Foreword. Cellular and molecular biology of non-conventional microbial fungi

Microbiology has been and still is a rich source of knowledge about the cellular and molecular biology of model organisms. Although the concept of model organism has arisen some criticisms, it is generally accepted that the feasibility of biochemical, genetic and other kinds of biological tools to be employed on some model organisms allows to carry out on them a wide spectrum of experimental approaches. Those approaches will lead to deep knowledge on their biology and to rise new possibilities to study the biology of other organisms for which no so accessible tools exist. In this context, easiness does not mean low level science but the ability to employ interdisciplinary experimental approaches to analyze a particular problem. Thus, two microorganisms are the paradigms of model organisms: Escherichia coli (from the early sixties) as a model prokaryote, and Saccharomyces cerevisiae (from the late seventies) as a model eukaryote. As a demonstration that this is the case think about the respective weighty bibles published on them which cover most of but still not all the biological aspects of these microorganisms (with Salmonella typhimurium as a friendly companion in one case).

However, biologists have to pay a toll for studying such model microorganisms. We study laboratory strains that may be far different from other strains of the same species. Molecular biology techniques have shown that E. coli K-12 is genetically very different from clinical E. coli strains, as well as that S. cerevisiae laboratory strains may be quite different among them and with respect to wine or beer strains. By the way, yeast researchers (both signants of this foreword being an example) tend to talk about genetic background differences to justify contrasting results among laboratories. It is interesting that we tend to forget these facts when doing research on model organisms, while explaining at the same time to our students at the basic microbiology course how atenuation is a technique that largely has been employed to develope vaccines! Beyond these anecdotes, real problems rise when other organisms important from an industrial, medical or merely biological point of view are not so easily approachable for study, and extrapollating experimental conclusions from model organisms is not so obvious. A fact to consider also in the new era of microbial genomics is the sequence differences among strains of the same species. While sequence comparisons among pathogenic and non-pathogenic strains might enrich our knowledge of the molecular basis of microbial pathogenicity, published bacterial genomic sequences up to this moment mostly correspond to a single laboratory strain of each species.

With all the above considerations in mind, we proposed to elaborate a monographic number on non-conventional microbial fungi as opposed to the S. cerevisiae standard, with the aim to introduce to not so thoroughly studied microbial fungi. Our definition of non-conventional microbial fungus justifies the inclusion of a pathogenic dimorphic yeast like Candida albicans, as well as the industrially relevant Yarrowia lipolytica, or the description of wine S. cerevisiae strains or a fungus with complex developmental stages as Ustilago maydis. Authors of the reviews demonstrate how difficulties in the application of previous cellular and-especiallymolecular biology approaches may be recompensed by a better knowledge of the biology of these organisms, with subsequent medical or industrial implications in some cases. We want to thank the authors of the reviews the work they carried out. They rapidly responded to our suggestions to present clear (and as short as possible!) descriptions on the respective microorganisms. For them is the merit of the results, and it is our responsibility the possible deficiencies that may arise while reading them. We expect that this monographic issue will broad the view of the readers on the biological diversity and interest of microbial fungi.

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