

GENOME EVOLUTION, JUNK DNA AND FUNCTIONAL VARIATION

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After having gained a thorough understanding of the structure and organization of model plant genomes such as those of *Arabidopsis thaliana* and rice, we have finally started to dig into the most interesting aspect of genome structure and evolution, i.e. its variations. Variation in DNA sequence is responsible for the genetic component of phenotypic variation, i.e. the component upon which both natural as well as artificial selection act. Estimates of intraspecific variation in transcribed regions due to nucleotide substitutions or small insertions/deletions (indels) were so far the only ones available. These sequence variants are usually either silent or affect the coding portions of the genes by causing aminoacid substitutions. Recent studies have started to shed light on sequence variation outside of genic regions due mainly to large indels caused by the presence/absence polymorphisms of transposable elements of different classes. In addition to LTR-retrotransposons, DNA transposons have been shown to be responsible for these polymorphisms, comprising *Helitrons*, CACTA and Mu-like elements that are capable of acquiring and piecing together fragments of plant genes that are often expressed. While this latter class of elements captures everyone's attention because of the potential for creating new genes through a sort of exon shuffling mechanism, the relevance of the large indel polymorphisms in intergenic regions for regulatory variation in flanking genes cannot be overlooked. From these studies it clearly appears that the recent movement of transposable elements of different classes has dramatically influenced genome and perhaps gene evolution in Angiosperm plants. Future analyses of the functional roles of intergenic sequence variation will tell us if we will need to pay more and more attention not only to genes but also to the "junk" DNA surrounding them.