**NMR dynamics study on the protein-induced Z-DNA and miRNA156a**

Joon-Hwa Lee

*Department of Chemistry, Gyeongsang National University, Jinju, Gyeongnam 660-701, Korea*

First topic of this study is the quantitative analysis of DNA binding and B-Z transition of the Z-DNA binding proteins (ZBPs) by NMR spectroscopy. Left-handed Z-DNA is a higher energy conformation than B-DNA and is induced by high salt, negative supercoiling, and complex formation with ZBPs, which have been identified in RNA editing enzyme (ADAR1), DNA-dependent activator of interferon regulatory factor (DAI), viral E3L protein and protein kinase containing Z-DNA binding domains (PKZ). The crystal structures of the Zα domains of these ZBPs in complex with 6-base-paired Z-DNA duplex revealed that one monomeric Zα domain binds to one strand of double-stranded (ds) Z-DNA, while a second monomer binds to the opposite strand, yielding 2-fold symmetry with respect to the DNA helical axis. In this study, we determined the solution structure of the free from of caZαPKZ by multidimensional heteronuclear NMR spectroscopy. We also performed NMR experiments on complexes of caZαPKZ with DNA duplexes, dT(CG)3 and d(CG)3 under various NaCl concentrations. We investigated changes in the conformation and dynamics of caZαPKZ induced by increment of NaCl concentration. Comparison of these results to those of ZαADAR1 provides the molecular basis for B-Z transition mechanism of ZBPs.

Second topic is base-pair opening dynamics of the primary miRNA156a. In plants, miRNAs are playing an important regulatory role in plant development. MiR156 is important regulator for flowering time control in the response to ambient temperature in Arabidopsis. The DCL1 enzyme processed primary miR156a into miR156/miR156\* duplex via a loop-to-base processing mechanism. Interestingly, some pairing mutants on the B5 bulge (P-B5 mutants) in the lower stem caused earlier flowering than wild-type pri-miR156a. Here, we have investigated the base-pair opening dynamics changes of the miR/miR\* duplex region induced by P-B5 mutations. This study provides insight into the molecular mechanism on the second cleavage reaction at lower stem structure by DCL1.