U1 is a particle composed of a short ribonucleic acid (small nuclear RNA, snRNA), seven proteins called Sm, also found in other similar to U1 particles, and three proteins specific to this ribonucleoprotein (U1-70K, U1-C, U1-A). U1 belongs to a family of ribonucleoprotein complexes found in the cell nucleus, called snRNPs (small nuclear ribonucleoproteins). Primary transcripts of genes encoding proteins (pre-mRNA) are composed of coding sections - exons, separated by non-coding sequences - introns. U1 snRNP participates in the process of cutting out introns from pre-mRNA, recognizing and binding to the place where the exon joins the intron, which is called the 5' splice site (5'ss). The binding of U1 snRNP to pre-mRNA is possible due to the complementarity of the U1 snRNA sequence with the 5'ss site. This reaction starts the process of cutting out introns called splicing. In addition to U1, four other snRNPs, U2, U4, U5 and U6, participate in pre-mRNA splicing. Together they form a large and dynamic complex called the spliceosome, catalyzing the reactions of cutting out introns and joining exonic sequences into mature mRNA. The participation of U1 in splicing is well known and is referred to as the so-called canonical function of this snRNP. Many years ago, however, it was noticed that in the cell nucleus the number of U1 is much greater than that of the other splicing snRNPs, although in the spliceosome all of these ribonucleoproteins occur in only one copy each. This suggested that U1 may have additional to participation in splicing functions. Indeed, work carried out on human cells has shown that U1, in addition to splicing, is responsible for inhibiting premature, incorrect polyadenylation of the transcript, or so-called telescripting. U1 has also been shown to be involved in the selection of polyadenylation sites at the end of the transcript, and demonstrated to regulate the association of long non-coding RNAs (lncRNAs) with chromatin. It has also been shown that U1 influences the rate of movement of Pol II during transcription. These additional functions of U1 are known as non-canonical functions of U1, and our knowledge of the mechanisms explaining the participation of U1 in these processes is close to zero. This applies primarily to plants, where we are only beginning to describe non-canonical functions of U1. Therefore, two laboratories, one headed by Dr. hab. Szymon Swiezewski from the Institute of Biochemistry and Biophysics of the Polish Academy of Sciences in Warsaw, the other under the supervision of Prof. dr. hab. Artur Jarmolowski from the Adam Mickiewicz University in Poznan, joined forces and decided to look for a common mechanism of non-canonical functions of U1. The project concerns selected non-canonical functions of U1 in plants : (i) splicing-dependent and -independent functions of U1 snRNP in transcription termination and polyadenylation, (ii) the role of U1 in co-transcriptional control of RNA quality in the cell nucleus, (iii) the dependence of transcription elongation rate on U1 snRNP. We hypothesized that all or at least most of the non-canonical functions of U1 can be explained by the influence of this snRNP on the kinetics of RNA synthesis by Pol II. We want to propose a common model of non-canonical functions of U1 snRNP. The project is based on preliminary results obtained in both laboratories, as well as the expertise of these teams in the field of RNA (laboratory in Poznan) and seed biology (Warsaw group). It is worth noting that the results of the project are general in nature, they do not describe only the processes occurring in plants, but refer to all eukaryotic organisms.