

# Microarray student

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In the cell cytoplasm, the ribosome reads the sequence of the Mrs. in groups of three bases to assemble the protein. D. What is the resulting primary sequence Of the protein you made in the interactive? Mennonite, Lucien, Aspartic Acid, Valise, Phenylalanine 2. Go to the " DNA Microfarad Virtual Lab" found at the university of Tutu's Learn-Genetics:

GeneticScienceLearning Center's website: <http://learn.Genetics.Utah>.

Du/content/labs/microfarad/ 3. Click on the microfarad slide to begin. Then choose Chapter 2 " Measuring Gene Expression" and go on through Chapter 3 " The Experiment".

Complete the interactive a first time without writing anything down. 4.

Answer the following questions as you work through the virtual DNA microfarad a second time. . What can scientists look for to see which genes are turned on in a particular cell? Provide an example. Scientists use DNA microfarad's that used techniques allowing the amount of Mrs. transcribed by each gene which allows scientists to determine which genes are expressed to a cell. To do so, they use PC to make copies of a gene and then DNA is placed on the microfarad.

An example of this is when the DNA microfarad's can be used to detect single nucleotide polymorphisms (Snaps). B. Why are tissue samples from healthy and cancer cells taken from the same patient? Both samples are elected to be able to compare the cells, look at differences in gene expression in cells that have the exact genetic blue print. C. How is RNA separated from the rest of the tissue? In order to be separated, RNA samples are mixed with organic solvents, and then they run through a vortex and centrifuge. D. Describe the process used to isolate Mrs. from the other types

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of RNA. RNA is different from other types of RNA because it is the only type that has Poly-A tails, having several adenine amino acids at the end of the molecule. E. Explain how samples are marked. Cancerous cells are red and healthy cells are green. . Why is it necessary to make a CDMA copy? Why is Mrs. not used? RNA is not used because DNA is a more stable compared to RNA Making a CDMA copy is necessary to visualize the CDMA later on. This is possible because when you make the CDMA copy, you incorporate a fluorescent label in the molecule. G.

Draw a diagram of the process of how labeled DNA copies are made. Label the important components of the process. Your diagram should be in color. Turned in. H. What does CDMA stand for and what was used as a template to create it? CDMA stands for complimentary DNA fragments. The reverse transcription of Mrs. allows for single stranded CDMA to be made. I. What happens once you apply the DNA from the two samples to the DNA microfarad? On the microfarad there are many identical copies of the same genes on certain spots, each spot represents a different gene. J. What does the red color indicate?

The red color indicates genes that were induced by elevated CA. K. What does the green color indicate? The green color indicates that the gene was strongly repressed by cancer cells. L. What does the yellow color indicate? The yellow color indicates that the gene was neither strongly expressed nor strongly repressed in cancer cells. . What conclusions can you make from microfarad data? Microfarad data is a collection Of DNA spots attached to a solid surface that's used to measure the expression levels of large numbers

of genes simultaneously or to genotype multiple regions of a genome. . Does every red spot mean that the genes in that spot are bad? Explain. Not every red spot is cancerous. Red spots on the merged image represent genes that have had their expression turned up or on in the cancerous tissues and are not expressed in normal cells, the they are not always cancerous. O. What are the limitations of DNA microfaradtechnology? The quality and amount of RNA remains a major challenge in the microfarad experiments. The amount of obtained tissue and the complexity of the tissue sample itself limit the quality and quantity of RNA that can be isolated.

Therefore, clinical studies that are published using the microfarad approach are performed in settings where biological samples are abundant and easily obtainable. 5. Complete the Paper Microfarad analysis that comes with the kit. Part II: Smokingand Lung Cancer Grandpa Joe, Judy Smith's father, has been a smoker for the past thirty years. Last year, Grandpa Joe came down with a cold that turned into pneumonia. It took him more than a month to recover. Thefamilyis very concerned he is going to develop lung cancer.

They heard about a study being conducted at the local hospital that is exploring lung-cancer associated genes in smokers and non-smokers. The family convinces Grandpa Joe to participate in the study in order to learn more about his risk for developing lung cancer. The study is investigating six genes thought to be involved with lung cancer using DNA microfarad technology. The researchers hope to compare gene expression of the six genes of interest between smokers and non-smokers in order to gain more knowledge of what causes a normal lung cell to become cancerous.

You have been assigned to the study. Your first task is to learn more about the six genes of interest. Below are descriptions for the six genes of interest:

Gene Name (and Symbol): Protein Function: Prediction: Gene 1: Human carcinogenicity antigen (CANDACE) This gene codes for a protein that is located in the extracellular matrix. This protein is involved with adhesion between cells and is thought to be a proto-oncogene and when over-expressed is an oncogene. Expressed in smoker. We predict that the CANDACE will progress to the form of a tumor or unable to harbor that potential.

Gene 2: Surfactant protein B (SFTSB) This gene codes for an extracellular protein. This protein enhances the rate of spreading and increases the stability of pulmonary surfactant, a lipid-rich material that prevents lung collapse by lowering surface tension at the air-liquid interface in the alveoli of the lungs. Expressed in the Smoker. This gene can possibly progress to spread a higher production of cells or possibly a higher rate of cancer, maybe in the lungs. Gene 3: p53 tumor suppressor (TP53) This gene codes for a protein that is located in the mitochondria and in the nucleolus.

This protein is involved with cell cycle checkpoints. This gene is a tumor suppressor gene and is thought to be the "Guardian of the Genome." Suppressed in the smoker. I predict this gene is unlikely to get cancer as it monitors cell production, etc. To prevent tumors. Gene 4: SRY This gene codes for a protein that is located in the nucleus. The protein that this gene codes for is testis-determining factor (TDF) which initiates male sex

determination. This protein has no function in lung cells. Not expressed in either. Non-smoker-? yellow.

This gene probably determines whether or not you get cancer based on cell production. Assume it contributes to getting cancer, unless in the lung cells, where there would be no increase or decrease in likelihood. Gene 5:

Stockroom IPPP (COPY AY) This gene codes for a protein that is located in the endoplasmic reticulum. The protein catalyzes reactions involved in drug metabolism and synthesizes cholesterol, steroids, and other lipids. The expression of this protein is induced by some polycyclic aromatic hydrocarbons (PARS), some of which are found in cigarette smoke.

Suppressed in smoker. This gene will contribute to causing cancer if deregulated because it controls cell signaling pathways. Gene 6: Clinical

3(SPEC) This gene codes for a protein that is located in the plasma membrane and extracellular matrix. The gene controls cellular response to damage and may control cellular growth regulation and apoptosis. This gene is considered to be a tumor suppressor gene for lung cancer.

Suppressed in smoker. This gene decreases your risk of cancer as it controls cell self-destruction and responds to damage or advances in cell growth 6.

Highlight or underline any interesting or important information about the function of each protein. 7. Predict how these genes will be expressed in a DNA microarray of a smoker versus a non-smoker. Would you expect the genes to be induced in the smoker (more expressed), suppressed in the smoker (less expressed), not expressed in either the smoker or the non-smoker, or expressed the same in both the smoker and non-smoker? In a

DNA microarray, I would expect these DNA genes to have a bit of diversity. I think Gene 1 and 2 will be likely induced as they can contribute to overall cell production, 4 would be unaffected as Mr..

Smith is testing for lung cancer, and 3, 5, and 6 to be suppressed as they work to control cell production and smoking destroys several of their functions. For example, Gene 6 works to control cell apoptosis-- if smoking ruins the chances for a cell to destroy itself, production can get out of control. 8. Record your predictions in the Prediction column of the above table. Part III: Microarray Wet Lab Now that you know more about the six genes of interest, your job is to perform a simulated DNA microarray using tissue samples taken from Grandpa Joe and a non-smoker's tissue samples.