Identification of a Potential Spindle Assembly Checkpoint Component Via Phosphorylation Motif Conservation

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Abstract. The spindle assembly checkpoint (SAC) is a highly regulated and critical aspect of the mitotic cell cycle. The SAC ensures that progression from metaphase to anaphase is stalled until there are correct attachments between microtubules and kinetochores on each sister chromatid. In the presence of an unattached kinetochore, phosphorylation of the outer *Saccharomyces cerevisiae* kinetochore protein, Spc105, by the kinase, Mps1, is an essential step required in the initiation of the SAC. Identification of the Spc105 MELT consensus motif, methionine (M), glutamic acid (E), leucine (L) and threonine (T), as a site of phosphorylation gave way to an in depth understanding of the essential signaling cascade that follows Mps1 kinase activity. Site directed mutagenesis, in which the phosphorylation site, serine or threonine, is replaced with the non-polar amino acid alanine, has shown that mutations to Mps1 phosphorylation sites on kinetochore proteins can lead to chromosome mis-segregation and aneuploidy in mitotic cells. To date, it is unclear which phosphorylation events are essential for kinetochore function and SAC regulation. There is evidence that Mps1 kinase activates many kinetochore proteins. However, all of the targets of the kinase have not been identified. I used the Protein Pattern Find tool from Bioinformatics.org to detect MELT motifs and thus Mps1 kinase targets within amino acid sequences of 59 *S. cerevisiae* kinetochore proteins. Molecular Evolutionary Analysis-across computing platforms bioinformatics software (MEGAX) was used to indicate conservation of the MELT consensus motifs within the fungi kingdom. Identification of highly conserved MELT consensus motifs of *S. cerevisiae* kinetochore protein, Stu1, suggests that Stu1 may be a potential novel substrate of the serine-threonine kinase, Mps1.