

Study on the stability of DNA triplex nano-assembly

- >Introduction of DNA triplex
- >Investigation of DNA triplex formation
- > How the DNA triplex can be stabilized?
- > The effect of CNT on the formation of triplex
- > The effect of synthetic compounds in the triplex stability

A DNA triplex is formed when pyrimidine or purine bases occupy the major groove of the DNA double Helix forming Hoogsteen pairs with purines of the Watson-Crick

basepairs. Annu. Rev. Biochem (1995) 64:65-95



Oligonucleotide-directed triple helix formation offers a means to target specific sequences in DNA and interfere with gene expression at the transcriptional level.



The formation of a three-stranded, or triple-helical, nucleic acid structure was first observed in 1957 when Felsenfeld et al demonstrated stable and specific binding of a single-stranded polyuridine oligonucleotide to a polyuridine/polyadenine duplex.

J. Am. Chem. Soc (1957) 79:2023–2024



TFO: Triplex Formation Oligonucleotide

The pyrimidine

bases

The purine bases



A TFO can be categorized depending on its base composition and binding orientation relative to its DNA target site.



TFO consisting of cytosine (C) and thymine (T) binds parallel to the purine-rich strand of DNA via Hoogsteen bonds. Protonation at N3 of cytosine is required for proper Hoogsteen bonding with N7 of guanine, but this occurs only under acidic conditions. Biochemistry (1988) 27:9108–9112





Antiparallel Orientation

TFO consisting of adenine (A), thymine (T), Guanine (G) binds antiparallel to the purine-rich strand in DNA via reverse Hoogsteen bonds and requires no base protonation and exhibits largely pH independent binding.

Proc Natl Acad Sci USA (1991) 88:8227-8231





ACCOUNTS OF CHEMICAL RESEARCH (2011) 44: 134–146



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Investigation of DNA triplex formation















	3'-GAAGAAGAAGAAGAAGAA-5'	15R(TFO)
	* * * * * * * * * * * * * * *	Hoogsteen base pairing
5'-TCGC	GAAGAAGAAGAAGAA CGCT- 3'	23R
	•••••	Watson-Crick base pairing
3'-AGCG	CTT CTT CTT CTT CTT GCGA-5'	23Y



Autoradiogram of the gel retardation assay (GRA) of 50 nM duplex, 23RY (lane 1) (with hot 23Y) and mixtures of duplex 23RYand 15R in different mole ratios 2:1 (lane 2); 1:1 (lane 3) and 1:2 (lane 4).

J. Biosci. (2012) 37:519–532







The responses of 10⁻¹² M target DNA by using the material of GSGHs

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3670–3676 Nucleic Acids Research, 2006, Vol. 34, No. 13 doi:10.1093/nar/gkl513

Carbon nanotubes selective destabilization of duplex and triplex DNA and inducing B–A transition in solution

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Premilat et al. have measured the major groove width of GC-DNA (~1.35 nm) and AT-DNA (~1.75 nm) through fiber X-ray diffraction. Eur. Biophys. J. (1991) 28, 574–582 Eur. Biophys. J. (2001) 30, 404–410

SWNTs (~1.1nm) we used were modified with carboxyl group. Carboxyl groups at the open end of SWNTs greatly increased their water solubility and may impact DNA binding to the modified nanotube surface.

Based on SWNTs size and their improved solubility, SWNTs should not bind to DNA minor grooves due to the narrower groove width. Alternatively, SWNTs may bind to the major groove and would fit better to GC-DNA major groove because AT-DNA major groove is too wide for SWNTs binding.

SWNTs selective destabilization of DNA



UV melting profiles of DNA: (A) poly[dGdC]:poly[dGdC], (B) ct-DNA, (C) poly[dAdT]:poly[dAdT] in the absence or presence of SWNTs. From right to left: 0, 1, 5, 10, 15, 20, 25 μ g ml⁻¹ SWNTs in pH = 7 solution.

It is obvious that GC-DNA and ct-DNA became unstable in the presence of SWNTs. Melting temperature Tm decreased 40°C for GC-DNA when SWNTs at 25 μ g ml⁻¹. The absorption after 80°C decreased showing the strong interaction of single strand DNA with SWNTs.

DNA triplex polydA. $(polydT)_2$

Tm1 was decreased in the presence of SWNTs but Tm2 did not change, indicating that SWNTs competed with the third strand binding to the duplex major groove of polydA:polydT, thus decrease the stability of Hoogsteen base pairs but not influence the duplex stability of polydA:polydT.



UV melting profiles of DNA triplex polydA (polydT)2 in the **absence** or presence of SWNTs: SWNTs 1 μ g ml⁻¹; 2 μ g ml⁻¹; 5 μ g ml⁻¹; 10 μ g ml⁻¹ in Tris buffer (10 mM Tris, 200 mM NaCl, pH=7.1). Normalized absorption changes at 260 nm were plotted against temperature.

Nucleic Acids Research, 2011, Vol. 39, No. 15 6835–6843 doi:10.1093/nar/gkr322

Stabilization of unstable CGC⁺ triplex DNA by single-walled carbon nanotubes under physiological conditions

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UV melting profiles of 1 mM d(CT)·d(AG) in the absence or presence of SWNTs: 5 μ g ml⁻¹ ,10 μ g ml⁻¹, 15 μ g ml⁻¹ in cacodylic buffer (1mM cacodylic acid /sodium cacodylate/200mM NaCl/pH 6.5).



Plot of Tm (the difference in the apparent Tm in the presence of SWNTs relative to $d(CT) \cdot d(AG)$. Filled circles are for the transition for dissociation of the third strand. Tm3-2 (triplex) duplex+single strand) is calculated by assuming a Tm3-2 of 4 °C in the absence of SWNTs (no transition seen). Open circles are for the duplex melting transition.

SWNT vs MWNT

As SWNTs can induce the perfect matched DNA triplex formation while MWNTs do not have the effect, which suggests the diameter of nanotubes is very important for DNA binding. MWNTs (10–20 nm-sized) are too large to bind to the major groove. In our previous study, SWNTs (1.1 nm sized) can bind to the groove of TAT DNA triplex and decrease the stability of TAT DNA triplex. In the present study, this selectivity can be attributed to the size of the groove and negatively charged carboxyl-modified SWNTs binding to the groove can further stabilize CGC+ DNA triplex.

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Research paper

Calorimetric and spectroscopic studies of aminoglycoside binding to AT-rich DNA triple helices

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Contribution from the Laboratory of Medicinal Chemistry, Department of Chemistry, Clemson University, Clemson, SC 29634, USA



Aminoglycoside antibiotics



Aminoglycoside can bind to RNA duplex, A-form DNA duplex, DNA-RNA hybrid duplex, DNA triplex, and RNA triplex.

Melting Curves of Aminoglycoside



Change in Tm $_{3-2}$ (rdb =0.67), where rdb =ratio of the drug/base triplet, on the stabilization of the polydA. 2polydT triplex melt in the presence of 150 mM KCl. Without any aminoglycoside present, the melting temperature of the triplex was 34.0 °C. Buffer conditions: 10 mM sodium cacodylate, 0.5 mM EDTA, pH 7.2. The melting rate was 0.2 °C/min. Number of amines in each drug is shown in parentheses.

Biochemistry 1993, 32, 14068-14074

Selectivity of Polyamines in Triplex DNA Stabilization[†]

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Structural specificity effects of trivalent polyamine analogues on the stabilization and conformational plasticity of triplex DNA

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Polyamines

Putrescine: $(H_2N(CH_2)_0NH_2) \rightarrow n=3$ Spermidine: $(H_2N(CH_2)_0NH(CH_2)_3NH_2)$ Spermine: $(H_2N(CH_2)_3NH(CH_2)_4NH(CH_2)_5NH_2)$ Cobalt hexamine $[Co(NH_3)_6^{3+}]$



FIGURE 2: Effect of putrescine (A) and spermidine (B) concentrations on the melting temperatures of triplex (T_{m1}) and duplex (T_{m2}) forms of DNA. The differences between T_{m2} and T_{m1} at each polyamine concentration are also plotted.

poly(dA). 2poly(dT)



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journal homepage: http://www.elsevier.com/locate/biophyschem

The stability of triplex DNA is affected by the stability of the underlying duplex

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The effect of backbone structure on polycation comb-type copolymer/DNA interactions and the molecular assembly of DNA

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Structural formulas of graft copolymers



Available online at www.sciencedirect.com



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Review

Chitosan microspheres as a potential carrier for drugs V.R. Sinha*, A.K. Singla, S. Wadhawan, R. Kaushik, R. Kumria, K. Bansal, S. Dhawan

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BCL2

AAA AAA GAG GAG AAG AAA AAA TTT TTT CTC CTC TTC TTT TTT



A proto-oncogene which encodes for 25KD protein which has a peculiar function of blocking programmed cell death without affecting proliferation.

- (i) a length of at least 18 nt for the target sequence, (ii) at least 40% guanine in the target sequence, (iii) no stretches of more than seven adenines.
- 7. Biochemistry (2002) 41:357–366

(iv) no long stretches of guanines (more than four) and no multiple repetitions of stretches of three or more guanines. 8. Biochemistry (1995) 34:278–284



The way the graphene sheet is wrapped is represented by a pair of indices (n,m). The integers n and m denote the number of unit vectors along two directions in the honeycomb crystal lattice of graphene.



The (n,m) nanotube naming scheme can be thought of as a vector (\mathbf{C}_h) in an infinite graphene sheet that describes how to "roll up" the graphene sheet to make the nanotube. In fact, a simple way to classify each nanotube structure is a vector which connects tow points on the graphene lattice and it is designated with Ch. T denotes the tube axis, and \mathbf{a}_1 and \mathbf{a}_2 are the unit vectors of graphene in real space.

$$d = \frac{a}{\pi}\sqrt{(n^2 + nm + m^2)}.$$









UV absorbance is a commonly used method and considered as the golden standard, it is limited by:

- 1) a relatively low sample throughput;
- 2) the need for relatively large amounts of oligonucleotides;
- 3) a relatively low switch in absorbance level upon melting;

4) the possibility for overlapping peaks for each strand composition in the melting profile

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RESEARCH PAPER

Attachment of biomolecules (protein and DNA) to amino-functionalized carbon nanotubes

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Functionalization of MWCNTs and attachment of biomolecules to the amino-functionalized MWCNTs



of amino f-MWCNTs-DNA