Role of U1 snRNP in Post-Transcriptional Regulation of Gene Expression

Anchilie Mangilet
University of Oldenburg

Splicing is a very important process in gene regulation where exons are combined, and intervening introns are removed to form a mature mRNA. This process is carried out by the spliceosome consisting of 5 small nuclear ribonucleoproteins (snRNPs) namely the U1, U2, U4, U5, and U6 and other axillary proteins. The U1 snRNP functions in the 5’ splice site selection during the initial step of splicing. In humans, the U1 snRNP also participate in other processes aside from splicing including polyadenylation, 3’ end processing and transcription. However, in plants very little is known about its function. The objective of this study is to determine the function of the U1 and identify its components in plants. To study the U1, we generated artificial microRNA targeting the two core protein subunits, the U1-70K and U1-C. Knockdown of these proteins resulted to pleiotropic developmental phenotypes as well as reduced tolerance to salt and cold stress. Transcriptomic analysis revealed global alternative splicing alteration in both knockdown lines. To identify the components of the U1 snRNP in plants we optimized an RNA centric approach called the Chromatin Isolation by RNA Purification (ChIRP). Using this technique, we were able to pulldown proteins involved in splicing as well as proteins involved in RNA transport, 3’ end processing and transcription. In conclusion, U1 snRNP is important in development and stress regulation in plants. We could also hypothesize that the plant U1 snRNP is also important in splicing and other RNA metabolism processes.