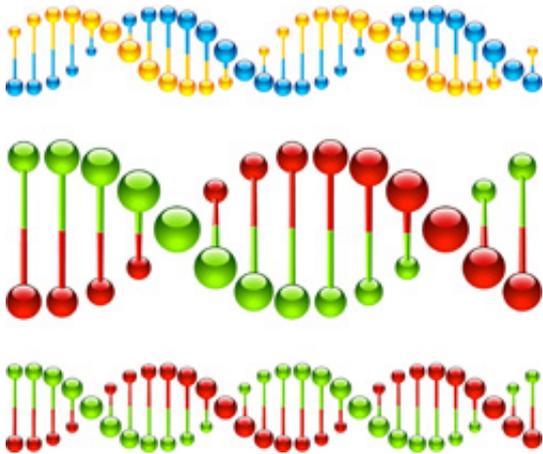


Mobile MITEs jump to fame in gene regulation

18 June 2012



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Moving genetic elements from one location to another in a genome makes for a very dynamic situation in terms of development and disease. An EU project has investigated a special type of micro transposable element and its impact on neighboring genes.

Movable [gene sequences](#) are a potent means of modifying a genome. These so-called transposable elements (TEs) or jumping genes can generate mutations by being placed in a strategic position in relation to a gene. They may also be the source of chromosomal rearrangements.

Making up over half of the DNA in an organism gives an idea of how important these transportable elements may be to [gene expression](#), development and evolution. The 'Regulation of transposable elements in plants and impact on genome evolution' (Transplant) project aimed to elucidate their role in the ubiquitous [model plant](#) Arabidopsis, commonly known as Shepherd's Purse.

The focus of the Transplant researchers centred in particular on miniature inverted repeat

transposable elements (MITEs). Present in large numbers in the genome and too small to encode a protein, MITEs constitute a special type of transposable element in the genome.

Project scientists wanted to ascertain the influence of MITEs on the expression of neighbouring genes. The project also aimed to analyze whether the miniature sequences played a role in organizing the genome.

Transplant researchers have developed appropriate bioinformatics tools to refine the information on the Arabidopsis genome. The influence of the transposable elements was also investigated. Continuing project research will focus on levels of methylation associated with selected MITEs to confirm the bioinformatics data so far collected.

Genomic progress has been meteoric since the first complex genetic regulatory mechanism was proposed on the lac operon some five decades ago. The scope for applications for [jumping gene](#) control is even more immense and spans the entire field of analysis of genomic structure and regulation.

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