

Internal friction of a migrating Holliday junction

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Friction within biomolecules has recently gained increasing interest. Here we present a method that allows to study the friction that occurs during fast, few nm-sized refolding processes of nucleic acids. Branch migration of a homologous Holliday junction serves as an ideal system where such friction can be investigated. In this four-arm DNA junction the opposing arms possess identical sequences with respect to the junction center. In the absence of external constraints the junction is mobile such that one pair of homologous arms can expand at the expense of the other in single base pair diffusive steps. We measure the dynamics of the branch migration process by stretching a torsionally constrained Holliday junction using magnetic tweezers and measuring the length fluctuations of the arms with high-speed videomicroscopy at ~ 3 kHz. Since DNA has a helical structure, branch migration causes twisting of the arms with one turn per helical pitch moved. This constrains the movement of the junction within the tweezers to ~ 10 bp. Single base pair diffusive steps are expected to occur on a sub-millisecond time scale and to be much smaller than the overall DNA length fluctuations. Thus they can not be directly resolved. However, power-spectral-density analysis of the length fluctuations is able to clearly resolve the overall dynamics of the branch migration process. Theoretical modeling considering the elastic coupling of DNA bending fluctuations and the junction movement allows to quantitatively determine the stepping rate and thus the friction of the branch migration process. We expect that our method is widely applicable to study local-scale molecular friction in biological systems.

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