

First genome-wide expression analysis yields better understanding of how leukemia develops

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In a collaborative study published Feb. 9, 2009, in the *Proceedings of the National Academy of Sciences* (PNAS), scientists performed a genome-wide expression analysis comparing highly enriched normal blood stem cells and leukemic stem cells, and identified several new pathways that have a key role in cancer development.

Many scientists believe the best way to eradicate cancer is to find therapies that target cancer's stem cells, the cells thought to be responsible for maintaining the disease. Most cancer treatments today fail to attack cancer at its root, which is why the disease can recur despite aggressive therapy.

Before the development of cancer stem cell therapies can take place, however, scientists must improve our understanding of the similarities and differences between biological networks active in leukemic stem cells and their normal cell counterparts

The PNAS paper showed that by using modern microarray technology, scientists could reveal a swath of stem-cell pathways - some of which were already well known and others not previously implicated in leukemia and other cancers. In fact, researchers identified 3,005 differentially expressed genes. Among them, a ribosome and T-cell receptor signaling pathway emerged as new players in the regulation of cancer stem cells.

The direct comparison of leukemic stems cells (obtained by consent from patients) to normal blood stem cells, also provides critical insight into the differences found in malignancy that may be used to develop targeted therapy, said Michael W. Becker, M.D., an assistant professor at the James P. Wilmot Cancer Center at the University of Rochester Medical Center. Becker was a co-first author.

Source: University of Rochester Medical Center

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