

eXtra Botany

Special Issue Editorial

Plant development and reproduction in a changing environment

Plants face the most diverse climatic conditions throughout their life cycle. As sessile organisms, they are remarkably resilient to adverse environments, which have been exacerbated in the current context of global change. The way in which plants sense and respond to various types of abiotic stresses varies depending on the severity of the stress and the developmental stage of the plant, affecting both vegetative and reproductive aspects. Understanding how plants respond and adapt to a changing environment is crucial for predicting and mitigating the impacts of climate change on ecosystems and ensuring the future survival and reproduction of plant species.

In this context, root hairs have become a relevant system for studying how plants modulate their growth in response to both cell-intrinsic and environmental stimuli. In their review article, [Lopez *et al.* \(2024\)](#) discussed new molecular components that regulate the transcriptional hub in root hairs. Root hairs are exposed to different environmental cues that involve the content of nutrients in the soil and hormonal stimuli that in turn influence the way in which the plant responds to different types of environmental stresses. By using the PlantConnectome database, the authors generated an updated view of root hair growth in these complex biological contexts.

Another fundamental aspect of development that is affected by environmental factors is the transition from vegetative to reproductive growth stages. In this regard, and given that environmental stresses have reduced crop productivity globally, there has been a growing interest and an increasing number of studies focused on the effect of stress on plant reproduction in recent years.

In this issue, [Li *et al.* \(2024\)](#) reviewed the genetic and epigenetic basis of phytohormone control of floral transition in plants and its integration with external environmental cues. Such integration is critical to regulate the timing of the developmental transition from the vegetative to the reproductive stage, and depends on the activity of specific transcription factors and epigenetic regulators. The precise regulation of flowering

time is coordinated by two critical regulators. FLOWERING LOCUS T (FT) and TERMINAL FLOWER (TFL) are members of the PHOSPHATIDYLETHANOLAMINE BINDING PROTEIN (PEBP) family of proteins that interact with transcriptional regulators, such as FLOWERING LOCUS D (FD). [Colleoni *et al.* \(2024\)](#) reviewed the role of PEBP family members not only as regulators of flowering time but also as emerging shapers of plant architecture across different species. In a new twist that adds more knowledge about key proteins in the regulation of these processes, [González-Suarez *et al.* \(2024\)](#) found that the ambient temperature during organ initiation strongly influences its size. This effect depends on FT-mediated signal integration, adding to the repertoire of developmental processes regulated by this pathway. Their work showed that increasing temperatures not only affect fertility, but also the size and seed number of fruits produced. In this sense, the regulation of FT expression represents a new opportunity to regulate these processes in a changing environment.

Sexual reproduction depends strictly on the viability of the gametophytes. In the current context of global warming, pollen grains have shown an enormous sensitivity to temperature increases. Therefore, research on the processes underlying the development and proper function of the male gametophyte is crucial. [Sede *et al.* \(2024\)](#) studied whether hydroxylation and subsequent O-glycosylation of Arabidopsis pollen leucine-rich repeat extensins (LRXs) are necessary for their proper function and cell wall localization in pollen tubes. By studying plants impaired in members of the 2-oxoglutarate-dependent dioxygenases family known as prolyl-4-hydroxylases (P4Hs), they found that their activity is required for pollen germination and pollen tube growth. Through immunoprecipitation–tandem MS analysis, they revealed a decrease in hydroxyprolines in the mutant pollen tubes, suggesting that P4H4 and P4H6 are required for pollen germination and for proper hydroxylation of LRX11, which is necessary for its localization at the cell wall of pollen tubes. After fertilization, the developing embryos are embedded in maternal tissues.

In their review, [Woudenberg *et al.* \(2024\)](#) analyzed the nurturing and protective roles that maternal tissues play in the control of embryogenesis across diverse land plants. These

nurturing, constraining, and protective roles include both direct and indirect effects that when studied through the lens of evolution, open up new and interesting questions for future research. However, even though they have a protective role, the maternal structures and thus the embryo embedded within them are not insensitive to variations in environmental conditions. Many of the most relevant processes that occur during embryogenesis, including developing and nutrient storage, are affected by environmental changes. With a focus on the current context of global warming, that includes increases in temperature and carbon dioxide concentrations, Escudero *et al.* (2024) discuss how variations in these parameters affect different aspects of embryogenesis, differentiating embryo autonomous processes, and maternal effects.

The development of the endosperm accompanies the development and growth of the embryo. However, depending on the species, the endosperm undergoes developmentally controlled programmed cell death (PCD) at specific time points of seed development or germination. This process exhibits a considerable diversity, both across different angiosperm taxa and within distinct endosperm tissues. In their review, Doll and Nowack (2024) provide an exhaustive overview of endosperm PCD mechanisms and regulation in angiosperms, shedding light on its relevance during seed development and seedling establishment. All these aspects that influence plant reproduction acquire a great relevance when food security is at risk due to the environmental changes that have occurred in recent years. In their review, Lv *et al.* (2024) synthesized the major advancements in unraveling the mechanisms underlying heat stress responses during maize sexual reproduction, which is directing new developing tools aimed to mitigate the effects that climate change is having on crop reproduction.

Drought is another major threat to global food security. In recent years, numerous studies have been aimed at discovering the molecular mechanisms underlying drought tolerance across species. In this issue, Antonietta *et al.* (2024) summarize the evidence for increased tolerance to water deficit in genotypes with delayed senescence, focusing on the physiological mechanisms and environmental conditions under which the stay-green trait may ameliorate stress tolerance and increase grain yield under stress.

Plants also have the challenge to adjust their growth and development to different conditions. The study of heat stress in plants and adaptation mechanisms such as the adjustments of protein synthesis is crucial for agriculture and environmental sustainability, especially in the context of climate change. High temperatures can negatively affect plant growth, reproduction, and productivity, thereby reducing crop yields. Knowing more about how plants respond and adapt to these environmental conditions and exploring adaptation strategies are essential to improve crop resilience. In this context, Lohman *et al.* (2024) describe various mechanisms that control protein translation in response to high temperature stress in plants, compared with yeast and metazoans, by modifying different components of

the translation machinery. Recent work also suggests an important role in these processes for the so-called stress granules or cytoplasmic biomolecular condensates. The authors provide a critical review of the role of these stress granules in translational regulation and the molecular processes associated with translation that could occur within them.

Another review that is part of this Special Issue is related to the study of stress adaptation in plants and the description of the mechanisms and proteins involved in it (Castellano *et al.*, 2024). It is widely known that the correct folding of proteins is crucial for them to acquire their tertiary structure, which is essential for their functionality and, therefore, for the correct functioning of all the biological processes in organisms, such as the occurrence of biochemical reactions that allow plants to grow, develop, and adapt to their environment. In some cases, the active conformation of a specific protein is obtained spontaneously. However, many proteins need the help of chaperones and co-chaperones to fold properly. These proteins help to maintain protein homeostasis under controlled conditions and during various stress responses. Castellano *et al.* (2024) reviewed the role of HOP (HSP70–HSP90 organizing protein). This is a family of co-chaperone proteins that is highly conserved and is essential in assisting HSPs in the folding of specific proteins. Previous studies carried out in mammals and yeast have revealed novel functions of HOPs and redefined their role in protein folding. In this article, the authors provide a detailed overview of the most important aspects of HOP regulation and function in other eukaryotic organisms and discuss whether these mechanisms are conserved in plants. Finally, the authors place special emphasis on the HOP clients described in plants and on the role of HOP in plant development and stress responses.

As we mentioned above, terrestrial plants have to face different adverse environments during their development and growth. One such adverse condition that plants must face are oxidizing environments, characterized by their heterogeneity and rapid fluctuations. In this sense, redox-dependent post-translational modifications emerge as a critical component of plant responses to stress. In this issue, El Baldouri *et al.* (2024) provided us with an evolutionary vision of the functions of CC-type glutaredoxins in the development of land plants and their adaptation to the environment. These glutaredoxins are of high relevance as they participate in the control of proper plant development and reproduction, and are mainly negative regulators of plant responses to biotic and abiotic stresses.

Bashir *et al.* (2024) provided an interesting approach to the reproductive biology of plants, specifically the olive tree (*Olea europaea* L.). The study of crop self-infertility and the concept of self-incompatibility are crucial to agriculture and plant reproductive biology. Self-incompatibility is a genetic mechanism that prevents self-fertilization and promotes genetic diversity by ensuring cross-fertilization between different individuals. This phenomenon is vital to maintain healthy and adaptable plant populations. When genetic diversity increases, plants

show greater resistance to diseases and pests, and are better able to adapt to environmental changes. The olive tree is a traditional Mediterranean tree species that has a wide range of local cultivars. Traditional olive plants are generally valued for their cultural importance. However, they often face challenges of economic sustainability. One of the drawbacks of these cultivars obtained by crossing is self-incompatibility, a common problem in olive production that could result in low fruit set and lower yields. Self-incompatibility was attributed to many genetic, physiological, environmental, and agronomic factors. These factors interlink to shape fertilization patterns, affecting both cultivated and wild olive species. In addition, it was reported that climatic conditions such as excessive rain or high temperatures can further affect pollination. Taking this into account, [Bashir et al. \(2024\)](#) provided an overview of the various factors that contribute to auto-infertility in olive plants, also focusing on recent advances in this area. Furthermore, the review explores the different strategies currently used to investigate self-incompatibility in the olive tree and future research required to address this problem. In agricultural crops, understanding and managing self-incompatibility can lead to improved yields and crop quality by optimizing pollination practices and selection of compatible varieties. In this way, the authors aimed to contribute to the development of sustainable olive production systems and the preservation of this vital component of Mediterranean culture.

Among other factors that influence the growth and development of plants, it is also important to highlight the existence of different genetic factors and growth regulators that act on gene expression, which allows plants to adapt to changing conditions, especially in the context of climate change. In this context, [Hardy and Balcerowicz \(2024\)](#) reviewed recent advances in the understanding of the essential role of untranslated regions (UTRs) in the post-transcriptional control of gene expression with respect to a plant's abiotic environment. In order to survive in a dynamic environment, plants continuously monitor their surroundings and adjust their development and physiology accordingly. These adjustments are driven by changes in gene expression, which is mainly attributed to transcriptional reprogramming. In this regard, UTRs act as key regulators in the environmental control of gene expression. In this work, the authors summarized the molecular mechanisms and signaling cascades controlled by UTRs, and discussed the role of UTRs in improving plant resilience against climate change.

It has also been reported that the regulation of chromatin function in eukaryotes plays a fundamental role in the control of the network of developmental regulatory genes. As sessile organisms, plants have developed sophisticated mechanisms to perceive and respond to environmental cues, orchestrating developmental programs that ensure adaptability and survival. A crucial aspect of this dynamic response involves the modulation of versatile gene-regulatory networks, which are mediated by various chromatin regulators. In this Special Issue, [Wang and Sung \(2024\)](#) reviewed this topic, describing the advances

in understanding the molecular mechanisms through which chromatin regulators integrate environmental signals and influence key aspects of plant development.

On the other hand, growth-regulating factors (GRFs) are key elements in the molecular machinery that controls plant growth and development, playing a fundamental role in the regulation of cell proliferation, differentiation, and morphogenesis. These transcription factors are responsible for activating specific genes involved in cell expansion and tissue formation, and determining the size and shape of plant organs. The importance of GRFs is related to their ability to improve plant performance by influencing desirable agronomic traits such as organ size, biomass production, and stress resistance, thus offering promising biotechnological applications. Here, the review of [Lazzara et al. \(2024\)](#) analyzed the complex molecular mechanisms that regulate GRF activity and how its natural and synthetic variants can impact plant growth and development. In addition, the work also discussed about how GRFs regulate gene expression and contribute to the control of organ growth and plant responses to a changing environment. The authors focused on the idea that to take advantage of the high biotechnological potential that GRFs have, it is necessary to better understand the functional diversity among GRF family members and the genetic networks they regulate them.

In their review, [Wittmer and Heidstra \(2024\)](#) draw a parallel between the resilience mechanisms of animals and plants. Both organisms exhibit remarkable abilities to regenerate damaged cells, either through the action of adult stem cells or by inducing somatic cells to revert to a stem-cell-like state. In this work, the authors reviewed different studies about cell regeneration in plants. A major scientific breakthrough was the discovery of induced pluripotent stem cells (iPSCs), which are reprogrammed from somatic cells by expressing different transcription factors. The creation of a genotype-independent iPSC system in plants would be useful to overcome current limitations in plant regeneration. This innovative approach could revolutionize plant biotechnology, enabling the enhancement of crucial traits such as yield and disease resistance.

Finally, the work by [Goeckeritz et al. \(2024\)](#) addressed a critical challenge in understanding floral development in *Prunus* to manipulate bloom time and to mitigate crop loss due to climate change. The authors analyzed flower development in sour cherries, revealing that genetic factors, specifically a major bloom time quantitative trait locus (QTL) on chromosome 4, significantly influence bloom timing. Notably, early-blooming trees exhibit consistently advanced floral development compared with late-blooming counterparts. Through genomic and transcriptomic analyses, the study identified candidate genes associated with late blooming, enabling a deeper understanding on the molecular mechanisms underlying this trait. This research provides not only a deeper knowledge of the molecular mechanisms underlying flower development in *Prunus* species, but also valuable insights for breeding programs aimed at developing climate-resilient cultivars with optimized bloom times.

The studies presented in this Special Issue highlight the importance of understanding how plant development and reproduction occur in the face of a changing climate. Elucidating the different mechanisms, metabolic pathways, and genetic factors that govern plant development and reproduction provides a crucial knowledge for developing resilient crop varieties and new strategies to mitigate the adverse effects of climate change.

Conflict of interest

The authors declare no conflicts of interest.

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