689, HJO690, HJO691, and HJO692. The mcp4Δ, mcp27Δ, and spo15Δ strains were derived from strains YF16412, YF17842 and YF12290, respectively (obtained from the Yeast Genetic Resource Center of Japan) (Nakase et al., 2008; Ohtaka et al., 2007, 2008).

To fluorescently label Ptl2, Isp3, or Mcp4, a two-step PCR method introducing the chromosomal GFP or mCherry tag was used (Hayashi et al., 2009). To visualize the FSM, integrating plasmids carrying mCherry-psyl1+ were introduced into the cells as described in Chikashige et al. (2006). GFP-tagged Meu14 or LifeAct was expressed from the lyy1–integrating plasmid.

Live-cell imaging of sporulating cells

After overnight incubation on ME plates, cells were re-suspended in EMM-N+55 medium. To disperse sporulating cells, suspensions were subjected by brief sonication (Handy Sonic; Tory Seiko, Tokyo, Japan); 20 µl of the cell suspension was then dropped onto lectin (0.2 mg/ml; Sigma-Aldrich, Tokyo, Japan)-coated 35-mm glass-bottomed culture dishes (MatTek, Ashland, MA, USA) to immobilize cells (Asakawa and Hiraoka, 2009). For imaging Latrunculin A-treated cells, Latrunculin A (Thermo Fisher Scientific, Tokyo, Japan) was added at a final concentration of 1 µM prior to cell immobilization. Cells undergoing sporulation were selected for live-cell imaging.

A DeltaVision microscope equipped with a CoolSNAP HQ2 charge-coupled device (GE Healthcare, Tokyo, Japan) was used for image acquisition. Optical section images were acquired at 0.5-µm focus intervals using an oil-immersion 60× objective lens (PlanApoN60x OSC, NA1.4; Olympus, Tokyo, Japan). Images were processed using the de-noising algorithm (Boulanger et al., 2009) and by constrained iterative deconvolution (Agard et al., 1989).

EM imaging

Cells were induced to sporulate on ME plates overnight, and aliquoted in monolayers on lectin-coated glass-bottomed culture dishes with addressing grids (grid size 50 µm; ibid, Bremen, Germany). Cells were fixed with 2% glutaraldehyde (Polysciences, Inc., Warrington, PA, USA) in 0.1 M phosphate buffer (pH 7.2) for 2 h at 4°C. Optical section images (0.2-µm intervals) of a cell of interest were obtained using the Olympus objective lens, as described above. EM observation was performed as described previously (Asakawa et al., 2010). Briefly, cells were post-fixed with a 1.2% KMnO₄ solution overnight at 4°C and embedded in Epon812. The epoxy block containing the same cells observed by fluorescence microscopy was trimmed according to the location on the coverslip. Serial sections with 80-nm thickness were stained with 4% uranyl acetate and a commercial ready-to-use solution of lead citrate (Sigma-Aldrich, St. Louis, MO, USA), and analyzed using a JEM1400 transmission electron microscope (JEOL, Tokyo, Japan). Adobe Photoshop CS4 (ver.11.0.1) was used for image processing.

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Competing interests

The authors declare no competing or financial interests.

Author contributions

H.-J.Y., T.H. and Y.H. conceived, designed, and interpreted experiments. H.-J.Y., T.H. and Y.H. wrote the manuscript, which was approved by all authors.

H.O. and T.K. performed the experiments and analyzed the data. H.-J.Y., T.H. and Y.H. declared no competing or financial interests.

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Supplementary information

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References


