IN BRIEF

A CLASSY RNA Silencing Signaling Mutant in Arabidopsis

RNA silencing in plants is associated with movement of a silencing signal from cell to cell and through the phloem. It is likely that the mobile silencing signals are RNA molecules: either short interfering RNAs generated by Dicer-like (DCL) RNaseIII enzymes or longer double stranded RNAs. Smith et al. (pages 1507–1521) describe a genetic screen designed to recover RNA silencing mutations in Arabidopsis that block or enhance the spread of silencing between cells. Their approach involved a silencing transgene expressed specifically in phloem companion cells such that a silencing phenotype observed in cells located away from vascular cells would require the spread of a silencing signal. Use of phytoene desaturase as the reporter of silencing allowed for a simple visual screen: movement of the silencing signal out of the phloem would lead to silencing in the surrounding mesophyll cells manifested as photobleaching. Use of this screen led to the identification of a novel SNF2-related gene, named CLASSY1, involved in the spread of silencing. CLASSY1 is in the same plant-specific family of SNF2 proteins as DRD1, which is implicated in DNA methylation and transcriptional gene silencing. It was also found that RDR2, NRPD1a, and NRPD2a, but not AGO4 or DCL3, were required for spreading of the silencing signal to surrounding tissues. The authors propose that AGO4 and DCL3 are involved in self-silencing of the target gene, whereas NRPD1a (a subunit of Pol IVa), RDR2, DCL4, and CLSY1 influence the spread of silencing via a signal amplification process in cells that receive the signal.

Bigfoot Genes and Plant Response to Environmental Change

Functional DNA sequence changes at a lower rate over evolutionary time and therefore is more highly conserved than sequence without function. In comparing homoeologous chromosomal regions having diverged from a common ancestor, a high degree of sequence similarity in noncoding regions is assumed to provide a measure of noncoding DNA function, where function is inferred from conservation. Conserved noncoding sequences (CNSs) have been studied extensively in mammals, and putative functions include matrix attachment regions, transcription factor (TF) binding sites, gene enhancers, and chromosome-level regulatory regions. The most recent tetraploidy event in Arabidopsis left numerous homoeologous regions. Freeling et al. (pages 1441–1457) conducted an alignment of homoeologous pairs that generated ~15,000 intragenomic CNSs. Analysis of this database identified 254 genes, called Bigfoot genes, located in CNS-rich chromosomal regions. Known TF binding motifs, such as the G-box, were found to be overrepresented in the CNSs, and the Bigfoot genes were found to be overrepresented for genes encoding TFs that respond to environmental signals. This suggests that Bigfoot genes may have a particular function in plant adaptation to environmental change.
Bigfoot Genes and Plant Response to Environmental Change
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