P081 CGH and SNP arrays enable detailed chromosome analysis without observing metaphase chromosomes

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We applied CGH and SNP arrays on the chromosome analysis in HL60 cells or TK6 cells. HL60 cells had a *c-myc* amplification as double minute chromosomes, which was detected as single peak in 8q24 region by the BAC-CGH array. The two deletion mutants of TK6 cell showed changes in dosage at tk regions. An additional deletion at 17pter was detected in one mutant. By using the HuSNP 10K Mapping array (Affymetrix), regions of the deletion in the TK6 mutants were identified as LOH (homo SNP calls) and changes in signal intensity. The SNP array identified a novel uniparental disomy in the HL60 subline, which could not be detected by any other methods. Amplification of the *c-myc* region in the HL60 cells were splitted into three peaks by the signal intensity analysis on the SNP chip, which was finally revealed as 8 separated amplicons by a custom oligo-CGH array containing 390K probes (NimbleGen). All deletion breakpoints could be cloned by PCR designed from the CGH data. The amplicon showed a complex rearrangement, suggesting a possible mechanism of *c-myc* amplification. CGH and SNP arrays can be used as an efficient tool for detailed chromosome analysis even without the preparation of metaphase chromosomes.

染色体を観ずに染色体を診る技術としてのCGHおよびSNPアレイの有用性

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P082 Proteomics approach for the detection of useful biomarkers in mutation research

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Proteomics is a promising but challenging approach for biomarker discovery. Its methodology is not well established as the transcriptome analysis by DNA microarray. We started establishing an efficient assay system for a comprehensive and comparative proteome analysis. As a widely used method, we applied the 2D gel electrophoresis on the liver homogenate samples from diethylnitrosamine-treated mouse. Several differently expressed spots were detected and those were subjected to the MALDI-TOF/TOF (AB4700) analysis for the protein identification. Peptide mass fingerprinting analysis identified hsc70, heat shock protein, actin as decreased spots and thioester S-methyltransferase as a shifted spot. For the more sophisticated approach, we tried the isotope-coded affinity tag (ICAT) analysis using the nano LC-MS/MS (Qstar-XL) system. As a model sample, we compared individual human liver cytosols for their protein composition. The MS/MS dependent analysis identified more than 50 proteins and some of them showed variation among samples. However, this approach has a limitation for the coverage of proteins. We are trying to establish the more efficient 2-step approach; initially by the TOF mass dependent differential analysis and followed by a focused identification of selected peptides by MS/MS analysis in additional run. For this purpose, we are also developing our original data visualization and analysis tools.

プロテオミクスを用いた変異原研究に有用なバイオマーカーの探索

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