ABSTRACT

Transcription of precursor mRNA (pre-mRNA) and its splicing were originally conceived as two separate processes. Using *Saccharomyces cerevisiae* as a model, it was shown that the assembly of the complex catalyzing pre-mRNA splicing (spliceosome) can occur cotranscriptionally, i. e., during the time before the termination of transcription by RNA polymerase II. Research on cotranscriptional splicing revealed that proteins involved in transcription and specific chromatin modifications may affect pre-mRNA splicing and its regulation. It is also possible that spliceosome assembly and chromatin modifications can affect each other.

Prp45, the yeast ortholog of the human transcription coregulator SKIP/SNW1, has been previously associated only with splicing. The results obtained in our laboratory suggest that Prp45 could be used as a regulator coupling the processes of transcription and splicing. We have shown that *PRP45* has genetic interactions with factors important for transcription elongation, as well as chromatin modifications, and that it affects early stage of spliceosome assembly.

The aim of this bachelor project was document the relationship between the physiological role of Prp45 and H3K4 trimethylation using chromatin immunoprecipitation. It was found that *prp45*(1-169) mutation does not markedly affect the trimethylation of histone 3 at lysine 4, which is characteristic for transcriptionally active genes.