

# DNA-DNA interactions and homology "recognition well"

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Mutual recognition of homologous sequences of DNA before strands exchange them is considered to be the most puzzling stage of homologous recombination<sup>1</sup>. In 2001, a mechanism was suggested for a double stranded DNA molecule to recognize from a distance its homologous match in electrolytic solution without unzipping.<sup>2</sup> Based on a theory of electrostatic interactions between helical molecules<sup>3,4</sup>, the difference in the electrostatic interaction energy between homologous duplexes and that between nonhomologous duplexes, called the *recognition energy*, was calculated. First experiments that have verified the existence of the predicted phenomena were published in Ref.<sup>5</sup>

Here we report a theoretical investigation of the form of the potential well (the first account of which was recently reported in Ref. 6) which DNA molecules may feel sliding along each other. This well, the bottom of which is determined by the recognition energy, leads to trapping of the molecular tracks of the same homology in direct juxtaposition. A simple formula for the shape of the well was obtained. The well is quasi-exponential. Its half-width is determined by the *helical coherence length*, introduced first in the same 2001 paper, the value of which, as the latest study shows, is close to 10 nm<sup>7</sup>.

In this talk various factors that may influence the shape of the well will be discussed together with several scenarios of possible single molecule experiments.

<sup>1</sup>Barzel A, Kupiec M Finding a match: how do homologous sequences get together for recombination? *Nature Reviews Genetics* 9:27-37(2008); Zickler D From early homologue recognition to synaptonemal complex formation. *Chromosoma* 115:158-174 (2006).

<sup>2</sup>Kornyshev AA, Leikin S (2001) Sequence recognition in the pairing of DNA duplexes. *Phys Rev Lett* 86:3666-3669 (2001).

<sup>3</sup>Kornyshev AA, Leikin S (1999) Electrostatic zipper motif for DNA aggregation. *Phys Rev Lett* 82:4138-4141 (1999)

<sup>4</sup>Kornyshev AA, Lee DJ, Leikin S, Wynveen A (2007) Structure and interactions of biological helices. *Rev Mod Phys* 79:943-996 (2007).

<sup>5</sup>Baldwin G, Brooks N., Robeson R., Goldar A., Wynveen A., Leikn S., Seddon J.M., Kornyshev A.A. . (2008) DNA double helices recognize mutual sequence homology in protein free environment. *J Phys Chem B* 112:1060-1064 (2008).

<sup>6</sup>Kornyshev A.A. and A.Wynveen A., The homology recognition well as an innate property of DNA structure, *Proc. Natl. Acad.Sci USA*, 106: 4683-4688 (2009).

<sup>7</sup> A.Wynveen; D.J. Lee; A. A. Kornyshev; S. Leikin, Helical coherence of DNA in crystals and solution, *Nucleic Acids Research* 36: 5540-5551 (2008).