

NHGRI *fact sheet*

DNA Microarray Technology

What is DNA microarray technology?

Although all of the cells in the human body contain the same genetic material, the same genes are not active in all of those cells. Studying which genes are active and which are inactive in different kinds of cells helps scientists understand more about how these cells function and about what happens when the genes in a cell don't function properly.

In the past scientists have only been able to conduct such genetic analyses on a few genes at once. With the development of DNA microarray technology, however, scientists can now examine thousands of genes at the same time, an advance that will help them determine the complex relationships between individual genes.

How does microarray work?

Microarray is based on a database of over 40,000 fragments of genes called expressed sequence tags (ESTs). Minuscule amounts of hundreds or thousands of these ESTs are arranged on a single microscope slide by a robot. Next the genetic messenger molecules, which signal the production of proteins, from a particular cell are labeled with fluorescent tags and allowed to hybridize, or bind, to the ESTs on the slide whose sequences are complementary to the those of the messengers. After a scanner measures the fluorescence of each sample on the slide, scientists can determine how active the genes represented by the ESTs are in the cell. Strong fluorescence indicates that many of the cell's messengers hybridized to the EST and, therefore, that the gene is very active in the cell. Conversely, no fluorescence indicates that none of the messenger molecules hybridized to the EST and that the gene is inactive in the cell.

Why do scientists use microarray?

Microarray technology will help researchers learn more about many different diseases—heart disease, mental illness, and infectious disease, to name only a few. One intense area of microarray research at the NIH is the study of cancer.

In the past, scientists have classified different types of cancer based on the organs in which the tumors develop. With the help of microarray technology, however, they will be able to further classify these types of cancer based on the patterns of gene activity in the tumor cells and will then be able to design treatment strategies targeted directly to each specific type of cancer.

Additionally, by examining the differences in gene activity between untreated and treated—radiated or oxygen-starved, for example—tumor cells, scientists can better understand how different types of cancer therapies affect tumors and can develop more effective treatments.