



ABSTRACT

“Impact of non-coding RNAs in root developmental plasticity”

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Long non-protein coding RNAs (npcRNA) represent an emerging class of riboregulators, which act either directly in this long form or are processed to shorter miRNA and siRNAs. Plant and animals use small RNAs (microRNAs and siRNAs) as guide for post-transcriptional and epigenetic regulation. In plants, miRNAs and trans-acting siRNA (tasiRNA) result from different biogenesis pathways but both interact with target transcripts to direct their cleavage. Genome-wide bioinformatic analysis of full-length cDNA databases allowed us to identify 76 *Arabidopsis* long npcRNAs. Eleven npcRNAs were antisense to protein-coding mRNAs whereas certain corresponded to miRNA or siRNA precursors. In addition, numerous 24-nt siRNAs matched to five different npcRNAs. To link them to root developmental plasticity, we have shown that abiotic stresses and hormone treatments in roots altered the accumulation of 22 of these npcRNAs.

Functional studies are ongoing to understand the regulatory mechanisms involving npcRNAs and their interacting RNA binding proteins in root tissues. We have identified an RNA-binding protein that interacts with an npcRNA that accumulates in nuclear “speckles” and controls auxin responses. In addition, one npcRNA expressed in root tissues corresponded to TAS3a, a tasiRNA precursor target of miR390. A feedback mechanism involving miR390/tasiRNAs and their ARF targets quantitatively controls lateral root emergence. Finally, the npcRNA43 locus was transcribed in sense/antisense orientation and its overexpression led to a developmental phenotype suggesting a novel compensatory mechanism mediated by an antisense RNA to control gene expression. We think that environmental control of long and small npcRNAs through interactions with RBPs may fine tune expression patterns of regulatory genes to modulate root developmental plasticity.