Abstract

One of the defining features of a eukaryotic cell is the presence of a nuclear envelope. This allowed the physical separation between nucleus and cytoplasm, although the presence of a variable number of openings called nuclear pore complexes (NPCs) allowed a constant flow of molecules and information between the two compartments. Certain molecules passively diffuse, but others need energy and specific interactions with transporters and components of the NPC to travel between through both compartments. The messenger RNAs (mRNAs) are among the molecules selectively exported from the nucleus to the cytoplasm. The physical separation between nucleus and cytoplasm isolates the processes of transcription and translation in eukaryotic cells, allowing the cell to select core transcripts competent for export and that will lead to a functional protein in the cytoplasm.

The right transcript levels in a cell, depending on the nutritional requirements, reproductive or relationship with the environment is essential for life. To this end, mechanisms regulating transcription, processing, stability, degradation, export or translation of the transcripts, are physically and spatially highly coupled in order to finely regulate the transcript levels in the cell.

In Saccharomyces cerevisiae, *SUS1* codes for a small protein of 11 kDa highly conserved in all eukaryotes. *SUS1* is part of the SAGA transcriptional co-activator, being a submodule component involved in chromatin remodeling. In addition, *SUS1* is one of the components of the TREX2 complex, wich interacts with the nuclear pore in the periphery of the nucleus and it is involved in the export of messenger RNAs. The presence of *SUS1* in both complexes allows the physical and spatial coupling phenomena of transcription and export of mRNAs. In addition, *SUS1* has two introns which is an unusual fact for the *S. cerevisiae* genome. Unlike other fungi or metazoans, the percentage of genes with introns in *S. cerevisiae* is very low (5%) and only 10 genes have more than one intron interrupting its coding sequence.

The unusual characteristics of *SUS1*, the role of Sus1 coordinating processes during mRNA biogenesis and its functional conservation in higher eukaryotes, led the research conducted in this dissertation.

In this work we studied in detail the biogenesis of *SUS1* transcripts. We have identified different factors, acting in *cis* and *trans* that are involved in regulating the expression of *SUS1* and function of the protein it encodes. On the other hand, we have studied the genetic relationship of *SUS1* with components of the 5 '$\rightarrow$ 3' cytoplasmic degradation machinery and expanded the knowledge about the role of *SUS1* during the biogenesis of mRNAs, not only in the nucleus but also in the cytoplasm.