

E103 **Immunogenic Epitope Mapping of Hantaan Virus Howang strain Nucleocapsid Protein by Nucleocapsid Protein Specific Monoclonal Antibodies**

Dae Yong Song^{1,2*}, Yong Kyu Chu² and Hak Ryul Kim¹
Department of Biochemistry and Physiology, Graduate School of
Korea University¹ and Asan Institute for Life Science²

Hantaan virus (HTNV) Howang strain is the member of the genus *Hantavirus* in the family *Bunyaviridae* and the causative agent of hemorrhagic fever with renal syndrome (HFRS). The nucleocapsid protein (NP) of *Hantavirus* has been shown to be highly immunogenic both in laboratory animals and in human. In this study, we aimed to find the immunogenic epitopes of NP HTNV Howang strain. We have already made 23 monoclonal antibodies (Mab) against HTNV Howang strain. Among them, 5 Mabs were confirmed to be specific against NP by Radio-labelled immunoprecipitation (RIP) assay. Mab #1 was reacted only with HTNV but Mab #12, 13, 14, 15 was reacted with both HTNV and Seoul virus (SEOV) by IFA. We expressed Poly-histidine tagged complete and truncated NPs of Howang virus in *E. coli* expression system by using pRSET expression vector, and purified them in native condition by Ni²⁺-chelated column. Thereafter, Purified complete and truncated NPs were tested with NP specific Mabs by western blot (WB).

As a result, Mab #1, 12, 13, 15 were detected by RIP and WB but Mab #14 was only detected by RIP. This means that Mab #1, 12, 13, 15 can recognize linear epitope but Mab #14 recognize conformational epitope. Mab #1 could recognize amino acids 246~290, and Mab #12, 13, 15 could recognize amino acids 45~64. We could assume the exact linear epitope by amino acid sequence analysis with in antigenic region among 4 serotypes of *Hantavirus*. Mab #1 recognition site may be 247~263, and this epitope is specific for HTN. Mab #12, 13, 15 recognition site may be 45~59, and this epitope is specific for HTN and SEO.

E104 **Biochemical comparison of antibacterial peptides from the common cutworm, *Spodoptera litura***

Chung Sik Choi*, Kwon Seok Chae, Hak-Ryul Kim
Department of biology, Korea University, Seoul, Korea

Antibacterial peptides were purified and characterized from the immune haemolymph of *S. litura*. Of the induced antibacterial peptides in response to bacterial injection, five molecules were finally purified by reverse phase FPLC. These peptides were eluted between 27.9-28%, 28.8-29.4%, 30.5-30.8%, 31.8-32.1%, 32.6-32.9% of acetonitrile, respectively. The purified peptides have antibacterial activity in vitro against a broad spectrum of Gram negative bacteria and Gram positive bacteria. And these peptides showed a similar structure of cecropin family, which were first named from *Hyalophora cecropia*. The amino acid sequence and other physicochemical characteristics were compared between these peptides.