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Lucy W. Barrett, Sue Fletcher, Steve D. Wilton

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There is now compelling evidence that the complexity of higher organisms correlates with the relative amount of non-coding RNA rather than the number of protein-coding genes. Previously dismissed as "junk DNA", it is the non-coding regions of the genome that are responsible for regulation, facilitating complex temporal and spatial gene expression through the combinatorial effect of numerous mechanisms and interactions working together to fine-tune gene expression. The major regions involved in regulation of a particular gene are the 5' and 3' untranslated regions and introns. In addition, pervasive transcription of complex genomes produces a variety of non-coding transcripts that interact with these regions and contribute to regulation. This book discusses recent insights into the regulatory roles of the untranslated gene regions and non-coding RNAs in the control of complex gene expression, as well as the implications of this in terms of organism complexity and evolution.?



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