Abstract Submitted
for the MAR17 Meeting of
The American Physical Society

3D Model of Cytokinetic Contractile Ring Assembly: Node-Mediated and Backup Pathways[1] TAMARA BIDONE, University of Chicago, DIMITRIOS VAVYLONIS, Lehigh University — Cytokinetic ring assembly in model organism fission yeast is a dynamic process, involving condensation of a network of actin filaments and myosin motors bound to the cell membrane through cortical nodes. A 3D computational model of ring assembly illustrates how the combined activities of myosin motors, filament crosslinkers and actin turnover lead to robust ring formation [Bidone et al. Biophys. J, 2014]. We modeled the importance of the physical properties of node movement along the cell membrane and of myosin recruitment to nodes. Experiments by D. Zhang (Temasek Life Sciences) show that tethering of the cortical endoplasmic reticulum (ER) to the plasma membrane modulates the speed of node condensation and the degree of node clumping. We captured the trend observed in these experiments by changes in the node drag coefficient and initial node distribution in simulations PM [Zhang, Bidone, and Vavylonis, Curr. Biol. (2016)]. The model predicted that reducing crosslinking activities in ER tethering mutants with faster node speed enhances actomyosin clumping. We developed a model of how tilted and/or misplaced rings assemble in cells that lack the node structural component anillin-like Mid1 and thus fail to recruit myosin II to nodes independently of actin. If actin-dependent binding of diffusive myosin to the cortex is incorporated into the model, it generates progressively elongating cortical actomyosin strands with fluctuating actin bundles at the tails. These stands often close into a ring, similar to observations by the group of J.Q. Wu (The Ohio State University).

[1]NIH R01GM098430

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Date submitted: 11 Nov 2016 Electronic form version 1.4