

# Preface

Transposable elements (TEs) are ubiquitous mobile DNA sequences found in both prokaryotic and eukaryotic genomes. They are able to insert at different positions of the genome, either by excising from one position and reinserting into another or by replicating into daughter copies. TEs are particularly abundant in plant genomes, where they can represent over 80 % of the bulk of large cereal genomes. Their discovery by B. McClintock, and the subsequent introduction of the notion of genome fluidity, was a major shift in our concepts on heredity. TEs can dramatically modify the structure of host genomes, affect genome sizes and generate genetic variation, not only by transposition but also by providing the raw material for genomic rearrangements due to their repetitive nature. Until recently, and in spite of B. Mc Clintock's seminal concept of "Controlling Elements," the impact of TEs on host genome function was merely regarded as circumstantial. A rather different representation has been brought to light in the last decade, which strongly argues that TEs may also act as pivotal factors in generating genic variation and modulating cellular gene expression. This book is intended at presenting the latest advances on the importance of TEs and on their impact on plant genome dynamics and function.

The TE research scene has recently seen major advances, with new tools such as Next Generation Sequencing (NGS) technologies opening tremendous possibilities for rapid global analyses of genomes at reduced costs. This has led to an exponential increase in the amount of TE-related data and to a deeper knowledge of their impact on host genomes. As a consequence, all plant researchers engaged in genomic studies are more or less unwillingly bumping into this wealth of TEs and are now realizing that these TEs cannot be discarded as annoying junk sequences anymore. TEs are encountered in both genomic and transcriptomic data, and in a tremendous variety of elements, including highly defective and deleted versions sometimes mobilized at surprisingly high levels via related copies, making their classification a difficult task. There is therefore a need for researchers to find guidelines to recognize and classify TEs and better understand their importance and potential impact.

This book is intended both for scientists familiar with the field and for nonspecialists. It is organized in 14 chapters written by recognized researchers and is centered, on one hand on how to recognize and study plant TEs, notably using NGS technologies, and, on the other hand, on how TEs impact plant genome structure and genome function, with a few final examples of exciting TE-mediated phenotypic impacts. The first few chapters cover important aspects of what are TEs and how they can be identified and analyzed. Chapter 1 covers recent developments in TE classification and annotation and tackles the complex issue of defining consistent guidelines, while Chap. 2 summarizes and compares computational tools available for TE identification and provides a road map for efficient annotation. Chapter 3 then explores how NGS technologies can be used to study TE-mediated genome size variations and evolutionary patterns that shape the TE compartment, and Chap. 4 describes the recent development of NGS technologies to monitor TE mobility. The three following chapters provide further insights on some of the best known plant TEs. Chapter 5 describes the predominant type of TEs found in plant genomes, the LTR retrotransposons, and the subtle functional interplay between their autonomous and nonautonomous versions, while Chap. 6 explores the intriguing possibility of the existence of plant endogenous retroviruses, and Chap. 7 updates our knowledge on the highly abundant miniature elements, MITEs, and their impact on plant genomes. Chapter 8 summarizes the current state of affairs for epigenetic mechanisms developed by plant genomes to control TE mobility and highlights the plasticity of these mechanisms. The two following chapters address the important issue of TEs in polyploid contexts: Chap. 9 summarizes current knowledge on TE involvement in the drastic structural and functional changes resulting from allopolyploidy, a major speciation process in the plant kingdom, while Chap. 10 compares the nature and evolution of TEs between polyploid sugarcane and other grass genomes. The four following chapters are dedicated to several striking mechanisms by which TEs have been exapted by host genomes to distil invaluable tools for modifying genome function. Chapter 11 describes how a fascinating type of TEs, Helitrons, can capture gene fragments and describes how such process can lead to new regulatory functions, and Chap. 12 reviews in detail how plant TE coding sequences have been frequently domesticated into functional cellular genes. Chapter 13 assesses current knowledge on the ubiquitous process of SINE exaptation for the production of regulatory RNAs, and Chap. 14 updates current data on plant LTR retrotransposon stress response and examines the possibility that LTRs could play a role in modulating host gene expression. Finally, the last two chapters present particularly striking examples of TE-associated phenotypic changes. Chapter 15 illustrates the role of the Rider LTR retrotransposon in several morphological and physiological changes in tomato, while Chap. 16 describes how small RNAs produced by a non-LTR retrotransposon are involved in the desiccation tolerance of resurrection plants.

The chapters were conceived and written autonomously, so that they can be read independently, even though this may have resulted in a few redundancies. Many other topics could have been covered, and many other beautiful examples of TE impact on plant genomes could have been exposed, however it was impossible to assemble all of the chapters that we would have liked to have in this volume, due to

lack of space. Nevertheless, we feel that the 14 chapters presented in this book provide altogether a global overview of the most interesting current advances in the field of plant TE studies, while providing a useful reference vademecum volume for all (highly welcomed!) newcomers to the field. We hope that they will feel the urge to better understand what are these repetitive sequences that compose more than half of their data and that, after consulting this book, they will become convinced that Transposable Elements are certainly not “junk,” but may actually be by far the most interesting and fun part of their data!

Finally, we wish to heartily thank all authors of this volume, that all have made substantial efforts to share our common passion with you and to provide excellent contributions. We also thank Stefan Hohmann for providing us the opportunity to compile this volume, the staff at Springer Verlag for their continuous help and support to make this book possible, and Tom Bureau for correcting this text.

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