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Investigation of mRNA Splicing in Saccharomyces cerevisiae using Microarrays

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Most genes in higher organism are split into separate modules (exons) by sequences that do not code for proteins; these are introns. When a gene is transcribed from DNA into mRNA, to act as a template for protein production, these need to be removed before a functioning protein can be produced. The intron is spliced out to produce an mRNA with a continuous coding sequence. The removal of introns is an important function for all of these cells, including S. cerevisiae. This is a yeast that is commercially important in baking and brewing. Although only 3.8% of this yeast's genes contain introns (an unusually low number), these account for a disproportionate 27% of the mRNAs produced [1,2]. Mutations in certain genes have an effect on both splicing and cell growth, this emphasises the vital role of splicing to the cell.

The small number of introns in this yeast, about 250 [2,3], from about 6250 genes in total, makes analysis of all of the introns feasible using systems biology techniques. Due to the conservation of splicing machinery from yeast to man, studies of splicing S. cerevisiae could provide insights into splicing defects implicated in human disease.

Microarrays with probes to diagnostic features of pre-mRNA splicing were used to monitor the splicing of all mRNAs [4]. These microarrays were used to investigate the factors involved in intron removal, including the effect of mutations, changes in growth conditions, and factors in the mRNA itself such as the composition and structures formed by the intron.

References

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