1153-92-481 **Mikahl Banwarth-Kuhn*** (mbanwarth-kuhn@ucmerced.edu), **Jordan Collignon** and **Suzanne Sindi**. *Study of the effect of individual cell behaviors on prion protein aggregation and colony structure and organization in yeast.*

Prion proteins are most commonly associated with fatal neurodegenerative diseases in mammals, but they are also responsible for a number of harmless phenotypes in yeast. The diseased state (or phenotype) in yeast arises when a misfolded form of a protein, i.e. prion, appears and, rather than be removed by cellular quality control mechanisms, persists. Mathematical models have previously been developed for studying prion aggregate dynamics in isolation. However, a major open question in prion biology is to understand how prion aggregates spread between cells within a whole colony or tissue. We introduce a novel, two-dimensional agent-based model of a budding yeast colony with detailed representation of cell-type specific biological processes, including budding, variation in cell-cycle length, and asymmetric protein segregation. The model is used to study how individual cell behaviors impact colony organization and structure as well as protein aggregation and propagation. In the model, spatial arrangement of cells is modeled using a center-based modeling approach and prion aggregate dynamics are simulated within each individual cell. The unified model may have the potential to predict mechanisms underlying experimentally observed phenomena such as sectored prion phenotypes. (Received September 03, 2019)