

# We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

4,800

Open access books available

122,000

International authors and editors

135M

Downloads

Our authors are among the

154

Countries delivered to

TOP 1%

most cited scientists

12.2%

Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index  
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?  
Contact [book.department@intechopen.com](mailto:book.department@intechopen.com)

Numbers displayed above are based on latest data collected.  
For more information visit [www.intechopen.com](http://www.intechopen.com)



---

# Sunflower Leaf Senescence: A Complex Genetic Process with Economic Impact on Crop Production

---

Sebastián Moschen, Agustín I. López Gialdi,  
Norma Paniego, Paula Fernandez and  
Ruth Amelia Heinz

Additional information is available at the end of the chapter

<http://dx.doi.org/10.5772/intechopen.68588>

---

## Abstract

Leaf senescence is a complex process controlled by multiple genetic and environmental variables. In different crops, a delay in leaf senescence has an important impact on grain yield through the maintenance of the photosynthetic leaf area during the reproductive stage. In sunflower (*Helianthus annuus* L.), the fourth largest oil crop worldwide, senescence reduces the capacity of plants to maintain their green leaf area for longer periods, especially during the grain filling phase, leading to important economic losses.

In crop species, taking into account the temporal gap between the onset and the phenotypic detection of senescence, identification of both, candidate genes and functional stay-green are indispensable to enable the early detection of senescence, the elucidation of molecular mechanisms and the development of tools for breeding applications.

In this chapter a comprehensive literature revision of leaf senescence process not only in model plant species but also in agronomical relevant crops is presented. Results derived from system biology approaches integrating transcriptomic, metabolomic and physiological data as well as those leading to the selection and characterization of stay green sunflower genotypes are included, making an important contribution to the knowledge of leaf senescence process and providing a valuable tool to assist in crop breeding.

**Keywords:** sunflower, candidate genes, leaf senescence, stay-green genotype, molecular markers

---

## 1. Introduction

Leaf senescence is an age-dependent complex process at the cellular, tissue, organ or organism level, leading to death at the end of the life span [1]. Annual plants as grain and oil crops undergo a visual process toward the end of the reproductive stage that is accompanied by nutrient remobilization from leaf to developing seeds [2]. Senescence process is controlled by multiple genetic and environmental variables, which has strong impact on crop yield [3]. Environmental factors such as light, nutrient availability, concentration of CO<sub>2</sub>, abiotic and biotic stresses caused by disease may affect the rate of senescence. In this context, not only environmental conditions but also biotic factors influence senescence, being this an irreversible process prematurely induced under these adverse conditions [4]. Moreover, reproductive growth is mentioned as a factor that usually impacts on leaf senescence, and particularly in sunflower, the lack of sinks delays the onset of senescence [5]. During this process, changes in gene expression result in a metabolic shift from anabolism to catabolism, which leads to decreased photosynthetic activity, progressive degradation of cellular structures and oxidative burst [6–8]. It has been documented that a delay in leaf senescence has a substantial impact on grain yield through the maintenance of the photosynthetic leaf area during the reproductive stage in different crops [3, 9, 10].

In sunflower (*Helianthus annuus* L.), the largest important oil crop worldwide, the senescence process reduces the capacity of plants to maintain their green leaf area for longer periods, especially during the grain-filling phase, affecting the yield and thus leading to economic losses [11, 12]. This production constraint has deepened since sunflower crop production has been gradually moved to marginal areas due to the rapid change of agricultural practices in crops such as soybean and maize, which have greatly increased their cultivated areas as a consequence of favorable commodity prices and because farmers found more profitable to sow transgenic crops with resistance to herbicides and insects [13, 14].

During the last years, many efforts have been achieved to build up useful functional genomics tools for cultivated sunflower involving physiological, transcriptional and metabolic profiles [15–23].

In crop species, considering the temporal gap between onset and phenotypic detection of senescence process, the availability of candidate genes and molecular markers to the early detection of senescence is indispensable to discriminate between early-senescent and late-senescent lines to be applied in the different context of breeding activities [24]. For example, the identification of functional stay-green genotypes for breeding applications and/or for elucidating molecular mechanisms involved in this complex trait.

## 2. Senescence and crop yields: stay-green genotypes

Senescence is an essential process for the normal growth and development of plants, being an important mechanism for the adaptation to several environmental conditions.

The hypothesis that a delay leaf senescence increases the productivity may be valid for most crops with regard to total biomass production and tuber crops, but this assumption is more controversial with respect to seed yields [3]. However, it has been documented that a delay in leaf senescence has a high impact on grain weight and quality in different crops, including sunflower [3, 5, 25, 26].

Stay-green is a regular term given to genotypes in which the senescence phenotype is delayed in comparison with a standard reference genotype. Stay-green genotypes could be classified into five different types taking into consideration functional or cosmetic stay-green [27, 28]. Functional stay-green genotypes have a photosynthetically active leaf area showing a delay in the onset of senescence (class A), or differing in the rate of the process (class B), whereas cosmetic stay-green genotypes are those in which the senescence proceeds normally but they show problems in chlorophyll degradation (class C), or the chlorophyll content does not decline due to rapid tissue death (class D), or they have a higher chlorophyll content with no change in onset or rate of senescence development (class E) [28]. Mature leaf is a net contributor of photosynthates to the whole plant. The carbon capture phase of the leaf is followed by a net organic nitrogen remobilization. The transition from carbon capture to nitrogen remobilization corresponds to the functional initiation of senescence [29]. In this sense, functional stay-green genotypes are present in those genotypes in which the C–N transition is delayed, or the transition occurs but the subsequent yellowing and N remobilization run slowly [29–31].

In this sense, functional stay-green genotypes could intercept more radiation, increasing photosynthesis and yield in crops with seeds rich in carbon compounds. However, a delay in the C–N transition could negatively affect the seed quality in crops with seed rich in protein compounds [30], such as soybean [32] and cowpea [33].

### **3. Study of leaf senescence process in sunflower**

Sunflower is the fourth most important oil crop worldwide and the second one in the Argentine. Moreover, Argentina is the third largest exporter of crude oil and the second of protein and pellet flour. The added value of oilseed industrialization contributes in the economy with US\$ 1400 million approximately, with a total production between 3.2 and 3.8 million tons of grain annually [34].

Sunflower is an annual monocarpic species in which reproductive phase exerts a strong control on leaf senescence and nutrient remobilization, affecting grain weight [35]. Potential yields of sunflower crop are far from the real ones in all Argentina productive regions. In Balcarce location, for instance (Southeast of Buenos Aires province), one of the best productive regions of Argentina, while the potential yields are estimated in 5000 kg ha<sup>-1</sup>, those obtained by the best producers only reach 3000 kg ha<sup>-1</sup>, and the average in the region ranges in 1800 kg ha<sup>-1</sup> [36]. Among the factors that contribute to the productivity gap, one of the most important is the inability of current hybrids to keep their green leaf area for long periods, limiting the incident

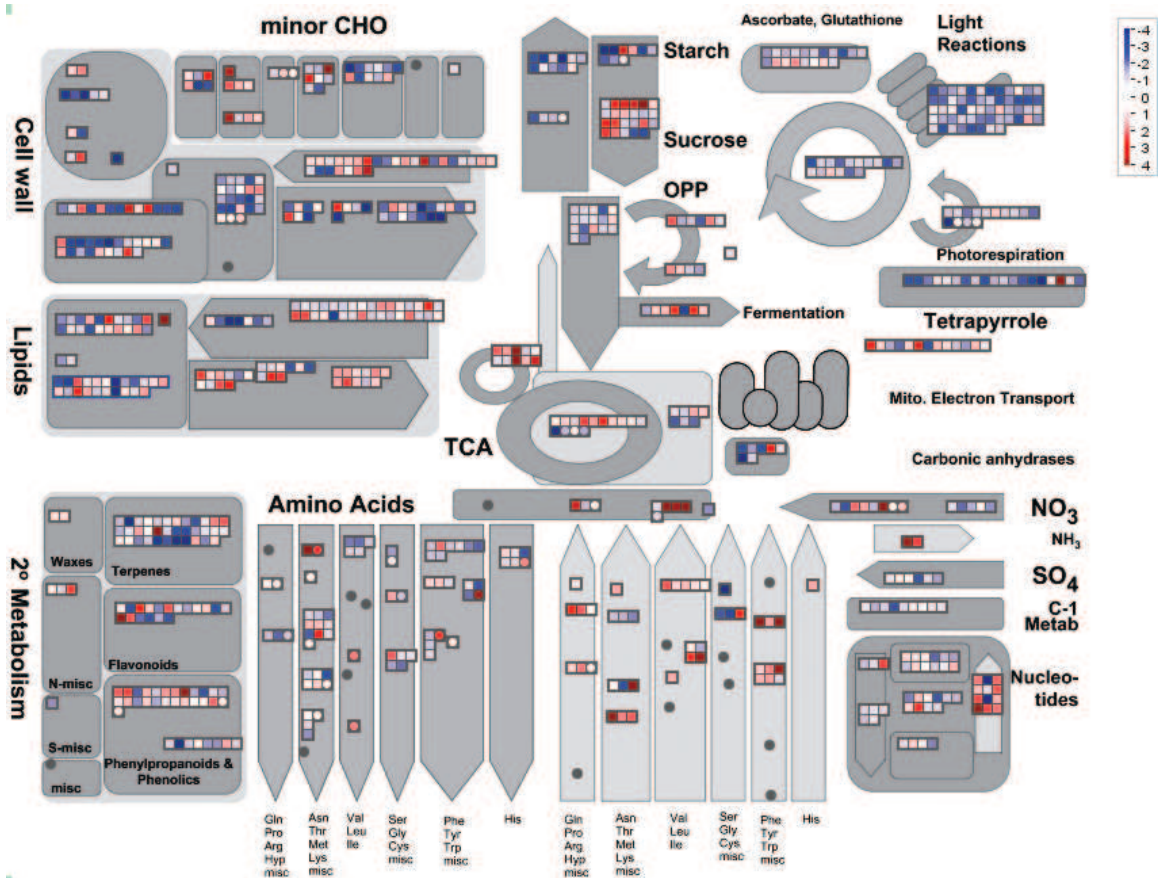
radiation capture during the grain-filling period and impacting negatively on the yield and oil concentration [12, 37].

Sunflower genome complexity characterized by long and highly similar repeats has slowed the pace of getting a complete genome reference. Recently, a high-quality assembly comprising 3.6 Gigabases has been achieved by means of PACBIO sequencing [38]. The reference genome together with extensive transcriptomic data from vegetative and floral organs is accessible at <https://www.heliagene.org/HanXRQ-SUNRISE>. In the last years, our group accomplished a series of transcriptional and metabolic profiling studies that were integrated into physiological, molecular and cytological analysis to contribute to the understanding of the senescence process in this crop and breeding genotypes against abiotic constraints [19–23, 39–41].

Through a system biology approach and using a commercial sunflower hybrid, we characterized the leaf senescence process by integrating transcriptomic and metabolomic analyses using both glasshouse and field conditions [22]. Our results revealed early metabolic changes before anthesis in the absence of the onset of the first visual senescence symptoms, with more pronounced changes observed when physiological and molecular variables were assessed under field conditions (**Figure 1**). Metabolite remobilization from mature and senescent leaves to the different sinks, particularly into seed development, affects their quality and quantity and is one of the most important aspects of crop improvement [3]. In this study, we showed a decrease of photosynthetic activity and cell growth before anthesis, whereas sucrose, fatty acid, nucleotide and amino acid metabolisms increased. The role of sugars in senescence has been widely discussed in recent years. Sugars are central elements of the source-sink relationships [42, 43] and have been reported as growth [44] and photosynthetic rate regulators [45]. However, the effect of sugars on senescence is controversial and differs between different species [1, 46, 47]. In sunflower, sugar content decreases during leaf development (**Figure 1**). This finding is in line with previous studies in tomato and higher plants, in which the photosynthetic rate dropped together with sugar levels in a mature leaf [48–50]. Furthermore, sunflower is a plant with a high demand for nutrient, especially sugars as substrate for oil synthesis, during the grain-filling phase. Likewise, low levels of sugars may increase production and/or ethylene sensitivity, which acts as senescence enhancer [51, 52].

Pathways related to nutrient recycling processes were also up-regulated. We found high expression levels of enzymes involved in recycling, such as asparagine synthetase and glutamine synthase, as well as the associated metabolites, asparagine and glutamine. These amino acids are involved in nitrogen and carbon transport between the different organs and are the most abundant amino acids in the xylem and phloem [53, 54], indicating a high recycling activity at early stages of leaf development.

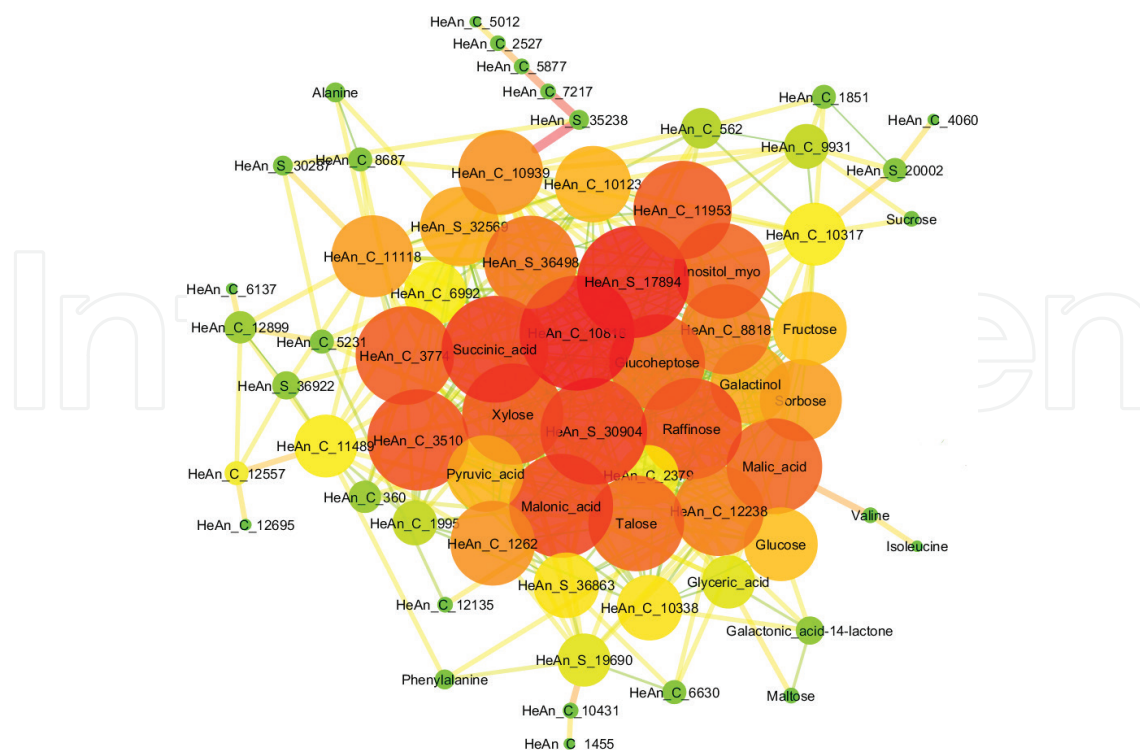
Transcription factors (TFs) are key proteins involved in the regulation of gene expression and signal transduction networks, regulating different biological processes and their function is crucial for triggering and/or controlling the different aspect of senescence process. Members of the NAC, AP2-EREBP, HB, bZIP and MYB transcription factor families showed high expression levels, and their expression level was highly correlated, suggesting their involvement in sunflower senescence. These results are in agreement with previous results described for *Arabidopsis thaliana* [55]. Particularly, we found a transcript with high sequence identity



**Figure 1.** Metabolism overview in the field experiment at pre-anthesis time. Genes and metabolites are represented by squares and circles, respectively. Color intensity corresponds to the expression ratio at logarithmic scale (red: up-regulated, blue: down-regulated) [22].

to *ANAC02* or *ATAF1*. This transcript might be associated with an upstream regulation of the signaling pathway involving *ORE1* and *EIN2* [56], thus activating their expression and inhibiting the expression of Golden2-like (*GLKs*) genes, which are necessary for chloroplast development and maintenance [57]. *ORE1* also acts as an antagonist of *GLK* protein, adding more complexity to this regulation pathway [57]. In *A. thaliana*, *ORE1* TF induces leaf senescence [58]. In addition, the micro-RNA *miR164* suppress *ORE1* transcript levels; *miR164* and *ORE1* may be regulated in a loop that would also involve *EIN2*, where *EIN2* would promote the expression of *ORE1* and would inhibit *miR164* [59]. In a previous work conducted in sunflower, expression profiles of candidate genes *Ha-EIN2* and *Ha-NAC01* (with high sequence identity to *ORE1*) were evaluated together with *miR164* levels [21] showing similar expression patterns to *Arabidopsis* and in line with the increase in the nutrient remobilization rate.

Moreover, using bioinformatic approaches and evaluating two different approaches for gene expression correlation analysis: Weighted Gene Correlation Network Analysis (*WGCNA*) and *BioSignature Discoverer* (*BioSD*, *Gnosis Data Analysis*, Heraklion, Greece), we integrated transcriptomic and metabolomic data [39]. *WGCNA* allowed the detection of 10 metabolites and 13 TFs (**Figure 2**), whereas *BioSD* allowed the detection of one metabolite and six TFs as potential biomarkers. Comparative analysis demonstrated that three transcription factors were detected



**Figure 2.** Integrated network of hubs metabolites and transcription factors detected by WGCNA [39]. 24 selected hubs metabolites and 82 TFs statistically significant during senescence were correlated ( $p$ -value  $< 0.0001$ ) and visualized in Cytoscape [60] by degree (node size and color) and edge weight (edge size and color).

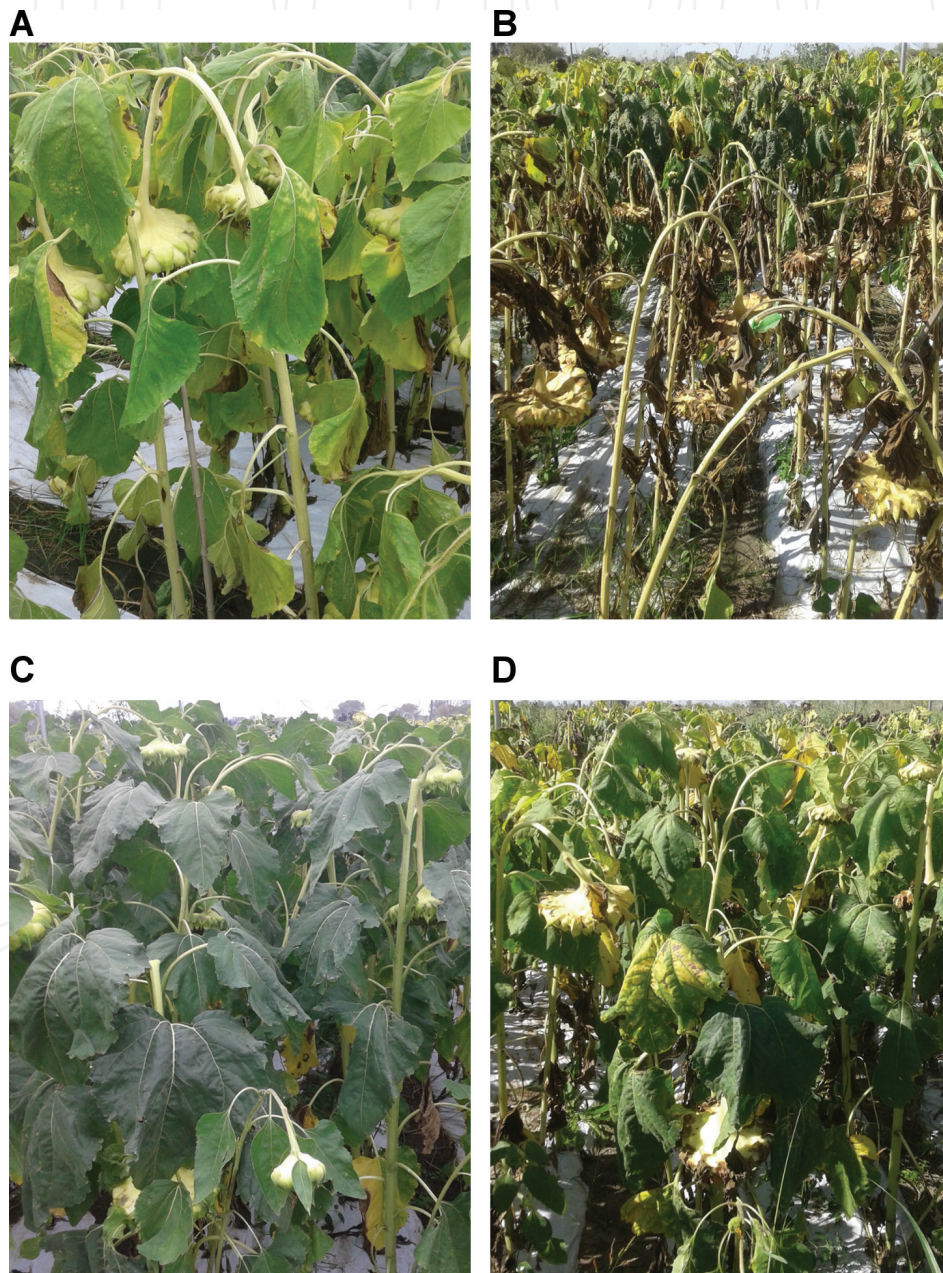
by both approaches, highlighting them as potentially robust biomarkers associated with leaf senescence in sunflower. This complementary use of network and BioSignature Discoverer analysis of transcriptomic and metabolomic data provided a useful tool for identifying candidate genes and metabolites, which may have a role in the triggering and development of the leaf senescence process.

Transcriptomic analysis in combination with metabolic profile is a comprehensive tool for the study of leaf senescence. These results suggest a complex regulatory network underlying this process. Thus, the identification of regulatory networks based on expression profiling is an important starting point for the detection of new key genes involved in the triggering of the senescence process in this crop.

#### 4. Selection of stay-green genotypes in sunflower

Given the importance of the stay-green genotypes selection for studies of this complex character, we performed a screening and selection of contrasting sunflower genotypes associated with early leaf senescence process evaluating 135 different genotypes from the INTA Sunflower Breeding Program (INTA Manfredi Sunflower Germplasm Collection) [61] growing under field conditions through a physiological, cytological and molecular approach.

Physiological measurement of growing cycle, anthesis time, number of leaves, plant size, evolution of total/dry leaf, green leaf area at anthesis time and SPAD was performed to select pairs of contrasting genotypes with very similar plant architecture, phenology and leaf area until anthesis, but with different senescence rate. This analysis allowed us to select 10 genotypes that were further evaluated, allowing the identification of two contrasting senescence inbred lines, R453 (early senescence genotype) and B481-6 (putative stay-green genotype) [23] (Figure 3).

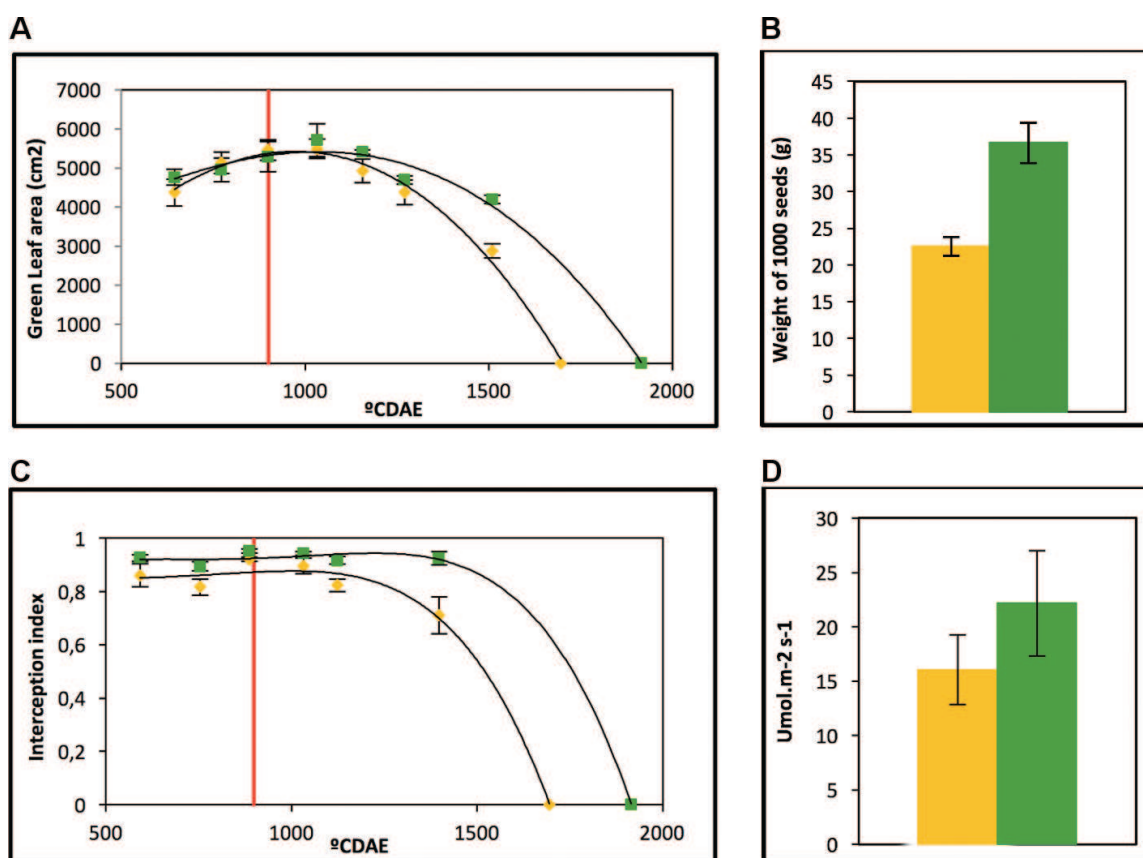


**Figure 3.** Phenotypic analysis of sunflower genotypes under field experiment. (A) and (B) early senescence genotype R453. (C) and (D) Stay-green genotype B481-6. Images (A) and (C) correspond to 15 days after anthesis and images (B) and (D) 30 days after anthesis.



At the physiological level, green leaf area evolution (GLA) is an indirect measurement of photosynthetically active leaf area, and its decrease has been reported as product of active chloroplast degeneration and chlorophyll degradation.

R453 and B481-6 displayed similar GLA evolution until anthesis. Then, GLA decreased abruptly in R453 and faster than the B481-6 genotype. GLA decline in B481-6, on the other hand, was gradual and reached complete senescence at 200 °CdAE later (**Figure 4A**). In sunflower, and many other monocarpic species, this senescence symptom is evident after anthesis, during grain-filling period, and is mainly due to source-sink relationships established at this stage of development [5, 20, 36, 62]. Radiation interception at the canopy level showed similar patterns with an early decrease in the early senescence genotype (**Figure 4C**). In grain crops, a delay in leaf senescence should have a positive impact on grain yield [3, 26]. Yield components were evaluated displaying significant differences in yield, with higher seed weight in the stay-green genotype (**Figure 4B**). These observations are in agreement with the expected for this trait suggesting a type B stay-green phenotype [28]. Moreover, photosynthesis measurement was performed 15 days after anthesis showing higher photosynthesis rate in the stay-green genotype (**Figure 4D**), supporting this finding.

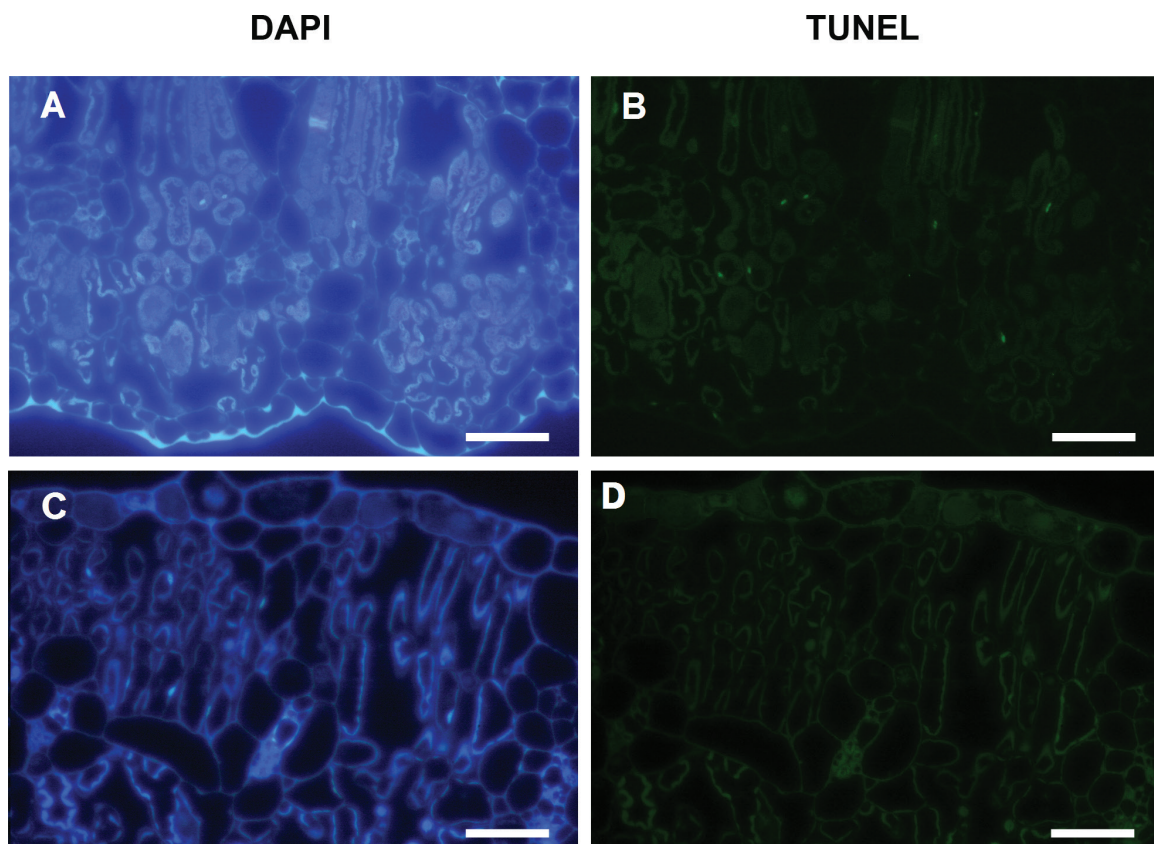


**Figure 4.** Physiological analysis of contrasting genotypes. R453 in orange and B481-6 in green colors. (A) Green leaf area (GLA); (B) yield; (C) radiation interception and (D) photosynthesis. °CdAE indicates thermal time after emergence. Red line in (A) and (C) indicates anthesis time for both genotypes.

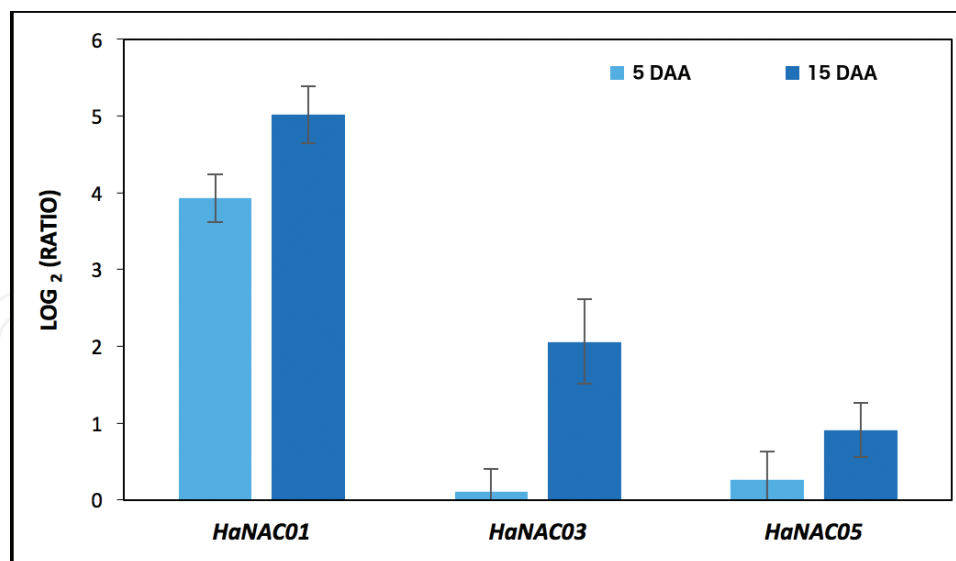
To confirm the senescence phenotype of the selected genotypes, we also performed cytological and molecular analysis. As senescence involves programmed Cell Death (PCD), nuclear DNA degradation associated with PCD can be detected in situ by TUNEL assay. In this sense, we analyzed mesophyll cells nuclei of both genotypes 10 days after anthesis. R453, with premature senescence phenotype, also showed TUNEL-positive nuclei, whereas B481-6, with stay-green phenotype, had TUNEL-negative nuclei (**Figure 5**). Mesophyll is the most photosynthetically active tissue of higher plants, having cells with high chloroplast and chlorophyll content and the cells in this tissue are affected firstly during senescence [9, 62, 63]. TUNEL-positive nuclei detection indicates that senescence process has already started in the early senescence genotype.

The gene expression pattern of the senescence-associated candidate transcription factors was evaluated for differences in the timing of senescence pathways activation between the early senescence and stay-green genotype [21, 22]. HaNAC01, HaNAC03 and HaNAC05 transcription factors were evaluated at two different times, 5 days after anthesis (DAA) and 15 days after anthesis (**Figure 6**). R453 showed higher expression levels of the three NAC transcription factor than B481-6, and its expression increased by 15 days post-anthesis.

Altogether, these findings highlight these genotypes as interesting potential candidates for further analysis of leaf senescence in sunflower. The B481-6 genotype showed a stay-green phenotype, also evidenced by cytological and molecular analysis and an increase of seed weight,



**Figure 5.** TUNEL assays of selected contrasting genotypes. (A) and (C): Nuclei visualization by DAPI staining. (B): TUNEL-positive nuclei in mesophyll cells of premature senescence genotypes (R453). (D): TUNEL-negative nuclei in stay-green genotype (B481-6) [23].



**Figure 6.** qPCR analysis of NAC transcription factors candidate genes. Relative transcript levels are shown as the ratio (log<sub>2</sub> scale) between the expression in the early senescence genotype (R453) in relation to the stay-green genotype (B481-6) in two different times 5 days after anthesis (DAA) and 15 days after anthesis [23].

which makes this genotype a potential candidate for the functional stay-green phenotype in comparison with R453 genotype.

## 5. Conclusions and perspectives

Integration of transcriptomic and metabolomics data arises as a powerful approach to identify pathways and candidate genes related to the senescence process in sunflower, an economically important oil crop without previous molecular information about this process. The results discussed in this chapter provide an important start point for understanding the senescence process and open new insights to explore alternative strategies and possibilities.

Moreover, by a combination of physiological, cytological and molecular analysis, we identified two senescence contrasting genotypes. B481-6 genotype showed a delay in senescence symptom evaluated both, under physiological and molecular measurement. This senescence delay, together with an increase in photosynthesis rate, leads to an increase in yield, highlighting this genotype as functional stay-green. These results together with a better understanding of the onset of the process will in turn impact on the development of different senescence management strategies and could help controlling the grain-filling process. All in all, these advances provide a valuable tool to assist in crop breeding, which represents a significant challenge for the future of agriculture attending to the increase in both, world population and climate risks that affect productivity.

## Acknowledgements

This research was supported by Research Projects of the Instituto Nacional de Tecnología Agropecuaria (INTA), ANPCyT and CONICET (MINCyT) and the DEANN Project (UE). Dr.

S. Moschen holds a postdoctoral fellowship from CONICET, Lic. A. I. López Gialdi holds a doctoral fellowship from CONICET, whereas Dr. N. Paniego, Dr. P. Fernandez, Dr. R. A. Heinz are career members of the Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET, Argentina) and INTA researchers.

## Author details

Sebastián Moschen<sup>1,2,3</sup>, Agustín I. López Gialdi<sup>2</sup>, Norma Paniego<sup>1,2</sup>, Paula Fernandez<sup>1,2,3</sup> and Ruth Amelia Heinz<sup>1,2,4\*</sup>

\*Address all correspondence to: heinz.ruth@inta.gob.ar

1 Instituto de Biotecnología, CICVyA, Instituto Nacional de Tecnología Agropecuaria, Hurlingham, Buenos Aires, Argentina

2 Consejo Nacional de Investigaciones Científicas y Técnicas, CONICET, Ciudad Autónoma de Buenos Aires, Argentina

3 Escuela de Ciencia y Tecnología, Universidad Nacional de San Martín, San Martín, Buenos Aires, Argentina

4 Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Ciudad Autónoma de Buenos Aires, Argentina

## References

- [1] Nooden LD. Whole plant senescence. In: AC L, editor. *Senescence and Aging in Plants*. San Diego, USA: Academic Press; 1988. pp. 392-439
- [2] Buchanan-Wollaston V, Earl S, Harrison E, Mathas E, Navabpour S, Page T, et al. The molecular analysis of leaf senescence--a genomics approach. *Plant Biotechnology Journal*. 2003;**1**:3-22. DOI: 10.1046/j.1467-7652.2003.00004.x
- [3] Gregersen PL, Culetic A, Boschian L, Krupinska K. Plant senescence and crop productivity. *Plant Molecular Biology*. 2013;**82**:603-622. DOI: 10.1007/s11103-013-0013-8
- [4] Lim PO, Woo HR, Nam HG. Molecular genetics of leaf senescence in Arabidopsis. *Trends in Plant Science*. 2003;**8**:272-278. DOI: 10.1016/S1360-1385(03)00103-1
- [5] Sadras VO, Echarte L, Andrade FH. Profiles of leaf senescence during reproductive growth of sunflower and maize. *Annals of Botany*. 2000;**85**:187-195
- [6] Guo Y, Cai Z, Gan S. Transcriptome of Arabidopsis leaf senescence. *Plant, Cell & Environment*. 2004;**27**:521-549
- [7] Agüera E, Cabello P, de la Haba P. Induction of leaf senescence by low nitrogen nutrition in sunflower (*Helianthus annuus*) plants. *Physiologia Plantarum*. 2010;**138**:256-267. DOI: 10.1111/j.1399-3054.2009.01336.x

- [8] Srivalli B, Khanna-Chopra R. The developing reproductive “sink” induces oxidative stress to mediate nitrogen mobilization during monocarpic senescence in wheat. *Biochemical and Biophysical Research Communications*. 2004;**325**:198-202. DOI: 10.1016/j.bbrc.2004.09.221
- [9] Thomas H. Senescence, ageing and death of the whole plant. *New Phytol*. 2013;**197**: 696-711. doi:10.1111/nph.12047
- [10] Kusaba M, Tanaka A, Tanaka R. Stay-green plants: What do they tell us about the molecular mechanism of leaf senescence. *Photosynthesis Research*. 2013;**117**:221-234. DOI: 10.1007/s11120-013-9862-x
- [11] Aguirrezabal LAN, Lavaud Y, Dosio GAA, Izquierdo NG, Andrade FH, González LM. Intercepted solar radiation during seedling determines sunflower weight per seed and oil concentration. *Crop Science*. 2003;**161**:152-161
- [12] Dosio GAA, Aguirrezabal LAN, Andrade FH, Pereyra VR. Solar radiation intercepted during seed filling and oil production in two sunflower hybrids. *Crop Science*. 2000;**1644**: 1637-1644
- [13] Moschen S, Radonic LM, Ehrenbolger GF, Fernández P, Lía V, Paniego NB, et al. Functional genomics and transgenesis applied to sunflower breeding. In: Arribas JI, editor. *Sunflowers: Growth and Development, Environmental Influences and Pests/Diseases*. Nova Science Publishers Inc., New York; 2014. pp. 131-164
- [14] Debaeke P, Casadebaig P, Flenet F, Langlade N. Sunflower crop and climate change: Vulnerability, adaptation, and mitigation potential from case-studies in Europe. *OCL. EDP Sciences*. 2017; **24**:1-15. DOI: 10.1051/ocl/2016052
- [15] Fernandez P, Paniego N, Lew S, Hopp HE, Heinz RA. Differential representation of sunflower ESTs in enriched organ-specific cDNA libraries in a small scale sequencing project. *BMC Genomics*. 2003;**4**:40. DOI: 10.1186/1471-2164-4-40
- [16] Paniego N, Heinz RA, Fernandez P, Talia P, Nishinakamasu V, Hopp HE. Sunflower. In: Kole C, editor. *Genome Mapping and Molecular Breeding in Plants*. Berlin Heidelberg: Springer-Verlag; 2007. pp. 153-177. DOI: 10.1007/978-3-540-34388-2\_4
- [17] Fernandez P, Rienzo J Di, Fernandez L, Hopp HE, Paniego N, Heinz RA, et al. Transcriptomic identification of candidate genes involved in sunflower responses to chilling and salt stresses based on cDNA microarray analysis. *BMC Plant Biology*. 2008;**8**:1-18. DOI: 10.1186/1471-2229-8-11
- [18] Peluffo L, Lia V, Troglia C, Maringolo C, Norma P, Escande A, et al. Metabolic profiles of sunflower genotypes with contrasting response to *Sclerotinia sclerotiorum* infection. *Phytochemistry*. Elsevier Ltd. 2010;**71**:70-80. DOI: 10.1016/j.phytochem.2009.09.018
- [19] Fernandez P, Soria M, Blesa D, DiRienzo J, Moschen S, Rivarola M, et al. Development, characterization and experimental validation of a cultivated sunflower (*Helianthus annuus* L.) gene expression oligonucleotide microarray. *PLoS One*. 2012;**7**:1-11. DOI: 10.1371/journal.pone.0045899

- [20] Fernandez P, Moschen S, Paniego N, Heinz RA. Functional approaches to study leaf senescence in sunflower. In: Nagata T, editor. *Senescence*. InTech Open Access Publisher, Croatia; 2012. pp. 69-88. DOI: 10.5772/1905
- [21] Moschen S, Bengoa Luoni S, Paniego NB, Hopp HE, Dosio GAA, Fernandez P, et al. Identification of candidate genes associated with leaf senescence in cultivated sunflower (*Helianthus annuus* L.). *PLoS One*. 2014;9:e104379. DOI: 10.1371/journal.pone.0104379
- [22] Moschen S, Bengoa Luoni S, Di Rienzo J, Caro M, Tohge T, Watanabe M, et al. Integrating transcriptomic and metabolomic analysis to understand natural leaf senescence in sunflower. *Plant Biotechnology Journal*. 2016;14:719-734. DOI: 10.1111/pbi.12422
- [23] López Gialdi AI, Moschen S, Villán CS, López Fernández MP, Maldonado S, Paniego N, et al. Identification and characterization of contrasting sunflower genotypes to early leaf senescence process combining molecular and physiological studies (*Helianthus annuus* L.). *Plant Sciences*. 2016;250:40-50. DOI: 10.1016/j.plantsci.2016.05.017
- [24] Diaz C, Purdy S, Christ A, Morot-Gaudry J-F, Wingler A, Masclaux-Daubresse C. Characterization of Markers to Determine the Extent and Variability of Leaf Senescence in Arabidopsis. A Metabolic Profiling Approach 1. *Plant Physiology*. 2005;138:898-908. DOI: 10.1104/pp.105.060764.898
- [25] De la Vega AJ, Cantore Ma., Sposaro MM, Trápani N, López Pereira M, Hall AJ. Canopy stay-green and yield in non-stressed sunflower. *Field Crops Research*. 2011;121:175-185. DOI: 10.1016/j.fcr.2010.12.015
- [26] Gregersen PL. Senescence and nutrient remobilization in crop plants. In: Hawkesford MJ, Barraclough P, editors. *The Molecular and Physiological Basis of Nutrient Use Efficiency in Crops*. Oxford, UK: Wiley-Blackwell; 2011. pp. 83-102
- [27] Thomas H, Smart CM. Crops that stay green. *Annals of Applied Biology*. Blackwell Publishing Ltd. 1993;123:193-219. DOI: 10.1111/j.1744-7348.1993.tb04086.x
- [28] Thomas H, Howarth CJ. Five ways to stay green. *Journal of Experimental Botany*. 2000;51:329-337
- [29] Thomas H, Ougham H. Senescence and crop performance. In: Sadras V, Calderini D, editors. *Applications for Genetic Improvement, Agronomy and Farming Systems*. 2nd ed. New York: Crop Physiology; 2014
- [30] Thomas H, Ougham H. The stay-green trait. *Journal of Experimental Botany*. 2014;65:3889-3900. DOI: 10.1093/jxb/eru037
- [31] Yoo S-C, Cho S-H, Zhang H, Paik H-C, Lee C-H, Li J, et al. Quantitative trait loci associated with functional stay-green SNU-SG1 in rice. *Molecules and Cells*. 2007;24:83-94. Available: <http://www.ncbi.nlm.nih.gov/pubmed/17846502>
- [32] Kumudini S. Trials and tribulations: A review of the role of assimilate supply in soybean genetic yield improvement. *Field Crops Research*. 2002;75:211-222. DOI: 10.1016/S0378-4290(02)00027-8

- [33] Ismail AM, Hall AE, Ehlers JD. Delayed-Leaf-Senescence and Heat-Tolerance Traits Mainly Are Independently Expressed in Cowpea. *Crop Science*. 2000;**40**:1049-1055.
- [34] ASAGIR. Asociación Argentina de Girasol [Internet]. Available: [www.asagir.org.ar](http://www.asagir.org.ar)
- [35] López Pereira M, Sadras VO, Trápani N. Genetic improvement of sunflower in Argentina between 1930 and 1995. I. Yield and its Components. *Field Crops Research*. 1999;**62**:157-166.
- [36] Dosio GAA, Aguirrezábal LAN. Variaciones del rendimiento en girasol. Identificando las causas. *Revista Agromercado, Cuadernillo de girasol*. 2004;**90**:7-10
- [37] Aguirrezábal LAN, Lavaud Y, Dosio GAA, Izquierdo NG, Andrade FH, González LM. Weight per seed and oil concentration in a sunflower hybrid are accounted for by intercepted solar radiation during a definite period of seed filling. *Crop Science*. 2003;**43**:152-161
- [38] Gouzy J, Mayjonade B, Grassa C, Carrere S, Sallet E, Legrand L, et al. Result of the de novo Sequencing of the Complex Sunflower Genome Using PacBio Technology (100X). XXIV Plant & Animal Genome Conference; San Diego, CA; 2016
- [39] Moschen S, Higgins J, Di Rienzo JA, Heinz RA, Paniego N, Fernandez P, et al. Network and biosignature analysis for the integration of transcriptomic and metabolomic data to characterize leaf senescence process in sunflower. *BMC Bioinformatics*. BioMed Central. 2016;**17**:174. DOI: 10.1186/s12859-016-1045-2
- [40] de la Mata L, Cabello P, de la Haba P, Agüera E. Growth under elevated atmospheric CO<sub>2</sub> concentration accelerates leaf senescence in sunflower (*Helianthus annuus* L.) plants. *Journal of Plant Physiology*. 2012;**169**:1392-1400
- [41] Agüera E, Cabello P, de la Mata L, Molina E, de la Haba P. Metabolic Regulation of Leaf Senescence in Sunflower (*Helianthus annuus* L.) Plants. In: Nagata T, editor. *Senescence*. InTech Open Access Publisher, Croatia; 2012. pp. 51-68. DOI: 10.5772/1905.
- [42] Balibrea Lara ME, Gonzalez Garcia M-C, Fatima T, Ehness R, Lee TK, Proels R, et al. Extracellular invertase is an essential component of cytokinin-mediated delay of senescence. *The Plant Cell*. 2004;**16**:1276-1287. DOI: 10.1105/tpc.018929
- [43] Roitsch T, González M-C. Function and regulation of plant invertases: Sweet sensations. *Trends in Plant Science*. 2004;**9**:606-613. DOI: 10.1016/j.tplants.2004.10.009
- [44] Smeekens S, Ma J, Hanson J, Rolland F. Sugar signals and molecular networks controlling plant growth. *Current Opinion in Plant Biology*. Elsevier Ltd. 2010;**13**:274-279. DOI: 10.1016/j.pbi.2009.12.002
- [45] Wingler A, Von Schaewen A, Leegood RC, Lea PL, Quick PW. Regulation of leaf senescence by cytokinin, sugars, and light. *Plant Physiology*. 1998;**116**:329-335
- [46] Wingler A, Masclaux-Daubresse C, Fischer AM. Sugars, senescence, and ageing in plants and heterotrophic organisms. *Journal of Experimental Botany*. 2009;**60**:1063-1066. DOI: 10.1093/jxb/erp067

- [47] Yoshida S. Molecular regulation of leaf senescence. *Current Opinion in Plant Biology*. 2003;**6**:79-84. DOI: 10.1016/S1369-5266(02)00009-2
- [48] Quirino BF, Noh YS, Himelblau E, Amasino RM. Molecular aspects of leaf senescence. *Trends in Plant Science*. 2000;**5**:278-282. Available: <http://www.ncbi.nlm.nih.gov/pubmed/10871899>
- [49] Jang JC, León P, Zhou L, Sheen J. Hexokinase as a sugar sensor in higher plants. *Plant Cell Online*. 1997;**9**:5-19. DOI: 10.1105/tpc.9.1.5
- [50] Dai N, Schaffer A, Petreikov M, Shahak Y, Giller Y, Ratner K, et al. Overexpression of *Arabidopsis* hexokinase in tomato plants inhibits growth, reduces photosynthesis, and induces rapid senescence. *The Plant Cell*. 1999;**11**:1253-1266. Available: <http://www.ncbi.nlm.nih.gov/pubmed/10402427>
- [51] Grbic V, Bleecker AB. Ethylene regulates the timing of leaf senescence in *Arabidopsis*. *The Plant Journal*. 1995;**8**:595-602. DOI: 10.1046/j.1365-313X.1995.8040595.x
- [52] Hoeberichts FA, van Doorn WG, Vorst O, Hall RD, van Wordragen MF. Sucrose prevents up-regulation of senescence-associated genes in carnation petals. *Journal of Experimental Botany*. 2007;**58**:2873-2885. DOI: 10.1093/jxb/erm076
- [53] Lea P, Mifflin B. Transport and Metabolism of Asparagine and Other Nitrogen Compounds within the Plant. In: Mifflin B, editor. *The Biochemistry of Plants*. Vol. 5. Amino Acids and Derivatives. Academic Press, New York, 569-607.
- [54] Urquhart AA, Joy KW. Use of Phloem exudate technique in the study of amino Acid transport in pea plants. *Plant Physiology*. 1981;**68**:750-754. Available: <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=425975&tool=pmcentrez&rendertype=abstract>
- [55] Balazadeh S, Riaño-Pachón DM, Mueller-Roeber B. Transcription factors regulating leaf senescence in *Arabidopsis thaliana*. *Plant Biology*. 2008;**10**:63-75. DOI: 10.1111/j.1438-8677.2008.00088.x
- [56] Balazadeh S, Garapati P, Xue G, Mueller-Roeber B. A transcription factor upstream of ORE1 and GLK1 integrates ABA signalling with drought-induced senescence. 6th European Workshop on Leaf Senescence 14-18 October INRA, Versailles, France. 2013
- [57] Rauf M, Arif M, Dortay H, Matallana-Ramírez LP, Waters MT, Gil Nam H, et al. ORE1 balances leaf senescence against maintenance by antagonizing G2-like-mediated transcription. *EMBO Reports*. 2013;**14**:382-388. DOI: 10.1038/embor.2013.24
- [58] Balazadeh S, Siddiqui H, Allu AD, Matallana-Ramirez LP, Caldana C, Mehrnia M, et al. A gene regulatory network controlled by the NAC transcription factor ANAC092/AtNAC2/ORE1 during salt-promoted senescence. *Plant Journal*. 2010;**62**:250-264. DOI: TPJ4151 [pii] 10.1111/j.1365-313X.2010.04151.x
- [59] Kim JH, Woo HR, Kim J, Lim PO, Lee IC, Choi SH, et al. Trifurcate feed-forward regulation of age-dependent cell death involving miR164 in *Arabidopsis*. *Science*. 2009;**323**:1053-1057. DOI: 10.1126/science.1166386



- [60] Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, et al. Cytoscape: A software environment for integrated models of biomolecular interaction networks. *Genome Research*. 2003;**13**:2498-2504. DOI: 10.1101/gr.1239303
- [61] Filippi CV, Aguirre N, Rivas JG, Zubrzycki J, Puebla A, Cordes D, et al. Population structure and genetic diversity characterization of a sunflower association mapping population using SSR and SNP markers. *BMC Plant Biology*. 2015;**15**:52. DOI: 10.1186/s12870-014-0360-x
- [62] Gan S, Amasino RM. Making Sense of Senescence (Molecular Genetic Regulation and Manipulation of Leaf Senescence). *Plant Physiology*. 1997;**113**:313-319. Available: [http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=158144&tool=pmcentrez&render\\_type=abstract](http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=158144&tool=pmcentrez&render_type=abstract)
- [63] Hörtensteiner S. Chlorophyll degradation during senescence. *Annual Review of Plant Biology*. 2006;**57**:55-77