

Preface

This manual describes technologies and experimental approaches often used in studies with fission yeast. In this Preface, we make a far-from-fully inclusive mention of some who have significantly contributed to these studies, excluding the Editors of course!

It has been 70 years since Øjvind Winge suggested to a young PhD student, Urs Leupold, that *Schizosaccharomyces pombe* may be a useful organism for genetic studies and more than 60 years since Murdoch Mitchison picked it as an ideal organism in which to ask the deceptively simple question, “How does a cell grow between one division and the next?” The prescient, elegant, and meticulous work of these forefathers laid the foundations for a fission yeast community that has placed this excellent model system at the forefront of many areas of fundamental biology.

The fusion of the Leupold and Mitchison approaches in pioneering genetic approaches to cell cycle control secured, for fission yeast, an enduring spot in the limelight of cell cycle research. This inspired Mitsuhiro Yanagida to place fission yeast at the forefront of mitosis research, while Anwar Nasim, Paul Russell, and Paco Antequera showed just how defining fission yeast studies can be in the arenas of DNA replication, repair, and checkpoints.

While this cell-cycle-driven roller coaster was setting off, studies by Richard Egel and Amar Klar of the most fundamental aspect of any genetic fungal system, mating-type switching, uncovered some fascinating biology surrounding DNA imprinting and silencing of nonexpressed cassettes. Understanding how cassettes were silenced was informed by the transposition of studies of position effect variegation from *Drosophila* to *S. pombe* by Robin Allshire and Amar Klar; these laid the foundations for *S. pombe*'s current preeminent position as the best single-cell model in which to address fundamental questions involving heterochromatin and the molecular basis for epigenetic inheritance. A similar rise to fame in the field of sexual differentiation was driven by Masayuki Yamamoto's desire to explain why Richard Egel's mutants failed to initiate meiosis. This ultimately led to Yoshinori Watanabe's seminal use of *S. pombe* to define the biology that sits at the heart of sexual reproduction: the molecular basis for chromosome partition in meiosis. A further phase of fission yeast sexual differentiation studies was propelled to fame by Yasushi Hiraoka's elegant and incisive work on the postreplicative recombination period of “horsetail” movement that Julie Cooper's studies have so elegantly shown is a gateway to understanding telomeres and global nuclear organization.

As with all organisms, genomics technologies heralded a new era in fission yeast research. Not only did the *S. pombe* genome sequence provide a definitive list of all genes to exclude the “what if another homolog exists?” question, but it opened the way for new and inspired approaches, pioneered by the Jürg Bähler and Nevan Krogan laboratories, to study uncloned genes individually and at the genome-wide level. Ever since the assembly of the initial drafts, Val Wood has been annotating and interrogating the *S. pombe* genome to develop what she ensures will remain a dynamic, ever-expanding, and invaluable database: pombase.org. Genomics work also inspired Nick Rhind to open the door to comparative studies and molecular interrogation of *S. pombe*'s cousins *S. octosporus*, *S. cryophilus*, and *S. japonicus*. The sequence comparisons alone and the pioneering interrogation of *S. japonicus* by Hironori Niki and Snezhana Oliferenko are already revealing some fascinating biology.

Such emphatic demonstrations of the utility of fission yeast are not unique. They stand alongside studies of the cytoskeleton, transcription, and cell wall biogenesis as just some of the areas where the malleability of this excellent model organism has been ruthlessly exploited to great gain. As we enter an era focused on noncoding RNA and renewed interest in metabolism and fungal diseases, we hope that more biologists will embrace fission yeast's endless potential for simple, direct, and incisive experiments in both novel and established fields.

Fission yeast is often described as a “simple eukaryotic model system”; however, nowhere is the complexity of biology exposed more extensively than in this “simple” model. Invariably, the ability to execute utterly conclusive, fully controlled experiments in fission yeast leads to the inevitable conclusion that “it is a bit more complicated than we thought” or “Oh. . . it is precisely the opposite result to the one we anticipated.” The greater the complexity, the greater the demand for the definition and malleability that systems such as the fission yeasts have to offer. We firmly believe that the definitive nature of experiments in these most malleable of model systems means that the list of landmark discoveries arising from fission yeast research will continue for many years to come. We hope that this manual will facilitate this exploitation of undiscovered riches.

The manual can be divided into two parts. The fundamental technologies that underpin core fission yeast research activity are covered in Chapters 1–10, whereas Chapters 11–18 cover technologies in key areas in which fission yeast is widely exploited. Although space limitations made it impossible to be as comprehensive as we would have liked, our ambition has been to provide both a useful resource to facilitate moves into new aspects of fission yeast biology for the experienced fission yeast laboratory and an easy entry point for newcomers to exploit the bounty fission yeast undoubtedly has to offer. We apologize for omissions but believe certain areas will be covered in the more dynamic technology review literature, which will undoubtedly surpass sections of this manual in years to come.

We would like to thank the fission yeast community for their support in compiling this manual. We are indebted to the authors for their enthusiasm in embracing the unenviable task of condensing accounts of their complex fields into such constrained Topic Introduction and Protocol formats. Their attention to detail and engagement made our task as editors a simple one. We are also deeply indebted to members of the community, too numerous to list, who provided extensive and useful comments to guide the evolution of each chapter. Special thanks go to Maria Smit, Maryliz Dickerson, and Richard Sever at Cold Spring Harbor Laboratory Press, whose positive, enthusiastic, and flexible approach made this manual an easy reality.

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