Noncanonical ATG8—ABS3 interaction controls senescence in plants

With the support by the National Natural Science Foundation of China, the research team led by Prof. Yu Fei (郁飞) at the State Key Laboratory of Crop Stress Biology for Arid Areas and College of Life Sciences, Northwest A&F University, uncovered a new senescence regulatory pathway controlled by ATG8—ABS3-mediated proteostasis, which was published in *Nature Plants* (2019, 5: 212—224, https://doi.org/10.1038/s41477-018-0348-x).

Senescence is an important biological process in plant growth, development and alternation of generations. During senescence, nutrients such as carbon and nitrogen are mobilized from the source organs (photosynthetic organs such as leaves) and reallocated to the sink organs (especially seeds), to ensure the reproductive success of plants. Despite the tremendous progress in understanding the control of life span and senescence in yeast and model animals, much less is known mechanistically in higher plants.

Dr. Yu's group found that the ABS3 subfamily MATE transporters promote plant leaf senescence and protein degradation, and the quadruple knock-out mutants of ABS3 subfamily *MATE* genes showed strong resistance to carbon starvation-induced plant senescence. The interaction between the ABS3 subfamily MATE proteins and the key protein ATG8 of the autophagy pathway in late endosomes is a prerequisite for ABS3 to promote senescence and protein degradation. This physical interaction of ATG8 with ABS3 does not depend on the classic autophagy pathway or cleavage of the carboxylic terminus of the ATG8 protein and phosphatidylethanolamine modification, suggesting a novel function of ATG8 that is independent of the classic autophagy pathway. Based on these data, the study proposes a model in which the ABS3-ATG8-mediated senescence-promoting pathway, together with the senescence-inhibiting autophagy pathway, achieves a balanced regulation of plant senescence. This is a new function of ATG8 found in plants independent of the classic autophagy pathway, and this pathway plays a conserved role in the model plant *Arabidopsis* and the main food crop wheat, providing important supports for potential future engineering of crop senescence traits.

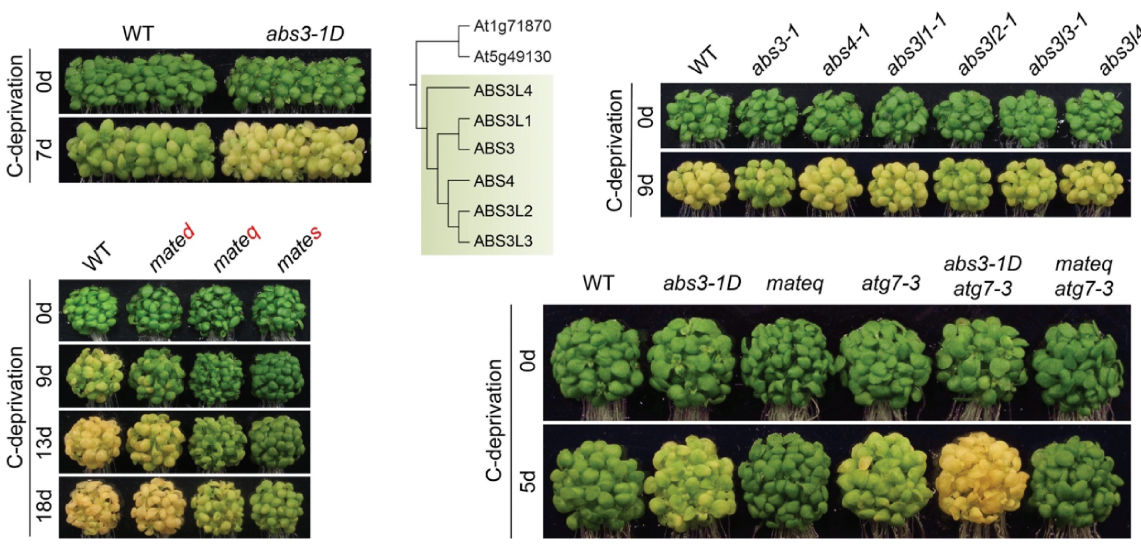

Figure ABS3 subfamily MATEs promote plant senescence. Gain-of-function mutant *abs3-1D* shows accelerated senescence. Loss-of-function mutants of ABS3 subfamily MATEs shows delayed senescence. Quadruple loss-of-function mutant *mateq* suppresses accelerated senescence of autophagy deficient *atg7-3* mutant.