

NEWS AND COMMENTARY

Transposon silencing

The extraordinary epigenetics of a transposon trap

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In a recent paper, Josse *et al.* (2007) bring us closer to understanding the molecular basis of a powerful defence system against selfish DNA.

During the twentieth century, a family of DNA transposons—*P* elements—invaded the genome of wild *Drosophila melanogaster* and rapidly spread worldwide, in one of the most dramatic and best-studied instances of conflict within the genome. *P* elements have a high rate of transposition when introduced into the genomes of naive strains, breaking chromosomes and causing sterility and aberrant development of the gonads. However, strains infested with *P* elements swiftly become able to suppress their transposition. This has been interpreted as the evolution of self-interested restraint on the part of the element, or of hyperparasitism by non-autonomous elements that can outcompete active ones, but recent work suggests that specialized genome defences against transposable elements are also of great importance in keeping *P* elements in check (Brennecke *et al.*, 2007).

The maternally inherited ability to prevent *P* elements from transposing is known as *P* cytotype, of which the telomeric-silencing effect (TSE) is a large component. This detects DNA sequences inserted into particular areas of heterochromatin at telomeres, and silences homologues of these sequences elsewhere in the genome. The system works so efficiently that two telomeric *P* elements will almost entirely suppress 80 or so other copies in the genome. In effect, the *Drosophila* telomere contains an intruder alarm, or a trap for transposons—which can also be sprung, inadvertently or otherwise, by genetic engineers when they introduce transgenes that integrate at the telomere.

Using flies in which a reporter *lacZ* transgene is silenced by the TSE, Josse *et al.* (2007) obtain a quantitative measure of its strength by assessing the proportion of egg chambers showing no *lacZ* expression. They find that the TSE

uses a cytoplasmic factor, which accumulates over several generations in the female germline. The evidence is in a peculiar pattern of non-Mendelian inheritance: in order for suppression to be fully effective, not only must a fly have a telomeric *P* element, but so must its female-line ancestors for the previous six generations. Over these six generations, the efficiency of silencing builds up gradually.

However, it does not matter which parent transmits the telomeric *P*. This rules out imprinting as a possible mechanism, so Josse *et al.* (2007) investigate whether RNA interference is responsible. By determining which of the several mutations in distinct RNAi pathways affect the TSE, they show that the epigenetic effect is probably based on repeat associated small interfering RNA, a recently discovered small RNA pathway implicated in transposon silencing in the germline (Vagin *et al.*, 2006).

The TSE is sensitive to the dosage of two proteins that are part of the telomere cap, which, like the variegated pattern of suppression, suggests that chromatin modelling may be involved.

Interestingly, a second putative genome defence system in *Drosophila* also involves loci in heterochromatin, in this case nested insertions of transposable elements near centromeres (Bergman *et al.*, 2006). Both these findings reinforce the already intriguing connection between RNAi-based gene regulation and heterochromatin (Bernstein and Allis, 2005). Heterochromatin has often been neglected in sequencing projects or assumed to be an inert genomic refuse tip, but it has become apparent in recent years (Dimitri *et al.*, 2004) that these genome regions warrant more intensive sequencing and research.

Although this study leaves many questions unanswered, it promises future directions. *P* elements are one of the best-understood transposable elements, and a highly tractable system with which the currently unknown molecular mechanics of the repeat asso-

ciated small interfering RNA-silencing pathway can be elucidated. This also offers a fascinating opportunity to explore genome defence systems from an evolutionary as well as molecular perspective, and to make use of interspecific comparisons, as species of *Drosophila* differ in their vulnerability to *P* element invasion (Daniels *et al.*, 1990). Given some advances in theoretical population epigenetics, we might even come to understand the evolutionary reasons why the TSE should have such an unusually long epigenetic memory.

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Editor's suggested reading

RNAi: a defensive RNA-silencing against viruses and transposable elements—all 3 versions N Buchon, C Vauray—**Heredity**, 2006—nature.com ... by PVX (Potato Virus X), interferes with **mobile** silencing signal ... the heritable silencing of an active **transposon** family. ... Viral **suppression** of systemic silencing ... Cited by 11—Related Articles—Web Search—BL Direct.

Steps in the evolution of heteromorphic sex chromosomes—all 3 versions D Charlesworth, B Charlesworth, G Marais—**Heredity**, 2005—nature.com ... evolve in several different ways, and that recombination **suppression** is favoured ... Transposable **element** accumulation is probably an early effect of restricted ... Cited by 26—Related Articles—Web Search—BL Direct.

Parasitism and the retrotransposon life cycle in plants: a hitchhiker's guide to the genome—F Sabot, AH Schulman—**Heredity**, 2006—nature.com ... can lead to overexpression or **suppression** of nearby ... A retrotransposable **element** from the mosquito *Anopheles gambiae* ... of Bs1, a maize retrovirus-like **transposon** ... Cited by 3—Related Articles—Web Search.

Patterns of hobo elements and their effects in natural populations of *Drosophila melanogaster* in ... —all 3 versions K Kikuno, K Tanaka, M Itoh, Y Tanaka, IA Boussy, S ... —**Heredity**, 2006—nature.com ... The findings suggest that the hobo element invaded Japanese populations in the mid-1950s, at about the same time as the **P element** invasion in Japan. ... Related Articles—Web Search.