ABSTRACT

Protein Prp45, the yeast ortholog of the human transcription coregulator SNW1/SKIP, has been previously associated only with the regulation of pre-mRNA splicing. However, our laboratory found that protein Prp45 genetically interacts not only with the proteins involved in pre-mRNA splicing, but also with factors important for transcription elongation and with chromatin modifying enzymes. Our data and the information about the human ortholog SNW1/SKIP suggest that Prp45 could serve as a regulator coupling splicing, transcription and chromatin state in *S. cerevisiae*.

The main aim of this diploma thesis was to find out whether the protein Prp45, which is essential for cotranscriptional assembly of the spliceosome, affects posttranslational modifications of chromatin on transcribed genes. Using chromatin immunoprecipitation, the influence of *prp45*(1-169) mutation on trimethylation of histone H3 at lysine 4 and acetylation of histone H3 at lysines 9, 14 and 18 on transcriptionally active genes was not confirmed. The other aim was to analyse the behavior of cells synchronized by α-factor by using flow cytometry. According to our results, *prp45*(1-169) mutation leads to the prolongation of the cell cycle. For the purpose of monitoring the dynamics of nucleosomes in *S. cerevisiae* strains, the system of induced expression of tagged histone H3 was introduced as part of the thesis.

Our results show that H3K4 trimethylation is not affected by the delay of splicing with respect to transcription. We assume that this modification is not directly involved in the coupling of these processes in *S. cerevisiae*.