

# **Preface for Nuclear Functions**

## **(eds. Pontes and Jin)**

Plants provide us with food and are the source of several other by-products such as compounds used in pharmaceuticals or biofuels. Therefore, it comes as no surprise that plants are crucial in solving major challenges now facing humanity, namely, food productivity/security, increasing energy demands, and environmental changes. There has been a dramatic increase for plant-derived food and feed products as the world population grows exponentially. Plants are also playing a role in filling our ever-increasing energy needs and these bio-energy crops are expected to provide a sustainable, CO<sub>2</sub>-neutral emission solution in the near future. Yet such crops will need to be compatible with food and feed agriculture production and must preserve Earth's ecosystems. So the question is: how can we face all of these challenges?

To meet our planet's needs, we need to improve and further develop sustainable methods for plant production by incorporating both biotechnology and sustainable agricultural practices. In this context, we must first establish a baseline understanding of different molecular and cellular mechanisms underlying plant development and response to stress, so we can then apply it to practical advances in plant production across the globe. Surprisingly, the biological networks underpinning plant yield are still poorly understood, particularly regarding the master regulator of cellular function: the nucleus.

The nucleus harbors the large majority of the plant's DNA, the linear sequence of which is the blueprint of every living organism. However, this is only the beginning: how this DNA is expressed and regulated depends on a variety of other interacting factors that play crucial roles in shaping its organization and function. With the sequencing of several plant genomes and recent advances in high-throughput technologies, plant nuclear biologists have been able to unveil many of the mechanisms underlying genome regulation.

For instance, epigenetic modifications, such as histone post-translational modifications and DNA methylation, directly impact gene expression and genome defense by regulating the organization and function of the genome. Importantly, while evolutionary processes take place at a timescale that does not allow plants to respond and adapt to climate-induced stress, we are starting to recognize that epigenetic mechanisms can confer phenotypic plasticity. Epigenetics enables a heritable control of

phenotypes that can change rapidly in response to environmental cues—sometimes over the course of just two to three generations. This epigenetic timescale of change has tremendous implications for how environmentally altered phenotypes are acquired and inherited at the organism and eventually at the population levels.

Another exciting recent discovery that came about through plant biology research is the previously unacknowledged role of noncoding small RNAs in gene expression. These small molecules have been increasingly recognized as players in the establishment of epigenetic modifications, as well as in genome defense and integrity. Noncoding small RNAs impact normal growth, development, and stress responses in diverse plant species, including staple crops such as rice and maize. Small noncoding RNAs are already playing key roles in plant biotechnology applications including directing the specific and enhanced expression of selected genes. These molecules are therefore of great interest in the context of bioengineering, and have enormous potential for enhancing crop productivity in a wide range of ecosystems. Yet, there is still a great deal left to learn about how small noncoding RNAs are integrated into plants' feedback loops, which direct epigenetic modifications throughout development and the stress response process.

Finally, genomes are dynamic structures as their functional properties are strongly determined by their spatial organization over time. Similarly, changes in higher order nuclear organization alter the functional properties of genomic regions. Various types of subcellular physical domains have been identified in the nucleus, the known nuclear bodies or subcompartments, and these structures are associated with transcription factors, RNA-processing proteins, and epigenetic regulators. Interestingly, these nuclear domains display different behaviors in response to the environment, yet it is still a matter of debate how nuclear organization functionally relates to plant biological processes.

The mechanisms and processes described above make it clear that a true understanding of genome function requires integrating the genomic sequence with what we are still discovering about how epigenetics, small noncoding RNAs, and dynamic nuclear organization modify genomes. It is the goal of this book to compile a series of landmark discussions on the recent advances in plant nuclear biology research and offer new perspectives into the functional relevance of the arrangement of genomes and nuclear processes that impact plant physiology and development. The following chapters will provide insights as to how genes are switched on/off and are tuned to specific expression levels, which will allow us to better predict plant phenotypes. Overall, a better understanding of the fundamentals of plant gene expression will aid in the more efficient design of numerous biotechnological applications and plant-breeding programs. This new knowledge will thus provide a foundation for solving both agricultural and environmental problems as well as developing practices that enable global sustainability. Lastly, plant biology is also relevant to human biology as several aspects of underlying mechanisms are conserved between both organisms. Understanding this shared biology will shed light on human diseases and could lead to better therapies for cancer and genetic diseases.

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