SI-2-2

INHIBITION OF HIV WITH INTRACELLULARLY EXPRESSED RNA DECOYS

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The purpose of this presentation is to describe the development of inhibitory genes and retroviral vector systems for gene therapy approaches to facilitate the immunological reconstitution of AIDS patient. Treatment of HIV infection with chemotherapeutic or biological agents has not been curative, prompting the development of alternative or complementary treatment strategies, including gene therapy. Since HIV, the etiological agent of AIDS, infects hemopoietic cells, insertion with vehicle including retroviral vector and intracellular expression of resistant genes in such cells could reduce, if not eliminate, the spread of the virus in the patient. Several HIV inhibitory genes have been described. However, a potential limitation of many strategies stems from the propensity of HIV to generate escape mutants. Here, I will describe the development an alternative intracellular inhibition strategy using retroviral vector against HIV, termed RNA decoy, which may be minimally affected by the variability encountered among HIV isolates. RNA decoys are short oligonucleotides corresponding to the HIV TAR or RRE sequences which function by inhibiting the binding of the HIV regulatory proteins *tat* or *rev* to the authentic TAR or RRE RNAs, respectively.

SI-2-3

GENOMIC DIVERSITY IN CORONAVIRUSES

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The polymerase chain reaction (PCR), restriction fragment length polymorphism (RFLP) and sequencing analysis were used to differentiate between serotypes of several avian infectious bronchitis viruses and transmissible gastroenteritis viruses. The S1 glycoprotein gene of approximately 1720 base pairs was amplified by PCR and digested with restriction enzymes. Eleven IBV strains were grouped according to the RFLP patterns. The identification of 26 IBV samples by PCR and RFLP agreed with the serotypes for traditional and variant IBV strains as determined by the virus neutralization test. The N-terminal half of the spike (S) glycoprotein gene and open reading frames (ORF) 3, 3-1 and 4 of transmissible gastroenteritis viruses (TGEV) and porcine respiratory coeonaviruses were analyzed using PCR and RFLP. They also were differentiated into several groups. Sequence analysis of a PCR product in the ORFs 3, 3-1 and 4 from virulent and attenuated Miller strains suggested that some differences in that region might be correlated with a change in virulence of TGEV isolates. Based on this study, there were genomic variations among TGEV and PRCV strains, which may explain the antigenic and virulence variations observed. Those methods were used to analyze IBV and TGEV strains isolated in Korea. They showed different RFLP patterns from U.S.A. strains.