Mathematical model of the role of CDC6 in CDK1 activation upon M-phase entry

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We focus our research on a clarification of the role of CDC6 protein in the entry into mitosis. In our biochemical experiments we have shown before that CDC6 acts as inhibitor of the major enzyme triggering the entry into mitosis, namely the kinase Cyclin-CDK1, during the activation of this protein complex upon mitotic entry. Moreover, CDC6 determines not only the dynamics of Cyclin-CDK1, but also a characteristic inflection of the activation curve at early stages of this process. This shape of the curve of Cyclin-CDK1 activation resembles the curve of microorganisms growth upon changing culture conditions known as diauxic growth. Thus, CDC6 seems to be the only factor responsible for the diauxic-type of growth of the activity of Cyclin-CDK1 kinase. The mathematical model, which we propose here concerns the relationship of the mentioned above proteins and CDC25 phosphatase, known as a major activator of CDK1 during mitotic entry. Thus, all regulatory proteins referred to herein are: kinase CDK1, its regulatory subunit cyclin B, the activator phosphatase CDC25 and the recently identified by us inhibitor CDC6. Our mathematical model is based on mass action kinetics. This model allows us to formulate a new hypothesis on a mutual interaction between CDC6 and CDK1, which determines the correct, diauxic-like dynamics of CDK1 activation upon mitotic entry.