## Determination of the Vaccine Induced Immunodominant Regions of Nucleoprotein Crimean-Congo Hemorrhagic Fever Virus

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Abstract : Crimean-Congo hemorrhagic fever virus (CCHFV) is a tick-borne virus in the family Bunyaviridae, genus Nairovirus. The CCHFV genome consists of three molecules of negative-sense single-stranded RNA, each encapsulated separately. The virion particle contains viral RNA polymerase (L segment), surface glycoproteins Gn and Gc (Msegment), and a nucleocapsid protein NP (S segment). CCHF is characterized by high case mortality, occurring in Asia, Africa, the Middle East and Eastern Europe. Clinical CCHF was first recognized in Turkey in 2002. The numbers of CCHF cases have gradually increased in Turkey making the virus a public health concern. Between 2002 and 2014, more than 8000 the CCHF cases have been reported in Turkey and mortality rate is around 5%. So, Turkey is one of the countries where the epidemy has become spread to the wider geography and the biggest outbreaks of CCHF have occurred in the world. We have recently developed an inactivated cellculture based vaccine against CCHF. We have showed that the Balb/c mice immunized with the CCHF vaccine induced the high level of neutralizing antibodies. In this study, we aimed to determine the immunodominant regions of nucleoprotein (NP) CCHFV Kelkit06 strain which stimulate T cells. For this purpose, pools of overlapping NP were used for an IFN- y ELISPOT assay. Balb/c mice were divided into two groups for the experiment. Two groups (n = 10 each) were immunized via the intraperitoneal route with 5, or 10 $\mu$ g of the cell culture-based vaccine. The control group (n = 6) was mock immunized with PBS. Booster injections with the same formulation were given on days 21 and 42 after the first immunization. The higher reactivity against the CCHFV NP pools 31-40 and 80-90 was determined in the two dose groups. In order to analyze the vaccine-induced T cell responses in Balb/c mice immunized with varying doses of the vaccine, we have been also currently working on CD4+, CD8+ and CD3 + T cells by flow cytometry.

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