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Next-generation sequencing test identified potential targets for pediatric cancer treatments

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A comprehensive genomic profiling test using next-generation sequencing has identified genomic alterations in more than half of pediatric cancer samples tested that would give clinicians potential targets on which to base individualized treatment decisions, according to results presented at the American Association for Cancer Research (AACR) special conference on "Pediatric Cancer at the Crossroads: Translating Discovery Into Improved Outcomes," held Nov. 3-6.

"During the last few years, we have seen many therapies that target specific genomic alterations become available for adult patients with cancer," said Matthew J. Hawryluk, Ph.D., senior director of corporate and business development at Foundation Medicine, in Cambridge, Mass. "Unfortunately, there is a lack of targeted therapies for pediatric malignancies."

"We were excited to discover that we could identify genomic alterations indicating a potential treatment option in 56 percent of the pediatric tumor samples that we analyzed using our FoundationOne genomic profiling product," said Hawryluk. "We will be launching a second product that more accurately reveals the types of genomic alterations that are key drivers for pediatric cancers, hematologic malignancies, and sarcomas."

FoundationOne is a next-generation sequencing-based genomic profiling

test that provides comprehensive analysis of more than 200 genes known to be altered in human cancers. Hawryluk and colleagues used the test to analyze 193 tumors from patients aged 21 years or younger with a wide variety of cancer types including sarcomas, solid tumors, and hematologic malignancies.

The test detected 361 genomic alterations among the patient samples. Seventy-five percent of patients had at least one genomic alteration, with an average of 2.5 alterations per patient. The test identified genomic alterations indicating a potential treatment option for 56 percent of the pediatric patients from whom the tumor samples were derived. Almost two-thirds of the alterations would not have been detected using available tumor type-specific tests, according to Hawryluk.

"We realize that this is an enormous unmet need, and we want to make these data available for researchers, physicians, and patients to demonstrate the importance of genomic profiling in pediatric cancers," Hawryluk said.

Hawryluk is an employee of Foundation Medicine, which funded the study.

More information: www.aacr.org/page34138.aspx

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