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Title: Intron specificity in pre-mRNA splicing

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Keywords: Intron-specific pre-mRNA splicing

Splicing regulation Alternative splicing Intron function Ubiquitin-like proteins

Issue Date: 2018

Publisher: Springer Ltd

Citation: Current Genetics, 64(4), pp. 777-784

Abstract:

The occurrence of spliceosomal introns in eukaryotic genomes is highly diverse and ranges from few introns in an organism to multiple introns per gene. Introns vary with respect to their lengths, strengths of splicing signals, and position in resident genes. Higher intronic density and diversity in genetically complex organisms relies on increased efficiency and accuracy of spliceosomes for pre-mRNA splicing. Since intron diversity is critical for functions in RNA stability, regulation of gene expression and alternative splicing, RNA-binding proteins, spliceosomal regulatory factors and post-translational modifications of splicing factors ought to make the splicing process intronspecific. We recently reported function and regulation of a ubiquitin fold harboring splicing regulator, Sde2, which following activation by ubiquitin-specific proteases facilitates excision of selected introns from a subset of multi-intronic genes in Schizosaccharomyces pombe (Thakran et al. EMBO J, https://doi.org/10.15252/embj.201796751, 2017). By reviewing our findings with understandings of intron functions and regulated splicing processes, we propose possible functions and mechanism of intron-specific pre-mRNA splicing and suggest that this process is crucial to highlight importance of introns in eukaryotic genomes.

URI:

https://link.springer.com/article/10.1007/s00294-017-0802-8 (https://link.springer.com/article/10.1007/s00294-017-0802-8)

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