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The impact of Helitrons



Shailesh Lal's research group is investigating the impact of transposable elements on the evolution and expression of the eukaryotic genome: the genetic information in multicellular, and even some single-cell, organisms. Transposable elements, sometimes known as jumping genes, are the most abundant entity of many eukaryotic genomes.

For example, almost half of the human genome consists of transposable elements that have been linked to many diseases, such as muscular dystrophy and cancer. These elements also confer antibiotic resistance in a broad spectrum of bacteria that cause disease. Despite their wide abundance, until recently virtually all known transposable elements were grouped into two classes based on their mechanistic mode of transposition (the movement of DNA sequences to different positions in the genome). Class I elements transpose via RNA intermediates, whereas elements of Class II transpose via DNA intermediates.

Lal's group is focusing specifically on the Helitron superfamily of novel transposable elements, which he first discovered in the maize genome. Helitrons differ fundamentally from other known families of transposable elements in both structure and the mechanism of transposition. Despite their wide abundance, these enigmatic elements remain undetected because, unlike generic transposable elements, Helitrons do not contain conserved sequences easily detected by computer-based database searches.

A potentially significant role for Helitrons is in the synthesis of new genes. The gene pieces captured by Helitrons are often transcribed into eclectic transcripts conjoining coding regions of several different genes. These elements are poorly understood despite their massive abundance, their structural diversity and the important role they apparently play in the evolution of eukaryotic genome. Although evidence for recent Helitron movement has been reported in maize, autonomous Helitron activity has not been reported. Helitrons are postulated to transpose via a so-called Rolling Circle (RC) mechanism involving strand replacement catalyzed by helicase and replicase enzymes encoded by an autonomous element. However, no experimental evidence in support of this hypothesis has been reported. Several models for gene piece capture have been proposed based on the structural features of Helitrons and the comparison of captured gene fragments of related elements. Again, no

supporting evidence is extant for any of the models proposed. A better understanding of these elements requires concrete evidence of their transposition in the present day genome, establishment of a system to assay their transposition and an analysis of additional indigenous Helitrons in other species.

Lal is using maize as a model system to study the mechanism by which these elements transpose and capture gene sequences. A better understanding of Helitron mediated movement and integration of large and diverse segments of DNA may aid in designing novel strategies for transformation and transgenic expression for animal and crop improvement.

Representative Recent Publications

1. Lal SK, Oetjens M, Hannah LC. 2009. Helitrons: Enigmatic abductors and mobilizers of host genome sequences. *Plant Science* 176:181-186.
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3. Jameson N, Georgelis N, Fouladbash E, Martens S, Hannah LC, Lal SK. 2008. Helitron mediated amplification of cytochrome P450 monooxygenase gene in maize. *Plant Mol Biol* 67:295-304.
4. Lal SK, Hannah LC. 2005. Plant genomes - Massive changes of the maize genome are caused by Helitrons. *Heredity* 95:421-422.
5. Lal SK, Hannah LC. 2005. Helitrons contribute to the lack of gene colinearity observed in modern maize inbreds. *Proc Natl Acad Sci USA* 102:9993-9994.
6. Gupta S, Wang BB, Stryker GA, Zanetti ME, Lal SK. 2005. Two novel arginine/serine (SR) proteins in maize are differentially spliced and utilize non-canonical splice sites. *Biochim Biophys Acta* 1728:105-114.
7. Gupta S, Gallavotti A, Stryker GA, Schmidt RJ, Lal SK. 2005. A novel class of Helitron-related transposable elements in maize contain portions of multiple pseudogenes. *Plant Mol Biol* 57:115-127.
8. Lal SK, Giroux M, Brendel V, Vallejos E, Hannah LC. 2003. The maize genome contains a Helitron insertion. *Plant Cell* 15:381-391.