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The dynamic interplay of Autophagy and plant development

Kranti M. Pawar*[1], BS Dilta[2], Arshi Sultanpuri[3], Rohit Verma[3], Priyanka Thakur[3], Ankita Thakur[3], Amandeep[3], Abhishek Tomar[3] and Ashish Kumar[3]

[1]Department of Seed Science and Technology, Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan, 173230 HP, India
[2]Department of Floriculture and Landscape Architecture, Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan, 173230 HP, India
[3]Department of Seed Science and Technology, Dr Y S Parmar University of Horticulture and Forestry, Nauni, Solan, 173230 HP, India

ABSTRACT

Plants have evolved intricate systems to recycle intracellular components essential for their metabolic processes and developmental changes, enabling efficient nutrient reuse and proper disposal of protein complexes, and malfunctioning organelles. One significant pathway in this process is autophagy, which employs specific vesicles to capture and transport cytoplasmic material to the vacuole for degradation[2]. Research highlights that selective autophagy plays a crucial role in maintaining homeostasis by recycling cellular components. In the early and intermediate developmental stages of maize (Zea mays) endosperm, autophagy influences seed maturation and nutrient storage, an area that warrants further exploration. A study utilizing quantitative real-time PCR identified autophagy-related gene (ATG) members in the pepper genome, analyzing their expression in response to heat and other abiotic factors. The results revealed 15 core ATG components, comprising 29 ATG proteins with conserved functional domains. Under normal conditions, the expression of CaATG genes exhibited specific patterns related to tissue type and developmental stage. Given the benefits of ATG genes, such as enhanced growth, increased yields, and improved stress tolerance, boosting their expression could offer significant agricultural advantages. Challenges of this study are Gene Families and Genetic redundancy, regulation specific to tissues and development, limited tools and markers. This review explores the potential of manipulating autophagy to enhance crop production under various environmental challenges[5].

Keywords: *Autophagy, ATG genes, Autophagic degradation, Selective autophagy, Stress response, Homeostasis, 15 core ATG components, 29 ATG proteins, CaATG genes.*

Introduction

In order to survive in changing environmental conditions plants—which normally live in a sessile state in open ecosystems—need to constantly modify their morphology physiology and metabolism [1]. They face a number of difficulties such as biotic stressors like pathogen attacks and herbivory abiotic stressors like drought extreme temperatures and salinity of the soil and nutritional deficits. These abiotic stressors have the potential to significantly impair plant productivity and growth two essential components of successful agriculture. This report aims to provide a comprehensive overview of recent advancements in our understanding of plant autophagy, focusing on the molecular mechanisms and physiological roles of autophagy-related genes (Atgs) and their associated proteins in various unfavorable environments. Understanding the intricate processes of autophagy is crucial for developing strategies to enhance plant resilience and productivity in the face of increasing environmental challenges. Through this exploration, we aim to highlight autophagy's pivotal role in enabling plants to adapt and thrive despite the myriad of stressors they encounter throughout their life cycle [7].

*Corresponding Author: **Kranti M. Pawar***

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Three primary forms of autophagy are seen in plants: mega-autophagy macro-autophagy and micro-autophagy. Via the tonoplast microautophagy directly consumes cytoplasmic components. Autophagosomes which are formed by macro-autophagy carry larger cargos for vacuole degradation. During programmed cell death mega-autophagy releases hydrolases and causes extensive cellular degradation. Each kind is essential for preserving cellular processes and boosting a plants resistance to environmental stressors [17].

Autophagy Machinery

About 40 conserved proteins from plants animals and fungi make up the autophagy machinery. These include kinases ubiquitin-like proteins and other autophagy-related proteins (ATGs) from more than seventeen families. ATGs organize into four major complexes in Arabidopsis thaliana: (i) the nutrient-deprivation-activated ATG1 kinase complex (ii) the phosphatidylinositol-3-kinase (PI3K) complex for phagophore formation (iii) the ATG9 complex for ER membrane recruitment and (iv) the ATG12 complex for cargo recruitment [3].

Unlocking the Secrets of ATG Genes in Crops

Identifying and characterizing autophagy-related genes (ATGs) is essential for enhancing crop resilience, with core ATG genes found in at least 14 species. This fascinating exploration reveals how plants adapt and thrive in challenging environments, showcasing the incredible potential of autophagy to boost agricultural productivity and sustainability [8].

Table 1: This information underscores the essential role of autophagy in diverse plant processes, especially in the face of environmental stressors [20]

Species	Related Processes
Apple (*Malusdomestica*)	Vegetative growth, senescence, abiotic stress response, metabolism
Banana (*Musa acuminata*)	Biotic stress response, hormone response, cell death
Barley (*Hordeumvulgare*)	Senescence, nutrient remobilization, microspore embryogenesis, cell death
Cassava (*Manihotesculenta*)	Biotic stress response
Common bean (*Phaseolus vulgaris*)	Nodule development
Foxtail millet (*Setariaitalica*)	Abiotic stress response
Grapevine (*Vitisvinifera*)	Abiotic stress response, fruit ripening
Maize (*Zea mays*)	Senescence, nutrient remobilization, seed development, abiotic stress
Rice (*Oryza sativa*)	Vegetative growth, senescence, nutrient remobilization, cell death
Soybean (*Glycine max*)	Nutrient remobilization, abiotic stress response
Tobacco (*Nicotianatabacum*)	Abiotic and biotic stress response, hormone response
Tomato (*Solanumlycopersicum*)	Anther development, abiotic and biotic stress response
Wheat (*Triticumaestivum*)	Phloem development, seed development, abiotic stress response

Strategies for Autophagy Monitoring

Assays for tracking different stages and possible substrates must be developed in order to evaluate plant autophagy. Fluorescent reporters have proven to be one of the most useful tools allowing for the quantitative measurement of autophagic flux as well as the visual identification of autophagic structures. Autophagic bodies particularly 1–2 μm vacuolar puncta stabilized by concanavalin A (ConA) are particularly detectable by confocal fluorescence microscopy. Furthermore confirming the transport of different organelles and ribosomes based on their distinct morphological features electron microscopy and three-dimensional tomographic imaging offer unmistakable proof of micro- and macro-autophagy [11].

Selective Autophagy: Protein aggregates organelles and pathogens are among the particular cytoplasmic components that selective autophagy targets for destruction. Numerous processes of selective autophagy that are present in animals also operate in plants according to rapidly developing research in this field. Initially believed to be a housekeeping function selective autophagy is now more widely acknowledged for its function in developmental transitions and stress tolerance [6].

Pathways for Selective Autophagy

There are other pathways for selective autophagy besides the ones that address metabolic emergencies. Lipid ATG8 mediates this specificity by attaching to a group of autophagy receptors that have different affinities for different types of cargo.

Aggrephagy: This process traps toxic and non-functional proteins into well-organized aggregates which is essential for maintaining protein homeostasis. When autophagy or the associated receptors are disrupted in plants big cytoplasmic aggregates build up and wait to be cleared [13].

Chlorophagy: During aging or starvation chlorophagy provides stable nitrogen and carbon while removing dysfunctional chloroplasts as a quality control mechanism. This procedure which is frequently triggered by severe photodamage integrates whole chloroplasts into ATG8-decorated autophagic vesicles for vacuolar delivery [9].

Mitophagy: Essential for both stress response and energy production mitophagy controls mitochondrial health. It makes sure that damaged mitochondria are removed because they can otherwise release reactive oxygen species (ROS) which can cause oxidative damage [12].

Pexophagy: Peroxisomes which are involved in a number of metabolic processes and are vulnerable to ROS damage are the target of pexophagy. During plant development the regulation of peroxisome turnover varies making the elimination of unused units necessary [15].

Ribophagy: In order to preserve resources during a nutrient shortage ribophagy selectively breaks down ribosomal subunits. This autophagic mechanism demonstrates how effectively plants store energy and amino acids [4].

Xenophagy: By identifying pathogen-associated molecular patterns (PAMPs) and triggering defenses that result in programmed cell death at infection sites plants use xenophagy as an immune response against a variety of pathogens thereby increasing resistance against biotic stress [10].

Functions of Autophagy in Crop Plants

Numerous studies have highlighted the significance of autophagy in various aspects of crop plant development, including stress response, hormonal regulation, infection, and cell death. This section elaborates on these roles [21].

During leaf senescence: Autophagy is essential during leaf senescence because it recycles nutrients from mature leaves to support developing organs especially seeds. This procedure makes nitrogen remobilization easier which is important for a number of crops. Enhanced autophagic activity is indicated by increased expression of ATG genes in senescent leaves particularly in aging maize leaves [14].

During seed development: Autophagy plays a critical role in reproductive development during seed development as evidenced by the upregulation of numerous ATG genes in maize endosperm and Arabidopsis siliques. In maize ATG8 lipidation peaks 18–30 days after fertilization signifying active autophagy. Furthermore as observed in wheat it facilitates the movement of seed storage proteins [16].

During Reproductive Development: Autophagy and Reproductive Development: Studies have connected autophagy to reproductive development especially in rice and wheat. In rice ATG7 and ATG9 mutants exhibit male sterility as a result of impaired nutrient provision during pollen development. Autophagy plays a critical role in hormone regulation and tapetum cell function impacting lipid metabolism and pollen germination which in turn impacts pollen shedding which is necessary for reproduction [22].

During Vascular Development: During Vascular Development: Research has linked autophagy to the development of reproductive organs particularly in rice and wheat. In ATG7 and ATG9 mutants disturbed nutrient provision during pollen development leads to male sterility in rice. Autophagy affects pollen shedding which is vital for reproduction tapetum cell function and hormone regulation as well as lipid metabolism and pollen germination [22].

During Nutrient Starvation: Autophagy responses to nutrient deprivation have been noted in various crops, including apple, barley, maize, and rice.

In apples, ATG18a overexpression improves nitrogen deficiency tolerance, enhances metabolic pathways like anthocyanin biosynthesis, and boosts nitrate uptake[23].

During Drought Stress: During Drought Stress: Another important environmental factor influencing plant health is drought stress. Early research in Arabidopsis showed that osmotic stress causes an increase in ATG18a expression which in turn promotes the formation of autophagosomes. ATG genes are upregulated in response to drought in a number of crops according to studies. The hypersensitivity to drought exhibited by mutants devoid of autophagic function such as atg5 and atg7 highlights the critical role autophagy plays in drought resilience [19].

During Plant-Microbe Interaction: In the course of plant-microbe interaction autophagy also responds to biotic stress by modifying disease resistance in a range of crops. ATG8 deletion in cassava increases resistance to Xanthomonas axonopodis whereas autophagy inhibition in bananas decreases resistance to Fusarium oxysporum. Recent research indicates that in plant-pathogen interactions autophagy may possess antibacterial and antimicrobial qualities [25].

During Symbiotic Interactions: Autophagy appears to be involved in symbiotic interactions with rhizobia in common beans (Phaseolus vulgaris). Enhanced autophagy is associated with higher levels of trehalose a metabolite that is produced during symbiosis. Autophagy and nutrient acquisition in symbiotic relationships may be related as inhibition of trehalose degradation increases nodule biomass and nitrogen fixation. To better understand autophagys function in these interactions more research is necessary [24].

Challenges of the study:

1. Gene Families and Genetic Redundancy

- Numerous ATG (autophagy-related) genes in plants are part of multigene families, in contrast to the single-copy genes present in yeast.
- This redundancy makes functional analysis more challenging, as eliminating one gene might not clarify its function due to compensation from paralogs.

2. Regulation Specific to Tissues and Development

- In plants, autophagy is precisely regulated both in space and time, changing with different tissues and developmental phases.
- Identifying basal autophagy separately from stress-induced autophagy is challenging because there are no specific, dynamic markers available.

3. Limited Tools and Markers

- Plant researchers have a more limited selection of specific antibodies, probes, and markers for investigating autophagy compared to those working with animal systems.
- It is particularly challenging to visualize autophagic flux (the active process rather than merely the buildup of autophagosomes) in plants.

4. Cross-Talk with Other Pathways

- Autophagy engages with hormonal signaling, metabolic processes, and immune responses, complicating the task of identifying the specific effects of autophagy.
- Separating the direct impacts of autophagy from its indirect functions necessitates advanced experimental design.

Future perspective:

1. Stress Tolerance and Crop Improvement

Plant resistance to abiotic stressors like heat salinity drought and nutrient shortage is increased by autophagy. Enhancing autophagy-related pathways through genetic engineering or selective breeding may result in crops that are more resilient to stress particularly in light of climate change. Adjusting autophagy to maximize yield under stress without causing growth penalties may be the main focus of future research.

2. Pathogen Defense and Plant Immunity

Through the breakdown of viral components or the control of immune signaling autophagy contributes to defense against pathogens such as bacteria fungi and viruses. Autophagy pathways may be the focus of future tactics to boost immune responses without inciting autoimmunity. New approaches to crop protection may result from a better understanding of selective autophagy (similar to xenophagy) in plant-pathogen interactions.

3. Genes and Synthetic Biology in Function

Autophagy-related genes (ATGs) can be precisely altered thanks to developments in CRISPR-Cas9 and other genome editing technologies. Customizable autophagy circuits that regulate the breakdown of particular proteins organelles or metabolites may be designed with the aid of synthetic biology. Finding new functional targets may be possible by mapping the interactomes and autophagy networks of different plant species.

Conflict of Interest:

- Autophagy-related genes and pathways are targets for developing stress-resistant or high-yield crops.
- Researchers or institutions might have financial stakes in biotechnology companies or patents related to autophagy.
- Studies funded by agribusiness companies or industry groups may have pressure (explicit or implicit) to produce favorable outcomes.

Conclusion

In inference, autophagy is integral to multiple physiological processes in crop plants, influencing nutrient remobilization, reproductive development, stress responses, and interactions with biotic and abiotic factors. As research continues to unveil its mechanisms, autophagy may present opportunities for enhancing crop resilience and productivity.

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References

1. Avin-Wittenberg T (2019) Autophagy and its role in plant abiotic stress management. Plant Cell Environ 42: 1045–1053.

2. Barros J, Chatt E, Augustine R, Mclughlin F, Li F, Otegui M and Vierstra R(2023) Autophagy during maize endosperm development dampens oxidative stress and promotes mitochondrial clearance. Plant Physiology193: 1395–1415.

3. Cao J, Liu C, Shao S and Zhou J(2020) Molecular mechanisms of autophagy regulation in plants and their applications in agriculture. Frontiers in Plant Science 11: 618944.

4. Denton D and Kumar S(2018)Ribophagy: new receptor discovered. Cell Research28: 699–700.

5. Fernandez RI and Carbajosa JV(2022)A view into seed autophagy: from development to environmental responses. Plants Journal11: 3247.

6. Ferretti G, Quarti J, Rangel L and Silva J (2022)Anticancer therapeutic strategies targeting p53 aggregation. International Journal of Molecular Sciences23: 11023.

7. Frake RA and Rubinsztein DC (2016) Yoshinori ohsumi'snobel prize for mechanisms of autophagy: From basic yeast biology to therapeutic potential. R. Coll. Physicians Edinb 46: 228– 233.

8. Izumi M, Hidema J and Ishida H (2015)Fromarabidopsis to cereal crops: conservation of chloroplast protein degradation by autophagy indicates its fundamental role in plant productivity. Plant Signal. Behav 10: 1101199.

9. Izumi M and Nakamura S (2017) Vacuolar digestion of entire damaged chloroplasts in *Arabidopsis thaliana* is accomplished by chlorophagy. Taylor and Francis Group 13: (7), 1239–1240.

10. Klapan K, Simon D, Karaulov A, Gomzikova M, Rizvanov A, Yousefi S and Simon H(2022) Autophagy and skin diseases. Frontiers in Pharmacology13: 844756.

11. Kurusu T, Koyano T and Hanamata (2014) Osatg7 is required for autophagy dependent lipid metabolism in rice post–meiotic anther development. Autophagy 10: 878–888.

12. Levanony H, Rubin R, Altschuler Y and Galili G (1992) Evidence for a novel route of wheat storage proteins to vacuoles. J. Cell Biol119: 1117–1128.

13. Li F, Chung T, Pennington J, Federico M, Kaeppler H, Kaeppler S, Otegui M and Vierstra RD (2015) Autophagic recycling plays a central role in maize nitrogen remobilization. The Plant Cell27: 1389–1408.

14. Li F and Vierstra RD (2012) Autophagy: A multifaceted intracellular system for bulk and selective recycling. Trends Plant Sci17: 526–537.

15. Liu Y and Bassham DC (2012) Autophagy: Pathways for self-eating in plant cells. Annu. Rev. Plant Biol63: 215–37.

16. Lv X, PuX, Qin G, Zhu T and Lin H (2014) The roles of autophagy in development and stress responses in arabidopsis thaliana. Apoptosis19: 905–921.

17. Marshall RS and Vierstra RD (2018) Autophagy: The master of bulk and selective recycling. Annual Rev. Plant Biol 69: 173–208.

18. Michaeli S, Galili G, Genschik P, Fernie AR and Avin–Wittenberg T (2016) Autophagy in plants–what's new on the menu? Trends Plant Sci21(2): 134–144.

19. Mizushima N (2020) Autophagy: Process and function. Genes Dev 21: 2861–2873.

20. Su W, Bao Y, Yu X, Xia X, Liu C and Yin W (2020) Autophagy and Its Regulators in Response to Stress in Plants. Int. J. Mol. Sci. 21: 8889.

21. Tang J and Bassham DC (2018) Autophagy in crop plants: what's new beyond arabidopsis? European Journal of Cell Biology8: 180162.

22. Yin Z, Pascual C and Klionsky DJ (2016) Autophagy: Machinery and regulation. Microbial cell3: 12.

23. Yue J, Sun H, Zhang W, Pei D, He Y and Wang H (2015)Wheat homologs of yeast ATG6 function in autophagy and are implicated in powdery mildew immunity. BMC Plant Biology15: 95.

24. Wang J, Milao S, Liu Y and Wang Y (2022) Linking autophagy to potential agronomic trait improvements in crops. International Journal of Molecular Sciences 23: 4793.

25. Zhai Y, Guo M, Wang H, Lu J, Liu J, Zhang C, Gong Z and Lu M (2016) Autophagy– a conserved mechanism for protein degradation, responds to heat and other abiotic stresses in *Capsicum Annuum (L).*Frontiers in Plant Science7: 131.

