produced equivocal survival benefits. We have used complementary DNA microarrays containing 9,216 genes to monitor gene expression in HNSCC tissue samples, adjacent normal margins and lymph node metastases. We extracted RNA from 46 surgically resected HNSCC tumor samples and compared it with cultured normal human adult keratinocytes. We are also comparing at least ten additional matched samples of primary and metastatic tumors from these same patients. Hierarchical clustering methodology has allowed us to classify these tumors on the basis of their gene expression patterns, and we are currently correlating these results with the clinical data collected for each patient. We have identified a group of genes that are generally overexpressed in these tumors, as well as genes that are diagnostic of specific tumor subtypes. Our results demonstrate that it is possible to classify HNSCC tumors based solely on global patterns of gene expression and to identify candidate genes that are the best predictors of tumor subtypes. We are studying these genes using other methodologies, such as tissue microarrays, to examine further their suitability as possible targets for drug treatment.

Bertoni, Francesco [22]

Construction of a chromosome 11q22–23 BAC/PAC contig to characterize deletions in lymphoproliferative disorders

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The application of technologies such as DNA microarrays and the ongoing human genome sequencing project will help the study of the genes underlying the pathogenesis of cancer. Chromosome 11q22–23 is frequently deleted in human solid and lymphoid neoplasms, such as breast and colorectal cancer, chronic lymphocytic leukemia and mantle cell lymphoma. Thus several cancer genes are likely to map to this region. To analyze the deletions in lymphoproliferative disorders, a PAC/BAC contig of chromosome 11q22–q23.3 was constructed, using as a guide the yeast artificial chromosome contig previously applied to characterize the deletions in patients affected by Jacobsen syndrome. BAC and PAC clones were identified and localized by screening of different human genomic libraries using the polymerase chain reaction, filter hybridization and database searches, using sequence-tagged sequences, expressed sequence tags or gene sequences known to map to the region of interest. The PAC and BAC end sequences were then used as new sequence-tagged sequences for database analysis or to design polymerase chain reaction primers after eliminating the repetitive elements using BLAST software. The assembled PAC/BAC contig stretches from D11S1897 to FRA11B. Construction of a transcript map to identify possible cancer genes is continuing. The ordered genomic clones will be used to analyze DNA samples of lymphoid tumors to determine regions of chromosome loss or amplification within the region of the contig using DNA microarray technology or the Invader assay.

Berx, Geert [23]

E-cadherin controlling epithelial differentiation in human carcinomas

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Acquisition of invasive and metastatic capabilities is frequently associated with loss of cell–cell adhesion. One of the major constituents of the cell-adhesion complex in epithelial cells is E-cadherin, a transmembrane protein involved in homotypic cell–cell adhesion. E-cadherin exerts a potent invasion-suppressing role in experimental tumor cell systems. Partial or total loss of E-cadherin expression apparently occurs in the majority of human carcinomas. Several different mechanisms seem to cause the loss of E-cadherin function, including transcriptional downregulation and mutational inactivation. E-cadherin mutations are already present at the early noninvasive *in situ* stage of lobular breast tumors, and E-cadherin germline mutations in cases of familial diffuse gastric cancer argue strongly in favor of a real tumor suppressor role for E-cadherin, in addition to its role as an invasion suppressor. The variety of effects on E-cadherin expression (such as epithelial cell morphology, cell polarization, and growth inhibitory and tumor suppressive effects) is not solely the result of cell–cell adhesion but implies that E-cadherin expression mediates complex signaling processes and transcriptional regulatory events. Therefore we set up cell models that mimic the E-cadherin deficiency in human carcinomas and analyzed them for differences in messenger RNA expression, using molecular indexing and microarrays. We are currently analyzing genes with differential expression in these matched tumor cell pairs (with and without E-cadherin expression) to determine their specific role in growth control and loss of cell differentiation during epithelial tumor progression.

Bharucha, Vandana [24]

Analysis of the CBFB, CBFA2 and AF-9 genes in familial acute myelogenous leukemia

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The cloning of chromosomal translocation breakpoints from sporadic leukemias has identified genes that are implicated in the pathogenesis of acute myelogenous leukemia (AML). Although common, such chromosomal translocations are not necessary for the development of leukemias, suggesting that other underlying genetic factors are involved in the early stages of leukemia development. Familial AML is extremely rare, and families with the disease provide a unique resource for the study of the genes involved in the initial stages of cancer development. We investigate a single family in which several members have developed AML. Three members (a mother and two offspring) are affected with AML M4eo, and a third offspring is affected with AML M2. The average age of onset in the children (7 years) is significantly lower than that for the mother (30 years). Transmission of the disease seems to be in an autosomal-dominant manner. The small size of the pedigree reduces the power of genome-wide linkage analysis and therefore we used a candidate gene approach. Initially three genes were selected for analysis based on their reported involvement in familial and sporadic AML: *CBFA2, CBFB* and *AF9.* We performed genotyping at these loci to identify shared haplotypes between affected individuals. We will also report the results of direct mutation analysis of the candidate genes.