

The mechanisms of plant aging

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European researchers investigated the molecular mechanisms that drive stress-related responses that cause aging and death in plants. The goal is to generate resilient crop varieties.

Unlike animals that can avoid stress, plants have evolved responses for evading factors that can be detrimental for growth and survival, environmental conditions and pathogens. This is often communicated through the production of [reactive oxygen species](#) (ROS), by-products of aerobic metabolism.

Low ROS levels mediate the responses towards stress while at higher concentrations they may lead to [programmed cell death](#). ROS also play a pivotal role during several developmental processes, including root hair growth and seed germination.

Scientists of the EU-funded Plantaging project wished to determine the role of ROS in plant senescence and aging and extend existing knowledge on the genetic determinants of the aging process. This was a collaborative undertaking between scientific groups from Bulgaria and New Zealand.

Biological aging in plants

Studies over the years have identified genes that accelerate senescence alongside others that delay senescence and thus extend lifespan. However, very little is known about how these genes interact and respond to specific environmental and developmental signals. In

addition, the developmental stage of a plant also affects its ability to withstand adverse [environmental conditions](#) or initiate senescence.

Planting researchers employed *Arabidopsis thaliana* mutants with extended or shortened life span as well as plants with extreme tolerance to abiotic stress. Abiotic stress contributors mainly comprise extreme temperatures, high salinity, water deprivation and pollutants including herbicides.

The team performed genome-wide studies including transcriptomics and metabolomics to investigate gene expression and metabolite level changes at different stages of development and under stress. They also examined how ROS-responsive genes react to oxidative stress. "We worked under the assumption that when a negative regulator of aging is overexpressed, the transgenic plants will have delayed senescence, while repression of such a gene would accelerate senescence," explains project coordinator Dr. Gechev. "The opposite will take place if a gene positively regulates senescence; its overexpression will accelerate biological aging," he continues.

Novel molecular cues on plant lifespan

Molecular, proteome and metabolome profiling provided important insight on how senescence-related genes regulate lifespan in plants. Genetic comparison between plants tolerant to abiotic stress and other stress-tolerant [plants](#) further produced significant information on the mechanism of [stress](#) response.

The consortium identified key [genes](#), metabolites, and lipid classes that are highly regulated during long-term darkness in the flowering plant *Haberlea rhodopensis*. Additionally, they sequenced the genome of the UV-tolerant plant *Pachycladon cheesemanii* and characterised its physiological and molecular responses to high doses of UV radiation.

Plant senescence is of considerable interest to agricultural practice as its manipulation has the potential to significantly influence crop tolerance to adverse conditions and improve yield. Project findings successfully uncovered new elements of the ROS regulatory pathway that modulate senescence in *Arabidopsis thaliana*.

Although too early to predict the impact on farming, Dr. Gechev envisages, "the enhanced knowledge on the mechanisms that regulate plant aging and senescence will contribute to more resistant crops and vegetables with extended shelf life."

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