



Gene network analysis of senescence-associated genes in annual plants and comparative assessment of aging in perennials and animals

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ABSTRACT

Aging, resulting from degenerative changes in cell metabolism, affects fecundity and longevity. To increase lifespan in animals or plants, manipulation in gene modification or pharmacology intervention has been proved to be as feasible approaches. NAD⁺, spermidine, and rapamycin, as well as genetic editing, bring to light at the tunnel end for the longevity in animals. In plants, the existing evidence suggests that they may share common aging signaling pathway with animals. However, as sessile organisms, plants got to cope with complex environmental changes and evolved specific signaling pathways. Here, we reviewed the latest research advances in plant aging to make a gene network analysis of senescence-associated genes in annual plant and perform a comparative assessment of aging in perennials as well as animals.

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1. Introduction

Along with sostenuto advances in science and technology, human's demands for health and longevity are never stopped. As an inevitable event in nearly all living organisms, aging involves complex regulatory processes and shows high diversity [1]. Distinctive phenotypic alterations and several hallmarks occur during animal aging, including the altered epigenetic regulation, affected proteostasis, deregulated nutrient sensing, stem cell exhaustion and intercellular communication alterations at the whole organism level, and the unstable genome, attrited telomere, dysfunctional mitochondria at the cellular level [2]. Premature cellular senescence might lead to the whole organism aging which is likely to shorten the lifespan [2–4]. In animals, a lot of efforts have been implemented for anti-aging research, mainly focused on pharmacology intervention and genetic modification. NAD⁺, a kind of nicotinamide nucleotides, rapamycin, spermidine, and resveratrol are proved administrations that can promote longevity [5–7]. Meanwhile, autophagy, a process of self-cannibalism, and melatonin-regulated circadian are also participated in the aging process [7–9]. Additionally, senescence-associated genes (SAGs)

also play critical roles in metabolism and inflammation (Sir2, the silent information regulator 2, encoding a histone deacetylase gene in *Saccharomyces cerevisiae*, and SIRT1, a mammalian homolog of Sir2, encoding an NAD⁺-dependent protein deacetylase), tumorigenesis (Hst2/SIRT2, a homolog of yeast Sir2), insulin secretion (a biological process that insulin is secreted by exocytosis and diffuses into islet capillary blood, SIRT4), ammonia detoxification (the ammonia is converted into a water-soluble compound known as urea, SIRT5), and DNA repair (SIRT6) [10–13], suggesting that aging is closely related to other physiological processes. Moreover, anti-aging attempts in animals offer important references for senescence research in plants which bear the burden for food security and healthy life.

Compared with animals, plants are sessile organisms, thus plant aging is influenced by the internal signaling transduction as well as the inescapable external stresses including the abiotic stresses such as drought, salinity, cold and waterlogging, and the biotic stresses such as pathogen and insects. The internal regulatory signaling of plants aging was partly similar to that of animals. For instance, lifespan can be extended in both animals and plants upon treatment with NAD⁺. NAD⁺ can improve virulent pathogen defense in the model plant *Arabidopsis* through elevating the production of reactive oxygen species (ROS) [14], and improve mitochondrial and stem cell function in model animal mice [15]. Plants' unmovable feature determines that they must cope with harsher external

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