

"Mouse genetic and epigenetic studies for identification genes involved in cancer development."

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日 時: 2003年12月17日(水)
午後4時30分 ~ 午後5時30分
場 所: A棟7階セミナー室

要旨:

Experimental mouse studies have been used successfully to identify genes responsible for complex genetic traits such as cancer. Our strategies to screen genetic changes and epigenetic changes involved in cancer development will be discussed.

First, DNA cytosine 5' methylation in genomic DNA is one of crucial factors in cancer development. To identify DNA methylation changes, we have analyzed mouse genome-wide methylation patterns by methylation sensitive Restriction Landmark Genomic Scanning (MS-RLGS). RLGS is a method for the two-dimensional display of 1,500-2,000 end-labelled DNA restriction fragments at one try. However, there are some difficulties to analyze 1,500-2,000 RLGS spots. To facilitate RLGS data analysis, we have developed computational software, Virtual image RLGS (Vi-RLGS). Vi-RLGS analyses the total genome sequence information, and indicates consequent RLGS spot patterns digested by restriction enzymes and DNA sequence information of each spots. The aspect and the application of the Vi-RLGS will be discussed.

Second, for the screening of DNA mutations, deletion, or amplification, relate to tumor development, we have performed two mouse-genetic approaches. In a F1 backcross study, hybrids of sensitive and resistant mouse strains have been analyzed. In a F1 dominant screening, heavy ion beam (HIB) mutagenized mice showing different cancer susceptibility have been analyzed. Recent results from these studies will be talked.

- Host -

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