MD simulations of oligonucleotide duplexes of peptide nucleic acid

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Peptide nucleic acid (PNA) is a DNA analogue in which the phosphodiester backbone has been replaced by a 2-aminoethyl-glycine backbone that is neutral and achiral (Figure 1). PNA is able to hybridize with high affinity and specificity to Watson-Crick complementary sequences of DNA, RNA, or other PNA strands. Since its discovery, PNA has shown great promise for use in the detection of gene mutations as well as gene-targeted drugs. Developing theoretical methods for examining the structure and stability of PNA·DNA duplexes is important for evaluating and improving diagnostic probes of PNA. Recent experiments have suggested that PNA·DNA duplexes are significantly stabilized when purine bases are present in the PNA strand rather than the DNA strand. These studies, however, could not elicit the origin of the different stabilities between purine-rich PNA versus pyrimidine-rich PNA heteroduplexes with DNA. Using molecular dynamics simulations, we analyze the helical structure of PNA·DNA with different sequences in comparison to pure DNA duplexes. The effects of duplex mismatches on the helical stability is also investigated and discussed.

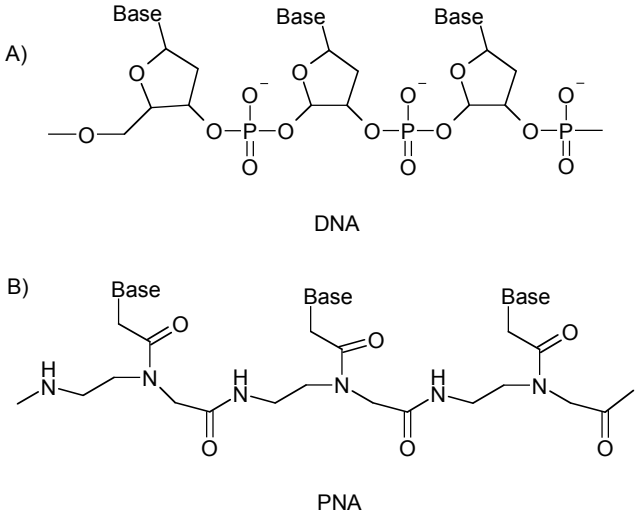

Figure 1