Abstract

Pre-mRNA splicing is a highly regulated cellular process. The tight cooperation of spliceosome and other splicing factors that enable pre-mRNA *cis*-elements interpretation results in precise pre-mRNA splicing regulation. Short conserved splicing sequences within introns represent an elementary and indispensable element for intron removal from primary transcript, yet they are not sufficient signals for efficient splicing events. Additional pre-mRNA features affect complex splicing regulation. We took advantage of strains with slightly disrupted spliceosome (*prp45*(1-169)) to study the effect of ACT1 and MAF1 intronic sequences on splicing efficiency. Here we show, that ACT1 intron region between branch point (BP) and 3' splice site (3'ss) maintains splicing efficiency in mutant cells. However, the specific element within this region was not determined. In addition, results implicate an alternative BP in splicing efficiency modulation in yeast *Saccharomyces cerevisiae*. Interestingly, this alternative BP is localized in ACT1 intron outside of the BP-3'ss region. Furthermore, splicing factors with potential influence on 3'ss selection were studied. Heterodimer composed of Slu7p and Prp18p participates in 3'ss positioning to the active site of the spliceosome. Splicing analysis of substrates with two competing 3'ss in strains bearing mutations in selected splicing factors confirms the impact of Slu7p and Prp18p on 3'ss selection. The results also indicate Cef1p involvement in proper 3'ss choice.

Key words: pre-mRNA splicing regulation, *cis*-elements, *ACT1*, *MAF1*, *Saccharomyces cerevisiae*