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Review on Role of Mobile Element in Crop Genetic Variability

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Abstract: Transposable elements make up a significant portion of plant genomes and are thought to play a key role in genomic reorganization and functional alterations. Transposable elements are known to cause a wide range of gene expression and function modifications in plants. This has led to the hypothesis that transposable element activity aided adaptive plant evolution. Transposons are controlled by a collection of mechanisms that identify and epigenetically quiet them, despite the fact that they are potentially very mutagenic. Two basic properties are shared by all transposable elements. The first is their ability to travel about the genome, which is why they're called mobile DNAs or transposable elements. The second is their ability to use this transposition to increase their copy number inside the genome, giving them a selective function that can make them selfish or parasitic DNAs. The distribution of transposable elements in the repeat-rich genomes of barley and bread wheat can be divided into three compartments (distal, interstitial, and proximal) that differ in age and type, gene density and function, and recombination frequency, implying that transposable elements are distributed differently in the repeat-rich genomes of barley and bread wheat. Transposable elements are thought to play a key role in genome organization and evolution. TEs have the potential to alter genomic structure and gene expression. Recombination between two TEs can result in chromosomal rearrangements or deletions of the interleaving genomic sequence. Transposition is regulated by the cellular processes that produce active transposase. Transposition regulation is unique to each element and encompasses transcription, differential splicing, translation, and protein-protein interaction regulation.

Keywords: DNA Transposon, Retrotransposon, Transposable Element

1. Introduction

Genetic entities capable of insertion from one region in a genome to another as a separate integrated unit are known as transposable elements [1]. TEs make up a large portion of eukaryotic genomes, particularly in plants, and can be used as a site for uneven and illegitimate recombination, resulting in changes such as deletions, insertions, frameshifts, inversions, translocations, and duplications [2]. As a result, it plays a significant role in genome structural patterning via transposition and/or recombination [3]. In 1983, Barbara McClintock was awarded the Nobel Prize in Physiology or Medicine for her work on maize genetics and cytogenetics, which led to the discovery of transposons [4]. Because TEs account for a high proportion of genome volume, it's assumed that they've had a role in genome size variations during speciation and evolution, as seen in plants like Drosophila and primates [5-7].

Transposable element activity can disrupt genes, mediate genomic rearrangements that result in genetic material translocation, duplication, or deletion, or influence proximal gene expression, all of which can have a substantial impact on genome structure and function [8, 9]. Because excessive transposable element activity is generally detrimental to an organism's fitness, genome defense mechanisms like as DNA methylation are used to suppress their activity [10, 11].

A considerable number of repetitive sequences may be found in most eukaryotic genomes. Waring and Britten used association studies to describe this phenomenon half a century ago [12, 13]. The majority of these repetitive sequences were discovered to have created in mobile

elements [14] though the proportion of the genome that is repetitive varies greatly between organisms, it ranges from 12% in Caenorhabditis elegans to 15% to 50% in mammals and more than 80% in some plants [15]. Given their huge contributions to genome sequences, it's not surprising that TEs have a significant impact on genome organization and evolution. Despite substantial progress in understanding the significance of TEs in a host genome, we are still far from having a complete picture of the delicate evolutionary interplay between invaders and the host genome. They also provide a number of challenges to the genomic community, including as detection and classification, genome assembly and annotation, genome comparisons, and mapping genomic variation. In general, transposable elements play a crucial role in genomic evolution.

2. Literature Review

2.1. Origin of Transposable Elements

All of the TE classes have a long ancestry, with obvious prokaryotic beginnings and a history of vertical descent [16]. Many bacterial TEs, on the other hand, are frequently transmitted horizontally, and a few TE families are transferred horizontally in some eukaryotic lineages. Plants have also reached similar conclusions. Due to high rates of DNA loss, distinct TE families can readily and frequently become extinct in specific lineages [17]. The widespread presence of transposable elements in all living creatures shows that these mobile DNAs have a long history. Transposable elements, on the other hand, are particularly likely candidates for horizontal transmission due to their mobility. They are frequently present on plasmids in bacteria and are triggered by the process of mating and concurrent DNA replication [18]. Retroviruses can easily spread among members of a species as well as between species. As a result, neither the time when these elements arose nor the particular procedures by which they arose are known. DNA transposable elements and retro elements, on the other hand, appear to be derivatives of separate evolutionary creations. The concept of selfish or parasitic DNA [19] suggests that the ability to amplify within a genome would be selected for any sequence and would give rise to such elements, possibly through multiple independent origins, as long as the host's fitness was not significantly harmed. Many additional plant species have highly analogous elements (with extremely similar TIRs and encoded transposase), as does the Ac/Ds maize family, as does the Spm/dspm (En/I) family [20]. Barbara McClintock discovered transposable elements while conducting maize studies in 1944. She dubbed them controlling components since they appeared to alter phenotypic features. The genetic community, on the other hand, was less than enthused about her discovery. "Genetic elements have been discovered in higher organisms that appear to be easily transferred from one place in the genome to another." McClintock described such elements in maize, identifying them by their regulatory functions. After another discovery, an underappreciated finding was brought back to life.

2.2. Evolution of Mobile Elements

All eukaryotic genomes contain transposable elements, which influence gene and genome evolution, structural rearrangement, and transcriptional regulation [21-23]. In many eukaryotes, transposable elements play a crucial role in genome evolution [24]. Beginning in the early twentieth century, genetic studies in eukaryotes like maize and Drosophila revealed mutations with transposable element characteristics. These and other Mutator transposable elements (TEs) are among the most mutagenic transposons known, due to their exceptionally high rates of transposition and proclivity for insertion at or near genes. The original Robertson's Mutator element (MuDR, 'Mutator Don Robertson') was discovered in maize, with Mutator lines having mutation frequencies 50 times greater than the natural rate of mutation [25]. The mutator system has a long history of application in the field of genetic engineering for both forward and reverse genetic screening, and it has impacted our understanding of host-transposon co-evolutionary interactions as a result of these qualities.

2.3. Classification of Mobile Elements

All transposable elements have two basic qualities in common. The first is their ability to move about the genome, which is why they're termed transposable elements or mobile DNAs. Second, they can employ this transposition to expand their copy number inside the genome, providing a selection role that can make them selfish or parasitic DNAs [26]. Based on their chromosomal integration technique, which reflects the protein-coding capabilities and organizational structure of each class and subclass of elements eukaryotic TEs are split into two basic groupings. Retrotransposons, also known as Class I elements, transpose by way of an RNA intermediate, which must be reverse transcribed before being incorporated into the genome. A Class I element (clade LINE-1) consists of a 5'-UTR with internal promoter activity and two Open Reading Frames (ORFs). ORF1 encodes a protein that binds to nucleic acids, whereas ORF2 produces a protein that lacks Long Terminal Repeats (LTR) and ends in a poly (A) [27].

To transpose Class II elements, a DNA intermediate is used [28]. Class II DNA elements are found in most eukaryotes, and despite their conservative transposition method, certain plants have been able to acquire significant copy numbers. In a Class II element, a transposase gene is flanked by Terminal Inverted Repeats (TIRs). The majority of the repetitive fraction of eukaryotic genomes is made up of Class II elements, which are present in multiple copies (commonly referred to as a TE family) and encode the machinery to aid their own transposition, usually in the form of a transposase (TPase) encoded by a single gene [29]. Wicker and colleagues developed a "cut and paste" transposition technique for Class II.

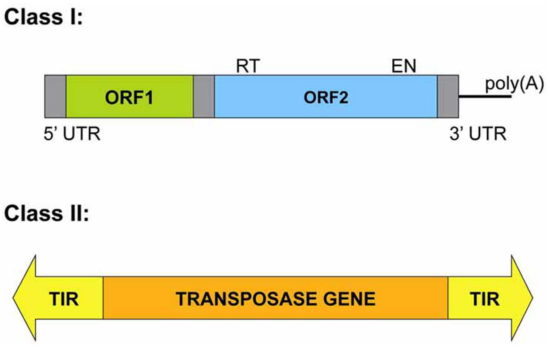

Figure 1. *Classes of Transposable Elements (TEs).*

2.4. Transposable Elements in Plants

Plant genomes, like those of pathogenic fungi and other filamentous pathogens, vary greatly in size and repeat content (transposable elements, simple and tandem repeats), with transposable elements accounting for 20% of the A. thaliana genome and up to 80% in cereals like wheat and maize [30]. In the repeat-rich genomes of barley and bread wheat, the distribution of transposable elements can be divided into three compartments (distal, interstitial, and proximal) based on age and type, gene density and function, and recombination frequency, implying that transposable elements play important roles in genome organization and evolution [31-33]. By comparing a subset of the recently sequenced 1135 A. thaliana genomes, researchers detected thousands of transposable element insertion and deletion variations [34, 35]. As it approaches the centromeres, transposable element density increases at peri centromeric regions, but gene density drops, a behavior seen in other plants such as wild rice [36].

In addition to genome expansion, transposable elements have been related to the majority of structural variations in the Arabidopsis population [37]. The researchers found 200 inversions in two rice species (wild and Asian rice), the majority of which are flanked by transposable elements. Because of their prevalence in plant genomes, transposable elements are usually regarded as important contributors to the creation of structural alterations such as genomic rearrangements, insertions, and deletions.

2.5. Transposable Elements Arrangement in Plant Genome

Because of the varied levels and degrees of specificity/bias for insertion or accumulation of distinct transposable elements, a plant genome can have many different configurations of components. Furthermore, different parts of a genome are likely to be arranged in quite diverse ways. Centrometric heterochromatin, for example, contains few if any genes but a large number of different types of repetitive DNA. The majority of these repetitive DNAs are expected to be mobile and will significantly outnumber Centro metric repeats [38]. According to one study, these TE are generally arranged as blocks of nested LTR-trotransposons intermixed with genic blocks of one to a few genes each in maize [39]. Only two other significant parts of complex plant genomes have been sequenced, and both sections were notable for their unusually high gene density.

2.6. Mechanism of Transposition

According to crystal structure comparisons, the catalytic domains of all three proteins are quite similar, bringing together the two aspartate and glutamate residues separated by 50 to 70 (D-D) and 35 (D-E) residues in the basic structure. This catalytic region is highly conserved across many integrases and is most likely responsible for the transphosphorylation essential for DNA breaking and strand transfer during the transposition process [40]. This method is divided into two parts. The ends of the transposable element are first cleaved at a specified place in the DNA, and then the complex of transposase-element ends is transported to a DNA target, where the strand transfer is accomplished by covalently attaching the element's 30 ends to the target DNA. The reaction's staggered phosphates produce a strand gap that varies in size depending on the element. This gap is eventually closed, most likely by host-dependent repair processes, resulting in the characteristic direct duplications seen at all transposable element terminals.

2.6.1. DNA Transposons

They are the most prevalent transposable elements in bacteria, and numerous families have been reported in fungi, ciliates, plants, worms, insects, fish, and humans [41]. The presence of two inverted repetitions flanking a DNA sequence encoding an enzyme known as transposase characterizes this family of transposable elements. This protein is involved in the "cut-and-paste" processing of DNA at the donor and target locations. In most cases, Transposase is the only prerequisite for transposition. As a result, transposition is frequently restricted to the regulation of this protein's expression.

2.6.2. Retrotransposons

Reverse transcriptase is encoded by retrotransposons, which are mobile components. Reverse transcription of this RNA template occurs in the cytoplasm, where a retro element-specific tRNA primes first-strand DNA synthesis and an oligopurine RNA molecule primes second-strand synthesis. Based on structural properties, these elements can be separated into long terminal repeat (LTR)-containing and poly (A)-containing transposons. LTR retrotransposons include two open reading frames (ORFs) containing gag (capsid proteins) and pol (protease, integrase, reverse transcriptase, and RNase H) proteins, and are identical to the pro viral form of vertebrate retroviruses. Some LTR retrotransposons, such as Drosophila's gypsy and tom, encode a third ORF that has been demonstrated to be physically and functionally comparable to vertebrate retrovirus envelope proteins. Retro elements of the poly (A) type lack LTRs and have an A-rich region at the 30 end. They normally have two ORFs, one for gag and one for pol proteins. The mechanism by which they are mobilized and integrated into the genome of their host, the nature of retro

element- and host-encoded factors that regulate this process, and the details of the relationship between transposons and their hosts that allows their reproduction and persistence in the genomes of all eukaryotes are all important questions in the biology of these elements.

2.7. Regulation and Control of Transposition

Transposition can be harmful to both the host and the transposon, whose replication and spread are dependent on the host's survival. As a result, finding techniques to reduce the impact of transposition on host fitness benefits both the host and the transposon [42, 43]. Transposition is regulated by the cellular processes that produce active transposase. Transposition is regulated at the transcriptional, differential splicing, translational, and protein-protein interaction levels, and is unique to each element.

The transposase can operate as a transposition inhibitor by reducing transposon activity when it reaches a certain concentration. Although the nature of this process is unknown, it has been detected in Tc1/mariner elements [44, 45]. It has been proposed that transposase monomers produce inactive or less active oligomers, lowering the transposition process' activity. The synthesis of transposase increases as the copy number of these elements grows in the host genome, and the mobilization of the transposon is inhibited by OPI.

2.8. Impact of Transposons on Plant Genome Structure

Transposons, in addition to their local impact on genes, can have a considerable impact on genome structure and gene expression on a global scale. Chromosome rearrangements or deletions of the interleaving genomic sequence can occur when two TEs recombine. Transposons, in addition to their local impact on genes, can have a considerable impact on genome structure and gene expression on a global scale [46]. Chromosome rearrangements or deletions of the interleaving genomic sequence can occur when two TEs recombine [47]. TE density is generally higher around centromeres and telomeres, despite the fact that some TEs preferentially insert in gene-rich chromosomal arms [48]. This is the result of several mechanisms interacting. Some TEs first insert into heterochromatin [48]. Gypsy-like retrotransposons do this most of the time, although most Copia-like retrotransposons and most DNA TEs tend to prefer euchromatin. Second, selection favors harmful insertions, concentrating TE insertions in gene-poor areas like as heterochromatic repetitive repeats. Finally, the rate of TE removal by intra- or inter-element recombination is reduced in the heterochromatic repetitive sections due to their lower recombination rate [49].

3. Conclusion

Transposable elements contribute to genome and transcriptome diversity by mediating structural variation and causing gene expression alterations as a result of changes in the local chromatin landscape, allowing for environmental adaptability. Genome and transcriptome diversity are governed by transposable elements, which also mediate the fast evolution of plant immune system components. As a result, the vast majority of studies revealing transposable elements' role have been descriptive in nature, demonstrating naturally occurring connections between transposable element occurrences and genome, transcriptome, and phenotypic variants.

TEs give more evidence that TEs are an endogenous system that provides a degree of evaluability, that the history of plant evolution would be considerably different without them, and that TE activity is responsible for a significant percentage of the genetic variety required for plant adaptation.

The widespread presence of transposable elements in all living creatures shows that these mobile DNAs have a long history. TEs are commonly present on plasmids in bacteria and are triggered by mating and concurrent DNA replication. The concept of parasite or selfish DNA suggests that the ability to amplify inside a genome would be selected for any sequence and would give rise to such elements, maybe through several independent origins, as long as this did not significantly affect the host's fitness.

DNA transposons and retrotransposons are the processes through which TEs transpose. DNA transposons are defined by the presence of two inverted repetitions flanking a DNA sequence encoding the transposase enzyme. At the donor and target sites, this protein is involved in the "cut-and-paste" processing of DNA. Reverse transcriptase is encoded by retrotransposons, which are mobile components.

References

[1] Kleckner, N (1977). Translocatable elements in prokaryotes. Cell 11: II.

[2] Lonnig WE, Saedler H (2002). Chromosome rearrangements and transposable elements. Annual Review of Genetics 36: 389–410.

[3] Vitte C, Panaud O. 2005. LTR retrotransposons and flowering plant genome size: emergence of the increase / decrease model. Cytogenetic and Genome Research 110: 91–107.

[4] McClintock, B (1950). The origin and behavior of mutable loci in maize. Proc. Natl. Acad. Sci. USA 36: 344–355. McClintock, B. 1984. The significance of responses of the genome to challenge. Science 226: 792–801.

[5] Sheen, F. M.; Levis, R. W (1994). Transposition of the LINE-like retrotransposon TART to Drosophila chromosome termini. *Proc. Natl. Acad. Sci. USA, 91* (26), 12510-12514.

[6] Frazer, K. A.; Chen, X.; Hinds, D. A.; Pant, P. V.; Patil, N.; Cox, D. R. Genomic DNA insertions and deletions occur frequently between humans and nonhuman primates. *Genome Res.,* 2003, *13* (3), 341-346.

[7] Locke, D. P.; Segraves, R.; Carbone, L.; Archidiacono, N.; Albertson, D. G.; Pinkel, D.; Eichler, E. E. (2003). Large-scale variation among human and great ape genomes determined by array comparative genomic hybridization. *Genome Res*, *13* (3), 347-357.

[8] Feschotte, C. and Pritham, E. J (2007) DNA transposons and he evolution of eukaryotic genomes. Annu. Rev. Genet. 41, 331–368 Fedoroff, N. V (2012) Transposable elements, epigenetics, and genome evolution. Science 338, 758–767.

[9] Lisch, D (2013). How important are transposons for plant evolution? Nat. Rev. Genet. 14: 49–61. doi: 10.1038/nrg3374.

[10] Feng, S. *et al*. (2010) Conservation and divergence of methylation patterning in plants and animals. Proc. Natl. Acad. Sci. U. S. A. 107, 8689–8694 5.

[11] Zemach, A. *et al*. (2010). Genome-wide evolutionary analysis of eukaryotic DNA methylation. Science 328, 916–919.

[12] Makalowski W (2001). The human genome structure and organization. Acta Biochim Pol 48 (3): 587–598 Pub Med Google Scholar.

[13] Britten RJ, Kohne DE (1968). Repeated sequences in DNA. Hundreds of thousands of copies of DNA sequences have been incorporated into the genomes of higher organisms. Science 161 (841): 529–540 Pub Med Cross Ref Google Scholar.

[14] Waring M, Britten RJ (1966). Nucleotide sequence repetition - a rapidly re associating fraction of mouse DNA. Science 154 (3750): 791–794 Pub Med Cross Ref Google Scholar.

[15] Consortium, C. e. S. Genome sequence of the nematode C. elegans: a platform for investigating biology. *Science,* 1998, *282* (5396), 2012-2018.

[16] SanMiguel, P.; Gaut, B. S.; Tikhonov, A.; Nakajima, Y.; Bennetzen, J. L.(1998). The paleontology of intergene retrotransposons of maize. *Nat. Genet*, *20* (1), 43-45.

[17] Xiong Y, Eickbush TH (1990). Origin and evolution of retro elements based upon their reversetranscriptase sequences. *EMBO J.* 9: 3353–62.

[18] Wicker T, Keller B (2007). Genome-wide comparative analysis of *copia* retrotransposons in Triticeae.

[19] Kim H-Y, Schiefelbein JW, Raboy V, Furtek DB, Nelson OE Jr (1987). RNA splicing permits expression of a maize gene with a defective *Suppressor-mutator* transposable element insertion in an exon. Proc Natl Acad Sci USA 84: 5863–5867.

[20] Doolittle WF, Sapienza C (1980). Selfish genes, the phenotype paradigm and genome evolution. Nature 284: 601–603.

[21] Hehl R, Nacken W, Krause A, Saedler H, Sommer H (1991). Structural analysis of *Tam*3, a transposable element from *Antirrhinum majus*, reveals homologies to the *Ac* element from maize. Plant Mol Biol 16: 369–371.

[22] Bennetzen, J. L (2000). Transposable element contributions to plant gene and genome evolution. Plant Mol. Biol. 42: 251–269. doi: 10.1023/A:1006344508454.

[23] Bucher, E., J. Reindeers, and M. Mirouze (2012). Epigenetic control of transposon transcription and mobility in *Arabidopsis*. Curr. Opin. Plant Biol. 15: 503–510. doi: 10.1016/j.pbi.2012.08.006.

[24] Lisch D. Mutator and MULE Transposons. Microbiol Spectr. 2015; 3: MDNA3– 0032.

[25] Fedoroff, N. V (2012) Transposable elements, epigenetics, and genome evolution. Science 338, 758 767.

[26] Walbot V (1991). The Mutator transposable element family of maize. Genet Eng (N Y).13: 1-37. PMID: 1369337.

[27] Orgel LE, Crick FHC: Selfish DNA (1980). The ultimate parasite. Nature 284: 604–607.

[28] Goodier, J. L.; Kazazian, H. H., Jr (2008). Retrotransposons revisited: the restraint and rehabilitation of parasites. *Cell,* 2008, *135* (1), 23-35.

[29] Finnegan DJ (1989). Eukaryotic transposable elements and genome evolution. Trends Genet 5: 103–107.

[30] Schnable, P. S. et al. (2009). The B73 maize genome: complexity, diversity, and dynamics. Science 326, 1112–1115.

[31] Daron, J. et al. (2014) Organization and evolution of transposable elements along the bread wheat chromosome 3B. Genome Biol. 15, 546.

[32] Choulet, F. et al. (2014). Structural and functional partitioning of bread wheat chromosome 3B. Science 345, 1249721–1249721.

[33] Mascher, M. *et al*. (2017). A chromosome conformation capture ordered sequence of the barley genome. Nature 544, 427–433.

[34] Quadrana, L. *et al*. (2016). The Arabidopsis thaliana mobile and its impact at the species level. Elife 5, 6919. Rice, and *Arabidopsis* reveals conserved ancient evolutionary lineages and distinct dynamics of individual *copia* families. *Genome Res.* 17: 107.

[35] Stuart, T. et al. (2016). Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. Elife 5, e60.

[36] Chen, J. et al. (2013). Whole-genome sequencing of Oryza brachyantha reveals mechanisms underlying Oryza genome evolution. Nat. Commun. 4, 1595.

[37] Kawakatsu, T. *et al*. (2016) Epigenomic diversity in a global collection of Arabidopsis thaliana accessions. Cell 166, 492–505.

[38] Jiang J, Nasuda S, Dong F, Scherrer CW, Woo S-S, Wing RA, Gill BS, Ward DC (1996). A conserved repetitive DNA element located in the centromeres of cereal chromosomes. Proc Natl Acad Sci USA 93: +14210–14213.

[39] SanMiguel P, Tikhonov A, Jin YK, Motchoulskaia N, Zakharov D, Melake-Berhan A, Springer PS, Edwards KJ, Lee M, Avramova Z, Bennetzen, JL (1996). Nested retrotransposons in the intergenic regions of the maize genome. Science 274: 765–768.

[40] Doak TG, Doerder FP, Jahn CG, Herrick AG (1994). A proposed superfamily of transposase genes: transposon-like elements in ciliated protozoa and a common “D35E” motif. *Proc. Natl. Acad. Sci. USA* 91: 942–46.

[41] Berg DE, Howe MM, eds (1989). *Mobile DNA*. Washington, DC: Am. Soc. Microbiol.

[42] Kleckner, N (1981). Transposable elements in prokaryotes. Annu. Rev. Genet. 15: 341.

[43] Vos JC, Baere ID, Plasterk HA. 1996. Transposase is the only nematode protein required for in vitro transposition of *Tc1*. *Genes Dev.* 10: 755–61.

[44] Lampe, D. J.; Grant, T. E.; Robertson, H. M (1998). Factors affecting transposition of the Himar1 mariner transposon *in vitro*. *Genetics, 149* (1), 179-187.

[45] Lohe, A. R.; Moriyama, E. N.; Lidholm, D. A.; Hartl, D. L (1995). Horizontal transmission, vertical inactivation, and stochastic loss of mariner-like transposable elements. *Mol. Biol. Evol*, *12* (1), 62-72.

[46] Weil CF, Wessler SR (1993). Molecular evidence that chromosome breakage by Ds elements is caused by aberrant transposition. The Plant Cell 5: 515–522.

[47] Hughes AL, Friedman R, Ekollu V, Rose JR (2003). Non-random association of transposable elements with duplicated genomic blocks in Arabidopsis thaliana. Molecular Phylogenetics and Evolution 29: 410–416.

[48] Contreras B, Vives C, Castells R, Casacuberta JM (2015). The impact of transposable elements in the evolution of plant genomes: from selfish elements to key players. In: Pontarotti P, ed. Evolutionary biology: biodiversification from genotype to phenotype. Cham: Springer International Publishing, 93–105.

[49] Zamudio N, Barau J, Teissandier A, *et al*. (2015). DNA methylation restrains transposons from adopting a chromatin signature permissive for meiotic recombination. Genes and Development 29: 1256–1270.