Genetic pattern that predicts leukemia relapse discovered

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A genetic pattern that predicts the likelihood of relapse in patients with one of the most aggressive forms of childhood leukemia has been discovered. Researchers publishing in the open access journal *Molecular Cancer* have identified a consistent pattern in five genes that has the potential to enable doctors to identify which patients would benefit from more aggressive treatment when first diagnosed with T-cell acute lymphoblastic leukemia (T-ALL).

Co-author Dr Alex Beesley of Perth's Telethon Institute for Child Health Research said "While up to 80% of children with T-ALL achieve complete remission, there are around 20% who relapse and whose prognosis can be very poor," Dr Beesley said. "In this study, we found a consistent pattern in the expression of five genes in patients that relapse. Importantly, this pattern was found to hold true across multiple patient cohorts, the first time that such a robust gene signature of this kind has been found for T-ALL. This gene signature would enable patients with T-ALL to be classified according to risk at the time of diagnosis."

Dr Beesley said the discovery had significant potential to improve outcomes for patients at high risk of relapse. "Patients identified using these markers could potentially be treated with more aggressive therapies from the outset to give them the best hope of achieving complete remission."

The research team analyzed bone marrow samples from children treated under the international Children's Oncology Group (COG) protocols.

They used gene-profiling (microarray) technology to model a five-gene classifier that accurately predicted clinical outcome in a cohort of 50 T-ALL patients. The five-gene classifier was further tested against three independent cohorts of T-ALL patients, using two different techniques (either quantitative RT-PCR or microarray gene expression), and could predict patients with significantly adverse clinical outcome in each.

Dr Beesley said the study also provided clues to the biological mechanisms leading to relapse in T-ALL, which could ultimately identify potential targets for new therapies to the disease.

T-ALL affects approximately 15% of newly diagnosed pediatric leukemia patients. The prognostic potential of the gene markers identified from this research will now be investigated as part of a large international Children's Oncology Group study of T-ALL patients undergoing the latest therapy.

More information: Gene-based outcome prediction in multiple cohorts of pediatric T-cell acute lymphoblastic leukemia: a Children's Oncology Group study
Amanda L Cleaver, Alex H Beesley, Martin J Firth, Nina C Sturges, Rebecca A O'Leary, Stephen P Hunger, David L Baker and Ursula R Kees
Molecular Cancer (in press), www.molecular-cancer.com/imedi … le.pdf?random=960475

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