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Single molecule analysis of B cell receptor motion during signaling activation IVAN REY SUAREZ, Univ of Maryland-College Park, PETER KOO, Harvard University, SHU ZHOU, BRITTANY WHEATLEY, WENXIA SONG, Univ of Maryland-College Park, SIMON MOCHRIE, Yale University, ARPITA UPADHYAYA, Univ of Maryland-College Park — B cells are an essential part of the adaptive immune system. They patrol the body for signs of infection in the form of antigen on the surface of antigen presenting cells. B cell receptor (BCR) binding to antigen induces a signaling cascade that leads to B cell activation and spreading. During activation, BCR form signaling microclusters that later coalesce as the cell contracts. We have studied the dynamics of BCRs on activated murine primary B cells using single particle tracking. The tracks are analyzed using perturbation expectation-maximization (pEM), a systems-level analysis, which allows identification of different short-time diffusive states from single molecule tracks. We identified four dominant diffusive states, two of which correspond to BCRs interacting with signaling molecules. For wild-type cells, the number of BCR in signaling states increases as the cell spreads and then decreases during cell contraction. In contrast, cells lacking the actin regulatory protein, N-WASP, are unable to contract and BCRs remain in the signaling states for longer times. These observations indicate that actin cytoskeleton dynamics modulate BCR diffusion and clustering. Our results provide novel information regarding the timescale of interaction between BCR and signaling molecules.

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