INTERNATIONAL JOURNAL OF CURRENT ADVANCED RESEARCH
ISSN: O: 2319-6475, ISSN: P: 2319-6505, Impact Factor: 6.614
Available Online at www.journalijcar.org
Volume 12; Issue 14(A); April 2023; Page No. 1888-1890
DOI: http://dx.doi.org/10.24327/ijcar.2023.1890.0416

Research Article

CHROMOSOMAL STUDY DOWN SYNDROME CHILDHOOD ASSOCIATED WITH ACUTE LYMPHOBLASTIC LEUKEMIA

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A R T I C L E I N F O

Article History:
Received 6th January, 2023
Received in revised form 15th February, 2023
Accepted 12th March, 2023
Published online 28th April, 2023

Key words:

Leukemia, Chromosomal Aberration, Down syndrome

A B S T R A C T

Background: Children with Down syndrome (CDS) are at increased risk of acute lymphoblastic leukemia (ALL) and chromosomal abnormalities. This research aims to determine which type of Down syndrome is most likely to cause acute lymphoblastic leukemia and what chromosomal changes are most likely to occur with this syndrome. in the city of Kut. **Methods**: 120 blood samples were taken, divided into 30 blood samples of healthy children, 30 Blood samples from children with acute lymphoblastic leukemia (only 30 cases with Down syndrome).and 30 cases of only patients with leukemia. These samples were compared with 30 blood samples of children with Down Syndrome as well as those diagnosed with acute lymphoblastic leukemia, stored in heparin tubes, and transferred to the private laboratory. The results were studied and numerical changes were found in the chromosomes, in addition to that he suffers from Down syndrome, and the type most susceptible to infection was the type of trisomy. Clinical notes, hematological parameters, and cytogenetic analysis were studied for all cases, and these cases were collected for Al-Zahria and Al-Karmah Hospital in Al-Kut for the period from 2019-2021. **Result**: Of the 30 children with DS who also had acute ALL, most of the studied cases were found to have trisomy 21 with 95%, followed by 4% of the transitional type and 1% of the mosaic type. Trisomy 21 types. The type, based on the literature, is likely to develop the most severe lymphoblastic leukemia. For chromosomal changes of the disease associated with this syndrome as well. Numerical changes were more common with the disease, with two groups, the first called hyperdiploid, and hypodiploid. **Conclusion**: Through the results, we concluded that the type of Down syndrome, chromosome 21, trisomy 21, is the most likely to develop acute lymphoblastic leukemia. Excessive chromosomal changes are the most chromosomal aberrations in these cases in the city of Kut. In addition to the absence of statistically significant differences in age and sex for the studied cases, the possibility is due to the lack of samples available for these cases in the city of Kut.

INTRODUCTION

Children with DS, causing trisomy 21, have a 50-fold vulnerability to acute leukemia in the first years of life[1]. Acute lymphoblastic leukemia (ALL) is very popular in children. Also, despite the increased possibility of acure, all major causes of death from childhood cancer remain. To find out the cause, patients must be diagnosed early and then appropriate treatment to get rid of leukemia[2,3].

Most research has found links betweenDS and leukemia over a 50-year period[4,5]. Several studies have proven that leukemia in patients with DS is 10 to 20 times higher than in the world population. DS increases the occurrence of both acute myeloid leukemia and acute lymphocytic leukemia, and transient leukemia caused by DS[6]. An additional chromosome 21 increases the vulnerability of ALL with DS. The role of trisomy 21 as an etiological factor for an increased risk of ALL is the most common acquired numerical abnormality in ALL[7,8].The lifetime probability of its onset in these children is two-stage, peaking first in the neonatal period and then again after 3-6 years. This increased risk may persist into adulthood[9]. According to studies, most of the cytogenetic types of Down syndrome are threatened by leukemia. The incidence of acute lymphoblastic leukemia is not different from acute non-glioblastoma leukemia in DS with age-related non-syndromic leukemia patients[10]. There is research that leukemia, Down syndrome, and other chromosomal changes within the family have in common. In these clans, there may be a family tendency toward non-separation [11]. Because of the increased prevalence of this syndrome, especially in recent years, accompanied by the spread of leukemia in these children, the idea of research came to shed light on the most common type in addition to the type of chromosomal abnormality prevalent in the city of Kut.

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MATERIAL AND METHOD

The research was conducted on children with Down syndrome who were transferred to Al-Zahria and AL-Karma Hospital, then 120 blood samples were taken, divided into 30 blood samples for healthy children,30 blood samples for children with acute lymphoblastic leukemia,30 cases only down syndrome, and 30 cases only leukemia patients. These samples were compared with 30 blood samples for children with Down syndrome Down in addition to those being diagnosed with acute lymphoblastic leukemia and stored in heparin tubes and transported to the special laboratory, from January 2019 to January 2021. The age From 1 to 12 years. Data collected included maternal and paternal age at the time of diagnosis and family history of the disease. Chromosomes were studied from collected peripheral blood, and cultures were harvested according to short-term cultivation using standard cytogenetic procedures with some modifications. Banding techniques were used to classify chromosomes: G-banding technique using trypsin (GTG banding)[12]. GTG domain chromosomes were classified based on the International System of Human Cytogenetic Nomenclature ISCN2005).

RESULT

The research included four groups, the first of which was for comparison with the main research group, the fourth group that collected Down syndrome and at the same time had acute leukemia, as shown in Table No. (1) through the results and in their study, it was found that most of the types Obtained she is of the trisomy type, and also most acute leukemias were diagnosed by her chromosomes, she is of the hyperploid type, and when compared with the fourth group, the chromosomal ones were diagnosed. 30 children with the syndrome who had leukemia at the same time found three groups of numerical chromosomal changes as shown in Table (2).

Table 1 Distribution the Result of 120 cases

groups	Number of cases	Gender M/F	Median age
Control groups	30	15:15	7
Leukemia patient groups	30	19:11	8
Down syndrome groups	30	15:15	8
Down syndrome with leukemia groups	30	18:12	7.3
Total	120	67:53	7.6

Table 2 Summarizing the result of Patient characteristics and chromosomal aberration for 30 Down syndrome patient's acute lymphocytic leukemia

Cytogenetic features	Number of patients Ds-ALL	Frequency %	Gender M/F	Medianage	Chromosomal numerical aberration
Hyperdiploid>46	18	60	15:8	8	60-80 aneuploidy
Hypodiploid<46	5	16.7	1:2	7	43-45 XX/XY
Psedodiploid<46>	7	23.3	2:2	7	45-47XX/XY
Total	30	100	18:12	7.3	

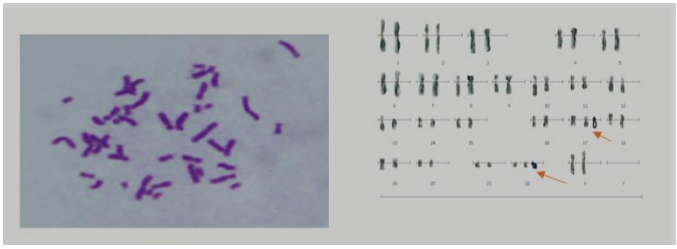

Figure 1 Chromosomal aberration of the patient

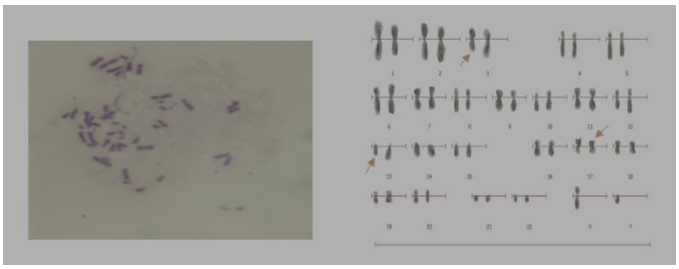

Figure 2 Chromosomal aberration of patient

DISCUSSION

Children with DS have a significantly bigger vulnerability to developing leukemia in childhood than children with no DS, but strangely, they havea smaller vulnerability to developing solid tumors[14]. "According to constitutional trisomy 21, DS is the most common cytogenetic abnormality at birth and occurs at a rate of 1/700 to 1/1000 of newborns"[15].Through this research, it was found that Trisomy 21 type is the most affected by acute lymphoblastic leukemia, since all samples collected were of this type. The frequency of acute lymphoblastic leukemia (ALL-DS) with DS is expected to be 1 in 300[16]. ALL-DS under the age of 5 is 40.7 times that of individuals of similar age with no DS. Also, up to the age of 30, the risk of ALL-DS remains higher than in people without Down syndrome[17]. Yet, different from patients with no DS, ALL-DS does not often exist in patients under the age of one. Therefore this result agrees with Madianin *et.al*. 2021 Children with DS are at anincreased risk of developing acute leukemia than children with no DS[18]. Literature studies are very few on the outcome, survival, and difficulties of treatment of those with DS and acute leukemia in the developing world. Three groups of numerical chromosomal changes were also found, and when compared with people who only had leukemia without Down syndrome also, there were three groups of numerical chromosomal changes: hyperdiploid, chromosomal hypodiploid, and pseudiploid type. There are many studies that indicated these numerical chromosomal changes. Haploid(loss of one or more chromosomes) is nearly 5% of all childhood cases while it is nearly 2.2% of those with constitutional trisomy 21[19]. Hyploidsis linked witha biggervulnerability of recurrence and isinfrequent in pediatric ALL cases[20]. "The cytogenetics of ALL-DS is different from the cytogenetics of ALL, which is not linked with DS". Children with ALL-DS have a lower frequency of favorable cytogenetics, including hyperdimers, trisomy 4, 10, and 17, and t (12; 21) translocations, in comparison with children with no DS[21]. Also, these ALL-DS offspring show an unfavorable frequency of translocations, including t (9; 22) and 11q23 (MLL) rearrangements. It is decreasing. Generally, these popularB-ALL gene rearrangements happen in nearly 60% of patients with non-DS, but only in about 20% of ALL-DS. Rather, ALL-DS possibly have a normal karyotype "except for the

constitutional trisomy 21"[22]. In people with a normal karyotype, DS-ALL is possibly low-high diploid and has common acquired changes such as + X and/or del (9p)[23,24]In people with relapse, ALL-DS has a lower event-free survival rate and lower general survival in comparison to people with ALL with no DS. This is often because of induced death and treatment-related mortality[25]. These recurrences often happen late (later than 6 months following treatment end)[25,26]. Conclusion This study found that chromosomal aberration consistsof three groups (hyperdiploid, hypodiploid, and pseudoploid).

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How to cite this article:

Sada Jasim Abdulameer (2023) 'Chromosomal Study Down Syndrome Childhood Associated With Acute Lymphoblastic Leukemia', *International Journal of Current Advanced Research*, 12(04), pp. 1888-1890.
DOI: http://dx.doi.org/10.24327/ijcar.2023.1890.0416