



Figure 1 Possible causes and consequences of uncontrolled movement of transposable elements (‘jumping genes’). Red and green boxes represent silenced and active transposons, respectively. a, A transposable element in the genome is typically silenced by methylation (addition of CH₃ groups) and probably by repressive chromatin structures — certain modifications of the proteins that bundle up the genome (purple ovals). b, When these controls are disrupted — for example, in plants with the *ddm1* mutation^{1,2} — the transposon is expressed (represented by a wavy line) and jumps about the genome at a much higher rate. c, Possible consequences of the transposon jumping into new sites elsewhere in the genome, such as into or nearby other genes (open rectangles).

The results of Miura *et al.*¹ and Singer *et al.*² provide striking support for the genome-defence model⁴. They show that at least two distinct kinds of transposon in *Arabidopsis* are activated and start jumping specifically in the context of reduced DNA methylation (Fig. 1). Both groups used *ddm1* (for ‘decrease in DNA methylation’) mutant plants, which have genome-wide decreases in methylation. The normal DDM1 protein is similar to some chromatin-remodelling proteins⁵, so the mutant plants may also have altered chromatin structures, another type of epigenetic modification.

Using a predictive bioinformatics approach, Singer *et al.*² identified a family of 22 transposons — related to maize transposons called Mutator elements — scattered throughout the *Arabidopsis* genome. At least one of these transposons readily hopped about the genome of *ddm1* mutants. By contrast, Miura *et al.*¹ started by investigating a morphological abnormality that arose spontaneously in an inbred lineage of *ddm1* plants. They showed that this defect was

caused by a transposon hopping into, and disrupting, a gene encoding a key protein involved in biosynthesis. The transposon was from the CACTA family, so called because the ends of these transposons have the DNA sequence CACTA. Miura *et al.* found three other related transposons in *Arabidopsis*, and at least two of the four jumped about avidly in *ddm1* plants.

Neither group found appreciable transposon movement in normal plants, indicating that methylation efficiently suppresses these mobile DNA elements. Moreover, a previous study found that the transcription of a different transposon is activated in *ddm1* plants⁹. Similarly, the expression of mouse transposons is activated in methylation-deficient animals^{10,11}. Collectively, these studies give considerable support to the genome-defence model⁴. Another implication is that loss of methylation of transposons may also result in increased transcriptional noise, regardless of the consequences for transposon movement.

Like any good experiment, these studies^{1,2} raise further questions, some specific and others broader. One is whether the *ddm1* mutation has effects on transposons — other than increased transcription — that might contribute to their increased mobility. For example, might it alter the chromatin structure at the transposons’ donor or target sites? The biochemical functions of the normal DDM1 gene are not yet certain, so the basis for methylation changes in *ddm1* mutant plants remains unclear. Another question is whether mutations in other *Arabidopsis* genes that alter methylation or chromatin structure will have similar consequences, or perhaps affect only particular subsections of the genome or classes of mobile elements.

Certainly, the new work^{1,2} will allow the generation of a practical resource, consisting of transposons sprinkled across the genome. This will be useful for investigating the possible consequences of transposon mobilization (Fig. 1), including gene disruption¹, altered gene transcription, chromosomal rearrangements and epigenetic instability¹².

It remains to be seen whether other *Arabidopsis* transposons are mobilized in methylation-deficient mutants. And it will be interesting to find out whether transposons in animal cells are mobilized by disrupting methylation patterns or chromatin structures. If so, this finding might give pause to those contemplating treating patients with drugs that perturb genome-wide epigenetic processes, such as chemotherapeutic drugs intended to ‘unsilence’ aberrantly hypermethylated and repressed genes in cancers.

These studies open new vistas on transposons and epigenetic controls, which together have shaped eukaryotic genomes through evolution, and provide a useful way of studying jumping genes. They also highlight the destabilizing effects of perturba-



100 YEARS AGO

The first sealed thermometer was made some time prior to 1654 by Ferdinand II., Grand Duke of Tuscany; he filled the bulb and part of the tube with alcohol, and then sealed the tube by melting the glass tip. Ferdinand and his brother, Leopold de Medici, promoted the establishment in Florence of the Accademia del Cimento, and the account of their experiments, published in 1667 and translated into English by Waller in 1684, contain descriptions of various thermometers made and used by the members. One of these old thermometers was given by the Grand Duke of Tuscany to the late Prof. Babbage, and is now in the Cavendish Laboratory at Cambridge. In England about the same time Boyle made experiments on thermometers. His ‘Lectures on Cold’ were published in 1665 in obedience to the command of the Royal Society, ‘imposed on me in such a way that I thought it would less misbecome me to obey it unskilfully than not at all. Especially since from so illustrious a company (where I have the happiness not to be hated) I may, in my endeavours to obey and serve them, hope to find my failings both pardoned and made occasions of discovering the truth I aimed at.’

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50 YEARS AGO

The publication of the Sanskrit manuscript of ‘Mānasōllāsa’ by King Sōmēśvara, son of King Vikramāditya VI of the later Chālukyas, in the Vikramāditya VI of the later Chālukyas, in the Gaekwad’s Oriental Series (Publication No. XXVIII, Baroda, 1925), has brought to light a chapter on angling which gives details, almost modern in practice, about this pleasant pastime. ‘Mānasōllāsa’ is an encyclopædic work and was composed in A.D. 1127. The kingdom of Sōmēśvara, comprised practically the whole of the Deccan plateau and included the Godavari, Narbada, Tapti and Kistna river systems... The work referred to here shows that the art of angling was developed in ancient India to a very high standard, for the methods described therein are quite in line with those used by anglers in India to-day. The gipsies of Europe, who use Mongolian, Hindi and other fragments of Asiatic languages, to-day practise the same methods as those described by King Sōmēśvara, and it is likely that they wandered from India to Europe and spread the art of angling there.

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