Journal of Leukemia
ISSN: 2329-6917
OPEN ACCESS Freely available online
Perspective

Comparison of Mortality Rate in Adults and Children with Acute Lymphoblastic Leukemia

Takagi Masatoshi*

Department of Pediatrics, Tokyo Medical University, Tokyo, Japan

DESCRIPTION

Acute Lymphoblastic Leukemia (ALL) is an antagonistic hematological cancer that affects children and adolescents more often than adults. The survival of ALL has improved, especially in pediatric patients, thanks to the introduction of treatment methods such enhanced chemotherapy, hematopoietic stem cell transplantation, and chimeric antigen receptor-T-cell immunotherapy. The prognosis for adult ALL cases, however, is still not good. A recurrence usually occurs within a few months of Complete Remission (CR) in about 30%-40% adult ALL patients, and about 50% of these patients eventually develop refractory leukemia, which has a dismal prognosis for cure and a 5-year Overall Survival rate (OS) of around 50%. Consequently, treating ALL in adults remains a difficult disease. ALL has been shown to progress due to aberrant genetic mutations and molecular abnormalities that impact cell differentiation, cell proliferation, and treatment resistance. In order to risk stratification and prognosis prediction, several biomarkers with significant roles in molecular etiology and clinical importance were found.

These biomarkers gave possible treatment targets and guided the choice of certain medicines. Notably, the prognosis of ALL patients with *BCR -ABL1* transcripts was improved by the use of Tyrosine Kinase Inhibitors (TKI). The detection of genetic abnormalities in ALL, including faulty DNA sequences, aberrant epigenetic changes, and abnormal gene expression, has recently expanded advancements in Next-Generation Sequencing (NGS) technologies including Whole-Exome Sequencing (WES) and RNA sequencing (RNA-seq). The poorer prognosis in ALL was partially caused by the high incidence of genetic subtypes that are unfavorable in adult patients. *BCR -ABL1* is a rare disease in childhood (2%-5% of patients), but it affects at least 25% of adults. Older children demonstrated a higher prevalence of somatic mutations and epigenetic regulator mutations than newborns in MLL-rearranged ALL. Additionally, while having the same genetic subtype as pediatric ALL patients, adult patients are less responsive to standard therapy.

The genetic variations and therapeutic responses between adult and pediatric ALL patients revealed unique leukemogenesis and pathophysiology in the two populations. According to earlier studies, adult patients had more gene alterations than pediatric ones. The Single Nucleotide Variant (SNV) is the most prevalent mutant type of the genomic profiling, which was consistent with what was reported in prior research. The median number of discovered gene mutations per sample in adult ALL was 19 (range: 1-53) and 4.5 (range: 1-19) in pediatric ALL. The most frequently altered genes in adult ALL were *NOTCH1*, *TTN*, and *IKZF1*, in that order. The most frequently mutated genes in paediatric ALL were *KRAS*, *NOTCH1*, *NRAS*, and *CREBBP* in that order. Genomic profiling's mutation frequency was equivalent to previously published data. The many center motor genes were eliminated using the bioinformatics tools. Adult ALL patients were more enriched for tumors metabolism and epigenetic changes, such as *IDH1* and *DNMT3A*, which may help to explain why the two populations' responses to treatment differed. *IDH1* mutations are most frequently found in myelodysplastic syndrome and acute myeloid leukemia.

Additionally, a little percentage of adult T-Cell Acute Lymphoblastic Leukemia (T-ALL) patients had *IDH1* mutations found. According to reports, *IDH1* mutations increased the metabolic profile of malignant T cells and likely had a role in the development of mouse T-cell malignancies. Mammalian DNA methylation throughout development depends on the DNA methyltransferase *DNMT3A*. According to reports, 65% of patients with T-ALL exhibited *NOTCH1* mutations, which led to ongoing activation of the *NOTCH1-MYC* pathway and further promoted the growth of the leukemic cells. *IKZF1* mutations were present in 15% of B-ALL patients and 70% of patients with Ph positive and Ph similar ALL, both of whom had poorer prognoses for survival. Low cardiorespiratory fitness was associated with a *TTN* gene variation in pediatric ALL. Poor information was provided for *TTN* mutations in adult-ALL, nevertheless. Notably, in our analysis, *TTN* mutations were found in adult-ALL patients but not in paediatric ALL patients.

Correspondence to: Semsei Agnes, Department of Genetics, Semmelweis University, Budapest, Hungary, E-mail: agnes@gmail.com

Received: 03-Apr-2023, Manuscript No. JLU-23-24739; **Editor assigned:** 06-Apr-2023, Pre QC No. JLU-23-24739 (PQ); **Reviewed:** 27-Apr-2023, QC No. JLU-23-24739; **Revised:** 04-May-2023, Manuscript No. JLU-23-24739 (R); **Published:** 11-May-2023, DOI: 10.35248/2329-6917.23.11.335

Citation: Agnes S (2023) Comparison of Mortality Rate in Adults and Children with Acute Lymphoblastic Leukemia. J Leuk. 11:335.