Retrotransposons and genetic diversity in crop plants

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Only a tiny proportion of the DNA of plants is comprised of genes. The vast majority of the average plant genome is 'non-coding' DNA, most which is made up from transposable elements more popularly known as transposons. As their name suggests, transposons have the ability to jump to new locations in their host genomes. Two major transposon classes exist in nature. The first of these, called retrotransposons or class I transposable elements, move by a 'copy and paste' mechanism, leaving the original 'donor' copy inttact. Class II transposons move by a 'cut and paste' mechanism. Retrotransposons themselves are very diverse, with three major groups identified, called *LINEs, copia* and *gypsy*, all of which are found in plants.

Retrotransposons as markers for biodiversity estimation and breeding. Retrotransposons make ideal genetic markers for plants, because they are ubiquitous, highly variable in their locations and very easy to detect. Several methods have been developed for converting retrotransposon insertions into molecular markers and we mainly use two of these, Sequencespecific Amplification Polymorphism³ (SSAP) and Retrotransposon-Based Insertional Polymorphism⁴ (RBIP). SSAP visualises each transposon insertion as a band on a gel and RBIP converts a single insertion into a fluorescent spot on a microarray (see Figure). We use SSAP markers for linkage mapping and biodiversity analysis in barley, wheat, lettuce and pea. RBIP was developed by us to characterise the overall genetic structures of complete germplasm collections, which contain thousands of samples. In the Figure 1536 pea samples, representing one half of the entire John Innes Pisum Germplasm Collection, have been scored for a single retrotransposon insertion. Very recently, we have adapted this method to score Single Nucleotide Polymorphism (SNP) markers.

References

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Figure 1 Retrotransposon-based molecular markers. a. *gypsy* SSAP markers in lettuce. Each column is a gel lane from the DNA of a single plant and each band represents a single retrotransposon insertion in the corresponding sample. b. A single *copia*-group retrotransposon insertion was scored in 1536 samples from the John Innes *Pisum* Germplasm Collection. A green spot indicates the presence of an 'occupied' allele (retrotransposon inserted at the locus), a red spot indicates an 'unoccupied' allele (retrotransposon absent from the locus) and yellow spots show the presence of both alleles in the sample.

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