Diversity of microbial growth strategies in a limited nutrient world

September 17 2013

The budding yeast, *Saccharomyces cerevisiae*, is a prime organism for studying fundamental cellular processes, with the functions of many proteins important in the cell cycle and signaling networks found in human biology having first been discovered in yeast.

Now, scientists from New York University have now developed a sophisticated assay to track cell growth at very low nutrient concentrations. The assay uses time-lapse microscopy to monitor individual yeast cells undergoing a small number of divisions to form microcolonies. The assay can measure the lag times and growth rates of as many as 80,000 individual microcolonies in a single 24-hour experiment, opening up a powerful new high-throughput tool to study the complex interplay between cell growth, division and metabolism under environmental conditions that are likely to be ecologically relevant but had previously been difficult to study in the laboratory.

The researchers studied growth rates and lag times in both lab strains and wild yeast by varying the amount of its prime carbon food source, glucose. They confirmed the prediction made over 60 years ago by Noble-prize-winning biologist Jacques Monod regarding changes in microbial growth rates with limited nutrients (the Monod equation). They also found significant differences among strains in both the average lag response (the amount of time it takes to transition from cell quiescence to restarting cell growth) and average growth rates in response to different environmental conditions.

In addition to average differences between strains and conditions, the powerful assay revealed metabolic differences among cells of the same strain in the same environment. Moreover, yeast strains differed in their variances in growth rate. According to the study's lead author, Naomi Ziv, "Heterogeneity among genetically identical cells in the same environment is a topic of increasing interest in biology and medicine. The different strain variances we see suggest that the extent of nongenetic heterogeneity is itself genetically determined."

Further investigations could pave the way to a more complete understanding of the genetics and metabolomics of cell growth in yeast and the underlying mechanisms relevant to other settings in which cells face challenging conditions, such as cancer progression and the evolution of drug resistance.

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Provided by Oxford University Press