

Preface

Plant Epigenetics: From Genotype to Phenotype

The Last Unicellular Common Ancestor (LUCA) has existed more than 1 billion years ago. During that time, the plant and animal kingdoms have evolved separately and adopted a multicellular system, with sophisticated pathways of development and capability for perfect adaptation to the environment. Today, in the era of genomics it is known that many developmental processes of plants and animals are similar, although they have evolved independently. The carriers of the logic in these two major lineages are different and show a complicated network of ancient protein and nucleic acid domains, but at the same time a very high conservation and similarity of chromatin proteins and regulatory mechanisms is observed. This, however, does not exclude differences of structure and functions of chromatin that exist between plants and animals. They have evolved very efficient and flexible but different adaptation mechanisms to the local environment in order to ensure survival and reproduction. The specific differences connected to lineage-specific features may provide strong information on the general mechanisms underlying the complexity and regulatory and integratory role of chromatin in all eukaryotes. During a movement towards their final differentiated states, various changes occur in cells due to genetic and environmental factors. Resulted altered properties of the cells have been memorized after each cell division.

Recent technological advances allow genome-wide analysis of DNA and histone modifications, which affect their structures, and have the potential to reveal the regulation mechanisms in plants on the level above nucleotide sequence. Those chemical changes allow the manifestation of multiple phenotypes encoded in the same DNA sequence. In this way, chromatin modifications contribute to variation at multiple levels, ranging from the expression of individual genes, to the differentiation of cell types, to population-level phenotypic diversity. In other words, that is epigenetics.

Formally, the term epigenetics is a combination of two words ‘epigenesis’ and ‘genetics’ and has been coined 75 years ago (Brilliant Jubilee) in 1942 by Conrad H. Waddington. He proposed epigenetics as the branch of biology that studies the causal interaction genes and their products, which brings the phenotype into being, and proposed the concept of the epigenetic landscape as a metaphor for cell differentiation. Currently, epigenetics is interpreted as the study of mitotically and/or meiotically heritable changes in patterns of gene expression that occur without alterations in DNA sequence. Generally, epigenetic studies are focused on chemical modifications of chromatin and their roles in transcriptional silencing. Epigenetic modifications contribute to phenotypic variation at multiple levels, from gene regulation to development, stress response, and population level phenotypic diversity and evolution. A lot of epigenomic features have been comprehensively profiled in health and disease across cell types, tissues and individuals.

Plant development particularly depends on epigenetics. They integrate various environmental signals into different phenotypic or growth responses. Therefore, an understanding of mechanisms of how epigenetic modifications affect the expression of genotype into phenotype in plants is of prime interest.

There are a number of epigenetic phenomena discovered in plants: (i) paramutation which describes the heritable change in expression status of an allele upon its exposure to an allele with the same sequence but displays a different expression status, (ii) nucleolar dominance that is a selective silencing of the ribosomal RNA genes inherited from one progenitor of a genetic hybrid, (iii) imprinting which is characterized by selective expression of genes inherited from only the maternal or the paternal parent, (iv) vernalization which induces flowering in plants in response to cold, (v) RNA-mediated homology-dependent technologies that have important contributions for plant genetic engineering, (vi) RNA-mediated DNA methylation that leads to gene downregulation and (vii) RNA-mediated mRNA degradation or inactivation.

Nowadays, genome sequences for Arabidopsis, rice, poplar, maize and many other plants are known and thus facilitate genome-wide analyses of DNA methylation and histone modifications and their relationships to coding as well as short (miRNAs, siRNAs) and long noncoding RNAs, which can function as epigenetic marks of transcriptional gene silencing and also a defence against transposable elements and viruses. Thus, plants are good model systems and stay as first line of discoveries in the fields of epigenetics.

To deeply discuss and present the frontiers of plant epigenetics, we brought together a diverse group of experts from academia, who working both from the bottom (mechanism) up and top (phenotype) down. We believe that these complementary approaches enable high-impact science.

In the book, there are 26 chapters, which present the current state of epigenomic profiling, and how functional information can be indirectly inferred is discussed. New approaches that promise functional answers, collectively referred to as epigenome editing, are also described. The book highlights the latest important advances in our understanding of the functions of plant epigenomics or new technologies for the study of epigenomic marks and mechanisms in plants. Topics include the deposition or removal of chromatin modifications and histone variants,

the role of epigenetics in development and response to environmental signals, natural variation and ecology, and applications for epigenetics in crop improvement. The chapters in this book are variable in nature, ranging from the complex regulation of stress and heterosis to the precise mechanisms of DNA and histone modifications, providing breakthroughs in the explanation of complex phenotypic phenomena. We hope that the chapters in this book present outstanding significance and will capture broad interest.

Berlin
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January 2017

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Plant Epigenetics

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2017, XI, 536 p. 53 illus., 48 illus. in color., Hardcover

ISBN: 978-3-319-55519-5