Retroposons, Retrovirus like element, Ty1 element in yeast

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RETROVIRUSLIKE ELEMENTS

- They are found in many different eukaryotes, **including yeast, plants and animals**.

- **Structure**: **they have a central coding region flanked by long terminal repeats, or LTRs, which are oriented in the same direction. The repeated sequences are typically a few hundred nucleotide pairs long.**

- Each LTR is, in turn, usually bounded by short inverted repeats. Because of their characteristic LTRs, the retroviruslike elements are sometimes called ***LTR retrotransposons.***

- **The coding region contains homologous of the *gag* and *pol* genes of retroviruses; *gag* encodes a structural protein of the virus capsule, and *pol* encodes a reverse transcriptase/integrase protein. They don't contain region homologous to *env*.**

- In the retroviruslike elements, the **"gag and pol" proteins play important roles in the transposition process.**

- One of the **best-studied retroviruslike elements is the Ty1 transposons from the yeast *Saccharomyces cerevisiae*.**

Structure of Ty1 Element

❖**Ty1 element is about 5.9 kilobase pairs long; its LTRs are about 340 base pairs long, and it creates a 5 bp target site duplication upon insertion into a chromosome.**

❖**Most yeast strain have about 35 copies of Ty1 element;** sometimes they also contain LTRs that have been detached from Ty1 elements. **These solo LTRs or delta sequences are apparently formed by recombination between the LTRs of complete Ty1 elements (Fig 1b)**

❖**The recombination event puts the central coding region and a portion of each LTR onto a circular molecule. When the circle leaves the chromosome, the remaining portions of the LTRs fuse, creating the solo delta sequence.**

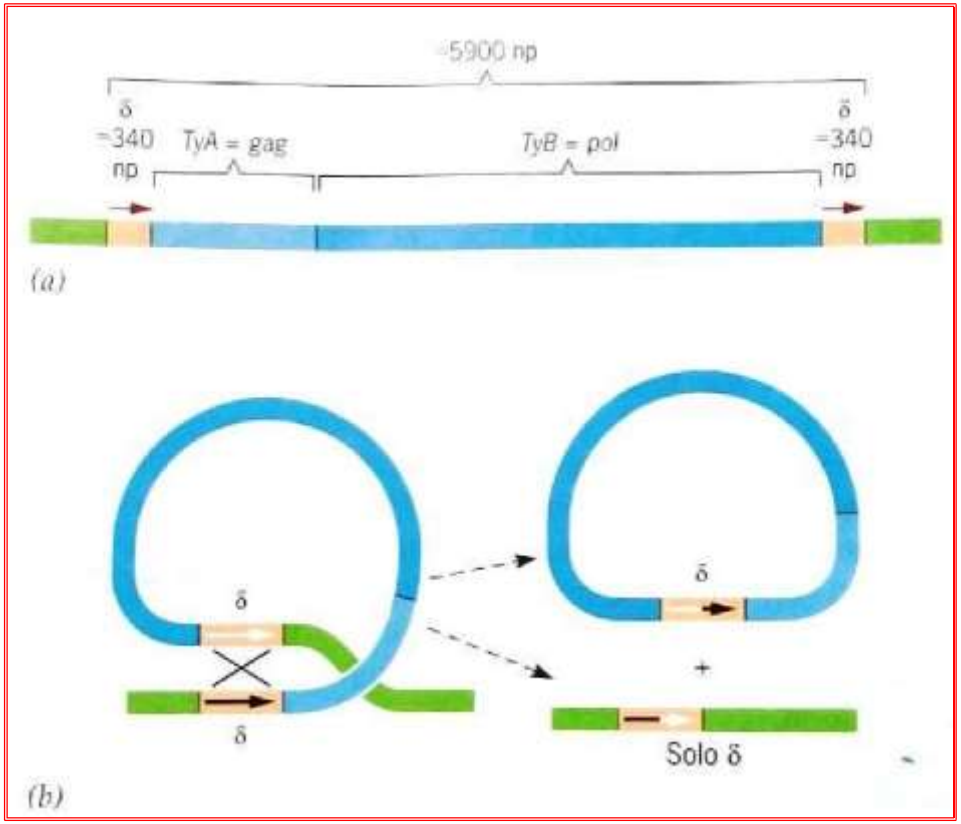

Fig 1: The retroviruslike element Ty1of yeast.
(a)Genetic organization of the yeast Ty1 element, showing the long terminal repeat sequences (LTRs, denoted by the Greek letter delta) and the **two genes (TyA and TyB).** Lengths of sequences are in nucleotide pairs (np)
(b)Formation of a solo delta sequence by homologous recombination between the delta sequences at the ends of the element.

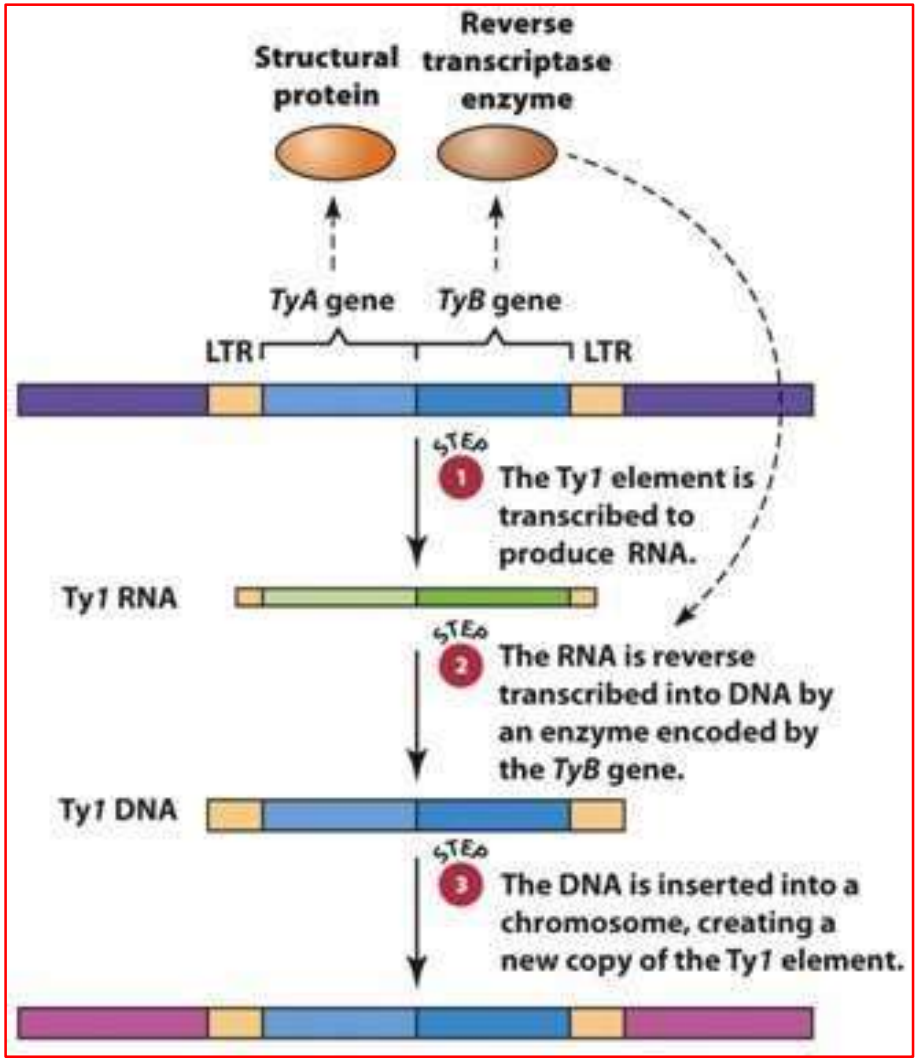

Fig 2: Transposition of the yeast Ty1 element

Transposition of the yeast Ty1 element

✓**Ty1 elements have only two genes, *TyA* and *TyB*, which are homologous to the *gag* and *pol* genes of the retroviruses.**

✓Biochemical studies revealed that the products of these two genes can form viruslike particle in the cytoplasm of the yeast cells.

✓**The transposition of Ty1 elements involves reverse transcription of RNA. After the RNA synthesised from Ty1 DNA, a reverse transcriptase encoded by the *TyB* gene uses it as a template to make double-stranded DNA.**

✓**Then the newly synthesised DNA is transported to the nucleus and inserted somewhere in the genome, creating a new Ty1 element.**

➢ **Retroviruslike element elements have also been found in *Drosophila*:**

***1)* *copia*,** so named because it produces copious amounts of RNA. **The *copia* element is structurally similar to the *Ty1* element of yeast.**

2) the ***gypsy* element**, another ***Drosophila* retrotransposons**, **is larger than *copia* element because it contains a gene similar to the '*env*' gene of retrovirus.**

Both the ***copia* and *gypsy* elements form viruslike particles inside *Drosophila* cells**; however, only the **particles that contain *gypsy* RNA can move across cell membranes, possibly because they also contain *gypsy's env* gene product.**

The ***gypsy* element** therefore appears to **be a genuine retrovirus**.

RETROPOSONS (NON-LTR RETROTRANSPOSONS)

❖**The retroposons, or non-LTR retrotransposons**, are a large and widely distributed class of retrotransposons, **including the *F,G,* and *I* elements of *Drosophila*** and several types of elements in mammals.

❖**These elements move through an RNA molecule that is reverse transcribed into DNA , probably by a protein encoded by the elements themselves.**

RETROPOSONS (NON-LTR RETROTRANSPOSONS) CONTD…..

❖ Although they create a target site duplication when they insert into a chromosome, **they do not have inverted or direct repeats as integral parts of their termini.**

❖Instead, **they are distinguished by a homogenous sequence of A:T base pairs at one end.** This **sequence is derived from reverse transcription of the poly(A) tail that is added near the 3′ end of the retroposons RNA during its maturation.**

❖**In *Drosophila*, the retroposons *HeT-A* and *TART* (for *t*elomere-*a*ssociated *r*etro*t*ransposons)** are **found at the ends (telomeres) of chromosomes, where they perform the critical function of replenishing DNA that is lost by incomplete chromosome replication.**

These **two elements transpose preferentially to the ends of chromosome, extending them by several kilobases.**

Eventually, the transposed sequences are lost by incomplete DNA replication, but then a new transposition occurs to restore them.

The *HeT-A* and *TART* retroposons therefore perform the important function of regenerating lost chromosome ends.

Thank You