Supplementary Material (ESI) for Chemical Communications

SUPPLEMENTARY INFORMATION, LUKEMAN, MITTAL & SEEMAN

Gel electrophoresis of A and B tiles

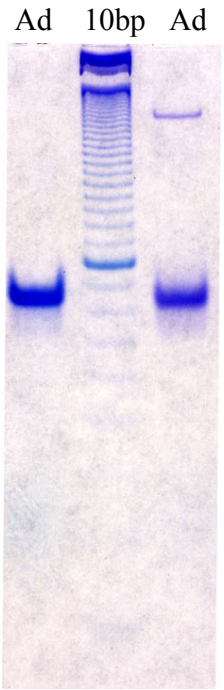
Formation of Hydrogen-Bonded Complexes

Complexes were formed by mixing a stoichiometric quantity (10pmols) of each strand as estimated by OD_{260}, in 40 mM Tris, 40 mM Acetic Acid, 12.5 mM Magnesium Acetate, and 2 mM EDTA (TAEMg) for a final strand concentration of 1 μM. This mixture was cooled over 5 h from 90 °C to room temperature in a 2 L water bath.

Nondenaturing gels of the A and B tiles .

All gels are 10% acrylamide (19:1 acrylamide:bis), TAEMg (10mM Mg) buffer and run at 25 V/cm, 20 °C. 10pm of each sample are loaded in each lane and after running the gel is stained in an aqueous formamide solution of Stains-All (Sigma). The marker lanes contain 3μg of either a 10bp ladder (USB) or 25bp ladder (USB) annealed in the same buffer system.

Figure 3 demonstrates the formation of the **Ad** and **Ap** tiles.



The slower moving band present in the **Ap** lane disappears at lower concentration. However, we use a 1μM initial tile concentration in the arrays (to maximize array size) - we therefore ran a gel under the same concentration conditions.

Figure 4 shows the formation of sub complexes of **Ap**. This demonstrates that the target band in the **Ap** lane is not one of these sub-complexes. The lanes labeled **Ap**-n contain all the strands present in **Ap** except strand n, where strand n is a strand defined by the nomenclature in the earlier supplementary information. 10bp is a 10-base pair ladder.

10bp **Ap**-1 **Ap**-2 **Ap**-3 **Ad** 10bp **Ap** **Ap**-4 **Ap**-5

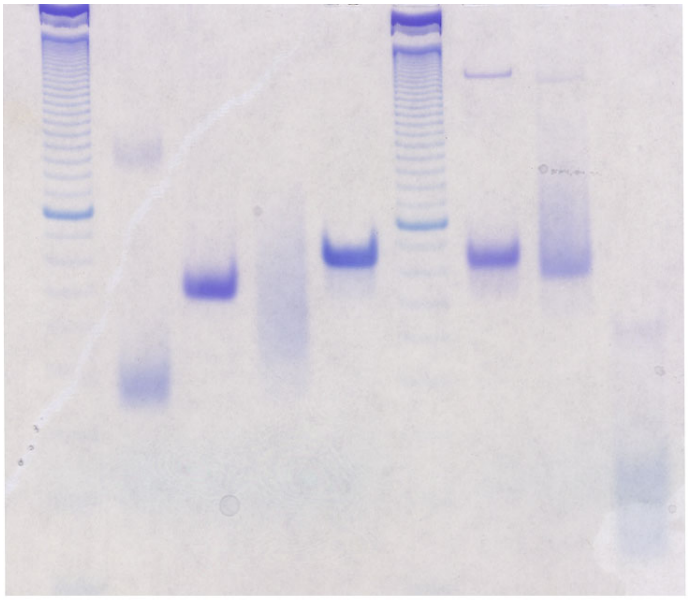
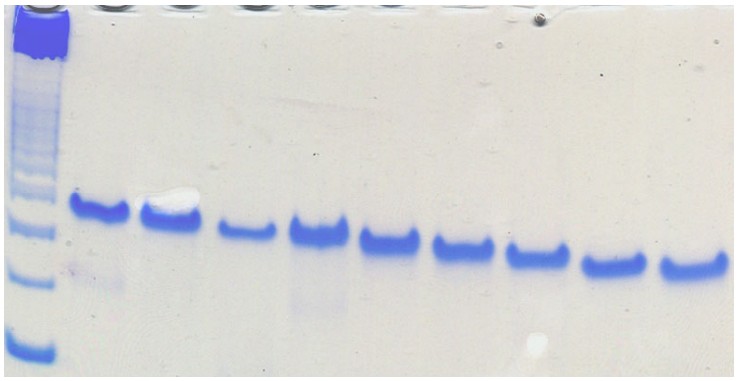


Figure 5 shows the formation of tiles **B0** through **B8**. 25bp is a 25-base pair ladder.

25bp **B8** **B7** **B6** **B5** **B4** **B3** **B2** **B1** **B0**



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Sequence information

Each tile consists of 5 strands.

A tile

The PNA A tile and the DNA A tile are identical except strand A2.2 and A2.4 are made of DNA and PNA respectively.

A2.1 (48mer)
GATGGCGACATCCTGCCGCTATGATTACACAGCCTGAGCATTGAC
ACG

A2.2 (15mer)
AATGCTCACCGATCA

A2.3 (48mer)
CGACCATGATCGGACGATACTACATGCCAGTTGGACTAACGGCG
CTAC

A2.4 (15mer)
CCGTTAGTGGATGTC

A2.5 (42mer)
TGTAGTATCGTGGCTGTGTAATCATAGCGGCACCAACTGGCA

B tile

Each tile consists of 5 strands.
In all the B tiles, the central strand (B1.5) is the same

B1.5 (42mer)
AGTACAACGCCACCGATGCGGTCACTGGTTAGTGGATTGCGT

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

B+ZERO

B2.1 (68mer)
CGTGCATCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAGTT
ACCGCATCGGACAGCAGCCTGAC
:
B2.2 (37mer)
GCCATCCGTCGATACGGCACCATGATGCACGGTAGCG

B2.3 (68mer)
AGTCGCACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGTAC
TACGCAATCCTGCCGTATCGACG

B2.4 (37mer)
TGGTCGGTCAGGCTGCTGTGGTCGTGCGACTCGTGTC

B+ONE

B2.1+ONE (69mer)
CGTGCATCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAGTT
ACCGCATCGGACAGCAGCCTTGAC

B2.2+ONE=B2.1 (37mer)

B2.3+ONE(69mer)
AGGTCGCACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGTA
CTACGCAATCCTGCCGTATCGACG

B2.4+ONE(39mer)
TGGTCGGTCAAGGCTGCTGTGGTCGTGCGACCTCGTGTC

B+TWO

B2.1+TWO (70mer)

CGTGCAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAGT
TACCGCATCGGACAGCAGCCCTGAC

B2.2+TWO (39mer)
GCCATCCGTCGAATACGGCACCATGACTGCACGGTAGCG

B2.3+TWO(70mer)
AGTCGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGTA
CTACGCAATCCTGCCGTATTCGACG

B2.4+TWO(39mer)
TGGTCGGTCAGGGCTGCTGTGGTCGTTGCGACTCGTGTC

B+THREE

PNAB2.1+THREE (71mer)
CGTGACAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAG
TTACCGCATCGGACAGCAGCCCTGAC

PNAB2.2+THREE(41mer)
GCCATCCGTCAGAATACGGCACCATGACTGTCACGGTAGCG

PNAB2.3+THREE(71mer)
AGTCGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGTA
CTACGCAATCCTGCCGTATTCTGACG

B2.4+THREE= B2.4+TWO

B+FOUR

PNAB2.1+FOUR (72mer)
CGTGACAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAG
TTACCGCATCGGACAGCAGCCCCTGAC

B2.2+FOUR = B2.2+THREE

PNAB2.3+FOUR (72mer)

AGTCCGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTGT
ACTACGCAATCCTGCCGTATTCTGACG

PNAB2.4+FOUR (41mer)
TGGTCGGTCAGGGGCTGCTGTGGTCGTTGCGGACTCGTGTC

B+FIVE

B2.1+FIVE (73mer)
CGTGACAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGAG
TTACCGCATCGGACAGCAGCCACCTGAC

B2.2+FIVE SAME AS AS B2.2+FOUR

B2.3+FIVE (73 mer)
AGTCCGGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTG
TACTACGCAATCCTGCCGTATTCTGACG

B2.4+FIVE (43mer)
TGGTCGGTCAGGTGGCTGCTGTGGTCGTTGCCGGACTCGTGTC

B+SIX

PNAB2.1+SIX (74mer)
CGTGACAAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCGA
GTTACCGCATCGGACAGCAGCCACCTGAC

PNAB2.2+SIX (43mer)
GCCATCCGTCAGAATACAGGCACCATGACTTGTCACGGTAGCG

B2.3+SIX (74mer)
AGTCCGGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTG
TACTACGCAATCCTGCCTGTATTCTGACG

B2.4+SIX = B2.4+FIVE

B+SEVEN

PNAB2.1+SEVEN (75mer)
CGTTGACAAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCG
AGTTACCGCATCGGACAGCAGCCACCTGAC

PNAB2.2+SEVEN (45mer)
GCCATCCGTTCAGAATACAGGCACCATGACTTGTCAACGGTAGCG

PNAB2.3+SEVEN (75mer)
AGTCCGGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTTG
TACTACGCAATCCTGCCTGTATTCTGAACG

B2.4+SEVEN = B2.4+SIX

B+EIGHT

PNAB2.1+EIGHT (76mer)
CGTTGACAAGTCATGGACTAACCAGTGCTCGCTGATTTTTCAGCG
AGTTACCGCATCGGACAGCAGCCACTCTGAC

PNAB2.2+EIGHT=PNAB2.2+SEVEN

PNAB2.3+EIGHT (76mer)
AGTCCTGGCAACGACCTGGCGTCTGTTGGCTTTTGCCAACAGTTT
GTACTACGCAATCCTGCCTGTATTCTGAACG

PNAB2.4+EIGHT (45mer)
TGGTCGGTCAGAGTGGCTGCTGTGGTCGTTGCCAGGACTCGTGTC