

Abstract Submitted
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Looping of anisotropic, short double-stranded DNA¹ HAROLD KIM, TUNG LE, Georgia Institute of Technology — Bending of double-stranded DNA (dsDNA) is associated with fundamental biological processes such as genome packaging and gene regulation, and therefore studying sequence-dependent dsDNA bending is a key to understanding biological impact of DNA sequence beyond the genetic code. Average mechanical behavior of long dsDNA is well described by the wormlike chain model, but sequence-dependent anisotropic bendability and bendedness of dsDNA can in principle lead to abnormally high looping probability at short length scales. Here, we measured the looping probability density (J factor) and kinetics of dsDNA as a function of length and curvature using single-molecule FRET (Förster Resonance Energy Transfer). For theoretical comparison, we calculated the J-factor using a discrete dinucleotide chain model, and also simulated it by Monte Carlo methods. We provide evidences that even when the intrinsic shape of dsDNA is accounted for, the wormlike chain model fails to describe looping dynamics of dsDNA below 200-bp length scale.

¹Georgia Tech FIRE program

Harold Kim
Georgia Institute of Technology

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