

Predicting New Prion Candidates in Yeast

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Abstract

Prions are infectious proteins capable of self-propagating and transmitting between organisms. Even though there is no homolog to the mammalian prion protein in yeast, several soluble proteins can form heritable aggregates de novo. These proteins provide a model system to investigate the nucleation, aggregation and propagation steps involved in the formation of a prion fibril. Several prion prediction algorithms have been developed to predict yeast proteins that have the propensity to form prions. One of these algorithms was previously developed in our laboratory (Prion Aggregation Prediction Algorithm, PAPA, Toombs et al., 2012). Therefore, we used PAPA to scan the yeast proteome to extract proteins that contain domains predicted to have prion activity (prion-like domains). These prion-like domains will be tested in four prion activity assays to assess their activity in vivo as well as in vitro. Here we provide preliminary evidence that we are successful at predicting yeast proteins that present prion activity in vivo. Following characterization of these prion-like domains, we will test the respective full-length proteins for prion activity using microscopy as well as developing phenotypic assays.

Keywords:

Ultimately we may identify new prion candidates in yeast by confirming PAPA's ability to predict prion proteins from the yeast proteome it allows the possibility to apply this methodology to other proteomes