

## **Abstract**

Until recently, the splicing and transcription were seen as almost independent processes. However, today a lot of studies provide plenty of evidence about their connection, even in the yeast *Saccharomyces cerevisiae*. The connection of these processes is particularly mediated by C-terminal domain of RNA polymerase II, which is consisted of tandemly repeated heptapeptide sequence – YSPTSPS. Amino acid residues of this heptapeptide sequence are specifically phosphorylated during transcription, which regulates transcription process and also the binding of specific factors. These factors are necessary for processing of the nascent transcript. Modifications of the primary transcript occur especially cotranscriptionally in higher eukaryotes, thus before the transcription is terminated and also before the functional mRNA is released.

Opinion on cotranscriptional splicing in *S. cerevisiae* were significantly changed in the last years. However, nowadays the splicing of pre-mRNA of most genes in *S. cerevisiae* is seen as cotranscriptional process. RNA polymerase II pauses within the terminal exons and this pausing event provides sufficient time for each spliceosomal component to assemble on the pre-mRNA and also for catalysis of splicing before the transcription termination.

**Keywords:** cotranscriptional splicing, RNA polymerase II, *Saccharomyces cerevisiae*, U snRNP, spliceosome, pre-mRNA