**RESEARCH ARTICLE**

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 are reservoirs of neutral lipids that act as important cellular energy resources. Using live-cell imaging analysis, we found that the lipid droplets of mother cells redistribute to their nascent spores. Notably, this process was actin polymerization-dependent and facilitated by the leading edge proteins of the forespore membrane. Spores lacking triacylglycerol synthesis, which is essential for lipid droplet formation, failed to germinate. Our results suggest that the lipid droplets are important for the sustenance of life in spores.

**KEY WORDS:** Actin, Forespore membrane, Lipid droplet, Septation initiation network, Spore, Germination

**INTRODUCTION**

Sporulation, scattering in the cytoplasm during meiosis I (Fig. S2, 18–18 min), but clustering around the two divided nuclei just before the 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 (*mug27*) produced FSMs that were small in size and frequently failed to enclose the nucleus during sporulation (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).

**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 disassembled 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 LEPs 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 (Fig. 3B, 0 min). Mug27 depletion resulted in inefficient inclusion of LDs by FSMs in these cells (Fig. 3B, 48 min, arrows). The similarity in the phenotype of Latrunculin A-treated cells and mug27Δ cells is consistent with a previous study reporting that Mug27 mediates 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).

Fig. 2. Actin polymerization is required for LD clustering. Time-lapse images of living cells expressing mCherry-Psy1 (red) and Ptl2-GFP (green): wild-type cell treated with DMSO (A), wild-type cell treated with Latrunculin A (final concentration of 1 µM) (B), and the mcp4Δ mutant (C). The arrowheads at 24 min indicate the FSM with few associated LDs. The arrows at 48 min represent LDs in the exterior of the forespores. The presented image is a representative example: the number of cells observed is 10 for (A), 12 for (B) and 15 for (C). Scale bar: 5 µm.

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

![Fig. 4. LDs are important for spore germination and spore wall integrity.](image)

| Tetrad (%) | Germination (%) |
|------------|-----------------|
| wild type  | 84              | 93               |
| mcp4Δ      | 85              | 95               |
| meu14Δ     | 20              | ND               |
| mug27Δ     | 65              | ND               |
| dga1Δ      | 82              | 95               |
| plh1Δ      | 85              | 93               |
| dga1Δplh1Δ | 84              | 17               |
| dga1Δplh1Δ + dga1Δ | 81 | 91 |
| dga1Δplh1Δ + plh1Δ | 82 | 94 |

(B) The dga1Δplh1Δ mutant possessed few LDs. The fluorescent dye BODIPY was used for LD labeling. The white dashed line outlines the sporulating cell. Scale bar: 5 µm.

(C) Examples of spore colony formation in the dga1Δplh1Δ mutant.

(D) Representative morphological changes of spore germination over time in the wild-type or the dga1Δplh1Δ spore. Scale bar: 6 µm.

(E) The germination defect of the dga1Δplh1Δ spores was time-dependent. The cells were subjected to sporulation on an ME plate for 2, 4, 8, or 16 days. At each time point, spore germination was assayed by tetrad dissection on the YES plate (three independent experiments per strain; 14 tetrads were dissected per experiment). Germination frequency = (number of germinated spores/number of total spores)\times100\%. The graph and the error bar represent mean and standard deviation, respectively.

(F) The spore wall was improperly assembled in the dga1Δplh1Δ mutant. Isp3-GFP was used to visualize the outermost layer of the spore wall. Isp3-GFP fluorescence signals were evenly distributed on the surface of the wild-type ascospores, whereas Isp3-GFP exhibited aggregate formation and uneven decoration of the ascospores of the dga1Δplh1Δ mutant. Scale bar: 5 µm.
viability in spore germination 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 dga1ΔiplhΔA 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 dga1ΔiplhΔA 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 dga1ΔiplhΔA 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 leucine (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 pAfa6-kanMX6 and primers HJO689, HJO690, HJO691, and HJO692. The mcp4Δ, mug2Δ7A, and spo13A strains were derived from strains F1Y614, F1Y7842 and F1Y1290, respectively (obtained from the Yeast Genetic Resource Center of Japan) (Nakase et al., 2008; Ohtaka et al., 2007, 2008).

To fluorescently label PIt2, 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-pys1+ were introduced into the cells as described in Chikashige et al. (2006). GFP-tagged Meu14 or LifeAct was expressed from the 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 pAfa6-kanMX6 and primers HJO689, HJO690, HJO691, and HJO692. The mcp4Δ, mug2Δ7A, and spo13A strains were derived from strains F1Y614, F1Y7842 and F1Y1290, respectively (obtained from the Yeast Genetic Resource Center of Japan) (Nakase et al., 2008; Ohtaka et al., 2007, 2008).

Live-cell imaging of sporulating cells
After overnight incubation on ME plates, cells were resuspended in EMM-N+5S medium. To disperse sporulating cells, suspensions were subjected by brief sonication (Handy Sonic; Tomy 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, Lutranculin 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., H.O. and T.K. performed the experiments and analyzed the data. H.-J.Y., T.H. and Y.H. wrote the manuscript, which was approved by all authors.

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### Supplementary materials

#### Table S1. Strains used in this study

| Strain   | Genotype                                      | Note          |
|----------|-----------------------------------------------|---------------|
| HJY766   | ade6-216 leu1-32 lys1-131 ura4-D18 lys1+::Pnmt-mCherry-psy1+ ptl2+::GFP-kan' | Figure 1, 2   |
| HJY593   | ade6-216 leu1-32 ura4-D18 lys1-131 mcp4+::mCherry-hph | Figure 1      |
| HJY250   | ade6-216 leu1-32 ura4-D18 lys1-131 cut11+::mCherry-hph lys1+::Pnda3-lifeAct-GFP | Figure 1      |
| HJY537   | ade6-216 leu1-32 lys1-131 ura4-D18 lys1+::Pmeu14-meu14+•-GFP | Figure 1      |
| HJY789   | ade6-M216 leu1-32 lys1-131 ura4-D18 mcp4Δ::ura4+ lys1+::Pnmt-mCherry-psy1+ ptl2+::GFP-kan' | Figure 2      |
| HJY805   | ade6-M216 leu1-32 lys1-131 ura4-D18 meu14Δ::ura4+ lys1+::Pnmt-mCherry-psy1+ ptl2+::GFP-kan' | Figure 3      |
| HJY795   | ade6-M210 leu1-32 ura4-D18 mug27Δ::ura4+ aur1'::Pnmt-mCherry-psy1+ ptl2+::GFP-kan' | Figure 3      |
| CRL493   | ade6-M216 leu1-32 lys1-131 ura4-D18            | Figure 4      |
| HJY595   | ade6-M216 leu1-32 lys1-131 ura4-D18 mcp4Δ::ura4+ | Figure 4      |
| HJY508   | ade6-M216 leu1-32 lys1-131 ura4-D18 meu14Δ::ura4+ | Figure 4      |
| FY17842  | ade6-M210 leu1-32 ura4-D18 mug27Δ::ura4+       | Figure 4      |
| HJY824   | ade6-M216 leu1-32 lys1-131 ura4-D18 dga1Δ::ura4+ | Figure 4      |
| Strain   | Genetic Marker                                      | Figure |
|----------|-----------------------------------------------------|--------|
| HJY825   | ade6-M210 leu1-32 lys1-131 ura4-D18 plh1Δ::kan†    | 4      |
| HJY836   | ade6-M210 leu1-32 lys1-131 ura4-D18 dga1Δ::ura4+ plh1Δ::kan† | 4      |
| HJY859   | ade6-M210 leu1-32 lys1-131 ura4-D18 dga1Δ::ura4+ plh1Δ::kan† lys1+::Pdga1-dga1+ | 4      |
| HJY863   | ade6-M210 leu1-32 lys1-131 ura4-D18 dga1Δ::ura4+ plh1Δ::kan† lys1+::Pnmt1-plh1+ | 4      |
| HJY847   | ade6-M216 leu1-32 lys1-131 ura4-D18 Isp3+::GFP-Nat† | 4      |
| HJY848   | ade6-M210 leu1-32 lys1-131 ura4-D18 dga1Δ::ura4+ plh1Δ::kan† Isp3+::GFP-Nat† | 4      |
### Table S2. Primers used in this study

| Primers | Sequence | Note |
|---------|----------|------|
| HJO423  | GAGTAAATATAAAGAGAAAC | *meu14Δ-Forward primer 1* |
| HJO424  | CCCACAGTCTAGAGGATCCGGTGGATT GTTTACGTTTCAG | *meu14Δ-Reverse primer 1* |
| HJO425  | GCCTTAACGAGCTAGTCGACTTATCATA ACAAACTAAGAAAC | *meu14Δ-Forward primer 2* |
| HJO426  | GAGATACAACCTCTGCAGGC | *meu14Δ-Reverse primer 2* |
| HJO684  | CTTTCCAATATCTCTGACTGTC | *dga1Δ-Forward primer 1* |
| HJO685  | CCCACAGTCTAGAGGATCCCTCCCGTT CTATATAATCGTG | *dga1Δ-Reverse primer 1* |
| HJO686  | GCCTTAACGAGCTAGTCGACATTATAT GAAGAAGTCTTC | *dga1Δ-Forward primer 2* |
| HJO687  | CGAAATTATATCTGACTGTC | *dga1Δ-Reverse primer 2* |
| HJO689  | CTAAGTAAAACCTGAGGAACCTC | *plh1Δ-Forward primer 1* |
| HJO690  | GAGGCAAGCTAAACAGATCTAGTTAAC TTTAAATATGAATTG | *plh1Δ-Reverse primer 1** |
| HJO691  | GTTTAAAAAGCTAGCTGAAATCAATCATT TACTTTAAATAATCC | *plh1Δ-Forward primer 2** |
| HJO692  | AGTGGAAACCTTTCAACCATCTC | *plh1Δ-Reverse primer 2* |

* The underlined portions represent sequences shared with the plasmid harboring *ura4* gene (Chikashige et al., 2006).

** The underlined sequences were shared with the pFA6a plasmids (Bähler et al., 1998).
Figure S1. Ptl2 localized to the LDs.

The fluorescence dye BODIPY493/503 (final concentration of 0.1 µg/ml) was used to stain the LDs. The mCherry-tagged Ptl2 co-localized to the BODIPY dye-stained regions in sporulating or non-sporulating cells, indicating that Ptl2 localizes at the LDs. The arrowhead indicates the non-sporulating cell and the arrows indicate the sporulating cell; scale bar = 5 µm.
Figure S2. The LDs clustered at the meiotic nuclei during meiosis II.

Meiotic progression was monitored using Cut11-mCherry (West et al., 1998). Cut11-mCherry outlines the nuclear envelope throughout meiosis, but labels metaphase SPB specifically. Meiosis I and meiosis II were recognized by identifying nuclear divisions. The numbers represent the time, in minutes, after metaphase I (at t = 0). The cell in metaphase I was recognized by the formation of two foci corresponding to Cut11-mCherry at the nuclear periphery. The white arrows at time points 36 minutes indicate that the LDs (Ptl2-GFP) clustered around the two divided nuclei just before the onset of meiosis II. At time point 66-78 minutes, the LD clusters partitioned with the nuclear division in anaphase II. The white arrows at time points 78 indicate that the LDs were partitioned into four clusters around the four nuclei; scale bar = 5 µm.
Figure S3. The LDs clustered at the nucleus during meiosis II, even without FSM assembly.

Representative images of the (A) wild-type cell or (B) the spo13Δ cell with LD cluster at the nucleus during meiosis II; Cut11-mCherry was used to label the nucleus, and BODIPY for staining the LDs. “ana” and “meta” represent anaphase and metaphase, respectively; scale bar = 5 µm.
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