Abstract

Saccharomyces cerevisiae, also known as a budding yeast, is one of the most used model organism in research of biochemical processes at the single cell level. Typically an exponential cell volume and population growth assumption is considered. Recently the adder model based on the uniform exponential growth of the cell volume with a constant volume added over the cell cycle was proposed for budding yeast based on the experimental measurements of cell volumes at the start and at the end of the cell cycle. However, multiple experimental studies of budding yeast report the non-uniform physiologically structured growth (PSG) instead with alternating intervals of exponential and logistic volume growth with duration of each phase dependent on the cell volume at the start of the phase. In this work we propose a model based on the PSG to resolve this apparent disagreement by showing that when changes in the cell volume are considered only between the volume at the beginning and at the end of the cell cycle, the PSG model exhibits similar behaviour to the adder model in most aspects. We also show that the number of cells in the population and the total volume of the population appear to grow exponentially when the cell volume growth govern by the PSG model despite its non-uniform structure of the single cell volume growth. We are also able to identify the multimodal stationary (homeostatic) cell volume distribution and the stationary fractal type cell volume distribution of cells at the start of their most recent cell cycle that differ from the distributions predicted by the adder model. One of the areas where the budding yeast is used as a model organism is the study of interactions of proteins from the Bcl-2 family that play a important role in the regulation of apoptosis, programmed cell death, in human cells. In the last part of this thesis we expanded the PSG model to incorporate mitochondrial volume growth to propose the model of interactions between proteins Bax and Bcl_{xL} and their effect on mitochondria at a single-cell level when co-expressed in yeast cells.

Key words: *Saccharomyces cerevisiae*, mathematical modelling, cell growth and division, Bcl-2 family proteins