Cyclic AMP induction of Dictyostelium prespore gene expression requires autophagy

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ABSTRACT

Dictyostelium discoideum amoebas display colonial multicellularity where starving amoebas aggregate to form migrating slugs and fruiting bodies consisting of spores and three supporting cell types. To resolve the cell signalling mechanism that controls sporulation, we use insertional mutagenesis of amoebas transformed with fusion constructs of spore genes and red fluorescent protein. We identified the defective gene in a mutant lacking spore gene expression as the autophagy gene Atg7. Directed knock-out of atg7 and of autophagy genes like atg5 and atg9 yielded a similar phenotype, with lack of viable spores and excessive differentiation of stalk cells. The atg7-, atg5- and atg9- cells were specifically defective in cAMP induction of prespore genes, but showed enhanced cAMP stimulation of prestalk genes at the same developmental stage. The lack of prespore gene induction in the autophagy mutants was not due to deleterious effects of loss of autophagy on known components of the cAMP pathway, such as cAMP receptors and their cAMP-induced phosphorylation and internalization, PKA and the transcription factors SpaA and GbfA, or to lack of NH3 production by proteolysis, which was previously suggested to stimulate the spore pathway. Our continued mutagenesis approach is the most likely to yield the intriguing link between autophagy and prespore gene induction.

1. Introduction

Autophagy is an ancient survival strategy that allows eukaryotic cells to survive starvation by enclosing and digesting cytosolic components and organelles. A large number of genes required for autophagy were initially identified in yeast and many proved to be deeply conserved in animals, plants and other eukaryotes. At the structural level, autophagy initiates with the formation of crescent-shaped double-membraned structures called phagophores, which enclose cellular contents and fuse at their termini to form an autophagosomal vesicle. The autophagosomal subsequently fuses with a primary lysosome to form an autolysosome where both the inner membrane and captured cargo are degraded and the catabolites are fed back into the cytoplasm by integral membrane permeases. At the molecular level, autophagy initiates when amino acid starvation blocks phosphorylation of Atg13 by the Target of Rapamycin C1 (TORC1) kinase, which prevents Atg13 from forming a complex with Atgs 1, 17, 29 and 31 and to initiate a phagophore assembly site (PAS). The phosphatidylinositol 3-kinase (PtdIns3K) complex consisting of Vps34, Vps15, Atg14 and 8 further regulate vesicle expansion (Feng et al., 2014; Mizushima et al., 2011; Yin et al., 2016).

Autophagy is also important for the multicellular life cycle of Dictyostelium amoebas, which survive starvation by aggregating to form fruiting bodies with dormant spores and dead stalk cells. Autolysosomes appear within 2 h of starvation and increase in number during aggregation. Thereafter, autolysosomes become less prominent in the presumptive spore cells and more numerous in the prestalk cells, where they finally fuse to form the plant-like vacuole of the stalk cells (Schaap, 1983; Schaap et al., 1981; Uchikawa et al., 2011). As a genetic model D. discoideum is particularly suitable for identification of essential components of the autophagy pathway, and up to date the roles of many components were identified, such as Atgs 1 and 13 of the Atg1 complex, Vps34, Vps15 and Atg14 of the PtdIns3K complex, Atgs 2 and 18 further regulate vesicle expansion (Feng et al., 2014; Mizushima et al., 2011; Yin et al., 2016).

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We investigate the signalling pathways that control prespore and spor differentiation and use mutagenesis of amoebas transformed with an mRFP tagged spore coat gene to identify pathway components. We spore differentiation and use mutagenesis of amoebas transformed with

Deletion of most of these genes prevents autophagosome formation and block autophagy mediated proteolysis. Lesions in vmp1 yield the most severe phenotype with cells failing to aggregate and block autophagy mediated proteolysis. Lesions in vmp1 yield amoebas that can aggregate, but there-after show delayed and abnormal development. Instead of one sorogen or slug, the aggregate gives rise to multiple small ones, which eventually turn into fruiting bodies with abnormal spores (Calvo-Garrido et al., 2010; Mesquita et al., 2017).

We investigate the signalling pathways that control prespore and spor differentiation and use mutagenesis of amoebas transformed with an mRFP tagged spore coat gene to identify pathway components. We recovered a mutant defective in sporulation, but overproducing stalk cells. The genetic lesion occurred in the atg7 gene and further analysis of a re-created atg7 knockout and knock-outs in atg5 and atg9 revealed that these genes were specifically required for induction of prespore gene expression, but dispensable for stalk cell differentiation in vivo and in vitro.

2. Materials and methods

2.1. Cell culture

 Dictyostelium discoideum Ax2 was cultured either in HL5 axenic medium (Formedium, UK) or on SM agar plates in association with Klebsiella aerogenes. For development, cells were distributed at 2.5 × 10⁶ cells/cm² on non-nutrient agar and for β-lactosidase assay on dialysis membrane supported by non-nutrient agar. atg9- cells (Tung et al., 2010) were obtained from the Dicty stock center http://dictybase.org/StockCenter/StockCenter.html.

2.2. Knock-out and expression constructs

To generate an atg7 knock-out vector, 5’ and 3’ fragments of the genomic region containing the atg7 gene were amplified using primer pairs atg7-5’/atg7-5’ and atg7-3’/atg7-3’ (Table 1), respectively, subcloned into vector pJet1.2blunt, and cloned into plasmid pLPBLP (Faix et al., 2004) using psth/BamHI for the 5’ fragment and HindIII/Sall for the 3’ fragment respectively. The plLPBLP-atg7KO vector was linearised with Scal and transformed into Ax2 cells.

To generate an atg5 knock-out vector, 5’ and 3’ fragments of genomic region of the atg5 gene was amplified using primer pairs atg5-5’/atg5-5’ and atg5-3’/atg5-3’ (Table 1, subcloned into pJet1.2blunt and cloned into plpBLP using psth/BamHI and HindIII/Sall digestion. The BamHI/ Sall fragment was excised from the vector and transformed into Ax2. Transformants were selected at 10 µg/ml blasticidin and diagnosed for atg7 or atg5 gene disruption by two PCR reactions (Fig. 1).

To generate wild-type and mutant atg7 expression constructs, the act15p-YFP fragment of pDD-NYPF was cloned into pExp4-Hyg (Yamada et al., 2018) using Sall/Xhol to generate Dd-NYPF-Hyg. The atg7 coding region was amplified from genomic DNA of Ax2 with primers atg7-f and atg7-r (Table 1), subcloned into pJet1.2blunt and cloned into pDD-NYPF-Hyg with EcoRI/Clal to create act15p-YFP-atg7. To generate a Cys563 to Ala point mutation, 5’ and 3’ atg7 fragments were amplified from act15p-YFP-atg7 using primers YFP-f and act7-mr and atg7-mf and 2Hterm-r (Table 1). After annealing the fragments, atg7cys563ala was amplified with atg7-f and atg7-r and cloned into Dd-NYPF-Hyg using EcoRI/Clal. Constructs were transformed into atg7- cells by electroporation and transformants were selected at 30 µg/ml hygromycin.

2.3. Western analysis of expressed proteins

Cells were lysed in SDS-sample buffer, proteins were separated on 4–12% polyacrylamide gels (Thermo Fisher Scientific, Whalham, MA), transferred to nitrocellulose and probed with anti-GFP antibody (Roche Applied Science, Penzberg, Germany), followed by HRP-conjugated anti-mouse antibody. YFP-positive bands were detected using SuperSignal West Pico Chemiluminescent Substrate (Thermo Fisher Scientific, Whalham, MA).

2.4. In vitro induction of stalk cell differentiation

Cells harvested from growth medium were resuspended in stalk salts (10 mM MES buffer pH 6.2, 2 mM NaCl, 1 mM CaCl₂) at 2 × 10⁶ cells/ml and distributed as 1.25 ml aliquots in a 6-well culture plate at 2.5 × 10⁶ cells/ml in 1 mM MgCl₂ in KK2 (20 mM potassium phosphate buffer, pH 6.2) and incubated in the presence and absence of 1 mM cAMP. For all genes, cells were developed on non-nutrient agar and for β-lactosidase assay on dialysis membrane supported by non-nutrient agar. atg9- cells (Tung et al., 2010) were obtained from the Dicty stock center http://dictybase.org/StockCenter/StockCenter.html.

Table 1

| Oligonucleotide primers used for plasmid constructs. |
|-----------------------------------------------|
| atg5-5’/f                                      |
| atg5-5’/r                                      |
| atg5-3’/f                                      |
| atg5-3’/r                                      |
| atg5KO1                                       |
| atg5KO2                                       |
| atg5KO3                                       |
| atg7-5’/f                                      |
| atg7-5’/r                                      |
| atg7-3’/f                                      |
| atg7-3’/r                                      |
| atg7KO1                                       |
| atg7KO2                                       |
| atg7KO3                                       |
| atg7KO1 /C1                                    |
| atg7KO2 /C2                                    |
| atg7KO3 /C3                                    |
| atg7KO4 /C4                                    |

Table 2

| Oligonucleotide primers used for plasmid constructs. |
|-----------------------------------------------|
| atg5-5’/f                                      |
| atg5-5’/r                                      |
| atg5-3’/f                                      |
| atg5-3’/r                                      |
| atg5KO1                                       |
| atg5KO2                                       |
| atg5KO3                                       |
| atg7-5’/f                                      |
| atg7-5’/r                                      |
| atg7-3’/f                                      |
| atg7-3’/r                                      |
| atg7KO1                                       |
| atg7KO2                                       |
| atg7KO3                                       |
| atg7KO1 /C1                                    |
| atg7KO2 /C2                                    |
| atg7KO3 /C3                                    |
| atg7KO4 /C4                                    |

For induction of prespore genes, cells were developed on non-nutrient agar at 12°C overnight and then at 22°C for a few hours until loose mounds had formed. Mounds were then dissociated, resuspended to 5 × 10⁶ cells/ml in 1 mM MgCl₂ in KK2 (20 mM potassium phosphate buffer, pH 6.2) and incubated in the presence and absence of 1 mM cAMP. For induction of ecmA, dissociated loose mound cells were resuspended in stalk salts at 3 × 10⁶ cells/ml and shaken with or without 1 mM cAMP and 100 mM DIF-1. For induction of cprB, cells were starved at 4°C overnight to induce aggregation competence and then shaken at 3 × 10⁶ cells/ml in KK2 with or without 1 mM cAMP. For all genes, cells were incubated with cAMP and/or DIF-1 for 4 h at 22°C and subsequently harvested for RNA isolation. The transcript levels of the different genes were analysed by RT-qPCR using the primers listed in Table 1 as described previously (Yamada et al., 2018).

To induce and assay cotC-gal, cells from dissociated loose mounds were resuspended at 3 × 10⁶ cells/ml in 1 mM MgCl₂ in KK2 and shaken for 6 h at 37°C in association with soil-grown Klebsiella strain Y4 (Yamada et al., 2018).
Table 2

| Oligonucleotide primers used for qRT-PCR. |
|-----------------------------------------|
| cotC-fl                                  |
| cotC-r                                  |
| pepA-fl                                 |
| pepA-r                                  |
| cprβ-fl                                 |
| cprβ-r                                  |
| emcA-fl                                 |
| emcA-r                                  |
| spaA-fl                                 |
| spaA-r                                  |
| ghA-fl                                  |
| ghA-r                                   |
| lg7-fl                                  |
| lg7-r                                   |
| carA-fl                                 |
| carA-r                                  |

NaH$_2$PO$_4$/Na$_2$HPO pH 7, 50 mM KCl, 5 mM MgSO$_4$, 2 mM MgCl$_2$, 2% β-mercaptoethanol and 5 mM chlorophenol red-β-D-galactopyranoside) and incubated at room temperature. OD$_{574}$ was measured at regular intervals using a microtiter plate reader.

Visualization of β-galactosidase expression in intact structures was performed using established procedures (Dingermann et al., 1989).

3. Results

3.1. Lesion of Atg7 impairs spore but not stalk differentiation in D. discoideum

In order to identify genes that control Dictyostelium sporulation, we performed REMI mutagenesis on Ax2 cells transformed with a fusion construct of mRFP and the spore coat gene cotC, expressed from its own promoter (Yamada et al., 2018) and screened for mutants with spore defects. CotC-mRFP is localized to Golgi-derived prespore vesicles in prespore cells and is exocytosed during fruiting body formation to be incorporated into the spore wall. We isolated a clone 10va3, which failed to form spores. The cells were slightly (~1 h) delayed in aggregation and more strongly in post-aggregative development, forming mounds with multiple early sorogens (a.k.a. first fingers) at 19 h, when the parental cells had nearly completed fruiting body formation (Fig. 2A). Expression of cotC-mRFP was undetectable in sorogens (Fig. 2B), suggesting that prespore differentiation is altered. The 10va3 sorogens eventually formed small fruiting bodies at 45 h on top of a basal cell mass, but cells in their spore heads were mostly round rather than elliptical as is the case for spores, and were not labelled with cotC-mRFP (Fig. 2C). Stalks contained vacuolated cells and thus stalk cell differentiation did not seem to be disturbed.

Sequencing of the genomic region flanking the inserted plasmid showed that the insertion in clone 10va3 occurred at a BamHI site in the atg7 gene. Knock-out of the atg7 gene was reported previously to result in loss of autophagy, formation of multi-tipped aggregates and defective spore differentiation (Otto et al., 2003), but a role for Atg7 in prespore gene expression was not reported. In addition, the formation of seemingly normal stalks in 10va3 was unexpected, since the autophagy gene atg1 is essential for stalk cell differentiation in vitro (Kosta et al., 2004). To analyse the role of Atg7 in cell differentiation in more detail, we created an atg7 knock-out by deleting a central region of the gene that contained about half of its Atg7-N and ThiF domains (Fig. 1A,C). The atg7- cells recapitulated the phenotype of clone 10va3 (Fig. 2D–F). Development was delayed several hours compared to parental Ax2 cells, but atg7- cells eventually formed small fruiting bodies with a thickened lower part. In contrast to the elliptical phase bright spores of Ax2, cells in atg7- spore heads were round and often phase dark. Most of these cells were not stained with calcofluor, a cellulose binding dye, although a fraction showed weak staining (Fig. 2F). Quantitation showed that only ~6% of atg7- cells produced detergent resistant spores, of which 1/3rd germinated to yield viable amoebas (Table 3). Malformation of the fruiting body and poor sporulation are consistent with the previously described insertion mutant of atg7- (Otto et al., 2003). We also confirmed that spore defects are cell-autonomous, since the atg7- cells did...
structures under phase contrast (top) and epifluorescence. Bar: 100 μm. C. Spores of terminal structures under phase contrast (top) and epifluorescence (bottom) illumination. Bar: 10 μm. D-F. Phenotype of the recapitulated atg7 knockout. Developing Ax2 and atg7-structures were photographed in situ (D) at 16, 24 and 46 h, or in case of atg7- also squashed under a coverslip (E). Bar: 50 μm. F. Spores and stalks from mature Ax2 and atg7- fruiting structures, stained with 0.002% Calcofluor and photographed under phase contrast and epifluorescence. Bar 10 μm.

**Fig. 2. Identification of atg7 by REMI mutagenesis and validation by gene knock-out.** A-C. Phenotype of parental strain Ax2/cotC-mRFP and REMI clone 10va3. A. Developing structures at 19 h and 45 h. Bar: 200 μm. B. Sorogens were photographed under phase contrast and epifluorescence. Bar: 100 μm. C. Spores of terminal structures under phase contrast (top) and epifluorescence (bottom) illumination. Bar: 10 μm. D-F. Phenotype of the recapitulated atg7 knockout. Developing Ax2 and atg7-structures were photographed in situ (D) at 16, 24 and 46 h, or in case of atg7- also squashed under a coverslip (E). Bar: 50 μm. F. Spores and stalks from mature Ax2 and atg7- fruiting structures, stained with 0.002% Calcofluor and photographed under phase contrast and epifluorescence. Bar 10 μm.

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**Table 3**

| strain | time (h) | detergent resistant spores (%) | germinating spores (%) | overall viable spores (%) |
|--------|----------|-------------------------------|------------------------|--------------------------|
| Ax2    | 25       | 149 ± 4                       | 85 ± 7                 | 127 ± 13                 |
| atg7-  | 43-49    | 6 ± 6                         | 32 ± 3                 | 2 ± 1                    |
| 1:1 Ax2/atg7- | 25 | 89 ± 50                       | 76 ± 19 (All)          | Ax2/3                   |

Axt2, atg7- and a 1:1 mixture of AX2 and atg7- cells were plated on 1 cm² nitrocellulose filters supported by NN agar at 2.5 × 10⁶ cells per filter. Filters were vortexed with 0.1% Triton-X100 when fruiting bodies had formed.

* Detergent resistant spores were counted and data are expressed as percentage of the plated cell number. Ax2 cells show >100% spores due to some cell division occurring during development.

* The detergent resistant spores were clonally plated on bacterial lawns, after 2-5 days emerging plaques were counted and expressed as percentage of the plated spores.

* The overall percentage of viable spores was determined as (fraction of triton-resistant x fraction of germinated spores) x 100.

* The genotype of the germinated spores was evaluated from the developmental phenotype.

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not form viable spores when mixed with Ax2 (Table 3).

Similar to clone 10va3, the atg7- fruiting bodies formed a stalk that penetrated the (pre)spore cell mass and connected to the basal cell mass (Fig. 2E and F). The cells inside the stalk were highly vacuolated and encapsulated in cellulose, although arrangement of the atg7- stalk cells was somewhat irregular compared to wild type. The cells in the expanded bottom region of the stalk eventually also vacuolated. These results show that Atg7 is essential for sporulation, while it is dispensable for stalk cell differentiation.

The earlier reports describing requirement for the autophagy protein Atg1 in stalk cell differentiation were based on cells differentiating in a monolayer in the presence of the polyketide DIF-1 (Kosta et al., 2004). To test whether Atg7 is required under these conditions, we rendered atg7-cells in monolayers competent to DIF-1 by pre-incubation with CAMP (Berks and Kay, 1990) and then stimulated cells with DIF-1. In contrast to atg1- cells (Kosta et al., 2004), atg7- and Ax2 cells readily vacuolated in response to DIF-1 (Fig. 3), although most vacuoles of the atg7- cells appeared to contain more material than those of Ax2. Both strains remained amoeboid in the absence of DIF-1. Apparently, Atg7 is not required for DIF-induced stalk cell vacuolation in vitro.

### 3.2. Expression of cell type markers in atg7-

The lack of cotC-mRFP expression in 10va3 sorogens (Fig. 2B) suggests that the abolished spore production is due to defective prespore differentiation. To examine cell differentiation in more detail, we transformed Ax2 and atg7- cells with fusion constructs of cell type specific promoters and the LacZ reporter gene (gal). The transformants were developed to early and late sorogens and fruiting bodies, and stained with X-gal to visualize β-galactosidase expression.

The prespore marker cotC-gal is expressed strongly in the posterior prespore region of Ax2 early culminants at 17 h, but at 17 and 24 h expression of cotC-gal in atg7- was very low and only detectable after prolonged staining with X-gal (Fig. 4A). At 24 h, cotC-gal expression was still very weak and confined to a short central region of the sorogen. In atg7- fruiting bodies, some cotC-gal expression was detected in the abnormal spores of the spherical heads. The prestalk markers ecmA-gal and ecmB-gal were expressed in the primary stalks of atg7- fruiting structures at about the same levels as in Ax2 cells. The vacuolating cell masses at the base of the atg7- stalks only started to express the prestalk
Fig. 3. Stalk cell induction in vitro. Ax2 and atg7- cells were pre-incubated for 6 h with 1 mM cAMP. After removal of cAMP, cells were incubated for 23 h with 100 nM DIF-1. Control cells received the DIF-1 solvent, 0.1% ethanol. About 70 cells per sample were photographed, with representative images shown in (A). Some of the typical stalk cell vacuoles are indicated by arrows. Bar: 20 μm. B. Percentages of vacuolated over total cells were determined from images. Means and SD of three experiments. Values for DIF-treated cells were not statistically different between Ax2 and atg7- (t-test, $P = 0.46$).

Fig. 4. Expression pattern of cell-type markers in atg7-. Ax2 and atg7- cells, transformed with cotC-gal (A), ecmA-gal (B) or ecmB-gal (C) were incubated on dialysis membrane supported by non-nutrient agar for the time periods shown above the images. Structures were fixed and stained with X-gal for 30 min at 22 °C for all structures, and also for 4 h at 37 °C for atg7-/cotC-gal structures as shown inside the images. Bar: 50 μm.
markers very late in fruiting body formation (Fig. 4B and C). Due to the overall delayed developmental programme of \( \text{atg7}^- \), its fruiting bodies started to form about 7 h later than in the \( \text{Ax2} \) parent.

3.3. Induction of post-aggregative genes by cAMP in \( \text{atg7}^- \)

Prespore differentiation requires cAMP in the micromolar range acting on cell surface receptors (cARs) (Schaap and Van Driel, 1985; Wang et al., 1988a), and for many prespore genes, also intracellular cAMP acting on PKA (Hopper and Williams, 1994). Very low \( \text{cotC} \) expression in \( \text{atg7}^- \) slugs (Fig. 4) prompted us to examine whether prespore gene induction by cAMP was impaired. Transcripts of the prespore genes \( \text{cotC} \) and \( \text{pspA} \), but not of the constitutively expressed gene \( \text{Ig7} \), strongly increased after 4 h of incubation with 1 mM cAMP in differentiation competent \( \text{Ax2} \) cells, but remained low in competent \( \text{atg7}^- \) cells and in the absence of cAMP (Fig. 5A,D). To assess whether defective cAMP induction of \( \text{atg7}^- \) cells was specific to prespore genes, we also tested the prestalk gene \( \text{ecmA} \) and the prestalk-enriched gene \( \text{cprB} \). \( \text{CprB} \) requires only cAMP for induction (Pears et al., 1985) and was induced in both \( \text{Ax2} \) and \( \text{atg7}^- \) cells, albeit that induction in \( \text{atg7}^- \) was 40% lower than in \( \text{Ax2} \) (Fig. 5B). \( \text{EcmA} \) is reported to require DIF-1 in addition to cAMP (Berks and Kay, 1990), and while effects of DIF-1 alone on \( \text{ecmA} \) induction were weak (Fig. 5C), induction by cAMP plus DIF-1 was high in both \( \text{Ax2} \) and \( \text{atg7}^- \) cells. These experiments show that \( \text{atg7}^- \) cells are specifically defective in cAMP induction of prespore gene expression.

3.4. Is defective sporulation the result of reduced autophagy in \( \text{atg7}^- \)?

The requirement of \( \text{Atg7} \) for cAMP induction of prespore gene expression suggests that autophagy is required for gene regulation. However, a role for \( \text{Atg7} \), independent of autophagy, was shown in starving mouse fibroblasts, where binding of \( \text{Atg7} \) to the \( \text{p}53 \) tumour suppressor was required for normal cell cycle arrest. This effect did not require the E1-like enzyme activity of \( \text{Atg7} \), which mediates its role in autophagy (Lee et al., 2012). To assess whether the effects of loss of \( \text{Atg7} \) in \( \text{Dictostelium} \) are independent from its role in autophagy, we complemented the \( \text{atg7}^- \) mutant with both intact \( \text{Atg7} \) and \( \text{Atg7} \) harbouring a Cys563 to Ala mutation, which abolishes its E1-like enzyme activity. Fig. 6 shows that only intact \( \text{Atg7} \) restores normal fruiting body formation and sporulation in the \( \text{atg7}^- \) mutants, indicating that the E1-like enzyme activity of \( \text{Atg7} \) is required for sporulation.

Several mutants in autophagy genes, such as \( \text{atg5} \), \( \text{atg6} \), \( \text{atg8} \) and \( \text{atg9} \) show a multi-tipped phenotype and spore defects (Otto et al., 2003, 2004; Tung et al., 2010). To assess whether specific defects in prespore gene induction are a general feature of autophagy mutants, we analysed the phenotype of \( \text{atg5}^- \) and \( \text{atg9}^- \) mutants in greater detail. \( \text{Atg5} \) acts as a
adenylate cyclase A (Theibert and Devreotes, 1986), PKA can potentially precocious sporulation being induced by overexpression of the PKA atg7–cells was determined as described in the legend to Table 1, with spores harvested from both 23 h and 44 h fruiting bodies. *: significantly different, P < 0.01. E. Lysates from atg7–, atg7–/akt15p-YFP-atg7 and atg7–/act15p-YFP-atg7/C563A cells were size-fractionated by SDS-PAGE and Western blots were probed with anti-GFP antibodies to visualize the YFP fusion proteins.

substrate in the first of the two steps of the ubiquitin-like system to conjugate Atg8 onto autophagosomes where Atg7 acts like an E1 enzyme, whereas Atg9 is required for recruiting lipid membrane in autophagosomal formation (Lamb and Tooze, 2016). We investigated cell differentiation in an existing atg9– and reactivated atg5– mutant (Fig. 1). During development on agar, atg9– and atg5– showed similar fruiting body defects as atg7–, with virtually absent spore formation, a relatively normal stalk with fully vacuolated and cellulose-encapsulated stalk cells and a large mass of basal cells that eventually also vacuolated (Fig. 7A–C). Similar to atg7–, cotC-gal expression was very low in atg9– and confined to a small region of the sorogens (Fig. 7D). Both ecmA-gal and ecmB-gal were expressed at similar levels in the primary stalk of developing fruiting bodies of Ax2 and atg9– (Fig. 7E and F). As was the case for atg7–, the enlarged bases of the atg9– fruiting bodies only expressed ecmA-gal and ecmB-gal very late in development.

cAMP induction of the prespore genes cotC and pspA was also absent among the atg5– and atg9– mutants, while crpR induction was 50% reduced. EcmA induction by cAMP and DIF was variable between experiments, but higher than in Ax2 (Fig. 8). Overall, these mutations in different aspects of the autophagy pathway all yielded the same phenotypic defects as atg7–, indicating that it is autophagy itself that is required for cAMP induction of prespore gene expression.

3.5. How does autophagy interact with cAMP induction of prespore gene expression?

The requirement of autophagy for cAMP-induced prespore expression could either result from i. cells not being competent to detect and process the cAMP signal, or ii. from autophagy being part of the cAMP signal transduction pathway by either producing a stimulator or degrading an inhibitor of prespore gene expression.

In addition to cAMP activation of cAMP receptors (cARs), cAMP activation of protein kinase A (PKA) is required for expression of many prespore genes and for spore maturation (Hopper et al., 1993), with precocious sporulation being induced by overexpression of the PKA catalytic subunit, PkaC (Mann et al., 1994). Because cARs also activate adenylate cyclase A (Theibert and Devreotes, 1986), PKA can potentially act downstream of cARs. We therefore examined whether PkaC overexpression can restore sporulation in atg7– and atg9–. Fig. 9 shows that PkaC overexpression in Ax2 caused precocious maturation of many spores at the sorogen base, before the prespore mass had ascended the stalk. However, no viable spores were formed in atg7– and atg9– overexpressing PkaC. To test whether the failure of PkaC to rescue sporulation in atg7– already acted at the stage of prespore gene induction, we compared cAMP induction of the prespore genes cotC and pspA between Ax2 and atg7– cells, both overexpressing pkaC-YFP. Fig. 9D shows that levels of cotC and pspA expression in response to cAMP stimulation remained very low in the atg7–/PkaC-YFP cells, indicating the pkaC does not act downstream of Atg7.

The cAMP receptors car1, 2 and 3 can largely complement each other’s function in mediating cAMP-induced prespore gene expression. However, car1, the only car, which, like prespore induction, is inhibited by adenosine, most likely mediates this process (Verkerke-VanWijk et al., 1998). We first tested whether expression of the car1 gene carA was defective in the atg7– mutant. Fig. 10A shows that carA transcript levels were only marginally reduced in atg7– during the first 12 h of development, indicating that its lack of cAMP-induced prespore gene expression is not due to lack of carA. During persistent stimulation with micromolar cAMP, car1 receptors are endocytosed and eventually degraded (Wang et al., 1988b). Autophagy was also reported to promote endocytosis of membrane receptors (Shin et al., 2016; Xu et al., 2016). We therefore tested whether Atg7 was required for internalization of car1, which could be part of the cAMP pathway activating prespore genes. We transformed both Ax2 and atg7– cells with a car1-GFP fusion construct, expressed from the constitutive act15 promoter (Xiao et al., 1997) and observed car1-GFP localization in the absence and presence of cAMP. Fig. 10B shows that car1-GFP remains mostly membrane localized in both Ax2 and atg7– cells, while staining at the cell periphery decreases. Upon persistent stimulation with cAMP, car1 is also phosphorylated, which causes a mobility shift on SDS-PAGE, followed by protein degradation (Vaughan and Devreotes, 1988). Fig. 10C shows that both Ax2 and atg7–, transformed with car1-GFP showed a mobility shift and subsequent degradation of
the cAR1-GFP. It is therefore unlikely that autophagy stimulates prespore gene expression by causing cAR1 internalization.

Protein degradation by autophagy yields ammonia, which was reported to promote spore differentiation (Bradbury and Gross, 1989; Gross et al., 1983). To investigate whether lack of ammonia caused defective cAMP-induced prespore gene expression in autophagy mutants, we treated atg7- and atg9- cells with cAMP and increasing ammonia concentrations. However, there was no restoration of cotC-gal induction by ammonia (Fig. 11).

We finally tested how loss of autophagy affected two transcription factors with roles in prespore gene expression. The transcription factor SpaA acts downstream of PKA to induce expression of some prespore genes and spore maturation (Yamada et al., 2018). GbfA was isolated as a protein binding to G-rich motifs in the prestalk gene cprB, and to be required for cAMP induction of this gene. Subsequent studies showed that it also interacted with G-rich motifs in prespore genes and was required for their cAMP-inducibility (Hjorth et al., 1989; Powell-Coffman et al., 1994; Schnitzler et al., 1994). Expression of gbfA is about 30%

Fig. 7. Developmental phenotypes of atg5- and atg9- in an Ax2 background. A-C. Developing structures. Atg5- and atg9- cells were developed on non-nutrient agar and terminal fruiting bodies were photographed in situ (A), or stained with Calcofluor, squashed under a coverslip and photographed under phase contrast (B, C left panel) or epifluorescence (C, right panel). Bar: 50 μm. D-F. Cell-type specific gene expression. Ax2 and atg9- cells, transformed with cotC-gal (D), ecmA-gal (E) and ecmB-gal (F) were incubated on dialysis membrane supported by non-nutrient agar for the time periods shown above the images. Structures were fixed and stained with X-gal for 30 min at 22 °C for all structures, and also for 4 h at 37 °C for some atg9-/cotC-gal structures as shown inside the images. Bar: 50 μm.
reduced in atg7- cells (Fig. 12A), which can account for the ~40% reduction of cAMP induction of cprB, but not the complete loss of cotC and pspA induction (Fig. 5). SpaA expression is about 60% reduced in atg7- cells (Fig. 12B), also not enough to account for complete loss of cotC induction. SpaA is only expressed in prespore and spore cells and we tested whether it was itself induced by cAMP. This was the case (Fig. 12C) with induction being ~70% reduced in atg7- cells, in agreement with its 60% reduced developmental expression. Overall, the effects of loss of Atg7 on spaA and gbfA expression are insufficient to account for the complete lack of prespore induction in atg7- cells.

4. Discussion

4.1. Disruption of autophagy prevents cAMP induction of prespore differentiation

A screen for mutants defective in spore differentiation identified Atg7, a component of the autophagy pathway as being essential for this process (Fig. 2). Further analysis showed that the atg7- mutant was specifically impaired in cAMP induction of prespore gene expression, but not in cAMP-induction of different classes of prestalk genes and in stalk cell differentiation (Fig. 5). Closer investigation of mutants lacking Atg5 and Atg9 revealed that they were also specifically defective in cAMP-induced prespore gene expression, indicating that the defect in atg7- mutants was due to loss of autophagy and not to a role of Atg7, unrelated to autophagy.

Because Dictyostelium cells go through multicellular development while starving, loss of autophagy, which essentially deprives cells of metabolites and sources of energy can be expected to interfere with several developmental processes, which is evident from the abnormal multi-tipped morphology of autophagy mutants and effects on expression of many classes of genes (Calvo-Garrido et al., 2010; Mesquita et al., 2017) (Fischer et al., 2019). Deleterious effects of loss of Atg7 and other autophagy proteins on spore formation was reported before (Otto et al., 2003, 2004; Tung et al., 2010). However, these studies focussed on resolving the autophagy pathway and did not study sporulation in detail. Loss of autophagy also prevents production of the spore maturation inducing peptide SDF-2 (Cabral et al., 2010), but unlike the cell-autonomous defect in prespore gene expression caused by loss of autophagy reported here, this is a non-cell autonomous defect that acts much later in development. Since spore differentiation requires a considerable investment in building materials for construction of the multi-layered spore wall, defective sporulation in autophagy mutants is to be expected. However, the early and specific effect of autophagy loss on cAMP-induced prespore gene expression is enigmatic.

4.2. Role of autophagy in stalk cell differentiation

The lack of effect of loss of autophagy genes on stalk cell differentiation was unexpected since autolysosome formation occurs much more prominently in prestalk than prespore cells, while fusion of autolysosomes is considered to cause formation of the large central vacuole of the stalk cells (Schaap, 1983; Uchikawa et al., 2011). Furthermore, loss of two other autophagy genes atg1 or vmp1 prevent cells from differentiating into stalk cells in vitro in response to DIF-1, an inducer of stalk cell differentiation (Calvo-Garrido and Escalante, 2010; Kosta et al., 2004). The atg7- mutant also showed normal DIF-induced stalk cell differentiation in vitro (Fig. 3), and, like atg5- and atg9-, formed somewhat disorganized, but otherwise normal stalks in vivo (Figs. 2 and 7), and this was also reported for vpsI3-mutants (Muñoz-Braceras et al., 2015).
The relatively normal stalk cell differentiation in \textit{atg7-}, \textit{atg5-}, \textit{atg9-}, \textit{vps13-} and likely all other autophagy mutants that still manage to form fruiting structures could be a consequence of the fact that unlike \textit{atg1}, these genes act more downstream in the autophagy pathway and might not inhibit autophagy altogether. Also non-canonical forms of autophagy that do not require Atg5 or Atg7 have been described (Arakawa et al., 2017; Dupont et al., 2017). Another explanation could be that both \textit{atg1-} and \textit{vmp1-} cells show early developmental arrest (Calvo-Garrido et al., 2008; Otto et al., 2004). In addition to autophagy, Vmp1 is also involved in organelle biogenesis, contractile vacuole function and protein secretion (Calvo-Garrido et al., 2008), and interference with these functions may preclude normal developmental progression. Apart from initiating phagophore formation, Atg1 regulates the activity of transketolase, an enzyme in the pentose phosphate pathway (Mesquita et al., 2015).

However, if autophagy does not cause stalk cell vacuolization, as the phenotypes of most autophagy mutants, except \textit{atg1-} and \textit{vmp1-}, suggest, than what does? One possibility is that the stalk vacuole is more akin to the large central vacuole of plants or fungi that fulfills a range of functions. While both the plant and fungal vacuoles also fuse with autophagosomes during the normal progression of autophagy (Yoshimoto and Ohsumi, 2018), the biogenesis of these vacuoles is not dependent on autophagy. \textit{Dictyostelium} may have as yet unnoticed protovacuoles that normally own much of their size increase to fusion with autophagosomes, but can also inflate in their own right.

### 4.3. Elimination of putative prespore pathway components that are affected by autophagy

While a pleiotropic effect of autophagy on the formation of normal viable spores is to be expected, direct involvement of non-specific
PKA overexpression neither rescued cAMP induction of prespore gene atg7, mound cells of Ax2 and highlight patches of internalised cAR1-GFP. Bar: 10 μm. A. cAR gene expression. Ax2 and atg7- cells were transformed with cotC-gal and developed into loose mounds. Cells were then dissociated in 20 mM potassium phosphate pH 7.4 containing 1 mM MgCl₂ and incubated with cAMP and increasing concentrations of NH₄Cl for 6 h. After cell lysis, expression of cotC-gal was analysed with a spectrophotometric β-galactosidase assay. Means and SD of two experiments performed in duplicate. Values for cAMP-treated Ax2 cells were significantly higher than for cAMP-treated atg7- cells at each of the NH₄Cl concentrations at P < 0.005.

expression in atg7-, nor sporulation in either the atg7- or atg9- mutant (Fig. 9), indicating that defective autophagy does not act by preventing PKA activation. This is further substantiated by the observation that cAMP induction of the prespore gene pspA, which does not require PKA, SpaA or CudA for expression (Hopper et al., 1993; Yamada et al., 2018) is also lacking in the atg7- mutant (Figs. 5 and 8). The transcription factor GβfA is required for cAR regulated expression of prespore and prestalk genes, particularly cprB (Hjorth et al., 1989; Powell-Coffman et al., 1994; Schnitzler et al., 1994). While gβfA expression is ~40% reduced in atg7- (Fig. 12A), this reduction can account for the similarly reduced cprB expression, but not for the complete absence of prespore gene expression (Figs. 5 and 8).

cAR1 phosphorylation and endocytosis accompany induction of prespore gene expression by micromolar cAMP and could potentially mediate this process (Vaughan and Devreotes, 1988; Wang et al., 1988b). However, neither cAR1 phosphorylation nor internalization were impaired in the atg7- mutant (Fig. 10). For autophagy to mediate cAMP-induced prespore gene expression, autophagy itself should be activated by cAMP. However, autophagic vesicles are actually down-regulated in prespore cells (Schaap, 1983). This leaves the possibilities that autophagy either produces a catabolite that is specifically required for the cAMP pathway or eliminates a pathway specific inhibitor. An obvious catabolite of protein degradation is ammonia, which is known to promote spore and inhibit Dictyostelium stalk cell differentiation (Bradbury and Gross, 1989; Gross et al., 1983) (Wang and Schaap, 1989). However, we could not restore cAMP induction in the atg7- mutant by co-incubation with ammonia (Fig. 11).

No further pathway components or inhibitors thereof are known, ending our options to identify the nature of the interaction between autophagy and prespore gene expression by a biased approach. Our current forward genetic strategy to identify sporulation genes, or a genetic screen for a suppressor of the atg7- phenotype is more likely to identify the prespore pathway components that are affected by loss of autophagy.
Fig. 12. Expression of transcription factors in the atg7- mutant. A. B. Developmental regulation. The RNAs isolated for analysis of cArX expression in Fig. 6 were used to study gbfA (A) and spaA (B) expression using spaA and gbfA specific primers (Table 2). C. CAMP induction. The RNAs isolated for analysis of carX expression in Fig. 5 were here analysed for spaA induction. Significant differences in expression between Ax2 and atg7- at the same developmental time (A,B) or after induction with cAMP (C) are marked with * for 0.01 < P < 0.05 and ** for P < 10^{-5}.

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