Evolution and consequences of transposable elements

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Recent studies on transposable elements (TEs) have shed light on the mechanisms that have shaped their evolution. In addition to accumulating nucleotide substitutions over evolutionary time, TEs appear to be especially prone to genetic rearrangements and vertical transmissions across even distantly related species. As a consequence of replicating in host genomes, TEs have a significant mutational effect on their hosts. Although most TE-insertion mutations seem to exert a negative effect on host fitness, a growing body of evidence indicates that some TE-mediated genetic changes have become established features of host species genomes indicating that TEs can contribute significantly to organismic evolution.

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Introduction

Evolutionary interest in transposable elements (TEs) may be focused on two distinct but interrelated phenomena: first, the structural and functional changes that occur among TEs themselves over evolutionary time, and second, the element-mediated evolutionary changes that occur within the host genomes in which TEs reside. In considering either of these phenomena it should be kept in mind that the term evolution refers to both a fact and a process. The fact that TEs have evolved and influenced the evolution of the host genomes in which they reside can often be documented by careful phylogenetic comparisons. Identification of the processes that underlie documented evolutionary changes is more problematic, but in some cases can be reasonably inferred by studying the mechanisms underlying the replication, movement and mutational consequences of TEs in contemporary species and laboratory strains. For this reason, anyone interested in the evolutionary potential of TEs should familiarize themselves with the many excellent reviews available on TE biology (e.g. [1,2]).

This review encompasses both of these areas of contemporary evolutionary interest in TEs. Discussion of each area is structured such that the relevant evolutionary facts (i.e. the structural/functional relationships which exist among TEs and their host genomes) are presented first, followed by a description of the evolutionary processes or mechanisms proposed to explain these facts. While papers published within the last year are featured, the critical background literature provides the necessary context for the issues discussed.

Transposable element evolution

TEs are classified into two major groups based on their mode of transposition. Class I, or retroelements, is made up of TEs that transpose by reverse transcription of an RNA intermediate. Class II, or DNA elements, consists of elements that transpose directly from DNA to DNA. Class I is further divided into two subclasses. Class I.1, the retrotransposons, have long terminal repeats (LTRs) and encode products with structural homology to the retroviral gag- and pol-encoded proteins. Class I.2, the non-LTR retrotransposons (LINE-like elements, poly(A) retrotransposons), also encode gag- and pol-like proteins but have no LTRs and carry a poly(A) tail at their 3' ends. Short interspersed elements (SINES) or Alu-like sequences transpose via an RNA intermediate but are not formally considered to be Class I elements because, unlike retroelements, they do not encode the reverse transcriptase (RT) necessary for their retrotransposition. SINES are thus the products of retroelements and not retroelements themselves. In this regard, they are similar to processed pseudogenes [3]. Recent evidence indicates that the RT activity responsible for the generation of SINES is provided by non-LTR retrotransposons [4**].

Class II elements are characterized by their small inverted terminal repeats of less than 100 bp bordering an internal transposase-encoding sequence which functions in a DNA-only mechanism of transposition. Some DNA elements can be heuristically organized into tentative subgroups based on the relative sequence similarities of their transposases. However, no overall

Abbreviations

LINE—long interspersed element; LTR—long terminal repeat; RT—reverse transcriptase; SINE—short interspersed element; snRNA—small nuclear RNA; TE—transposable element.
Evolutionary relationship has, as yet, been established among the diverse groups of DNA elements.

**Evolutionary patterns in TE evolution**

Extensive effort has gone into establishing plausible evolutionary relationships among the vast diversity of TEs thus far isolated from eukaryotic species. Comparison of the structural and phylogenetic relationships that exist among TEs and their hosts reveals some interesting patterns or trends that shed light on the processes underlying TE evolution.

**Class I or retroelements**

Retroelements all encode amino acid sequences with similarity to the RT of retroviruses [5,6]. RT is an ancient protein which is present in both prokaryotes and eukaryotes [7], and structural studies suggest that it may have been the progenitor of DNA polymerases [8]. It is postulated that RT activity played a critical role in the evolutionary transition from RNA-based to DNA-based genetic systems [9,10]. Comparisons of conserved regions of the RT-encoding sequences from a broad diversity of retroelements have allowed the establishment of probable evolutionary relationships (recently reviewed in [4**,5,11]). One major branch of the RT-based retroelement tree contains msDNA-producing (multicopy single-stranded DNA-producing) elements (bacterial retroelements or retrons), group II introns and all of the non-LTR retrotransposons. The second major branch consists of the LTR-containing retroelements, that is, retroviruses, LTR retrotransposons, caulimoviruses and hepadnaviruses. The LTR retrotransposons are further divided into the Ty1-copia group and the Ty3-gypsy group. In addition to sequence differences, the splitting of LTR retrotransposons into two subgroups is further supported by diagnostic structural differences. The Ty1-copia group elements have their integrase domain located upstream of the RT domain, in contrast to the more typical relationship (i.e., RT domain located upstream of integrase domain) characteristic of all retroviruses and Ty3-gypsy group elements. This modular rearrangement between these two groups suggests that segment shuffling or rearrangements in addition to nucleotide substitutions may play a significant role in retroelement evolution. This contention is further supported by other sequence alignment studies showing that a retroelement phylogeny based on ribonuclease H sequences is not congruent with a phylogeny based on RT sequences [11]. Incongruities of this type suggest that xenologous recombination events (i.e., the replacement of a resident gene by a homologous gene) have occurred among retroelements over evolutionary time. Recent evidence that xenologous recombination has occurred during the evolution of the *Drosophila microtia* retrotransposon [12] lends further credence to the view that it may be a relatively common feature of retroelement evolution.

If it is assumed that bacterial retrons are representative of the most ancient retroelements as previously suggested [13,14], then the RT-based tree should be rooted on this branch. When this is done, the non-LTR elements fall out as the apparent progenitors of the LTR-containing retroelements [4**]. This is consistent with Temin's original proviral hypothesis [15,16], which states that retroviruses evolved from cellular TEs.

When the RT-based phylogeny of retroelements is compared with phylogenetic relationships previously established among the host organisms in which retroelements are located, some dramatic inconsistencies arise. For example, the plant Ty3-gypsy group elements *IPG7* and *del9* isolated from *Pinus radiata* and *Lilium longiflorum* respectively, are sequentially more similar to yeast Ty3 and several *Drosophila* elements than to other plant elements [5]. Likewise, a Ty1-copia group element recently isolated from herring (*Clupea harengus*) is highly homologous to elements present in yeast and *Drosophila* despite the vast spans of time separating vertebrates from these species [17]. Other examples of these sorts of inconsistencies are not infrequent among retroelements (e.g., 118*10*), and may support the contention that this class of TEs is relatively frequently transferred across species (and perhaps kingdoms) boundaries over evolutionary time. It should be noted, however, that in at least some cases, incongruent phylogenies can be explained by alternative hypotheses consistent with vertical inheritance [119]. Direct evidence for the horizontal transmission of non-LTR retroelements comes from the study of the *Drosophila* L1 elements. This family of non-LTR retroelements is widely distributed among *Drosophila* species but has invaded *D. melanogaster* sometime within the last 20–60 years [20].

SINES form another group of TEs which rely on RT for mobilization but do not themselves encode the enzyme [21]. SINES are typically small (about 300bp in length), but are present in high copy number ranging from 50,000 to 300,000 per genome. They are derived from RNA polymerase III transcripts and thus may carry promoter sequences. Some are capable of being transcribed in vitro by RNA polymerase III. As RNA polymerase III is responsible for transcribing small nuclear RNAs (snRNAs), tRNAs and 5S rRNA, it is reasonable to assume that SINES may have originated by reverse transcription of one of these classes of cellular RNAs sometime in their evolutionary past. A family of SINES in humans called Alu elements (because they contain a unique Alu restriction site near their 5' end) can be transcribed in vitro by RNA polymerase III into an snRNA with homology to the 7SL RNA component of the signal recognition particle, which plays a key role in the intracellular localization of proteins. Thus it seems likely that Alu elements were originally derived from 7SL RNA-like molecules. The *Bombyx mori* SIN*E, Bm-1*, is homologous to a U1 snRNA suggesting that the snRNA may have served as the progenitor of *Bm-1* elements [22]. Most other SINES appear to have originated from tRNAs [21].

Recent evidence suggests that if the RT of a non-LTR retrotransposon becomes associated with another RNA, reverse transcription and integration of a DNA copy of the RNA can result [4**]. This is facilitated by the fact
that a significant component of the binding of the integration complex of non-LTR retrotransposons with its RNA involves the poly(A)-rich 3' end. This has led to the hypothesis that actively transposing non-LTR retrotransposons are the most likely source of the enzymatic machinery necessary to generate SINES and processed pseudogenes [4**].

Class II or DNA elements
DNA elements all share the same basic design of short inverted repeats bordering one or more open reading frames, at least one of which encodes a transposase. Transposition of DNA elements occurs via a DNA intermediate rather than the RNA intermediate characteristic of retroelements. The following is a brief overview of evolutionary significant features of some major groups of DNA elements.

Mariner-like elements
The Drosophila mariner element was first discovered in connection with an unstable eye color mutant in Drosophila mauritiana [23]. Southern blot surveys established that mariner is present in five of the eight species of the Drosophila melanogaster subgroup and sporadically in other species of the subgenus Sophophora [24*]. Outside the Sophophora subgenus, mariner was reported in several species of drosophilid, Zaprionus [25], and in Hyalophora cecropia, a moth species very distantly related to Drosophila [26]. The mariner element from Zaprionus tuberculatus was sequenced and shown to be significantly more closely related to the Drosophila elements than chromosomal genes like Adh (alcohol dehydrogenase), suggesting that mariner had most likely been introduced into Z. tuberculatus by horizontal transfer [25].

Using degenerate primers designed to represent regions of amino acid conservation between the putative transposase genes of the D. mauritiana and II. cecropia mariner elements, Robertson [27**] recently employed polymerase chain reaction methodology to amplify equivalent regions of presumed mariner elements from 10 insect species representing six additional phylogenetic orders. Alignments of the conceptual translations of at least six clones of mariner PCR fragments from each of the 12 species resulted in a phylogenetic tree with four clearly distinct groupings indicating that mariner-like elements consist of at least four major subfamilies. The degree of divergence between elements representing these subfamilies indicates that some of the elements have been separated for more than 200 million years. The presence of elements from more than one distantly related subfamily within the same genomes of a number of insect species indicates that extensive horizontal as well as vertical transmissions must have occurred over the evolutionary history of this group of DNA elements.

Tc1-like elements
Tc1 is a DNA element first isolated from Caenorhabditis elegans and found to be highly conserved among all members of this species thus far examined [26]. Using a Tc1 probe, a homologous element called Barney was isolated from the closely related nematode species Caenorhabditis briggsae [29]. The coding regions for the putative transposases of Tc1 and Barney show 70% homology. The Drosophila DNA element HB1 is 30% homologous to Tc1 within its putative transposase-encoding region [29]. Recently, the DNA element Ubu has been isolated from several Hawaiian Drosophila species [30**]. By inserting three gaps of 1–8 nucleotides in length and two deletions of 1 bp and 10 bp in the Ubu sequence, the entire 273 protease coding region of Tc1 aligns with a 273 amino acid sequence of Ubu with 40% identity [31]. When Barney is aligned with Ubu (again by allowing some gaps and deletions), the two elements show 38% amino acid identity. Alignment of HB1 with the modified Ubu sequence requires three additional deletions. When aligned in this way, Ubu and HB1 show 32% identity in amino acid sequence. The fact that Ubu transposase sequence is more similar to the transposases carried by the nematode elements than the Drosophila HB1 transposase would seem to suggest horizontal transmission. However, as the HB1 element is apparently transpositionally defective [32], it may be evolving at a significantly different rate from the active Tc1, Barney and Ubu elements. A Tc1-like element has recently been reported in the hagfish (Eptatretus stouti) [33]. This element, called Tes1, encodes a transposase with sequence similarity to the C. elegans and Drosophila Tc1-like elements. The widespread distribution of Tc1-like elements with sequence similarity suggests that horizontal transfer may have occurred over the evolution of this group. However, within the Hawaiian Drosophila, there is no evidence that horizontal transmissions have taken place [30**].

Ac-like elements
The maize Ac elements are members of yet another apparently ancient class of DNA elements with a wide phylogenetic distribution. The transposase of maize Ac elements has recently been shown to have significant sequence similarity with Drosophila hobo elements and Tam 3 elements from snapdragon (Antirrhinum majus), indicating that the Ac-like elements may be ancient or that a horizontal transfer of Ac-like elements may have occurred between plants and animals [34]. Drosophila hobo elements were first isolated from D. melanogaster [35,36] but have subsequently been found in other members of the melanogaster subgroup and in two species of the more distantly related montium subgroup [37]. The presence of hobo in the montium subgroup seems best explained by horizontal transfer [38*]. Horizontal transfer also seems to be the best explanation of the distribution of hobo among D. simulans, D. mauritiana and D. melanogaster. Simmons [39] compared the sequences of hobo elements from these three species and found that they were nearly identical. These data strongly suggest that the same element was introduced into these three species relatively recently. The hypothesis that hobo is prone to horizontal transmission between species is further supported by the recent finding of a hobo element...
in the common house fly, Musca domestica [40]. On the other hand, sequence comparison of Ac elements from maize and pearl millet (Pennisetum glaucum) indicate that Ac-like elements were present in the common ancestor of these two species around 25-40 million years ago [41]. Thus, Ac-like elements represent an ancient class of DNA elements which have probably undergone repeated horizontal transfers over their evolutionary history.

P-like elements

Drosophila P elements were the first class of transposable elements shown to be horizontally transferred across species [42]. They apparently first arose within the willistoni group of Drosophila, endemic to the New World tropics. The introduction of P elements into D. melanogaster probably occurred soon after the chance introduction of this species into the New World during the early part of this century [43]. There is only a single nucleotide difference between P elements isolated from D. melanogaster and D. willistoni despite the fact that these species are separated by 40 million years of evolution. This fact, coupled with the observation that P elements have not been found in any other member of the melanogaster subgroup, is compelling evidence that P was introduced into D. melanogaster by horizontal transfer [42].

P-like elements have been found in a number of Drosophila species outside the melanogaster subgroup, and in the distantly related Scaptomyza pallida [44,45]. The sequences of the P elements in these species show only slight homology to the elements in D. melanogaster and the willistoni subgroup. This indicates that P-like elements were probably present in the ancestors of Drosophilidae species. It has recently been demonstrated that at least three separate horizontal transmissions of P-like elements need to be invoked to account for the distribution of the elements among contemporary Drosophila and dipteran species [44]. Thus P-like elements are also an apparently ancient class of DNA elements that have experienced a number of horizontal transfers over their evolutionary history.

The fact that P elements can be horizontally transferred has taken on added significance with the finding that these elements are sometimes able to capture and transpose chromosomal (host) genes [46]. This raises the possibility that P elements may have the potential to mediate the horizontal transmission of chromosomal genes.

**Mechanisms underlying transposable element evolutionary change**

The evolutionary mechanisms underlying nucleotide substitution (i.e. selection, drift, etc.) are presumably the same as those postulated for chromosomal genes (e.g. [47]). It should be noted, however, that the mutation rate associated with retroelements is significantly higher than that of DNA elements because RT has no proofreading capacity. Retroelements may also be especially prone to xenologous recombination because two full length RNA genomes are typically packaged within the retroelement capsid. If by chance these two RNA molecules represented different retroelement genomes, inter-element recombination may occur. Indeed such inter-element recombination events apparently occur with relative frequency among infectious retroviruses [48].

Perhaps the most remarkable and unexpected finding that has come out of the phylogenetic analyses of TEs is the relative frequency with which both retroelements and DNA elements have apparently been transferred horizontally between species [49]. For closely related species that are able to hybridize, introgression may be invoked to account for the horizontal transmission of elements. However, to account for horizontal transfers between more distantly related species, some biological vector is probably involved [50]. Perhaps the most obvious candidates are infectious viruses.

When a virus infects a TE-containing cell, the TE could integrate into the viral genome and be subsequently transferred with the vector into another species. This hypothesis was supported by the isolation of an insect baculovirus containing a copia-like retrotransposon [51]. Since that time a number of additional baculoviruses have been isolated that have TEs inserted within their genomes (L. Miller, personal communication). As baculoviruses are characterized by their ability to infect a broad spectrum of insect species [52], they may well play a role in the horizontal transmission of TEs in insects. Further research is needed to establish whether or not viruses are factors in the horizontal transmission of TEs in other animals and plants.

Recently, parasitic mites have been identified as potential vectors of TEs in Drosophila [53]. It is proposed that the mite's mouth parts may play a role analogous to a laboratory microinjection needle for introducing foreign DNA into Drosophila embryos.

**The consequences of transposable elements on host genome evolution**

Mutation is the underlying source of all evolutionary change. It is now generally recognized that the majority of all spontaneous mutations having significant phenotypic effect are associated with TE insertions [54,55,56]. The range of biological consequences that TE insertions have on host genome structure and function is nothing short of amazing. TE-mediated effects can influence all aspects of the phenotype, including life history traits such as aging [57]. TE-mediated changes may have a number of evolutionary consequences ranging from significant morphological and behavioral changes [58] to speciation [59]. TE-insertion mutations have been associated with alterations in chromosome structure, recombination, replication and gene regulation. For example, interactions between Drosophila hobo elements have recently been shown to be responsible for chromosomal rearrangement mutations in this species [60,61].
Similarly, hotspots for meiotic recombination in mice have recently been associated with retroelement LTRs [62]. These data support earlier findings in maize and yeast associating chromosomal breakpoints and recombination hotspots with TEs (e.g. [63,64]).

Many mutations affecting the regulation of gene expression are attributable to the insertion of TEs. There is a long list of examples of TE insertions into 5' flanking regions having an effect on transcriptional initiation in a temporal-specific or tissue-specific manner [65*]. Such regulatory changes may be due to the read-through of transcripts initiated in the TE promoter or to the presence of negative or positive enhancer-like sequences within the element. TE insertions can also result in regulatory changes by altering gene splicing patterns (e.g. [66,67*]). Indeed, the fact that some TEs behave like primitive introns has prompted the hypothesis that they played a role in intron evolution [68*,69*]. Inserted TEs in some genes have been shown to contain termination and polyadenylation signals which alter patterns of expression (e.g. [70]).

**Evidence that transposable elements influence the evolution of their hosts**

Although it is clear that TEs are capable of causing mutational changes which have the potential to influence many aspects of host genome evolution, this, in itself, does not constitute proof that they play a significant evolutionary role. Indeed, much has been made of the fact that TE-insertion mutations usually appear to reduce the fitness of their hosts and so may not be expected to exert any positive role in organismic evolution [71,72]. The very low frequency of TE-insertion mutations in most natural populations seems consistent with this view and can be explained as the result of a constant transposition rate being balanced against negative selection (1731; however, see 174* for an alternative view).

These arguments notwithstanding, the view that TEs do contribute to the evolution of their hosts is strengthened by recent demonstrations that at least some evolutionary differences in genome structure and function are TE-mediated. For example, there are a number of documented cases of evolutionary differences in patterns of gene expression which are attributable to the insertion of TEs.

The mouse Sip gene is a member of the murine histocompatibility complex and arose by tandem duplication of the fourth component of the complement C4 gene. Sip and C4 maintain considerable sequence homology but display marked differences in their tissue-specific patterns of expression. Efforts to identify the cis-regulatory sequences responsible for this regulatory difference culminated in the discovery that the operative enhancer sequence is contained within the LTR of a cryptic retroviral-like element [75]. The inserted element has accumulated a large number of nonsense mutations, including several stop mutations, which indicates that the retroviral-like element has not been reproductively active for millions of years. Due to the idiosyncracies of RT-mediated retroviral replication, the LTRs are sequentially identical at the time of the insertion event. Thus, the fact that there is considerable sequence divergence between the 5' and 3' LTRs of the element inserted adjacent to the Sip gene indicates that the original insertion event occurred several million years ago [76**].

The rat oncomodulin gene is related to a larger family of rat albumin genes but is unique in that it is expressed in extra-embryonic tissue like the placenta. The sequence responsible for the tissue-specific expression of the oncomodulin gene is contained within a solo LTR related to LTRs associated with the intracistemal A-particle family of endogenous retroviruses in mice [77,78]. Another LTR with similarities to the same retrovirus family has also been shown to be the promoter of the MIPF gene in the Balb-C strain of mice [79,80].

The human Amy 1 gene is a member of the human amylase gene family. Other members of this gene family are expressed in the pancreas. A cryptic retroviral-like element positioned 5' to the Amy 1 gene has resulted in the gene being expressed only in salivary gland [76**,81]. Comparison of the sequence divergence which has occurred between the two LTRs located upstream of the Amy 1 gene indicates that the insertion event occurred about 45 million years ago.

SINE elements have also been implicated in regulatory evolution. For example, the human beta-1 alpha globin gene has been shown to utilize a truncated Alu sequence as part of its promoter [82]. An Alu sequence located 5' to the human epsilon globin gene negatively regulates expression in a tissue-specific manner [83].

TEs may contribute to the evolution of termination signals as well. For example, the polyadenylation signals of several genes have recently been shown to be derived from TEs [84,85,86*].

The role played by TEs in regulatory evolution may not always be as easily documented as in the examples cited above. As only a relatively small subregion of a TE may be responsible for imposing novel cis-regulatory effects on adjacent chromosomal genes, it may be that only these short stretches of regulatory sequences will be preserved by natural selection over long spans of evolutionary time. Thus the 'footprints' of evolutionarily significant TE insertion mutations may have relatively short half-lives and be difficult to detect in comparisons between homologous genes with variant regulatory phenotypes. In this regard, it may be relevant to note that nearly every enhancer and other control sequence known to be critical for proper regulatory expression of eukaryotic genes has been identified in one or more TEs. Thus, there may exist an evolutionary relationship between regulatory sequences carried by TEs and those contained within the control regions of eukaryotic genes [88]. This type of correlation extends beyond transcriptional control sequences. It has recently been shown, for example, that there is significant similarity between the termini of invertebrate Tc-1-like elements and the signal sequences of the vertebrate immunoglobulin somatic recombination pathway [87].
Several functions underlying chromosome structure in *Drosophila* have recently been shown to involve TEs. For example, the recently discovered DNA element *Bari J*, has been implicated as contributing to the structure of centromeric heterochromatin in *D. melanogaster* [88*]. *Drosophila HetA* elements, which are found exclusively in the telomeric regions of *D. melanogaster* chromosomes have recently been shown to be involved in the phenomenon of chromosome healing in this species [89*]. In addition, a retroelement has recently been associated with the phenomenon of Y chromosome degeneration in *D. miranda* [90,91].

The evolutionary significance of chromosomal inversion polymorphisms has long been recognized in *Drosophila*. It has recently been shown that the breakpoints of many inversions endemic to Hawaiian populations of *D. melanogaster* contain hobo elements [92*]. Similarly, the *copia* retroelement has recently been associated with endemic inversion breakpoints in French *Drosophila* populations (C Biemont, personal communication).

Mechanisms potentially involved in the establishment of transposable element insertion mutants in populations and species

For many years TEs were regarded as purely parasitic or 'selfish' DNA playing no positive role in the evolution of their hosts [93–95]. The accumulating evidence that TEs can influence the evolution of their hosts is leading evolutionary geneticists to explore alternative views and explanatory models (e.g. 96*–98*).

Recent laboratory studies of yeast populations indicate that TE-insertion alleles may not always be negatively selected against but may occasionally increase the fitness of their carriers [99*]. This finding is consistent with earlier studies of bacterial and *Drosophila* populations [100–102]. Thus, it remains plausible that natural selection may occasionally lead to the fixation of TE-insertion mutants. However, the available evidence suggests that TE-insertion mutants are almost always either selectively neutral or selected against [71,72,103]. Thus, it may be that the establishment of TE-insertion mutants in populations and species is by non-selective mechanisms. In this regard, it may be relevant to note that the rate of TE-insertion mutations is not always low and constant, as assumed in many population genetic models [74*]. Emerging evidence suggests that TE-mediated mutations can episodically arise at very high frequencies (e.g. [104–106]). This may be due, at least in part, to the fact that transposition is not a random, but a host-regulated process. Molecular and genetic studies indicate that both the expression and transposition of TEs fall under host genetic control (e.g. [107–112]). Significant increases in rates of transposition have been associated with inbreeding (e.g. [113,114,115*]), interstrain and inter-specific crosses (e.g. [59*,116]), and environmental factors and stress (e.g. [117*,118,119*,120–122]). Each of these phenomena can be explained as resulting from the disruption of host-mediated controls. Episodically high mutation rates coupled with the chance effects of inbreeding could result in the fixation of TE-insertion alleles that would not otherwise be favored by natural selection.

In addition to controlling the expression and transposition of TEs, host genes have been identified which are capable of suppressing the mutant phenotypes associated with retrotransposon insertion mutations [123,124]. It has recently been postulated that the existence of such 'suppressor genes' in natural populations at low to moderate frequency may shield retroelement insertion mutants from negative selection [98*]. Periods of severe inbreeding associated with genetic bottlenecks or founder events may lead to the chance fixation of retroelement insertion variants and the simultaneous loss of suppressor alleles [58]. Thus, the presence of a TE-mediated structure or function in a species does not necessarily imply that it was brought to fixation by natural selection.

We are far from understanding all of the mechanisms that may influence the establishment of TE-insertion mutants in populations and species over evolutionary time. However, as we continue to learn more about the complex interactions existing between TEs and their host genomes, we should be in a better position to understand the evolutionary processes involved.

Conclusion

Current evolutionary interest in TEs focuses on two areas: changes that have occurred among TEs over evolutionary time, and the consequences TEs have had on host genome evolution. Incongruities between TE phylogenies and the phylogenies of their host species suggest that horizontal transfers have been a common feature of TE evolution. Current data indicate that xenologous recombination events have occurred over the evolutionary history of retroelements. A number of evolutionary changes in gene regulation and chromosome structure and function have been shown to be TE-mediated. Much remains to be learned concerning the mechanisms by which TE-insertion alleles become established in populations and species. Natural selection remains a viable possibility in some cases, but increasing attention is being given to non-selection models for the establishment of TE-insertion mutants.

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References and recommended reading

Papers of particular interest, published within the annual period of review, have been highlighted as:

• of special interest
•• of outstanding interest


An excellent overview of the biology of non-LTR retroelements.


A concise review of an interesting new Drosophila retrotransposon, microPT, which displays an unusual mechanism of autoregulation.


A summary of the extent of Ty1-copia group retrotansposons in eukaryotes, and a comparison of models for the evolution of these elements in light of recent phylogenetic data.


An extensive survey of the variation among copia-like elements in cotton —this can be explained without invoking horizontal transfer.


A summary of data related to the potential evolutionary significance of J elements.


The authors present a summary of mariner sequence diversity among the D. melanogaster subgroup. The results suggest that mariner was present in the ancestor of the D. melanogaster subgroup and was lost in some of the lineages.


Sequence comparison among mariner element transposase sequences isolated from six orders of insects indicates that vertical as well as horizontal transmission has occurred during the evolution of this family of elements.


An analysis of sequence similarities between Ubu elements within and between Hawaiian Drosophila species shows a grouping of the two pairs of most closely related species but shows a much larger variation within the most recently diverged species than expected, indicating that Ubu may have been activated at the time of formation of each species as it colonized the newly formed islands of the Hawaiian archipelago.

A concise summary of the evidence in support of the horizontal transfer of genes across species boundaries.


56. Shapiro J: Natural Genetic Engineering in Evolution. In Transposable Elements and Evolution. Edited by McDonald JF, Dordrecht: Kluwer Academic Publishers; 1993:325-337. It is hypothesized that evolution is primarily based upon the rearrangement of basic genetic motifs, analogous to the manipulations of contemporary genetic engineers (see Shapiro, this issue, pp 845-848).


59. PONTIVEROS A: Generic Instability and Rapid Speciation: Are They Coupled? In Transposable Elements and Evolution. Edited by McDonald JF, Dordrecht: Kluwer Academic Publishers; 1993:242-253. Evidence is presented of high rates of chromosomal rearrangement produced by inbreeding and interspecific crosses which are probably TE-mediated. The results are considered within the context of speciation.


61. A hobo element in the Notch locus of the X chromosome interacts with other hobo elements in the same chromosome to produce Notch mutations. Nearly all of the mutations are associated with deficiencies, inversions and other rearrangements, and hobo elements are present at each breakpoint.


In situ hybridization and genomic Southern analysis of recessive lethal mutations that occurred on derivatives of an unstable X chromosome (Xc) indicate that hobo elements are responsible for the instabilities.


64. ROTHSHIN R, ARTHUR W, WALLIS J, RUNNE H, THOMAS B: The Genetic Control of Recombination Between Repeated
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An extensive overview of the literature relevant to TEs and evolution coupled with a theory as to how TEs and host genomes may co-evolve.


A summary of work showing that maize retrotransposons inserted into genes can induce new patterns of splicing.


Review of studies in Drosophila and maize indicating that some TEs are spliced from pre-mRNA and thus behave as introns. The relevance of these results to models of intron evolution is discussed.


Excellent overview of data indicating that TEs elements may have contributed to the evolution of eukaryotic introns.


A critical review of various theoretical population genetic models to account for the frequency and distribution of TEs in natural populations.


An excellent summary of examples of TEs having played a role in the regulatory evolution of a mouse gene and a human gene.


84. Harenzcz, Johnson L: Polyadenylation Signall of the Mouse Thymidylate Synthase Gene was Created by Insertion of an L1 Repetitive Element Downstream of the Open Reading Frame. Proc Natl Acad Sci USA 1990, 87:2531-2535.


87. Discovery of a new and widely dispersed TE in maize which may contribute to the evolution of gene expression.


A Tcl-like TE from Drosophila melanogaster is frequently clustered in a heterochromatic region close to the centromere of the second chromosome where it may play a functional role.


A study demonstrating that the Bar-A transposable element is involved with the 'healing' of broken chromosome ends in Drosophila melanogaster.


A study demonstrating that the "healing" of broken chromosome ends in Drosophila melanogaster.


A model is proposed to explain the differences in abundance of TEs between prokaryotes and eukaryotes.

Evidence is presented that the mutational spectrum generated by Ty transpositions in yeast may, due to their target specificity and gene regulatory capabilities, possess a higher frequency of adaptively beneficial mutations than spectrum resulting from other types of mutations.

The stability of 11 families of TEs is examined in natural populations. and Somatic Excision Rate of mariner Transposable Element in Three Natural Populations of Drosophila. Genet Res 1992, 60:105-114.


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The excision rate of an inactive mariner element was significantly affected by temperature in two out of three strains of Drosophila derived from natural populations.


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