SUPPLEMENTAL INFORMATION

Two dimensional LNA/DNA arrays: estimating the helicity of LNA/DNA hybrid duplex

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Materials Custom DNA oligonucleotides were purchased from Integrated DNA Technology (www.idtdna.com). The 15 base LNA strands were purchased from Sigma Proligo (Proligo France SAS, Paris, France). All strands were purified by denaturing PAGE and the desired bands were cut from the gel, eluted and precipitated from ethanol. The concentration of each strand was measured and estimated by measuring OD_{260}.

Assembly of the complexes. The complexes were formed by mixing a stoichiometric quantity of each strand involved in the complex in 1x TAE/Mg buffer (20 mM Tris, pH 7.6, 2 mM EDTA, 12.5 mM $MgCl_2$). The final concentration of DNA was 1.0 μM. The mixture was cooled slowly from 90 °C to room temperature in 2 L water placed in a styrofoam box over 16 hours to facilitate hybridization.

AFM Imaging. Imaging was performed under 1xTAE/Mg in a fluid cell on PicoPlus AFM (Molecular Imaging) in AAC mode, using the tip on the thinner and shorter cantilever of the NP-S tips (Veeco Inc.). A piece of freshly cleaved mica (Ted Pella, Inc.) was first assembled as the bottom of the fluid cell on the sample plate. Then a 2 μL of the sample (10 times diluted in 1xTAE/Mg buffer, 0.1 μM) was added to the spot. Finally, 400 μL 1xTAE/Mg buffer was added onto the mica in the fluid cell.

Melting temperature measurement. 1.4 mL of the complex (complete AD and AL tile or the partial tiles) was formed as described above and the sample transferred to a quartz cuvette with the 1xTAE.Mg buffer used as a blank. Thermal melting of the complexes were monitored at 260 nm on a Cary UV-vis spectrometer using built-in peltier temperature control. The temperature was incremented at 0.1 °C/min.

DNA sequences The sequences in reference S1 were used.

A tile: Each tile consists of 5 strands
The LNA A tile (AL) and the DNA A tile (AD) are identical except the strands A2.2 and A2.4 are made of LNA and DNA respectively.
A2.1 (48mer)
GAT GGC GAC ATC CTG CCG CTA TGA TTA CAC AGC CTG AGC ATT GAC ACG
A2.2 (15mer) AAT GCT CAC CGA TCA
A2.3 (48mer)
CGA CCA TGA TCG GAC GAT ACT ACA TGC CAG TTG GAC TAA CGG CGC TAC
A2.4 (15mer) CCG TTA GTG GAT GTC

A2.5 (42mer)
TGT AGT ATC GTG GCT GTG TAA TCA TAG CGG CAC CAA CTG GCA

B tile: Each tile consists of 5 strands.
In all the B tiles, the central strand (B1.5) is the same
B1.5 (42mer)
AGT ACA ACG CCA CCG ATG CGG TCA CTG GTT AGT GGA TTG CGT

As one ascends the series, there is an extra base added to one of the sides of the DX molecule. This means that one of the crossover stands can remain the same as the previous molecule in the series.

B0 tile
B2.1.0 (68mer)
CGTGCATCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAGTT
ACCGCATCGGACAGCAGCCTGAC
B2.2.0 (37mer) GCCATCCGTCGATACGGCACCATGATGCACGGTAGCG
B2.3.0 (68mer)
AGTCGCACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGTAC
TACGCAATCCTGCCGTATCGACG
B2.4.0 (37mer) TGGTCGGTCAGGCTGCTGTGGTCGTGCGACTCGTGTC

B1 tile
B2.1.1 (69mer)
CGTGCATCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAGTT
ACCGCATCGGACAGCAGCCTTGAC
B2.2.1=B2.2 (37mer)
B2.3.1(69mer)
AGGTCGCACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGTA
CTACGCAATCCTGCCGTATCGACG
B2.4.1(39mer) TGGTCGGTCAAGGCTGCTGTGGTCGTGCGACCTCGTGTC

B2 tile
B2.1.2 (70mer)
CGTGCAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAGT
TACCGCATCGGACAGCAGCCCTGAC
B2.2.2 (39mer) GCCATCCGTCGAATACGGCACCATGACTGCACGGTAGCG
B2.3.2(70mer)
AGTCGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGTA
CTACGCAATCCTGCCGTATTCGACG
B2.4.2 (39mer) TGGTCGGTCAGGGCTGCTGTGGTCGTTGCGACTCGTGTC

B3 tile
B2.1.3 (71mer)
CGTGACAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAG
TTACCGCATCGGACAGCAGCCCTGAC

B2.2.3(41mer) GCCATCCGTCAGAATACGGCACCATGACTGTCACGGTAGCG
B2.3.3(71mer)
AGTCGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGTA
CTACGCAATCCTGCCGTATTCTGACG
B2.4.3= B2.4.2

B4 tile
B2.1.4 (72mer)
CGTGACAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAG
TTACCGCATCGGACAGCAGCCCCTGAC
B2.2.4 = B2.2.3
B2.3.4 (72mer)
AGTCCGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGT
ACTACGCAATCCTGCCGTATTCTGACG
B2.4.4 (41mer)
TGGTCGGTCAGGGGCTGCTGTGGTCGTTGCGGACTCGTGTC

B5 tile
B2.1.5 (73mer)
CGTGACAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAG
TTACCGCATCGGACAGCAGCCACCTGAC
B2.2.5 = B2.2.4
B2.3.5 (73 mer)
AGTCCGGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTG
TACTACGCAATCCTGCCGTATTCTGACG
B2.4.5 (43mer)
TGGTCGGTCAGGTGGCTGCTGTGGTCGTTGCCGGACTCGTGTC

B6 tile
B2.1.6 (74mer)
CGTGACAAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGA
GTTACCGCATCGGACAGCAGCCACCTGAC
B2.2.6 (43mer)
GCCATCCGTCAGAATACAGGCACCATGACTTGTCACGGTAGCG
B2.3.6 (74mer)
AGTCCGGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTG
TACTACGCAATCCTGCCTGTATTCTGACG
B2.4.6 = B2.4.5

B7 tile
B2.1.7(75mer)
CGTTGACAAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCG
AGTTACCGCATCGGACAGCAGCCACCTGAC
B2.2.7 (45mer)
GCCATCCGTTCAGAATACAGGCACCATGACTTGTCAACGGTAGCG
B2.3.7 (75mer)

AGTCCGGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTG
TACTACGCAATCCTGCCTGTATTCTGAACG
B2.4.7= B2.4.5

B8 tile
B2.1.8 (76mer)
CGTTGACAAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCG
AGTTACCGCATCGGACAGCAGCCACTCTGAC
B2.2.8=B2.2.7
B2.3.8 (76mer)
AGTCCTGGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTT
GTACTACGCAATCCTGCCTGTATTCTGAACG
B2.4.8 (45mer)
TGGTCGGTCAGAGTGGCTGCTGTGGTCGTTGCCAGGACTCGTGTC

A2.2, all DNA or all LNA, was used in the melting experiment. The sequence of the 7 base complementary strand is A2.2CS (7mer), 5'-TGATCGG-3'.
As a partial A tile, A2.1, A2.3 and A2.5 were used in the three-strand complex and A2.3 and A2.5 were used in the two-strand complex.

Reference:

S1. P. S. Lukeman, A. C. Mittal and N. C. Seeman, *Chemical Communications*, 2004, 1694-1695.