Poster 12

## NMR Studies of the Panhandle Structure of the Influenza Virus RNA

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The influenza A viruses which are the most severe and common among the influenza viruses have highly conserved 3' and 5' terminal sequences of genomic RNA called panhandle. The conserved panhandle RNA linked by UUCG tetraloop was studied by NMR spectroscopy. The panhandle is partially double-stranded and involved in initiation and termination of transcription, switching from transcription to replication as well as packaging. The panhandle structure was studied by Cheong *et al.* but the conserved sequences were modified so the results were argued against. This study was initiated to certify this point by using the unmodified panhandle RNA which was available by the trans cleaving hammerhead ribozyme.

Overall conformation looks like that of Cheong *et al.* In U3AG/U27UG(I) and A7ACAA/U22GCU(II) which have been known as the important binding sites of the influenza RNA polymerase, the region (I) is base paired and the region (II) seems to have no base pairs or very weak base pairs which cannot not be identified.

All base pairs except UUCG tetraloop stem melt between 30 and 35 degree implying that both region (I) and (II) are single-stranded in physiological conditions which were proposed by the fork model. However, since the influenza virus RNA polymerase would stabilize both regions, the *in vivo* panhandle structure might be different from the *in vitro* case so it needs further investigation at the stage of polymerase binding.

Cheong, H.K., Cheong, C., Choi, B.S.(1996), Secondary structure of the panhandle RNA of influenza virus A studied by NMR spectroscopy, *Nucleic Acids Res.* 24:4197–4201