

P005 Target identification of AtXRN4, a cytoplasmic 5' to 3' exoribonuclease

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Among eukaryotes, mRNA decay pathways have been primarily dissected in yeast in which most transcripts are first deadenylated and then subjected to 3' to 5' or 5' to 3' decay. In the latter pathway, Xrn1p, a member of the 5' to 3' exoribonuclease family (XRN), plays a central role. XRN homologs are present in multicellular organisms indicating that XRN-mediated mRNA degradation may be conserved. However, recent *in vitro* studies in mammalian system argue for the pivotal role of the exosome. Accordingly, the functional contributions of Xrn1p homologs in decay pathways of higher eukaryotes remain a mystery. In Arabidopsis, since AtXRN4 is the sole cytoplasmic member of this XRN family, it has the highest potential to be the functional homolog of Xrn1p. To assess its putative role in degrading mRNAs, T-DNA knockout mutants in the *AtXRN4* gene were isolated. Homozygous *xrn4* plants were then analyzed using microarray technology. The identification of several putative targets will be presented to provide *in vivo* evidence that XRN function in mRNA degradation in multicellular eukaryotes, and likely have a role in specialized mRNA decay pathways. Funded by the NSF and DOE.