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Contour-Based Data Analysis: Loading Rate Dependence in Dynamic Catch of Integrin-Ligand Bonds

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Abstract: Cell-matrix interactions guide various cell behaviors, including proliferation, differentiation, migration, etc. Integrins, as a known transmembrane mechanosensor, undergo conformational changes in response to mechanical stimuli, and manipulate cell-matrix chemical-mechanical coupled signaling transduction [1]. The integrin-ligand bond kinetics has gain increasing attention among researchers. Independent studies showed that the integrin-ligand bond has been reported to be reinforced by the applied force *f*, while the loading rate *df/dt* had little effect on the bond lifetime [2].

We previously observed a dramatic increase in bond lifetime beyond a loading rate threshold for the integrin α2β1-DGEA bond, by introducing AFM (Atomic Force Microscopy) -based SCFS (single-cell force spectroscopy) and contour-based data analysis algorithm [3].

Here, we used AFM SMFS (single-molecule force spectroscopy)/SCFS [4] and contour-based data analysis to study the kinetic properties of α2β1-DGEA and α5β1-RGD bonds. Both bonds possessed loading-rate-dependent lifetimes on a molecular level and in living cells.

In conclusion, with the help of AFM force spectroscopy and contour-based data analysis, we illustrated the complex relationship between the rupture force and the loading rate of the integrin-ligand bonds. At least two subunits of the integrin family showed loading-rate-dependent dynamic catch with their ligands. It worth more efforts on whether loading-rate-strengthened receptor-ligand bond is a general property of the integrin family.

Keywords: Integrin; receptor-ligand bond kinetics; atomic force microscopy; loading rate

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