

Preface

Eukaryotic gene expression is tightly controlled at multiple levels and coordinates the expression of proteins governing related biological processes, i.e. cellular growth and differentiation. Some of the molecular mechanisms controlling these gene networks are conserved among eukaryotes while others are absent or have evolved differently. This generates interesting diversity from the point of view of biologists trying to understand life, as well as challenging diversity from the point of view of those who attempt to control biology for the improvement of health, the environment or the economy.

It is estimated that more than one million fungal species exist on Earth. These include organisms of great importance for industry, medicine and agriculture. Despite their diversity in live styles (free-living, saprophytic, parasitic and mutualistic), fungi share common features distinctive from plants and animals and have been grouped taxonomically as an independent eukaryotic kingdom. Currently, more than 250 fungal species have been sequenced and this number will grow exponentially in the coming decade, thanks to efforts such as the 1,000 Fungal Genomes Project (<http://1000.fungalgenomes.org/>). Although the knowledge generated at a molecular level is clearly ahead on unicellular fission and budding yeasts, filamentous fungi represent invaluable tools for understanding additional features of complex eukaryotes such as multicellular development, pathogenesis, natural product synthesis, small RNA-mediated gene silencing, DNA methylation and programmed cell death. Their manageable genome sizes and vast diversity provide excellent tools and helpful insights to understand common and new regulatory mechanisms of gene expression, including their evolutionary perspective.

This advanced book on “Fungal RNA Biology” is a reflection of the work of many talented colleagues and individuals, whose collaborative efforts have made this project possible. We are really grateful to the authors for the effort involved. This book tries to cover the most relevant aspects and groundbreaking studies over the recent years on RNA-mediated mechanisms in model unicellular yeasts and filamentous fungi. Fifteen chapters, written by experts in their fields, describe the RNA-dependent processes that take place in a fungal cell, ranging from formation of coding and non-coding RNAs to mRNA splicing, export, localisation, degradation and translation. Other aspects related to RNA metabolism and gene expression are also covered such as ribosomal RNA biogenesis, gene silencing,

involvement of tRNA modifications in protein synthesis and heterochromatin regulation. Two methodological chapters based on biochemical and bioinformatic approaches conclude the book. This book highlights the commonalities and particularities of the fungal RNA machinery and RNA-dependent processes with higher eukaryotes, including remaining questions and future challenges in this area. Accordingly, it is a valuable resource for students and researchers studying RNA-dependent processes.



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