Identify potential sites of phosphorylation on \textit{S. cerevisiae} Cdc28 through examining evolutionary conservation

Eric Waters and Dr. Jack Vincent
Division of Sciences & Mathematics, University of Washington | Tacoma, Tacoma, WA 98402

Introduction

Phosphorylation plays a critical role in the regulation of many cellular processes including cell cycle, growth, apoptosis and signal transduction pathways. Cdc28/CDK1 kinase is an essential kinase for regulation of the cell cycle. It is a member of the Pkc superfamily of kinases. The phosphorylation of Cdc28 in budding yeast is a checkpoint for G1 progression of the cell cycle. Cdc28 has the ability to self-phosphorylate and is able to phosphorylate other substrates and kinases within the cell cycle. The phosphorylation of Cdc28 relates to checkpoints that are go or no go to proceed to the next phase of mitosis. Signaling between kinases is done by the process of phosphorylation and dephosphorylation of Cdc28.

Approach

\textit{Saccharomyces cerevisiae} has multiple kinases involved in the process of cell division. Our goal is to use Bioinformatics to find possible links of crosstalk between Cdc28, Ipl1 and Mps1 kinases. By comparing conservation at known phosphorylation sites. We will be looking at Cdc28 phosphorylation sites since it's the master regulator in mitotic cell division. Each kinase has specific roles during cell division process.

Methods

We will use blast protein database searches to locate possible conserved sequences between the following kinase proteins Cdc28, Ipl1, Mps1. To determine if there is correlation between the kinases that will link homologs to each kinase. We will access the biogrid database at https://thebiogrid.org to identify sites of phosphorylation to determine possible sites linkage between Cdc28, Ipl1 and Mps1 kinases. The purpose is to find possible links to crosstalk between kinases during Mitosis. Examine conserved sequences within Cdc28/CDK1 between organism of multiple kingdoms for possible evolutionary links within Eukaryotic life.

Method I: Identify known sites of phosphorylation for Cdc28 within \textit{S. cerevisiae} species.
Method II: Identify known sites of phosphorylation for Cdc28 within the Fungi kingdom excluding \textit{S. cerevisiae} species.
Method III: Identify known sites of phosphorylation for Cdc28 within the Fungi kingdom excluding all Fungi species.

Biogrid information

Identifying the linkage of phosphorylation between Cdc28, Ipl1 and Mps1 kinases was not determined by using bioinformatics. Well conserved sites of phosphorylation were found within the \textit{S. cerevisiae} species, the fungi kingdom and primates. Site 46 is identified as a Serine residue Site 169 is identified as a Threonine residue Site 190 is identified as a Serine residue Site 191 is identified as a Threonine residue

Results

There is full conservation of known phosphorylation locations within Cdc28/CDK1 kinase. The conservation of phosphorylation locations seems to have a profound impact on eukaryotic life as we know it. These locations were observed from \textit{S. cerevisiae} to \textit{H. sapiens}. The evolutionary impacts from single cell organisms to multicellular are present with the findings of this Bioinformatics survey. Proper cell division requires equal distribution of genetic material to ensure proper conservation of genetic information to future generations of any species. In future studies into the mechanism of phosphorylation at these locations will help to further our understanding as why they are so important to the cell cycle.

References


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