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Study: Genetic mutations found in 8.5% of children with cancer

November 24, 2015

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Article type: News

Topics: Cancer/Neoplastic, Genetics

Roughly 8.5% of children with cancer were found to have mutations in cancer-predisposing genes, and most of those did not have a family history of the disease, according to a new study.

Researchers say the findings could allow them to detect and treat cancer at earlier stages.

“This paper marks an important turning point in our understanding of pediatric cancer risk and will likely change how patients are evaluated," corresponding author James R. Downing, M.D., president and CEO of St. Jude Children’s Research Hospital, said in a news release. “For many pediatric cancer patients, comprehensive next-generation DNA sequencing of both their tumor and normal tissue may provide valuable information that will not only influence their clinical management but also lead to genetic counseling and testing of their parents and siblings who may be at risk and would benefit from ongoing surveillance.”

The research stems from the St. Jude Children’s Research Hospital – Washington University Pediatric Cancer Genome Project and is published in the paper “Germline Mutations in Predisposition Genes in Pediatric Cancer” (Zhang J, et al. N Engl J Med. Nov. 19, 2015, www.nejm.org/doi/pdf/10.1056/NEJMoa1508054).

Researchers sequenced the whole genome, whole exome or both in 1,120 pediatric cancer patients to check for mutations in 565 genes associated with cancer. They also performed an in-depth analysis of 60 genes known to increase cancer risk when altered.

About 8.5% of the children had germline mutations that were deemed pathogenic or probably pathogenic compared to 1.1% of adults from the 1000 Genomes Project who were not known to have cancer.

Of the children with such mutations who had information available on their family, 40% had a family history of cancer. Experts previously thought these mutations were found only in families with strong histories of cancer.

Prevalence of these mutations was highest in children with non-central nervous system (CNS) solid tumors (16.7%) followed by CNS tumors (8.6%) and leukemia (4.4%).

The genes most commonly mutated were TP53, APC, BRCA2, NF1, PMS2 and RB1. Researchers said they were surprised to find mutations in the breast and ovarian cancer genes BRCA1 and BRCA2 and germline mutations in six patients with Ewing sarcoma.

St. Jude plans to continue to analyze genetic mutations through its new clinical research study Genomes for Kids and refer children with certain germline mutations to the new St. Jude Hereditary Cancer Predisposition

Clinic.

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