CGH MICROARRAY IN HEAD AND NECK TUMORS

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Deletions and amplifications through the genome frequently contribute to alterations in the expression of tumour- suppressor genes and oncogenes and is recognized as a key event during oncogenesis. CGH and, more recently, CGH arrays is providing a great deal of information to access genome wide variations as a function of tumor as well as tumor biology. To establish this technology in our lab, we performed CGH array using genomic DNA from Head and Neck tumors and reference genomic DNA. Differentially labeled DNA was co-hybridized to a cDNA microarray containing approximately 5.000 human genes. Following hybridization, we scanned the microarray to produce a pseudocolour image. The objective of this study is standardizing the CGH technique that goes from the DNA labeling through statistical analysis. DNA digestion was performed with two restriction enzymes, DpnII and EcoRI. The direct labeling protocol uses the fluorophores Cy3 and Cy5 and the hybridization protocol reveal data that exceeds our quality control. We are now performing hybridizations with a series of 20 DNAs derived from head and neck tumors and our goal is to correlate genomic alterations with gene expression levels.