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Commentary

Short Note on *Saccharomyces cerevisiae*

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DESCRIPTION

Saccharomyces cerevisiae has been a key for the study of infectious diseases, comprising dsRNA viruses, ssRNA viruses, and prions. Studies of the mechanisms of virus and prion replication, virus structure, and structure of the amyloid filaments that are the base of yeast prions have been at the forefront of such studies in these classes of infectious bodies. Yeast has been predominantly useful in defining the interactions of the infectious elements with cellular components: chromosomally encoded proteins essential for blocking the propagation of the viruses and prions, and proteins intricate in the expression of viral constituents. *Saccharomyces cerevisiae* is the best studied eukaryote and a valued tool for most aspects of basic research on eukaryotic organisms. This is due to its unicellular nature, which often simplifies matters, offering the combination of the facts that nearly all biological functions found in eukaryotes are also existing and well preserved in *S. cerevisiae*. In addition, it is also easily amenable to genetic manipulation. Moreover, unlike other model organisms, *S. cerevisiae* is simultaneously of great significance for various biotechnological applications, some of which date back to thousands of years. *S. cerevisiae's* biotechnological efficacy resides in its unique biological characteristics, i.e., its fermentation ability, accompanied by the production of alcohol and CO_2 and its resilience to adverse circumstances of osmolarity and low pH. Among the most prominent applications including the use of *S. cerevisiae* are the ones in food, beverage -particularly wine- and biofuel production industries. Under favorable conditions, strains of *Saccharomyces cerevisiae* have produced up to 18 percent (by volume) of alcohol, although 15 to 16 percent is the usual limit.

The mannoprotein which is a major component of the cell wall of *Saccharomyces cerevisiae* is an effectual bioemulsifier. Mannoprotein emulsifier was extracted in a high yield from whole cells of fresh bakers' yeast by two methods, by autoclaving in neutral citrate buffer and by digestion with Zymolase, a beta-1,3-glucanase. Heat-extracted emulsifier was cleansed by ultrafiltration and contained approximately 44% carbohydrate (mannose) and 17% protein. Treatment of the emulsifier with protease removed emulsification. Kerosene-in-water emulsions were stabilized over a broad range of circumstances, from pH 2 to 11, with up to 5% sodium chloride or up to 50% ethanol in the aqueous phase. In the presence of a low concentration of various solutes, emulsions were stable to three cycles of freezing and thawing. An emulsifying agent was extracted from each species or strain of yeast tested, comprising 13 species of genera other than *Saccharomyces*. Yeast from the manufacture of beer and wine was established to be a potential source for the large-scale production of this bio emulsifier.

Pseudohyphal development in both haploid and diploid strains of *Saccharomyces cerevisiae* reflects concerted changes in altered cellular processes: budding pattern, cell elongation and cell adhesion. These changes are triggered by environmental signals and are controlled by numerous pathways which act in parallel. Nitrogen deprivation, And possibly other stresses, activate a MAP kinase cataract which has the transcript factor Ste12 as its final target. A cAMP-dependent pathway, in which the protein kinase Tpk2 plays a particular role, is also necessary for the morphogenetic switch. Both pathways contribute to regulate the expression of the MUC1/FLO11 gene which encodes a cell-surface flocculin required for pseudohyphal and invasive growth. The MAP kinase cascade could also control the action of the cyclin/Cdc28 complexes which affect both the budding pattern of yeast and cell elongation. An additional protein which excites filamentous growth in *S. cerevisiae*; while its mode of action is unknown, it may be controlled by a cAMP-dependent protein kinase, as occurs with the homologous protein Efg1 from *Candida albicans*, which is essential for the creation of true hyphae. Morphogenesis in different yeast genera share common elements, but there are also significant differences. Although a complete picture cannot yet be drawn, limited models may be proposed for the interaction of the regulatory pathways, both in the case of *S. cerevisiae* and in that of *C. albicans*. In recent decades, fungal infections have come out as an important health problem accompanying with more people who present deficiencies in the immune system, such as HIV or transplanted patients. *Saccharomyces cerevisiae* is one of the developing fungal pathogens with a unique characteristic: its presence in many food products. *S. cerevisiae* has a perfectly good food safety

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record compared to other microorganisms like virus, bacteria and some filamentous fungi. However, humans unknowingly and inadvertently ingest large viable populations of *S. cerevisiae* (home-brewed beer or dietary supplements that comprise yeast).

In the last few years, researchers have studied the nature of *S. cerevisiae* strains and the molecular mechanisms correlated to infections.