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|  | A substantial number of oncogenes and tumor-suppressor genes have already been discovered. However, genome analysis techniques suggest that the number of such genes may be strikingly large, and there is much to be discovered. It is important to find regions in the genome of recurrent aberrations in chromosomes. An aberration is a location on a chromosome that has deviated from the normal. A number of such regions have been identified in human cancers but the functional consequences of most of these abnormalities are not yet known. Identification of the affected genes in these regions, knowledge of their functions, and association of these genes with tumor progression is essential to fully understand the growth and progression of tumors. (Genome Changes and Gene Expression in Human Solid Tumors, by Joe W. Gray and Colin Collins)    My research project is to identify chromosome aberration patterns and identify genes that occur significantly in breast cancer tissue. I am concentrating on specific locations on chromosomes that have already been noted by CGAP to be potentially important locations for breast cancer causing genes.    There are twenty-two different chromosomes, and each have a double copy. There are also two sex chromosomes for a total of forty-six chromosomes in every cell. To specify where a chromosomal aberration is, the chromosome’s number is stated. The chromosome can further be divided because it has two arms, the longer arm is called q, and the shorter arm is called p. Each cytogenetic location is given a number to specify the exact location the aberration has occurred on the chromosome. When dyeing a chromosome, there will be many stripes, altering dark and light colors. These divisions on the chromosomes are divided into bands. For example, 11p15 means that the cytogenetic location is on chromosome number 11, it is on the shorter arm of the chromosome, and is located at band number 1, and sub-band number 5. There are many cytogenetic locations on chromosomes that are thought to be involved in the development of cancer. There may be genes in these regions that are differentially expressed through mutations.    The first step of my project is to choose 3 to 4 important recurrent chromosome aberrations in breast cancer from the Mitelman Database of Chromosome Aberrations. This is done by selecting aberrations by the criteria of how frequently they occur and by being in a region that contains many genes.    Second, I will find the list of genes that are mapped to the cytogenetic band of each chromosome aberration, by using the Gene Finder on CGAP. A second program called Virtual Northern has data on the relative expression levels of each gene in normal versus cancer tissue. The expression levels are given in terms of EST’s. An EST, or expressed sequenced tag, is a tag of the messenger RNA, made by the gene. By counting the number of EST’s in a tissue, this is equivalent to counting the number of messages transcribed from the gene, and this is what we mean by expression level. The EST’s are counted by sequencing a cDNA library made from a tissue. cDNA stands for copy DNA and is made by mRNA from reverse transcription. For each gene, four numbers are given by the Virtual Northern program. (Note: Northern refers to a gel analysis of mRNA and the name is a play on the term Southern, which refers to the last name of the man who first analyzed DNA by gels.) The numbers are the counts for the EST’s specific to the gene in normal and cancer tissue, and the total number of ESTs for all genes expressed in normal and cancer tissue.    Third, I downloaded the expression level data (EST counts) for each gene into Excel to analyze the data. Differential expression is when the number of ESTs per gene is statistically different between normal tissue and cancerous tissue. A single gene might express just one message or a few hundred. A gene in normal tissue that has a significantly different level of expression than the same gene in cancer tissue is a gene that I am going to analyze further for a functional role in cancer. Because this gene is different in cancer than normal tissue, the gene may be a factor in the development of the cancer. After I have identified the statistically significant differentially expressed genes in breast tissue, I study each gene from a website called Locus Link, which provides extensive information about individual genes, such as their functions and whether they can be targeted by drugs.    I have selected this topic because I have an interest in the study of pharmacology and cancer, so this project exposes me to the frontier of drug discovery and I am able to use the same resources that professional cancer researchers use. My project is only examining a small part of this new and exciting part of cancer research. There is still an overwhelming amount of research that needs to be done. Cancer researchers know that cancer is still the second most common cause of death for people of all ages. One in nine women will develop breast cancer at some point in her life. This is why cancer researchers have a tremendous drive to continue working hard to find answers.  <[Back](http://docs.google.com/intro3.html)> |
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