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Activation of CD22 a Potential Novel Marker for Ovarian Cancer

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Abstract

CD22 is a gene that codes for a protein by the same name. This protein is normally expressed on the surface of B-cells, where it participates in the cell's survival. In related studies, CD22 as been shown to appear on cancerous lung cells. It is suspected that this is also true for cancerous ovarian and pancreatic cells due to a chromosome abnormality common to all of these cancers.

The primary hypothesis is that inappropriate activation of the CD22 gene gives a tumor cell an advantage to metastasis to lymph nodes and bone. This research tests this hypothesis by comparing the expression of CD22 expression on B-cell lines with several ovarian cancer cell lines to determine expression patterns and by characterization of normal and aberrant CD22 receptor substrate interactions on bone marrow stromal cells.

This research has great significance. It will provide valuable information on the expression of CD22 on tumors, which can in turn be used as a new target for antibody directed therapy. Antibody therapy for this protein also has great potential in lung and pancreatic cancers, as it is tailored with

Results

Figure 1: Primers for PCR

This cDNA is a 133 base pair fragment without the intron, which is much shorter than the genomic CD22 sequence at several thousand base pairs.

The primers designed in this study were carefully chosen so that the exact desired region of the genome would be targeted, rather than include sequences from neighboring genes or even neighboring chromosomes. Using primers on cDNA instead of genomic DNA also excludes introns from the sequence.

Figure 2: Gel Electrophoresis

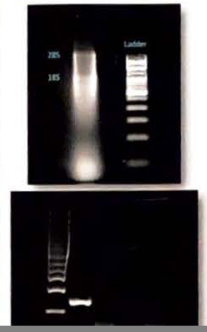
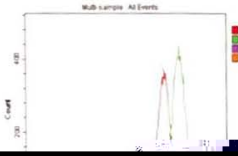


Figure 3: Flow Cytometry



Population	Mean CD22 FITC FITC-A
Ramos IgG1 (Control)	53065.2
Ramos CD22	108305.4
PA-1 IgG (Control)	26848.1
PA-1 CD22	30215.5

Flow cytometry has only been performed with one cell line (PA-1) thus far, as seen in figure 3. Ramos cells acted as the positive control for this experiment. For both Ramos cells and the cancerous ovarian cells, two

Discussion

What Has Been Observed So Far

In qualitative analysis of the total RNA prior to performing reverse transcription (Figure 2a), there are two bands and evidence of ribosomal RNA at varying lengths, indicating the RNA is intact at this stage. Figure 2b depicts a gel that was run following reverse transcription and PCR amplification. While fainter compared to the Ramos (B-cell) band, a definite band is present for the PA-1 cDNA. This asserts that CD22 is expressed inappropriately in cancerous PA-1 ovarian cells; however, it is not expressed at the levels seen in the Ramos cells.

PA-1 ovarian cells are the only cells that have been analyzed thus far via flow cytometry. The difference in means between the IgG PA-1 control and the PA-1 CD22 population lends confidence to CD22 surface expression in this cell line. Flow cytometry has yet to be optimized for this experiment, and more cell lines and negative controls will be analyzed using flow cytometry. Hela, the negative control used, proved to be a poor control upon flow cytometry.