

## **S1-5**

Mechanism for the Hepatitis B virus HBx-mediated regulation of host cell signaling

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The X-gene product(HBx) of Hepatitis B virus plays essential roles in viral replication and the generation of hepatocellular carcinoma. These functions of HBx is believed to be mediated through alteration of host cell signal transduction. HBx is known to activate the ras/Map kinase, Jnk as well as NF- $\kappa$ B signaling pathway. In addition, we have previously shown that HBx also activates Jak1/STAT signaling pathway. Here, we investigated whether the reported activation of multiple signaling pathways by HBx is mediated through Jak1 tyrosine kinase and found: 1)HBx associates with Jak1 directly in vivo. 2)The natural inhibitor of Jak1, Jab, blocked the HBx-induced transcriptional activation through AP-1, SRE, NF- $\kappa$ B and stat. 3) HBx induces tyrosine phosphorylation of raf, but not src and shc. The tyrosine phosphorylation of raf is blocked by the overexpression of Jab. 4)HBx-induced elevation of GTP-bound ras level is diminished by Jab. 5)HBx-induced cell proliferation is blocked by Jab. >From these results, we conclude that the promiscuous signal activation by HBx is mediated through direct association and subsequent activation of Jak1 tyrosine kinase.

## **S2-1**

Genome Analysis of *Zymomonas mobilis* ZM4

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We have reported the physical map of *Zymomonas mobilis* ZM4 containing ribosomal transcription unit which are clustered around 50 min. region (Gene 206, 223-228, 1998). The size of *Zymomonas* genome is about 2Mbp. We determined nucleotide sequence of 350kbp around 50min to 5min region of the physical map. Analysis of the 350Kbp sequence of *Zymomonas mobilis* ZM4 shows: 13 known genes in *Zymomonas* which belong to 4% of total analyzed 350Kbp, 115 homologous genes to the reported genes from other organisms, 40%, 84 unidentified ORFs, 22%, and 34% of unknown sequences. The number of nucleotide of *rrnA* is 5270bp, *rrnB* 4880bp, and *rrnC* is 5230bp. The molecular organization of all three ribosomal transcription units (*rrnA-C*) was order of 5'-16s rRNA-tRNA Ile - tRNAAla - 23s rRNA - 5s rRNA - tRNA<sup>fmet</sup> - 3'. the secondary structures of ribosomal RNA will be discussed. The status of Korean genome project of microorganism will be presented shortly.