Check for updates

Received: 29 October 2023 | Revised: 15 January 2024 | Accepted: 16 January 2024

DOI: 10.1111/jmi.13267

Journal of Microscopy RMS

THEMED ISSUE ARTICLE

Mitophagy in plants: Emerging regulators of mitochondrial targeting for selective autophagy

Patrick J. Duckney[1] | **Pengwei Wang**[2] | **Patrick J. Hussey**[1]

[1]Department of Biosciences, Durham University, Durham, UK

[2]Key Laboratory of Horticultural Plant Biology, College of Horticulture and Forestry Sciences, Huazhong Agricultural University, Wuhan, China

Correspondence
Patrick J. Hussey, Department of Biosciences, Durham University, Durham, UK.
Email: p.j.hussey@durham.ac.uk

Abstract

The degradation and turnover of mitochondria is fundamental to Eukaryotes and is a key homeostatic mechanism for maintaining functional mitochondrial populations. Autophagy is an important pathway by which mitochondria are degraded, involving their sequestration into membrane-bound autophagosomes and targeting to lytic endosomal compartments (the lysosome in animals, the vacuole in plants and yeast). Selective targeting of mitochondria for autophagy, also known as mitophagy, distinguishes mitochondria from other cell components for degradation and is necessary for the regulation of mitochondria-specific cell processes. In mammals and yeast, mitophagy has been well characterised and is regulated by numerous pathways with diverse and important functions in the regulation of cell homeostasis, metabolism and responses to specific stresses. In contrast, we are only just beginning to understand the importance and functions of mitophagy in plants, chiefly as the proteins that target mitochondria for autophagy in plants are only recently emerging. Here, we discuss the current progress of our understanding of mitophagy in plants, the importance of mitophagy for plant life and the regulatory autophagy proteins involved in mitochondrial degradation. In particular, we will discuss the recent emergence of mitophagy receptor proteins that selectively target mitochondria for autophagy, and discuss the missing links in our knowledge of mitophagy-regulatory proteins in plants compared to animals and yeast.

KEYWORDS

Arabidopsis, autophagy, contact site, homeostasis, mitochondria, mitophagy, plant, stress, TraB, TRB1

1 | INTRODUCTION

Mitochondria are a major metabolic organelle with key roles in ATP generation, metabolic biosynthesis and catabolism, redox homeostasis and cell signalling.[1,2] Homeostatic maintenance of functional mitochondrial populations is fundamental to Eukaryotic life, and removal and degradation of mitochondria is an important cellular mechanism for mitochondrial quality control. Across Eukaryotes, it has been documented that mitochondrial degradation has diverse and important functions including the turnover of damaged mitochondria during stress,

This is an open access article under the terms of the Creative Commons Attribution-NonCommercial-NoDerivs License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made.
© 2024 The Authors. *Journal of Microscopy* published by John Wiley & Sons Ltd on behalf of Royal Microscopical Society.

the control of metabolism during cell development and differentiation, immune responses and the prevention of paternal mtDNA inheritance.[3]

A major route for the degradation of subcellular components (including mitochondria) is the autophagy pathway, in which cargos destined for degradation are encapsulated in a membrane-bound autophagosome and targeted to the vacuole (in plants and yeast) or lysosome (in animals). Autophagy is a tightly regulated process coordinated by a large number of autophagy-regulatory proteins, which control the progression of autophagy over a series of key stages, including (i) the initiation of a pre-autophagosome membrane structure, or 'phagophore', (ii) the recognition and binding of selected cargo to the phagophore membrane, (iii) the expansion of the phagophore membrane to engulf and sequester cargo in the autophagosome and, (iv) targeting and fusion of the autophagosome to the vacuole. The specific targeting of certain subcellular components for autophagic degradation is known as selective autophagy and is inherent to the regulation of specific subcellular processes or appropriate responses to specific stresses. The discernment of mitochondria for selective autophagic degradation (referred to as mitophagy) is well understood in yeast and animal model systems as the protein regulators that target mitochondria for autophagic degradation have been widely characterised.[3] However, in plants the mechanisms that regulate mitophagy and their importance to plant life present a gap in our knowledge, as the protein regulators of plant mitophagy have remained elusive until recently.

We will discuss the emerging field of mitophagy in plants, its importance, mechanisms of regulation and the proteins that selectively target mitochondria for encapsulation within autophagosomal membranes (Figure 1). We will discuss the gaps in our understanding of plant mitophagy in comparison to animals and yeast and speculate upon potential plant protein regulators that may fill these missing links.

2 | THE EVIDENCE FOR MITOPHAGY IN PLANTS AND ITS IMPORTANCE TO PLANT LIFE

Early indicators of the existence of mitophagy in plants has been derived from ultrastructural cell analysis, in which mitochondria have been observed encapsulated in autophagosome-like double membrane structures, and the presence of mitochondria in the vacuole.[4–7] Further evidence for the autophagic degradation of mitochondria can be drawn from the colocalisation of fluorescently labelled mitochondria with markers of autophagy-regulatory proteins in live cells. For example, mitochondria have been seen to colocalise with members of the ATG8 family of autophagy cargo recruitment proteins, and the autophagy scaffolding protein, ATG11, in Arabidopsis.[7–12] Moreover, mitochondria internalised into the vacuole can be seen to colocalise with ATG8-labelled autophagosomes, indicating a link between vacuolar degradation of mitochondria and the autophagy pathway.[9,10] Evidence for mitophagy in plants has been decisively demonstrated using autophagy-defective mutants, in which targeting of mitochondria to the vacuole and their degradation is impaired, underscoring the dependence of mitochondrial degradation on the autophagy pathway.[7,8,10,13]

It is becoming increasingly clear that mitophagy has diverse functions in plants. As in animal and yeast model systems, a major role for mitophagy in plants is homeostatic mitochondrial quality control, through the clearance and recycling of damaged mitochondria to maintain 'healthy' populations of functional mitochondria. Under nonstressed conditions, plants undergo a basal level of mitophagy to maintain mitochondrial homeostasis[7,10] but the importance of mitophagy is particularly evident in the responses of plants to environmental stresses that cause mitochondrial damage. For example, mitochondrial stress induced through pharmacological mitochondrial depolarisation (including 2,4-dinitrophenol; DNP, or carbonyl cyanide-p-trifluoromethoxyphenylhydrazone; FCCP) results in the increased autophagic degradation of mitochondria. In autophagy and mitophagy-defective mutant lines however, vacuolar degradation of mitochondria is impaired resulting in the accumulation of damaged mitochondria in the cytoplasm.[7,10] As a result, mitophagy-defective mutants show reduced recovery following mitochondrial stress treatments, stemming from their inability to recycle nonfunctional mitochondria.[10] Mitophagy has been proposed to recycle mitochondria damaged during high UV-B stress.[9] Autophagy-defective mutants are hypersensitive to UV-B treatment and accumulate large numbers of damaged mitochondria.[9,14] Interestingly, while Dundar et al. (2020) and Nakamura et al. (2021) observed accumulation of damaged mitochondria following UV-B treatment, Kacprzak and Van Aken (2022) demonstrated mitochondrial degradation was not induced by UV-B treatment. These authors have highlighted that broader stresses including nitrogen starvation, heat shock and hypoxia are not triggers for mitophagy, instead reporting that mitophagy is triggered by mitochondrial-specific stresses. These mitochondrial stresses included pharmacological treatments that induce mitochondrial depolarisation (DNP, FCCP), impair mitochondrial protein import (MitoBlockCK-6; MB) and mitochondrial translation (doxycycline; Dox). Kacprzak and Van Aken (2022)[15] suggest clearing of damaged mitochondria by mitophagy is important for plant responses to carbon starvation

13652818, 0, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/jmi.13267 by Test, Wiley Online Library on [08/02/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

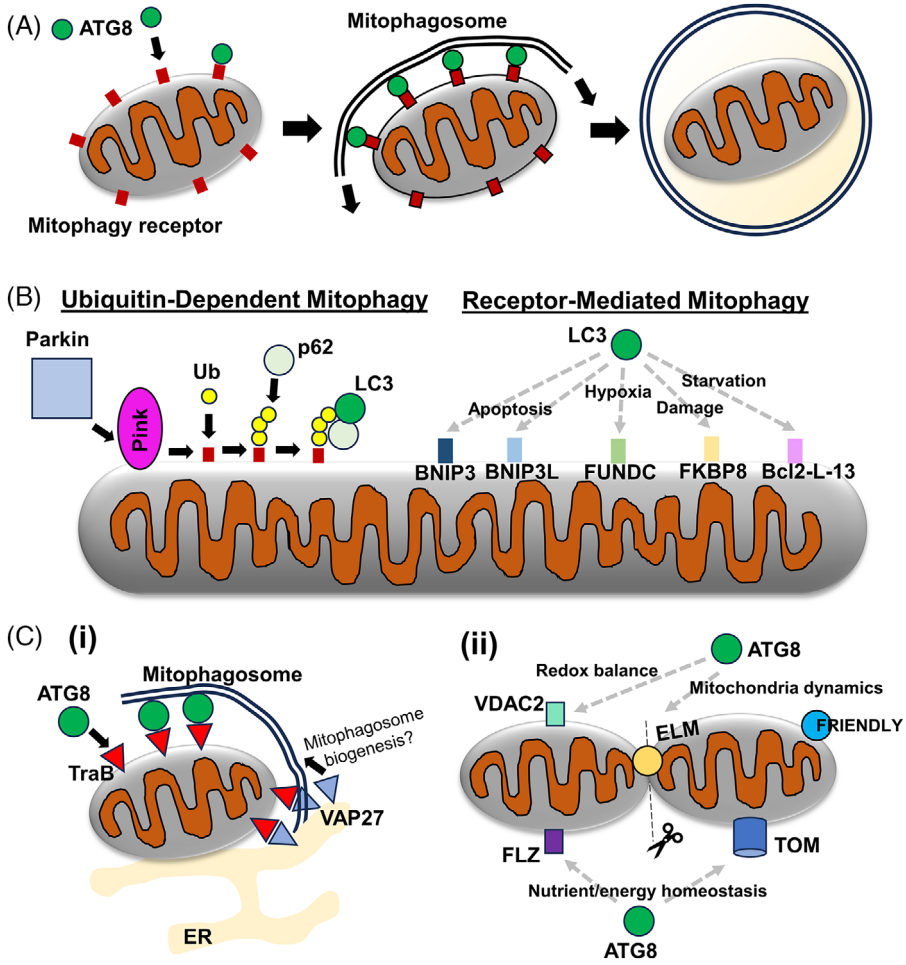

FIGURE 1 Mitophagy: the selective targeting of mitochondria for autophagic degradation. (A) The autophagy-regulatory protein, ATG8, recognises cargo for degradation. Mitophagy receptor proteins recruit ATG8 to the mitochondrial membrane. Recruitment of the autophagy machinery to the membrane drives the expansion of the mitophagosome and the encapsulation of mitochondria in a membrane-bound autophagosome. (B) Targeting of mitochondria for autophagy in mammals. In ubiquitin-dependent mitophagy (in response to oxidative stress, or mitochondrial depolarisation), Parkin activates PINK, which polyubiquitinates (Ub) mitochondrial membrane proteins resulting in the recruitment of p62 and LC3. In receptor-mediated mitophagy, several mitophagy receptor proteins recruit LC3 in response to various cell stresses. (C) Mechanisms of mitophagy in plants. (i) ATG8 is recruited to the outer membrane of damaged mitochondria by TraB-family proteins to drive autophagosome biogenesis. At ER-Mitochondrial Contact Sites, TraB proteins also interact with VAP27, which may drive mitophagosome biogenesis. (ii) Putative mitophagy receptors in Arabidopsis may interact with and recruit ATG8 through ATG8-Interacting Motif (AIM) domains, likely to regulate mitophagy in response to specific stresses. The mitochondrial organising protein, FRIENDLY, may link mitophagy to mitochondrial dynamics through yet-unknown mechanisms.

through a homeostatic metabolic balancing mechanism. During the daytime photosynthetic period, cellular energy and ATP are generated chiefly in the chloroplasts, but during dark photosynthetic periods the function of ATP production is carried out through mitochondrial respiration. Therefore, increased levels of mitophagy likely serve to maintain maximal mitochondrial quality and increases capacity for mitochondrial energy production.[15] From current observations, it seems a major role for mitophagy during stress is the homeostasis of mitochondrial quality.

Autophagic degradation of mitochondria plays important roles in several aspects of plant development. Mitophagy is important for spermeogenesis in the liverwort *Marchantia polymorpha* and achieves developmentally programmed reduction of mitochondrial populations necessary to generate functional spermatozoids.[13] It has been reported that mitophagy is important for male fertility and reproduction in Arabidopsis, and likely serves to maintain functional populations of mitochondria to meet the energy demands of rapidly growing pollen tubes.[12] A role for mitophagy in plant development appears likely and various regulators of mitophagy are linked to plant growth. Mutants defective in mitophagy such as *vap27* and TRB1 dominant negative mutants exhibit defects in plant growth

13652818, 0, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/jmi.13267 by Test, Wiley Online Library on [08/02/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

and development.[10,11] In maize, autophagy is important for endosperm development and functions to clear dysfunctional mitochondria, maintain redox homeostasis, and support cell metabolism.[16] Additionally, mitophagy appears to function during plant senescence.[8,15,17] Whereas organelles such as chloroplasts are degraded and recycled early during senescence, mitochondria are preserved to assist in the recycling of nutrients. It is hypothesised that mitophagy maintains mitochondrial function throughout senescence to maximise mitochondrial support of metabolic recycling.[15]

Mitophagy also appears to be important in the regulation of plant metabolism; and mutants of TraB-family mitophagy proteins exhibit defects in starch metabolism and ATP synthesis.[10,11] It remains to be determined if these metabolic defects are linked to the impairment of mitophagy and loss of homeostatic mitochondrial quality control.

3 | PROTEIN REGULATORS OF PLANT MITOPHAGY

As a specialised form of autophagy, plant mitophagy is, unsurprisingly, dependent on much of the core autophagy machinery that regulates nonspecific ('or bulk') autophagy. Induction of bulk autophagy using AZD8055, an inhibitor of the autophagy-repressing protein, TOR, resulted in constitutive mitophagy and enhanced degradation of mitochondria under nonstressed conditions.[15] Much of these core autophagy regulators are conserved across Eukaryotes and are implicitly necessary for the initiation, biogenesis and transport of the autophagosome. The ATG1/ATG13 kinase complex is a sensor of upstream signals that promote autophagosome biogenesis.[18,19] ATG1/ATG13 interact with the scaffolding protein, ATG11, which is proposed to recruit ATG1 to the pre-autophagosome structure, is important for targeting of mitochondria to the vacuole.[8,15,17] It is currently unknown exactly how the ATG1/ATG11/ATG13 complex regulates the targeting of mitochondria to the vacuole in plants, as their exact functions in autophagosome biogenesis and vacuole-targeting remain to be elucidated. However, it appears that at least one likely role of the complex is the encapsulation of mitochondria in the autophagosome, as mutants of *atg1* and *atg13* are impaired in the closure of the autophagic vesicle body.[18] Regulators of autophagosome biogenesis, ATG5, ATG7 and ATG12,[16,20] are important for the autophagic degradation of mitochondria.[7,8,10,15,16] ATG5, ATG7 and ATG12 are important for the lipidation of ATG8 proteins and their embedding into the autophagosome membrane, where they bind cargo for degradation and drive autophagosome biogenesis.[16,20–22] Recognition of mitochondrial proteins by ATG8 is important to promote its recruitment to the outer mitochondrial membrane (OMM) and target mitochondria for autophagic degradation.[10]

The specificity of mitochondrial degradation during mitophagy requires mechanisms to specifically target mitochondria to the autophagosome separately from other cell components. Protein regulators that specify mitochondria for selective autophagic degradation have long remained elusive in plants. Recently however, the TraB-family proteins, TRB1 and TRB2, have emerged as plant mitophagy receptors. TRB1 specifically localises to the OMM and recruits ATG8 to drive the encapsulation of mitochondria in the autophagosome membranes (Figure 2).[10,11] Similarly, TRB2 also localises to the OMM and interacts with ATG8, and therefore likely also functions to recruit ATG8 to the OMM.[10] Interestingly, TRB2 also localises to the cytosolic face of the ER; however, its function here remains to be explored.[10] TraB proteins likely have dual functions in the regulation of mitophagy, through their roles as ER-Mitochondrial Contact Site (EMCS) proteins. TraB proteins regulate EMCS through interaction with ER-integral, VAP27. In plants, VAP27 regulates autophagosome biogenesis in complex with the actin-regulatory protein EH1/Pan1, T-PLATE and clathrin endocytic machinery.[23] A potential role for TraB proteins could be to engage the mitochondria with this autophagic machinery at the ER membrane to facilitate their encapsulation in autophagosome membranes. In animal and yeast model systems, EMCS are also important in the regulation of mitophagy, likely serving as a membrane source for the developing mitophagosome.[24] It is possible that ER-mitochondrial tethering by TraB proteins and VAP27 may facilitate lipid transfer to the mitophagosome in plants.

Mitochondrial positioning and organisation may also be important for mitophagy. In mutants of FRIENDLY, mitochondria are abnormally distributed in the cytoplasm and form large clusters,[25,26] and *friendly* mutants are impaired in mitophagy.[7,27] Currently, it is not clear whether FRIENDLY has a direct role in promoting mitophagy through regulating mitochondrial organisation, or whether observed defects in mitophagy are an indirect consequence of abnormal mitochondrial clustering.

4 | MISSING LINKS: THE GAPS IN OUR UNDERSTANDING OF MITOPHAGY IN PLANTS

Our understanding of the regulation of mitophagy in plants lags behind that of mammalian model systems, as many of the plant-equivalent protein regulators of

13652818, 0, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/jmi.13267 by Test, Wiley Online Library on [08/02/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

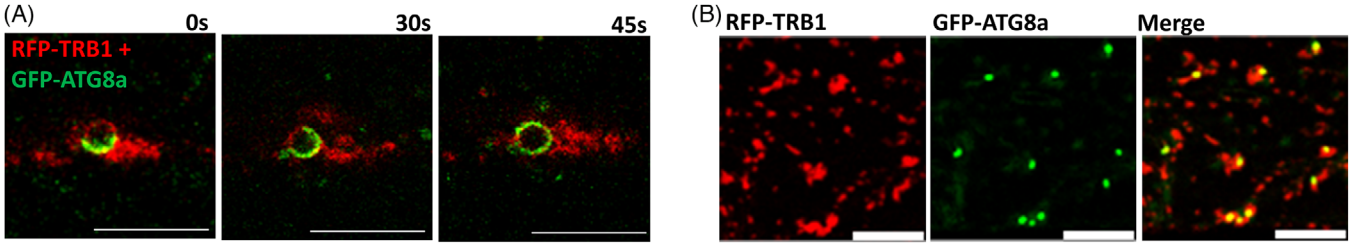

FIGURE 2 TRB1 is a mitophagy receptor protein in plants. (A) TRB1 recruits ATG8a to the mitochondrial outer membrane, resulting in the encapsulation of mitochondria in the autophagosome. Time course image of *Arabidopsis* stable transgenic lines co-expressing RFP-TRB1 and GFP-ATG8a under mitochondrial stress conditions (mitochondrial depolarisation induced by 2,4-dinitrophenol treatment). Over time, ATG8-labelled autophagosome membranes envelop the TRB1-labelled mitochondria, resulting in its encapsulation. (B) Selection of mitochondria for autophagic degradation by TRB1. Colocalisation of TRB1-labelled mitochondria and ATG8a-labelled autophagosomes indicates targeting of mitochondria for degradation by autophagy, and their encapsulation in autophagosome vesicles. TRB1 functions to promote the recruitment of ATG8 proteins to the mitochondrial membranes to target them for degradation. Images modified from Li et al. (2022).[10] Scale bars = 10 μm.

mitophagy have not been characterised, or are not present in plants. In mammals, mitophagy is initiated at the OMM by the ubiquitination-dependent, PINK1-PARKIN pathway. Upon mitochondrial depolarisation (induced by oxidative stress or pharmacological treatment), PTEN-Induced Kinase 1 (PINK1) recruits and activates the E3 ubiquitin-ligase, PARKIN, through phosphorylation. Subsequent ubiquitination of OMM proteins by PARKIN facilitates the recruitment of the autophagy adaptor protein, p62, which interacts with ATG8-family proteins to target mitochondria to the autophagosome.[28–30] Presently, no equivalent regulators of ubiquitin-dependent mitophagy have been identified in Arabidopsis,[31] and it remains to be determined if this strategy is used to clear damaged mitochondria in plants.

Mammals and yeast also employ numerous OMM mitophagy receptor proteins, which interact with ATG8-family proteins (referred to as LC3; Microtubule Associated Protein Light Chain 3 in animals) through cytosolic AIM domains. Mammalian OMM-integral BCL2-INTERACTING PROTEIN 3 (BNIP3) and BNIP3-LIKE (BNIP3L)/NIX interact with LC3 under control of phosphorylation of their AIM domains. Recruitment of LC3 to the OMM by BNIP3 and BNIP3L promotes mitophagy in order to control apoptosis.[32–34] Likewise, the OMM-integral FUN14 Domain Containing Protein 1 (FUNDC1) interacts with LC3 in a phosphorylation-dependent manner, and is important for hypoxia-induced mitophagy.[35] OMM-localised FKBP8 (FK506-Binding Protein 8) recruits LC3 to the mitochondria following mitochondrial damage, dependent on the FKBP8 AIM domain.[36] Mammalian Bcl2-Like-Protein 13 (Bcl2-L-13) is conserved with the yeast mitophagy receptor protein, ATG32, and can rescue starvation-induced mitophagy in yeast *atg32* mutants. Bcl2-L-13 recruits both LC3 and ULK1 autophagy-regulatory proteins to the OMM to target mitochondria for selective autophagy.[37] Studies on mammalian systems demonstrate diverse mechanisms of mitophagy to control different cellular functions, and considerable complexity in the cell signalling pathways that regulate mitophagy receptors though phosphorylation. Future investigation of mitophagy receptors in plants is likely to identify diverse mechanisms regulating mitophagy to coordinate cell function during plant development and stress responses. As the first plant mitophagy receptors are only recently becoming characterised, it remains to be determined whether their activity is controlled by posttranslational modification during stress.

In addition to TraB mitophagy receptors, putative AIM domains have been identified in 11 further Arabidopsis OMM proteins, indicating their potential roles as mitophagy receptors.[6] Their future investigation is likely to advance our understanding of how mitophagy is regulated and the functions of mitophagy in plants. Broda et al. have noted AIM domains to be present in several subunits of the mitochondrial TOM (Translocase of the Outer Membrane) protein importer complex, including TOM40, TOM20-2, TOM20-3 and DGS1 (DGD SUPPRESSOR 1). DSG1 functions in mitochondrial lipid homeostasis, and it is possible that this complex may link mitochondrial turnover to cell nutrient signalling.[38] Mitochondrial ATG8-interacting FLZ (FCS-Like Zinc Finger) proteins may also link mitophagy to cell energy sensing. FLZ proteins repress the energy-sensing SnRK1 kinase complex, and are likely degraded by mitophagy during carbon starvation. Their degradation during nutrient stress results in the release of SnRK1 signalling from inhibition.[39] It is possible that FLZ proteins may regulate mitophagy in response to nutrient starvation in relationship with SnRK1, however this possibility remains to be explored. VOLTAGE DEPENDENT ANION CHANNEL 2 (VDAC2) calcium channels also contain predicted AIM domains[6] and have roles in

13652818, 0, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/jmi.13267 by Test, Wiley Online Library on [08/02/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

mitochondrial ROS signalling and homeostasis.[40] During oxidative stress, OMM-localised VDAC2 may be involved in initiating mitophagy in response to mitochondrial depolarisation to clear damaged mitochondria. The putative AIM-containing protein ELONGATED MITOCHONDRIA 1 (ELM1) also has intriguing implications in the regulation of mitophagy, potentially linking mitochondrial degradation to the dynamics of mitochondria fission. ELM recruits mitochondrial scission proteins DYNAMIN-RELATED PROTEIN 3A (DRP3A) and DRP3B to the OMM to mediate mitochondrial fission.[41] In mammals, mitochondrial fission mediated by DRP proteins is widely speculated to be an important step in mitophagy through mechanisms that are not completely understood. For example, it has been hypothesised that mitochondrial fragmentation facilitates encapsulation of mitochondrial components into autophagosome membranes[42,43] or conversely, may protect mitochondria from autophagy through preventing the accumulation of Parkin.[44] It is possible that in plants, ELM1 may function to link mitophagy to mitochondrial dynamics with yet-unknown functions.

5 | CONCLUSION

It has long been understood that mitophagy is an important mechanism of mitochondrial degradation and quality control in mammals and yeast. In contrast, mitophagy has remained poorly understood in plants until recently. It is becoming apparent that plant mitophagy is an important mechanism of mitochondrial homeostasis to recycle damaged mitochondria during stress and maintain mitochondrial function to support cell growth and plant development.

Plant mitophagy has remained enigmatic as the protein regulators that target mitochondria for degradation are only recently emerging. Plant mitophagy is driven by the core autophagy machinery including the ATG1/ATG13 complex, ATG11, ATG5, ATG7 and ATG8. Selective targeting of mitochondria for degradation is regulated by mitophagy-specific proteins. Recently, the first plant mitophagy receptor proteins have been characterised,[10] advancing our understanding of the regulation of mitophagy and its importance in plants. Putative mitophagy receptors may link the regulation of mitophagy to several cell processes including mitochondrial organisation and dynamics, ER-mitochondrial interactions, as well as nutrient and ROS homeostasis. Future characterisation of plant mitophagy receptors and regulators will advance our understanding of how plants regulate mitochondrial function and quality control, and the importance of mitophagy to plant life.

ORCID

Pengwei Wang https://orcid.org/0000-0001-8882-3447
Patrick J. Hussey https://orcid.org/0000-0003-2094-5725

REFERENCES

1. Welchen, E., Canal, M. V., Gras, D. E., & Gonzalez, D. H. (2021). Cross-talk between mitochondrial function, growth, and stress signalling pathways in plants. *Journal of Experimental Botany*, *72*(11), 4102–4118.
2. Van Aken, O. (2021). Mitochondrial redox systems as central hubs in plant metabolism and signalling. *Plant Physiology*, *186*(1), 36–52.
3. Onishi, M., Yamano, K., Sato, M., Matsuda, N., & Okamoto, K. (2021). Molecular mechanisms and physiological functions of mitophagy. *Embo Journal*, *40*(3), e104705.
4. Toyooka, K., Okamoto, T., & Minamikawa, T. (2001). Cotyledon cells of Vigna mungo seedlings use at least two distinct autophagic machineries for degradation of starch granules and cellular components. *Journal of Cell Biology*, *154*(5), 973–982.
5. Kwon, S. I., Cho, H. J., Jung, J. H., Yoshimoto, K., Shirasu, K., & Park, O. K. (2010). The Rab GTPase RabG3b functions in autophagy and contributes to tracheary element differentiation in Arabidopsis. *Plant Journal*, *64*(1), 151–164.
6. Broda, M., Millar, A. H., & Van Aken, O. (2018). Mitophagy: A mechanism for plant growth and survival. *Trends in Plant Science*, *23*(5), 434–450.
7. Ma, J., Liang, Z., Zhao, J., Wang, P., Ma, W., Mai, K. K., Fernandez Andrade, J. A., Zeng, Y., Grujic, N., Jiang, L., Dagdas, Y., & Kang, B. H. (2021). Friendly mediates membrane depolarization-induced mitophagy in Arabidopsis. *Current Biology*, *31*(9), 1931–1944.
8. Li, F., Chung, T., & Vierstra, R. D. (2014). AUTOPHAGY-RELATED11 plays a critical role in general autophagy- and senescence-induced mitophagy in Arabidopsis. *Plant Cell*, *26*(2), 788–807.
9. Nakamura, S., Hagihara, S., Otomo, K., Ishida, H., Hidema, J., Nemoto, T., & Izumi, M. (2021). Autophagy contributes to the quality control of leaf mitochondria. *Plant & Cell Physiology*, *62*(2), 229–247.
10. Li, C., Duckney, P., Zhang, T., Fu, Y., Li, X., Kroon, J., De Jaeger, G., Cheng, Y., Hussey, P. J., & Wang, P. (2022). TraB family proteins are components of ER-mitochondrial contact sites and regulate ER-mitochondrial interactions and mitophagy. *Nature Communications*, *13*(1), 5658.
11. Duckney, P., Li, C., Hussey, P. J., & Wang, P. (2023). TraB, a novel plant ER-mitochondrial contact site protein functions as a mitophagy receptor in plants. *Autophagy*, *19*(7), 2148–2150.
12. Yan, H., Zhuang, M., Xu, X., Li, S., Yang, M., Li, N., Du, X., Hu, K., Peng, X., Huang, W., Wu, H., Tse, Y. C., Zhao, L., & Wang, H. (2023). Autophagy and its mediated mitochondrial quality control maintain pollen tube growth and male fertility in Arabidopsis. *Autophagy*, *19*(3), 768–783.
13. Norizuki, T., Minamino, N., Sato, M., Tsukaya, H., & Ueda, T. (2022). Dynamic rearrangement and autophagic degradation of mitochondria during spermiogenesis in the liverwort *Marchantia polymorpha*. *Cell Reports*, *39*(11), 110975.
14. Dündar, G., Teranishi, M., & Hidema, J. (2020). Autophagy-deficient Arabidopsis mutant atg5, which shows ultraviolet-B

13652818, 0, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/jmi.13267 by Test, Wiley Online Library on [08/02/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

sensitivity, cannot remove ultraviolet-B-induced fragmented mitochondria. *Photochemical & Photobiological Sciences*, *19*(12), 1717–1729.
15. Kacprzak, S. M., & Van Aken, O. (2022). Carbon starvation, senescence and specific mitochondrial stresses, but not nitrogen starvation and general stresses, are major triggers for mitophagy in Arabidopsis. *Autophagy*, *18*(12), 2894–2912.
16. Barros, J. A. S., Chatt, E. C., Augustine, R. C., McLoughlin, F., Li, F., Otegui, M. S., & Vierstra, R. D. (2023). Autophagy during maize endosperm development dampens oxidative stress and promotes mitochondrial clearance. *Plant Physiology*, *193*(2), 1395–1415.
17. Li, F., & Vierstra, R. D. (2014). Arabidopsis ATG11, a scaffold that links the ATG1-ATG13 kinase complex to general autophagy and selective mitophagy. *Autophagy*, *10*(8), 1466–1467.
18. Suttangkakul, A., Li, F., Chung, T., & Vierstra, R. D. (2011). The ATG1/ATG13 protein kinase complex is both a regulator and a target of autophagic recycling in Arabidopsis. *Plant Cell*, *23*(10), 3761–3779.
19. Chen, L., Su, Z. Z., Huang, L., Xia, F. N., Qi, H., Xie, L. J., Xiao, S., & Chen, Q. F. (2017). The AMP-activated protein kinase KIN10 is involved in the regulation of autophagy in Arabidopsis. *Frontiers in Plant Science*, *8*, 1201.
20. Chung, T., Phillips, A. R., & Vierstra, R. D. (2010). ATG8 lipidation and ATG8-mediated autophagy in Arabidopsis require ATG12 expressed from the differentially controlled ATG12A AND ATG12B loci. *Plant Journal*, *62*(3), 483–493.
21. Fujioka, Y., Noda, N. N., Fujii, K., Yoshimoto, K., Ohsumi, Y., & Inagaki, F. (2008). *In vitro* reconstitution of plant Atg8 and Atg12 conjugation systems essential for autophagy. *Journal of Biological Chemistry*, *283*(4), 1921–1928.
22. Martens, S., & Fracchiolla, D. (2020). Activation and targeting of ATG8 protein lipidation. *Cell Discovery*, *6*, 23.
23. Wang, P., Pleskot, R., Zang, J., Winkler, J., Wang, J., Yperman, K., Zhang, T., Wang, K., Gong, J., Guan, Y., Richardson, C., Duckney, P., Vandorpe, M., Mylle, E., Fiserova, J., Van Damme, D., & Hussey, P. J. (2019). Plant AtEH/Pan1 proteins drive autophagosome formation at ER-PM contact sites with actin and endocytic machinery. *Nature Communications*, *10*(1), 5132.
24. Böckler S and Westermann, B. (2014). Mitochondrial ER contacts are crucial for mitophagy in yeast. *Developmental Cell*, *28*(4), 450–458.
25. Logan, D. C., Scott, I., & Tobin, A. K. (2003). The genetic control of plant mitochondrial morphology and dynamics. *Plant Journal*, *36*(4), 500–509.
26. El Zawily, A. M., Schwarzländer, M., Finkemeier, I., Johnston, I. G., Benamar, A., Cao, Y., Gissot, C., Meyer, A. J., Wilson, K., Datla, R., Macherel, D., Jones, N. S., & Logan, D. C. (2014). FRIENDLY regulates mitochondrial distribution, fusion, and quality control in Arabidopsis. *Plant Physiology*, *166*(2), 808–828.
27. Kacprzak, S. M., & Van Aken, O. (2023). FRIENDLY is required for efficient dark-induced mitophagy and controlled senescence in Arabidopsis. *Free Radical Biology and Medicine*, *204*, 1–7.
28. Narendra, D., Tanaka, A., Suen, D. F., & Youle, R. J. (2008). Parkin is recruited selectively to impaired mitochondria and promotes their autophagy. *Journal of Cell Biology*, *183*, 795–803.
29. Narendra, D. P., Jin, S. M., Tanaka, A., Suen, D. F., Gautier, C. A., Shen, J., Cookson, M. R., & Youle, R. J. (2010). PINK1 is selectively stabilized on impaired mitochondria to activate Parkin. *PLoS Biology*, *26*, e1000298.
30. Geisler, S., Holmström, K. M., Skujat, D., Fiesel, F. C., Rothfuss, O. C., Kahle, P. J., & Springer, W. (2010). PINK1/Parkin-mediated mitophagy is dependent on VDAC1 and p62/SQSTM1. *Nature Cell Biology*, *12*(2), 119–131.
31. Ren, K., Feng, L., Sun, S., & Zhuang, X. (2021). Plant mitophagy in comparison to mammals: What is still missing? *International Journal of Molecular Sciences*, *22*(3), 1236.
32. Hanna, R. A., Quinsay, M. N., Orogo, A. M., Giang, K., Rikka, S., & Gustafsson, Å. B. (2012). Microtubule-associated protein 1 light chain 3 (LC3) interacts with Bnip3 protein to selectively remove endoplasmic reticulum and mitochondria via autophagy. *Journal of Biological Chemistry*, *287*(23), 19094–19104.
33. Rogov, V. V., Suzuki, H., Marinković, M., Lang, V., Kato, R., Kawasaki, M., Buljubašić, M., Šprung, M., Rogova, N., Wakatsuki, S., Hamacher-Brady, A., Dötsch, V., Dikic, I., Brady, N. R., & Novak, I. (2017). Phosphorylation of the mitochondrial autophagy receptor Nix enhances its interaction with LC3 proteins. *Scientific Reports*, *7*(1), 1131.
34. Marinković, M., & Novak, I. (2021). A brief overview of BNIP3L/NIX receptor-mediated mitophagy. *FEBS Open Biology*, *11*(12), 3230–3236.
35. Liu, L., Feng, D., Chen, G., Chen, M., Zheng, Q., Song, P., Ma, Q., Zhu, C., Wang, R., Qi, W., Huang, L., Xue, P., Li, B., Wang, X., Jin, H., Wang, J., Yang, F., Liu, P., Zhu, Y., … Chen, Q. (2012). Mitochondrial outer-membrane protein FUNDC1 mediates hypoxia-induced mitophagy in mammalian cells. *Nature Cell Biology*, *14*(2), 177–185.
36. Bhujabal, Z., Birgisdottir, Å. B., Sjøttem, E., Brenne, H. B., Øvervatn, A., Habisov, S., Kirkin, V., Lamark, T., & Johansen, T. (2017). FKBP8 recruits LC3A to mediate Parkin-independent mitophagy. *Embo Reports*, *18*(6), 947–961.
37. Murakawa, T., Okamoto, K., Omiya, S., Taneike, M., Yamaguchi, O., & Otsu, K. (2019). A Mammalian Mitophagy receptor, Bcl2-L-13, recruits the ULK1 complex to induce mitophagy. *Cell Reports*, *26*(2), 338–345.
38. Li, L., Lavell, A., Meng, X., Berkowitz, O., Selinski, J., Van de Meene, A., Carrie, C., Benning, C., Whelan, J., De Clercq, I., & Wang, Y. (2019). Arabidopsis DGD1 SUPPRESSOR1 is a subunit of the mitochondrial contact site and cristae organizing system and affects mitochondrial biogenesis. *The Plant Cell*, *31*(8), 1856–1878.
39. Yang, C., Li, X., Yang, L., Chen, S., Liao, J., Li, K., Zhou, J., Shen, W., Zhuang, X., Bai, M., Bassham, D. C., & Gao, C. (2023). A positive feedback regulation of SnRK1 signaling by autophagy in plants. *Molecular Plant*, *16*(7), 1192–1211.
40. Sanyal, S. K., Kanwar, P., Fernandes, J. L., Mahiwal, S., Yadav, A. K., Samtani, H., Srivastava, A. K., Suprasanna, P., & Pandey, G. K. (2020). Arabidopsis mitochondrial voltage-dependent anion channels are involved in maintaining reactive oxygen species homeostasis, oxidative and salt stress tolerance in yeast. *Frontiers in Plant Science*, *11*, 50.
41. Arimura, S., Fujimoto, M., Doniwa, Y., Kadoya, N., Nakazono, M., Sakamoto, W., & Tsutsumi, N. (2008). Arabidopsis ELONGATED MITOCHONDRIA1 is required for localization of DYNAMIN-RELATED PROTEIN 3A to mitochondrial fission sites. *Plant Cell*, *20*(6), 1555–1566.
42. Twig, G., Elorza, A., Molina, A. J., Mohamed, H., Wikstrom, J. D., Walzer, G., Stiles, L., Haigh, S. E., Katz, S., Las, G., Alroy, J.,

13652818, 0, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/jmi.13267 by Test, Wiley Online Library on [08/02/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Wu, M., Py, B. F., Yuan, J., Deeney, J. T., Corkey, B. E., & Shirihai, O. S. (2008). Fission and selective fusion govern mitochondrial segregation and elimination by autophagy. *Embo Journal*, *27*(2), 433–446.

43. Kageyama, Y., Hoshijima, M., Seo, K., Bedja, D., Sysa-Shah, P., Andrabi, S. A., Chen, W., Höke, A., Dawson, V. L., Dawson, T. M., Gabrielson, K., Kass, D. A., Iijima, M., & Sesaki, H. (2014). Parkin-independent mitophagy requires Drp1 and maintains the integrity of mammalian heart and brain. *Embo Journal*, *33*(23), 2798–2813.
44. Burman, J. L., Pickles, S., Wang, C., Sekine, S., Vargas, J. N. S., Zhang, Z., Youle, A. M., Nezich, C. L., Wu, X., Hammer, J. A., & Youle, R. J. (2017). Mitochondrial fission facilitates the selective mitophagy of protein aggregates. *Journal of Cell Biology*, *216*(10), 3231–3247.

How to cite this article: Duckney, P. J., Wang, P., & Hussey, P. J. (2024). Mitophagy in plants: Emerging regulators of mitochondrial targeting for selective autophagy. *Journal of Microscopy*, 1–8. https://doi.org/10.1111/jmi.13267

13652818, 0, Downloaded from https://onlinelibrary.wiley.com/doi/10.1111/jmi.13267 by Test, Wiley Online Library on [08/02/2024]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License