

Scientific Session II

## NMR and Molecular Modeling Studies on the Structures of DNA Oligomers with AA Mismatches

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NMR and molecular modeling studies on the deoxyribonucleic acids having AA mismatches were performed to understand the structural changes accompanied by base-pair mismatches and associated thermodynamics. The two palindromic duplexes synthesized chemically, 5'-d(CGACAATTGACG) (named as GC12) and 5'-d(CGAGAATTCACG) (named as GG12), have different nearest neighbor sequences to the AA mismatches. When they form duplexes, the sequences near the AA mismatches (shown by boxes) are  $\begin{matrix} 5'-dG & \boxed{A} & C \\ & C & \boxed{A} & G \end{matrix}$  for GC12 and  $\begin{matrix} 5'-dG & \boxed{A} & C \\ G & \boxed{A} & C \end{matrix}$  for GG12. Essential part of the present study lies in elucidation of the structural and thermodynamic differences between these two molecules.

The global structures of the two molecules closely resemble the B-form, but their local conformations near and at the mismatched residues were quite different from each other.

Both of the mismatched adenines in GC12 were found to be stacked into the helix. On the other hand one of the mismatched adenines in GG12, which is surrounded by guanines, was found to be partially looped out of the helix, while the other adenine surrounded by cytosines was stacked into the helix. In GC12, a hydrogen bond between the mismatched adenines was observed, but GG12 did not contain any hydrogen bond in the mismatch. Thermodynamically, GC12 was found to be more stable than GG12 [ $\Delta\Delta G^\circ = -1.3$  kcal/mole at 298K], which can be ascribed to the formation of the hydrogen bond. Thermally, the melting temperature of the internal bases of GC12 is higher by about 7°C than that of GG12.

The conformational changes of these molecules were also investigated at low pH. The result indicate that GC12 unambiguously assume parallel-stranded duplex at pH 4, but GG12 exists as a mixture of antiparallel and parallel duplexes below pH 5.