Modeling specific interaction of polyamines with DNA double helix

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The interactions of natural polyamine molecules (putrescine^{2+}, spermidine^{3+}, and spermine^{4+}) with the DNA fragment (CGCGAATTCGCGAATTCGCG) have been studied using atomistic molecular dynamics simulation [1]. The results show that polyamine molecules prefer to be localized in the groove of the double helix characterized by the lowest width. The widths of grooves of the double helix were found to depend on the sequence of nucleotide bases, and this in turn induces the polyamine to bind preferentially to some nucleotide sequence motifs. In the case of the considered DNA fragment the narrowest region is the minor groove in A-tract, and the polyamines were found to reside the longest time in this region. To further characterize the binding preference, we developed a phenomenological model showing that the electrostatic interactions are the most important driving force in this phenomenon, making it even more prominent for polyamines with higher charges. Thus, the present study explains the specificity of polyamine interactions with A-tract region of the DNA double helix which is observed in experiments.

1. Perepelytsya S., Uličný J., Laaksonen A., Mocci F. Pattern preferences of DNA nucleotide motifs by polyamines putrescine^{2+}, spermidine^{3+}, and spermine^{4+}. Nucleic Acids Research, 2019, 47, 6084-6097.