

P021 Specific subsets of mRNA molecules associate with the U2AF⁶⁵ and PTB splicing factors

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mRNA binding proteins are increasingly viewed as multifunctional entities, playing multiple roles in different steps of the gene expression pathway. The polypyrimidine tract binding (PTB) protein is a paradigm of this. Although it has been originally identified as an alternative splicing factor, it is also known to be involved in the regulation of translation and cytoplasmic localization of some viral and cellular mRNAs. U2AF⁶⁵ is an essential splicing factor involved in the recognition of introns during the early steps of spliceosome assembly. We have previously shown that U2AF⁶⁵ shuttles between the nucleus and the cytoplasm and hypothesized that this shuttling activity may occur in association with a specific subset of mRNA molecules, whose metabolism may be regulated by U2AF⁶⁵.

Here we describe a new U2AF⁶⁵-associated RNA complex and identify the population of mRNA molecules present in it by RNA immunoprecipitation assays coupled to microarray analysis. We have performed a similar analysis for PTB associated mRNAs. We find that U2AF⁶⁵ associated mRNAs are enriched in transcription factors and genes related to cell cycle regulation, DNA packaging and RNA metabolism. In contrast, mRNAs enriched in PTB immunoprecipitation experiments encode proteins associated to intracellular transport, cytoplasmic compartments and metabolism. RT-PCR analysis of specific genes confirms the results obtained by microarrays and the spliced status of the RNA molecules. We are currently exploring the functional significance of these interactions.