The various steps of posttranscriptional regulation including splicing, 3´end cleavage and polyadenylation, and decay are tightly coordinated to shape the plant transcriptome. We have shown that active 5´splice sites affect polyadenylation of miRNA precursors in *Arabidopsis thaliana*. Moreover, we observed interactions between U1 snRNP, a ribonucleoprotein particle recognizing 5´splice sites, and the CFI complex as part of the 3´end cleavage and polyadenylation machinery. Here, we investigate coupling between splicing and 3´end processing globally. We propose that the crosstalk between U1 snRNP and the CFI complex plays an important role in defining the use of polyadenylation sites. We will determine *in vivo* targets of the CFI subunits genome-wide using individual nucleotide resolution crosslinking and immunoprecipitation recently established for plants and determine binding motifs. In parallel, we will perform 3´end sequencing on mutants defective in the CFI subunits. This will reveal for the first time which of the CFI subunits control polyadenylation. Cross-referencing the *in vivo* binding data and transcriptomic data will enable us to determine CFI binding sites involved in the choice of poly(A) sites and CFI sites located in the vicinity of 5´splice sites. From these data, we will select candidate genes for a functional analysis. To identify proteins mediating the crosstalk between U1 snRNP and CFI we will immunoprecipitate tagged CFI subunits and identify co-purified proteins by mass spectrometry. A function of the proteins that are part of U1 snRNP or interact with both, U1 snRNP and CFI in the control of polyadenylation will be analyzed. For this, corresponding mutants will be obtained assayed for alterations in polyadenylation. Our results will greatly improve our knowledge of polyadenylation control in Arabidopsis and unravel novel functions of U1 snRNP besides its role in splicing. This will significantly advance our understanding of gene regulation in general, a process fundamental in plant adaptation to changing environments. Our project is based on complementary expertise in RNA processing and interest in polyadenylation in both groups that will lead to a fruitful collaboration. The project will also benefit from a mutual exchange of state-of-the art techniques developed in each group.