

Genome-wide efforts have recently revealed that a large fraction of the DNA in human and other eukaryotic genomes is transcribed. The functional analysis of such ‘dark matter transcripts’ led to the identification of so-called long non-coding RNAs (lncRNAs) with regulatory potential, though the functionality and specific roles of most lncRNAs are still not well understood. LncRNAs are >200 nt transcripts, and results from animal model systems suggested various roles in developmental patterning processes. However in plants, functional roles of lncRNAs in development are largely uncharacterized. Our preliminary analyses resulted in the identification of 25078 lncRNAs in the model plant *Arabidopsis thaliana*, and more than 7.7% (1925/25078) of these lncRNAs are expressed in a tissue-specific manner. The goal of this proposal is to characterize the developmental dynamics of lncRNAs during plant reproductive development at genome-wide scale, and to identify lncRNAs with critical roles in developmental gene regulation in plants. For this purpose, we collected large genome-wide mRNA and chromatin sequencing datasets in the model plant *Arabidopsis* that we plan to analyze using the HLRN resources.