

New tools for prediction of disease progression in acute childhood leukemia

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(PhysOrg.com) -- Researchers at Uppsala University and University Children's Hospital in Uppsala have devised powerful new tools for typing cells from children with acute lymphatic leukemia and for prediction of how children with leukemia will respond to chemotherapy. The study was recently published in electronic form by the prestigious hematological journal *Blood*.

Acute leukemia is the most common form of [childhood cancer](#). The new study shows that [DNA methylation](#) is a promising tool for predicting disease progression. DNA methylation is a so-called epigenetic change in the genome. Epigenetic changes are alterations of the genomic DNA that do not affect the DNA sequence - as opposed to hereditary mutations.

The present study analyzed DNA methylation of the DNA of bone marrow cells from 400 children with acute lymphatic leukemia (ALL) from the Nordic countries. These samples are unique in an international perspective. During many years pediatric oncologists in the Nordic countries have collected detailed information about the patients and documented it in a Nordic database.

On the basis of a preliminary analysis of 8,000 human genes, the scientists selected 400 genes for analysis of DNA methylation. Methylation analysis of only 40 genes allowed subtyping of [leukemic cells](#) from the patients with a similar accuracy as is achieved by cytogenetic methods routinely used today. The researchers also identified groups of [genes](#) whose DNA methylation levels correlated

with the treatment response in ALL patients.

The studied was directed by Professor Ann-Christine Syvänen at Uppsala University and Professor Gudmar Lönnnerholm from Uppsala University Children's Hospital.

“Our findings indicate that analysis of DNA methylation of a limited number of methylated bases in DNA can be used as markers in a DNA test to identify those groups of patients who will not respond to leukemia treatment,” says Professor Ann-Christine Syvänen.

Despite recent dramatic improvements in methods of treatment for acute childhood leukemia, certain groups of patients do not respond to chemotherapy and suffer relapses.

Human DNA contains tens of millions of bases that can be methylated. Hopefully the results from the study will also contribute to an increased understanding of epigenetic mechanisms that cause [leukemia](#). Epigenetics is a new research field for which technology for genome-wide studies has become available only recently.

More information: bloodjournal.hematologylibrary.org/

Source: Uppsala University ([news](#) : [web](#))

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