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Mechanisms and Dynamics of Collagen Assembly[1] JINHUI TAO, RAYMOND FRIDDLE, DEBIN WANG, JIM DE YOREO, Lawrence Berkeley National Laboratory — Collagen is the major structural protein of bone, dentine and it template the nucleation of biomineral phases. Both collagen conformation and architecture on substrate are critical for its function. We studied the mechanism of collagen I assembly on mica by in-situ AFM. At acidic condition, assembled architecture evolved from random fibers to co-aligned fibers and finally to bundles as the K^+ concentration increased from 100 to 300mM. XPS and NEXAFS showed the concentration of K^+ within the collagen layer increased and the intensity of absorption peak due to π^*(C=O) resonance decreased with higher K^+ concentration. The magnitude of collagen-mica (C-M) and collagen-collagen (C-C) interactions were measured by dynamic force spectroscopy. The free energy ΔG_b for C-M and C-C at 200mM K^+ were 13.7kT and 1.4kT, while ΔG_b at 300mM K^+ were 5.7kT and 12.3kT, respectively. The switch from co-aligned fibers to 3D bundles is driven by the reversal in the magnitude of C-C and C-M interactions. Our results indicate K^+ complex with C=O of collagen and its effect on the strength of collagen-collagen bridging is the likely source of architecture control.

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