

A triptych of the evolution of plant transposable elements

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Transposable elements (TEs) constitute the majority of angiosperm DNA, but the processes that govern their accumulation remain mysterious. Here we discuss the three major forces that govern the accumulation of TEs, corresponding to the three panels of a triptych. The first force, transposition, creates new copies of TEs, but is regulated by both host- and TE-specific mechanisms. The second force, deletion of TE DNA, is capable of removing vast swaths of genomic regions via recombination processes, but we still have very little insight into how deletion varies across species and even among TE types. Finally, we focus on the often-ignored third panel of our triptych – the population processes that determine the ultimate evolutionary fate of TE insertions.

Transposable elements constitute the majority of plant genomic DNA

Angiosperm genomes vary over 1000-fold in size, and this variation correlates strongly with transposable element (TE) content (Figure 1). For plant species with relatively small genomes, like *Brachypodium distachyon* and *Arabidopsis* spp., DNA derived from TEs usually constitutes 20–30% of the genome [1,2]. Species with larger genomes have commensurately larger proportions of TE-derived DNA (Figure 1), including > 85% of the genomes of maize (*Zea mays* sp. *mays*) and barley (*Hordeum vulgare*) [3,4]. When one considers that the average size of a diploid angiosperm genome is ~6400 Mb (<http://data.kew.org/cva/kew/>) and that the larger genomes in Figure 1 are more typical of higher plants, the surprising conclusion is that most extant angiosperm DNA is derived from TEs.

Recent comparative genomic studies have highlighted the rapidity with which genome size can change due to TE activity. For example, maize, *Gossypium* spp., and a relative of rice (*Oryza australiensis*) have at least doubled in genome size within the last ~5 million years due to the proliferation of TEs [5–7]. The process can be so rapid as to be detectable within species; the two sequenced maize genomes differ in size by 22%, with 90% of this difference due to the accumulation of repetitive elements [8]. Differences in genome size appear to be largely attributable to class I TEs [5–7], which are retroelements that ‘copy and paste’ through an RNA intermediate [9]. The large contribution of class I elements is not surprising, because retroelements constitute ~90% of the TE fraction in

species like maize, *Arabidopsis thaliana*, and rice [10,11]. Nonetheless, class II elements, which proliferate via a ‘cut and paste’ mechanism [9], also contribute to differences in genome size [12].

Given the rapidity by which TEs can differentiate genomes within and between species, the study of TE dynamics is critical for understanding the evolution of plant genome size, structure and function. Yet, despite heightened knowledge from comparative studies about the empirical distribution of TEs among plant genomes, we still know little about the balance of the evolutionary forces that have created this distribution [13]. In this review, we discuss major aspects of TE evolution by invoking the analogy of a triptych, a three-paneled work of art. Each panel of a triptych may be assessed on its own, but each is also essential to the meaning of the whole. In this case, the panels correspond to the three main forces that govern TE dynamics: transposition, TE removal and, most importantly, population processes such as natural selection. Together, these forces determine the distribution of TEs in plant genomes.

Control of TE transposition

The propensity for rapid differentiation of genome size between species and individuals suggests that transposition must be frequent and ongoing. Yet, little is known about absolute rates of transposition because few described elements have been observed to be active in their plant host. It has therefore been difficult to characterize transposition rates experimentally. The few exceptions include: the *Mutator* (*Mu*) transposon, for which activity reaches one transposition event per element per generation in active maize lines [14]; the *Associator/Dissociator* (*Ac/Ds*) system, with transposition rates measured to be ~10⁻⁶ per locus per tested chromosome [15]; and *mPing*, whose transposition rate was estimated on average to ~56 new copies in rice *F*₁ and *F*₂ individuals [16].

Despite the dearth of rate estimates, our understanding of the factors that affect transposition is growing rapidly. For example, a recent ground-breaking study [17] tested the ability of autonomous *mariner*-like elements to transpose *stowaway* nonautonomous MITEs. After examining 119 different *mariner*-like × *stowaway* combinations, the authors found only four cases (3%) where the autonomous element successfully transposed the non-autonomous element. In one of these four cases, the nonautonomous element transposed at ~3000-fold higher levels than its

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Plant Transposable Elements Alaskan Aviation History

O. Nelson



Plant Transposable Elements Alaskan Aviation History:

Plant Transposable Elements O. Nelson, 2012-12-06 Transposon tagging can work Even though most of our understanding about the factors that contribute to a successful tagging experiment has been accumulated from a limited number of experiments using different transposable elements in different genetic backgrounds it is still possible to draw some conclusions regarding the best experimental strategies for gene tagging In our experience Spm has proved to be a good element for transposon tagging The frequency of recovering mutable alleles induced by Spm is not significantly different from that for Ac Ds or for Mu 6 summarized in Ref 22 and varies from about 10 to 10⁻⁸ Spm has the unique advantage however in that all of the members of this family that have been examined thus far are homologous to each other at the DNA level Therefore by combining molecular analysis with genetic segregation it is possible to identify and isolate alleles that are due to insertions of either autonomous or nonautonomous Spm elements There are definite steps one can take to increase the chances of detecting a transposition into the gene of interest The most important step is to select a genetic background in which the desired phenotype will be easy to screen If the phenotype is not likely to be mutable then tester lines should be constructed so as to contain flanking markers that can aid in subsequent segregation analyses Subject Guide to Books in Print, 1997 **Books in Print**, 1991 **Library of Congress Subject Headings** Library of Congress, Library of Congress. Subject Cataloging Division, Library of Congress. Office for Subject Cataloging Policy, Library of Congress. Cataloging Policy and Support Office, 1975 **Books In Print 2004-2005** Ed Bowker Staff, Staff Bowker, Ed, 2004 **Bibliography of Agriculture with Subject Index**, 1988-10 Bibliography of Agriculture, 1998 **Animal Behaviour Abstracts**, 2002 **Biological & Agricultural Index**, 1990 Forthcoming Books Rose Army, 1989 A Bibliography of Alaska Aviation Dale Stirling, 1985-01-01

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Table of Contents Plant Transposable Elements Alaskan Aviation History

1. Understanding the eBook Plant Transposable Elements Alaskan Aviation History
 - The Rise of Digital Reading Plant Transposable Elements Alaskan Aviation History
 - Advantages of eBooks Over Traditional Books
2. Identifying Plant Transposable Elements Alaskan Aviation History
 - Exploring Different Genres
 - Considering Fiction vs. Non-Fiction
 - Determining Your Reading Goals
3. Choosing the Right eBook Platform
 - Popular eBook Platforms
 - Features to Look for in an Plant Transposable Elements Alaskan Aviation History
 - User-Friendly Interface
4. Exploring eBook Recommendations from Plant Transposable Elements Alaskan Aviation History

- Personalized Recommendations
- Plant Transposable Elements Alaskan Aviation History User Reviews and Ratings
- Plant Transposable Elements Alaskan Aviation History and Bestseller Lists
- 5. Accessing Plant Transposable Elements Alaskan Aviation History Free and Paid eBooks
 - Plant Transposable Elements Alaskan Aviation History Public Domain eBooks
 - Plant Transposable Elements Alaskan Aviation History eBook Subscription Services
 - Plant Transposable Elements Alaskan Aviation History Budget-Friendly Options
- 6. Navigating Plant Transposable Elements Alaskan Aviation History eBook Formats
 - ePub, PDF, MOBI, and More
 - Plant Transposable Elements Alaskan Aviation History Compatibility with Devices
 - Plant Transposable Elements Alaskan Aviation History Enhanced eBook Features
- 7. Enhancing Your Reading Experience
 - Adjustable Fonts and Text Sizes of Plant Transposable Elements Alaskan Aviation History
 - Highlighting and Note-Taking Plant Transposable Elements Alaskan Aviation History
 - Interactive Elements Plant Transposable Elements Alaskan Aviation History
- 8. Staying Engaged with Plant Transposable Elements Alaskan Aviation History
 - Joining Online Reading Communities
 - Participating in Virtual Book Clubs
 - Following Authors and Publishers Plant Transposable Elements Alaskan Aviation History
- 9. Balancing eBooks and Physical Books Plant Transposable Elements Alaskan Aviation History
 - Benefits of a Digital Library
 - Creating a Diverse Reading Collection Plant Transposable Elements Alaskan Aviation History
- 10. Overcoming Reading Challenges
 - Dealing with Digital Eye Strain
 - Minimizing Distractions
 - Managing Screen Time
- 11. Cultivating a Reading Routine Plant Transposable Elements Alaskan Aviation History
 - Setting Reading Goals Plant Transposable Elements Alaskan Aviation History
 - Carving Out Dedicated Reading Time
- 12. Sourcing Reliable Information of Plant Transposable Elements Alaskan Aviation History

- Fact-Checking eBook Content of Plant Transposable Elements Alaskan Aviation History
- Distinguishing Credible Sources
- 13. Promoting Lifelong Learning
 - Utilizing eBooks for Skill Development
 - Exploring Educational eBooks
- 14. Embracing eBook Trends
 - Integration of Multimedia Elements
 - Interactive and Gamified eBooks

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