**P020** Genetic Analysis on a Collection of Colorectal Cancer Cell Lines

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76 cell lines are being cultured and maintained in our laboratory. These cell lines represent various colorectal carcinomas and would help us to decipher the genetic pathways involved in the pathogenesis of colorectal cancer. Comprehensive genetic information has been accumulated for most of them. This includes: karyotyping of the cell lines, LOH information on each chromosome arm with a coverage of, on average, one microsatellite marker per 10 CM; microsatellite instability status of each cell line; mutation analysis of tumour suppressor genes and oncogenes including *APC, TP53, K-RAS, E-Cadherin, β-catenin, SMAD4, TGF-β receptor*, *CHK1*, *MLH1*, and *MSH2*; and methylation status of the promoter regions of genes including *MLH1, MSH2, P16, P14* and *P15*. Our current research focuses include: a), detailed studies of the expression and function of p53 in our panel of cell lines with a combination of DHPLC mutation screening of the p53 gene, sequencing of the cDNA of p53 and assessing the function of p53 by testing the induced expression of phosphorylated p53 and p21 after γ radiation treatment of cells; b, expression analysis of specific subgroups of colorectal cancer cell lines using microarray technology (Affymetrix). Results from these two aspects will be presented and discussed.