Abstract

Protein Prp22 is a DEAH box RNA helicase, which plays two distinct roles in pre-mRNA splicing: it participates in second transesterification step (ATP independent function) and it releases mature mRNA from the spliceosome (ATP dependent function). Prp45p, yeast ortholog of the human transcription co-regulator SNW/SKIP, is an essential splicing factor, it is included in spliceosome throughout the splicing reaction. Mutant *prp45*(1-169) genetically interacts with some alleles of NTC complex and second step splicing factors, one of them is also gene *PRP22*. Here we present, that mutants *prp22*(-158T) and *prp22*(-327A), which are synthetically lethal with *prp45*(1-169), express lower amount of Prp22p due to the mutation in upstream regulation region. Mutants *prp22*(-158T), *prp22*(300PPI) and *prp22*(-327A) affect splicing of pre-mRNA with mutation in 5´ss with respect to sequence of the second exon. N-terminal mutants *prp22*(Δ301) and *prp22*(Δ350) are synthetically lethal with *prp45*(1-169). Synthetic lethality is possibly caused by lower efficiency of Prp22 recruitment to the spliceosomes, which is no more viable for cells.