Investigating Modification of an RNA-Binding Protein in Pathogenic Yeast using Mass Spectrometry

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Slr1, an SR-like RNA-binding protein in the pathogenic yeast *Candida albicans*, has been shown previously by the McBride lab to be critical for normal virulence in a mouse model of disease. Sequence homology with other proteins has suggested that Slr1 may transport mRNA, and experimental evidence gathered by the McBride lab supports this model. We hypothesize that Slr1 may be phosphorylated near the C-terminus of the protein, and that this modification in turn may regulate Slr1 mediated RNA transport. To determine which amino acid(s) is/are phosphorylated, I have adopted an approach where I first purify Slr1 and then analyze it using a Liquid Chromatography-Mass-Spectrometer (LC-MS). Using this method, I have identified a known phosphorylation site on ovalbumin, but to date, purification has not yielded sufficient quantities of Slr1 for LC-MS analysis. Following optimization of the purification protocol, however, recent, preliminary results indicate that I may have a sample that could be analyzed by LC-MS in the near future.

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