Abstract Submitted
for the MAR13 Meeting of
The American Physical Society

Model of Capping Protein and Arp2/3 Complex Turnover in the Lamellipodium Based on Single Molecule Statistics LAURA MCMILLEN, Lehigh University, MATTHEW SMITH, UCL London/Max Planck Institure-CBG Dresden, DIMITRIOS VAVYLONIS, Lehigh University — Capping protein (CP) and Arp2/3 protein complex regulate actin polymerization near the leading edge of motile cells. Actin and regulatory proteins assemble near the leading edge of the cell, undergo retrograde flow, and dissociate into the cytoplasm as single subunits (monomers) or as part of multiple actin subunits (oligomers.) To better understand this cycle, we modeled the kinetics of actin CP and Arp2/3 complex near the leading edge using data from prior experiments [Miyoshi et al. JCB, 2006, 175:948]. We used the measured dissociation rates of Arp2/3 complex and CP in a Monte Carlo simulation that includes particles in association with filamentous and diffuse actin in the cytoplasm. A slowly diffusing cytoplasmic pool may account for a big fraction of CP, with diffusion coefficients as slow as 0.5 $\mu m^2/s$ [Smith et al. Biophys. J., 2011,101:1799]. Such slow diffusion coefficients are consistent with prior experiments by Kapustina et al. [Cytoskeleton, 2010, 67:525]. We also show that the single molecule data are consistent with experiments by Lai et al. [EMBO J., 2008, 28:986]. We discuss the implication of disassembly with actin oligomers and suggest experiments to distinguish among mechanisms that influence long range transport.

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Date submitted: 09 Nov 2012 Electronic form version 1.4