Landmark study sequences most childhood cancer samples from single cancer type ever

Scientists from St. Jude Children's Research Hospital in United States (US), have created a roadmap of the genetic mutations present in the most common childhood cancer, acute lymphoblastic leukemia (ALL), claiming they have sequenced the most childhood cancer samples from a single cancer type ever.

The landmark study, published September 1, 2022 in the journal *Nature Genetics*, is the first to supply a comprehensive view of the genomics of all subtypes of ALL, which the researchers hope will serve as a foundational guide for physicians and scientists to understand disease development and improve patient outcomes with treatments.

Their research included 2,574 pediatric ALL patient samples, the largest such cohort ever published. By comparison, earlier studies have typically studied hundreds of samples, or fewer.

The samples, collected over more than a decade in collaboration with the Children's Oncology Group, were subjected to a combination of whole-genome, whole-exome, or transcriptome sequencing. The researchers compared the sequences to find patterns in the mutations, which they contend can serve as roadmaps to understand how the cancer develops and how it may respond to treatment.

"In this study, we were able to comprehensively define the number and type of recurrently altered genes that are found in childhood ALL," co-corresponding author Dr. Charles Mullighan, from the St. Jude Department of Pathology, said in a statement. "Because of the scale of the study, we could identify many newly implicated genes that have not been reported in leukemia or cancer at all, and to show that they fall into several new cellular pathways."

The data from the paper can be accessed by other scientists on the St. Jude Cloud, within the pediatric cancer data portal (PeCan) database. - **www.scienceboard.net, September 2, 2022**