

An Overview of Transposable Elements and their Impact on some Insect Host Genomes

Wiem BEN AMARA*

PhD in Genetics and Molecular Biology, Research Laboratory of Biochemistry and Biotechnology, Department of Biology, Faculty of Sciences of Tunis, University of Tunis El Manar, Tunisia

*Corresponding Author: Wiem BEN AMARA, PhD in Genetics and Molecular Biology, Research Laboratory of Biochemistry and Biotechnology, Department of Biology, Faculty of Sciences of Tunis, University of Tunis El Manar, Tunisia.

The history of Transposable elements (TEs) has started in 1951 with the discovery of the Ac (Activator) and Ds (Dissociation) elements by Barbara McClintock, that she considered to be at the origin of mutations leading to genetic instabilities in the color of corn kernels [1]. These discoveries, for which McClintock was awarded the Nobel Prize in 1983, revolutionized the notion of genome stability to demonstrate that it is dynamic and fluid [2]. Thus, transposable elements are defined as repeated DNA sequences dispersed in the genome that are capable of moving from one site to another and multiplying in an autonomous or non-autonomous way. These mobile DNA sequences have several impacts on the genomes they invade and are key players in their evolution and diversity [3-5].

Eukaryotic TEs are divided into 2 major classes according to their transposition mechanism [6]: Class I elements or retrotransposons move via an RNA intermediate according to the "copyand-paste" model, whereas Class II elements or DNA transposons transpose via a DNA intermediate according to the "cut-and-paste" model.

TEs are at the origin of different chromosomal rearrangements that they induce as a result of ectopic recombination taking place between homologous regions of copies. Various studies have been carried out on TEs-induced chromosomal rearrangements and have demonstrated their implication in translocation, duplication and deletion phenomena [7-9]. These rearrangements will be at the source, not only of the change in the architecture of genomes but also of their size evolution.

TEs constitute innovative sequences by bringing to the host genome new genetic information corresponding to regulatory regions such as promoters and splicing sites. As so-called "control elements" [10,11], TEs can contribute to the regulation of gene exReceived: February 27, 2023 Published: April 01, 2023 © All rights are reserved by Wiem BEN AMARA.

pression according to their insertion sites. Indeed, insertion near genes can influence their expression through their own regulatory regions and thus this gene will be expressed under the control of the promoter of the TEs near it.

In *Drosophila simulans*, variations in emitted courtship songs have been shown to be due to an intronic insertion of a TE into a gene (slo) encoding an ion chain thus altering its splicing [12].

The rearrangements and modifications caused by TEs are not always deleterious. Indeed, they can be recruited or domesticated by the host genome to perform biological functions that are vital to the cell. Domestication involves TEs in different biological functions and processes such as immunology [13], regulation of apoptosis, cell cycle control as well as in mammalian reproduction [14-16].

Chromosomal rearrangements and changes in genome architecture created by TEs could be the source of differentiation between species and the creation of biological barriers[17]. For example, in *Drosophila*, hybrid dysgenesis creates barriers that can lead to the speciation [18].

In insects, some TEs have been found to be fixed in the genome species, in particular in *Drosophila melanogaster* [19] and are therefore used as genetic markers to study the polymorphism of their insertion sites within the different populations of a given species or between two neighbouring species in order to estimate the date of their speciation or to predict their evolutionary history. Studies conducted by Boulesteix, Simard [20] have shown that the insertion polymorphism of some TEs, notably the non-LTRs, differs between the two molecular forms M and S forms of the mosquito *Anopheles gambiae* (Diptera: Culicidae). In addition, the polymor-



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phism of the insertion sites of the SINE-type element is used as a genetic marker of choice to better characterize the divergence of the X chromosome between populations of these two molecular forms in *Anopheles* [21]. These TEs also play adaptive roles for insect hosts during their evolution, especially in the Drosophilidae [22].

Otherwise, the ability of transposable elements to mobilize has allowed them to be used as biotechnology tools for transgenesis and mutagenesis to control insect pests or disease vectors. These technologies aim either to genetically modify the insects in question by blocking the genes involved in virulence or in the development of pathogenicity, or to suppress an entire population of insects of insects by generating sterile males or females carrying dominant alleles of lethality [23]. P-elements are the first vectors used to transform embryonic or germline cells in Drosophilidae [24]. In non Drosophilidae, three major elements have been used for transgenesis.

- *PiggyBac* elements are the most widely used vectors for transformation in insects of various orders [25] including Coleoptera and Diptera [26,27].
- The mariner-like *Minos* element that has been used to transform some species of Tephritidae including the olive fly *Bactrocera oleae* [28] and the corn rootworm *Diabrotica virgifera* (Coleoptera: Chrysomelidae) [29].
- The Hermes element of the *hAT* superfamily from the housefly *Musca domestica* [30].

It should be noted that the choice of vector depends largely on the genome's repertoire of transposable elements and the activity of the elements of the families in question.

The TEs used as a vector to transform host cells must not have homologous copies same group in the genome in question. Therefore, the annotation of TEs and the study of the dynamics of the different populations of these elements is a crucial step for the analyses that follow. This is facilitated by the accessibility of sequenced genomes and the development of bioinformatics tools. More recently, many genomes have been used to annotate TEs in economically important insect pests like Hessian fly [31], the cotton bollworm [32] and whitefly [33] to localise the TEs insertion sites around virulence or insecticide resistance genes. TEs are mining in large number of insect genomes and have been annotated using a big variety of bioinformatics tools and methods. Nevertheless further analyses should follow these annotations and results of annotations should be treated with caution regarding evolution and adaptations of host species for more reliability and accuracy.

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