stenosis (SVAS). Patients with WS show allelic loss of *ELN*, exhibiting a submicroscopic deletion at 7q11.23. While the involvement of elastin mutation in isolated SVAS is indisputable, the nature of the relationship between SVAS and WS in terms of mutational basis is less clear. In this study, we present the results of deletion mapping in classic WS and isolated SVAS patients. RAG mouse cells were hybridized with lymphoblastoid cells of WS or SVAS patients to allow their deletion breakpoints to be more finely mapped. Hybrids containing the deleted chromosome 7 from each case were screened for the presence of D7S1816, 5C19R, D7S489C, D7S489B, *ELN*, *LIMK1*, D7S2472, D7S1870, D7S489A, *HIP1* and D7S2518 in the order from centromere to telomere. Our results show that the proximal deletion breakpoint was between 5C19R and D7S489C and the distal deletion breakpoint was mapped between D7S489A and HIP1 in WS patients. On the contrary, the deletion in isolated SVAS patients was confined within the gene *ELN*. The deletion size in our WS patients is greater than that in any published data. We believe that these results would make the genotype-phenotype matching possible through cloning the genes within the deleted region and, therefore, provide valuable informations to fully understand the WS and SVAS pathogenesis.

## F107 신장 투명세포육종 세포주 (CCSK-2)의 제작 및 특성분석

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신장의 투명세포육종은 소아 신장종양의 약 4-5%를 차지하는 매우 드물고 악성도가 심한 종양으로서 최근 연구결과 병리학적으로 윌름씨 종양과는 상이한 특징을 갖는 것으로 밝혀졌으며, 성인에서는 발생률이 극히 낮고 대부분 12개월에서 36개월의 소아에서 호발하는 질환이다. 본 연구에서는 19세 남성환자의 신장 종양조직으로부터 신장의 투명세포 육종세포주(CCSK-2) 개발을 시도하였다. CCSK-2는 생체외 MEM 배지에서 약 48시간의 세포배가 시간을 나타냈으며, 면역화학염색에서 vimentin에 강한 양성을 보였으나 desmin, smooth muscle actin, S-100, cytokeratin에 대해서는 음성인 것으로 관찰되었다. 이러한 결과는 확립된 세포주가 투명세포로부터 유래된 육종세포라는 사실을 강하게 시사해주고 있다. 또한 CCSK-2에서는 E-cadherin, KAI-1 및 종양억제 유전자인 p53의 발현이 억제되었고, VHL, WT-1 및 DCC는 정상 신세포주와 유사한 발현양상을 나타내었다. 향후 CCSK-2 세포주는 신장의 투명세포육종의 분자생물학적 특성 연구 및 새로운 항암성 약제 개발에 유용한 재로로서 사용될 것으로 기대된다.

## F108 Sequence analysis of variations in the 5'-nontranslated region of the cardio/non-cardiovirulent Coxsackievirus B3 (CVB3) isolated in Korea

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The 5'-nontranslated region (NTR) of enteroviruses contains an internal ribosome entry site (IRES), which facilitates translation initiation of the viral open reading frame in a 5'- (m7GpppN) cap-independent manner, and cis-acting signals for positive-strand RNA replication. For several enteroviruses including Coxsackievirus B3 (CVB3), the 5'-NTR has been shown to determine the virulence phenotype. Particularly, the cardiovirulence of CVB3 has been known to be greatly influenced by the secondary structure of the 5'-NTR. We have analyzed the nucleotide sequences and compared the secondary structures of 5'-NTR of 14 non-cardiovirulent isolates and one cardiovirulent

isolate with the Nancy strain (ATCC-VR 30) as a reference. The nucleotide sequence homologies of 5'-NTR of intra-isolates (14 isolates) were 99.0-99.8% regardless the year of isolation. On the other hand, homologies between 14 isolates and the Nancy strain were 84.0-84.7%. In addition, nucleotide sequence of 5'-NTR of one isolate, which was isolated from the patient with acute myocarditis showed very high homology (96.0%) with the reference strain with cardiovirulence. The 5'-NTR of all the viruses retained identical primary clover-leaf (CL) structure with additional unique stems and loops depending on their cardiovirulence. Taken together, these results indicated that the secondary structure of 5'-NTR of CVB3, which resulted from nucleotide divergences, is responsible for a determination of cardio/non-cardiovirulent phenotype in a murine model for acute myocarditis.

## F109 Genomic Determinants of Cardiovirulence in Coxsackievirus B3

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Coxsackievirus B3 (CVB3) infections can cause myocarditis in humans and are implicated in the pathogenesis of dilated cardiomyopathy. The natural genetic determinants of cardiovirulence for CVB3 have not been fully identified, although using strains engineered in the laboratory, cardiovirulence determinants have been identified in the CVB3 5' nontranslated region (5'NTR) and capsid. The 5'NTRs of the non-cardiovirulent CVB3 Korean isolates and cardiovirulent Nancy strain were examined to determine their influence on the cardiovirulence phenotype. In order to exactly identify CVB3 cardiovirulence determinants, infectious full-length cDNA clones of CVB3K and Nancy strain were constructed using mammalian expression vector pCDNA 3.1 (-). The recombinant constructs consisted of the full-length viral cDNA stably inserted into the pCDNA3.1 (-) vector under control of CMV immediate early transcriptional element. Intratypic chimeric virus was constructed in which 5'NTR sequences of the infectious cDNA copy of the cardiovirulent CVB3 Nancy strain genome were replaced by homologous sequences from the noncardiovirulent CVB3K. This chimeric virus (Chi-CVB3) was transfected into Cos7 and hCAR (Human Coxsackievirus and Adenovirus Receptor expressed cell) cells by the lipofectamine reagent and the infectious progeny virus was harvested. The myocarditic potential of chimeric virus was determined using an established murine model of inflammatory heart disease. Chimeric virus was screened for cardiovirulence by inoculation into Balb/c mice. Sections of hearts removed at 7 days postinoculation were examined for evidence of myocarditis by light microscopy and Enterovirus-specific PCR assayed for the presence of virus. These results indicate that 5'NTR plays an important role in the cardiovirulence determinants of CVB3.

## F110 Effects of inhibitors on Apoptosis and Adaptive Response Induced by Ultraviolet Radiation in HeLa S3 Cells

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The present study was performed to elucidate the effects of inhibitors on apoptosis and adaptive response induced by Ultraviolet Radiation (UV) in HeLa $S_3$ cells. After treatment of the cells with UV, cells were incubated with three kinds of inhibitors for various times. DNA fragmentation induced in cells were not