Physical and Structural Basis for the Strong Interactions of the –ImPy–Central Pairing Motif in the Polyamide, f-ImPyIm

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Figure S1 - CD and T_M control experiments for the NMR experiments.
Table S1 - Assignment of DNA base and polyamide protons.
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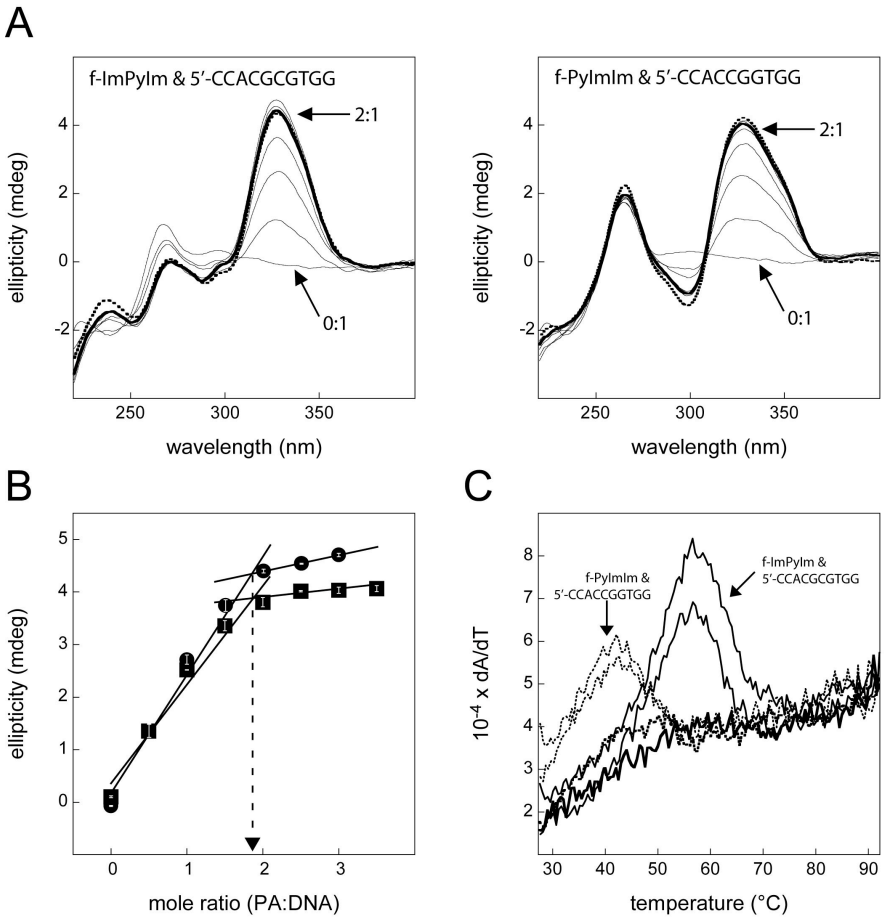

Supplemental Material, Figure S1
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Figure S1. CD and T_M control experiments for the NMR experiments. A. Titration of f-ImPyIm into $(CGCGnmr)_2$ (left panel) and f-PyImIm into $(CCGGnmr)_2$ (right panel). Solid lines indicate the titration of fresh triamide into fresh DNA at 0.5:1 mole ratio increments until 2:1 and 2.5:1 (thick solid lines) were reached for f-ImPyIm and f-PyImIm, respectively. Spectra from samples taken from the NMR tubes are overlayed (dashed lines). These samples were diluted so that the DNA concentration was ~9 μM. B. Induced peak ellipticity as a function of triamide to DNA ratio. Circles are f-ImPyIm: $(CGCGnmr)_2$ and squares are f-PyImIm:$(CCGGnmr)_2$. The arrow indicates the ratio at which the DNAs are saturated. C. Thermal denaturation studies with 2:1 f-ImPyIm: $(CGCGnmr)_2$ (solid lines) and 2.5:1 f-PyImIm:$(CCGGnmr)_2$ (dashed lines). Thick solid and dashed lines indicate the broad melting of $(CGCGnmr)_2$ and $(CCGGnmr)_2$, respectively. The complex peaks with the higher dA/dT values are from freshly prepared samples and the lower of the two lines are from diluted NMR samples.

Table S1 - Assignment of DNA base and polyamide protons.

S1A. f-ImPyIm & 5'-CCACGCGTGG[a]

DNA H	free (ppm)	bound (ppm)	f-ImPyIm H	free (bound)	bound (ppm)
C_1H5	6.00	5.98	formyl	8.10	8.22
C_1H6	7.81	7.81	Im–H (N-term)	7.12	7.68
C_2H5	5.79	5.80	Im–CH_3 (N-term)	3.86 or 3.83	3.95
C_2H6	7.65	7.62	Py–H (H3*)[b]	6.96	7.57
A_3H2	7.90	7.81	Py–H (H5*)	6.65	6.96
A_3H8	8.36	8.45	Py–CH_3	3.70	3.94
C_4H5	5.35	5.45	Im–H (C-term)	7.12	7.74
C_4H6	7.28	7.48	Im–CH_3 (C-term)	3.86 or 3.83	3.95
G_5H8	7.90	7.91	CH_2 (β to tail)[c]	3.92	4.09
C_6H5	5.37	5.68	CH_2 (α to tail)	3.40	3.55
C_6H6	7.32	7.10	N–$(CH_3)_2$	3.00	3.04
G_7H8	7.94	7.74			
T_8CH_3	1.53	1.64			
T_8H6	7.19	6.82			
G_9H8	7.85	7.80			
G_9H8	7.85	7.80			

S1B. f-PyImIm & 5'-CCACCGGTGG[a]

DNA H	free (ppm)	bound (ppm)
C_1H5	6.05	5.98
C_1H6	7.88	7.82
C_2H5	5.87	5.80
C_2H6	7.73	7.64
A_3H2	7.93	
A_3H8	8.40	8.45
C_4H5	5.35	5.44
C_4H6	7.37	7.68
C_5H5	5.89	6.09
C_5H6	7.71	7.96
G_6H8	7.96	
G_7H8	7.75	
T_8CH_3	1.46	1.61
T_8H6	7.20	
G_9H8	7.86	
G_9H8	7.86	

a. The DNA is sequentially numbered from 5' to 3'.
b. The asterisk indicates protons from pyrrole moieties.
c. The tail is the dimethylamino moiety.

Table S2. The solvent accessible surface areas (SASA) were calculated with GRASP (39) using the Cornell et al. radii with a probe radius of 1.7683 _ (40).

	Polar (A_p)	Non-polar (A_{np})	Total (A_{total})
Complex	2244	1853	4098
Free ligand 1	223	749	973
Free ligand 2	204	760	964
Free DNA	2271	1650	3921
Change (_)	-454	-1306	-1760
$\_Cp_{SASA}$[a]	-354 ± 70 (Eq. 3)[b] -470 ± 40 (Eq. 4) -444 ± 69 (Eq. 5)		

a. The area unit is $\_^2$.
b. The $\_Cp_{SASA}$ values (cal/(mole_K)) are for two ligands. Reported $\_Cp = \_Cp_{SASA} / 2$.