Retrospective Study of B Lymphoblastic Leukemia to Assess the Prevalence of TEL/AML1 in South India: A Study of 214 Cases and Review of Literature

Sandhya Devi G. 1  Faiq Ahmed 1  Manasi C. Mundada 1  Rachna Khera 1  Lavanya Nambaru 1
Krishnamohan Mallavarapu 2  Pavan Kumar Boyella 2  Veerandra Patil 2  Pallavi Suresh Laddha 2
Senthil J. Rajappa 2

1 Department of Laboratory Medicine, Basavatarama Indo American Cancer Hospital and Research Institute, Hyderabad, Telangana, India
2 Department of Medical Oncology, Basavatarama Indo American Cancer Hospital and Research Institute, Hyderabad, Telangana, India

Address for correspondence Dr. G Sandhya Devi, PhD, Department of Pathology, Basavatarama Indo American Cancer Hospital, Hyderabad 500034, Telangana, India
(e-mail: sandhyag@induscancer.com).

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Abstract

Introduction  Translocation t(12;21)(p13;q22), a recurrent and an invisible chromosomal abnormality, resulting in TEL/AML1 gene fusion, associated with good prognosis, has been described to be a common abnormality, in children with B-acute lymphoblastic leukemia (B-ALL).

Objectives  The initial observation of very few TEL/AML1 positive patients at this center on testing by fluorescence in situ hybridization (FISH) led to study the prevalence of the abnormality, compare with the global distribution, and evaluate clinical, pathological, molecular, and cytogenetic features in TEL/AML1 positive patients.

Materials and Methods  A retrospective study of all B-ALL patients tested for TEL/AML1 gene fusion during the period January 2009 to November 2020 was undertaken. Clinicopathological, molecular, cytogenetic, treatment, and follow-up details were collected. All publications dealing with TEL/AML1 gene rearrangement were reviewed post Google and PubMed search.

Results  TEL/AML1 gene rearrangement was assessed by FISH in 178 patients and by reverse transcription polymerase chain reaction in 36 patients and detected as the sole abnormality in 8.4% patients with additional genetic abnormalities noted on FISH evaluation. Normal karyotype was noted in 14/18 (77.7%) of these patients and 2 had complex karyotype. Complete blood count revealed hemoglobin to range from 35 to 116 g/L (median: 74 g/L), white blood count: 1.01–110 × 10^9/L (median: 7.8 × 10^9/L), platelet counts: 10–115 × 10^9/L (median: 42 × 10^9/L), blast count in peripheral smear: 0–98% (median: 41%). Immunophenotyping demonstrated 94.4% were CD34 positive, common acute lymphoblastic leukemia associated antigen (CALLA) positive with aberrant expression of CD13, CD33, CD56, singly or in combination in 58.8%.

Keywords

► TEL/AML1
► t(12;21) fluorescence in situ hybridization
► acute lymphoblastic leukemia (ALL)
► RT-PCR

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Thieme Medical and Scientific Publishers Pvt. Ltd., A-12, 2nd Floor, Sector 2, Noida-201301 UP, India
Introduction

Detection of recurrent genetic abnormalities in hematological malignancies by fluorescence in situ hybridization (FISH) is part of routine standard of care. Recurrent cryptic translocation t(12;21)(p13;q22) in pediatric B-acute lymphoblastic leukemia (B-ALL) is associated with specific clinicopathological characteristics and favorable prognosis. Assessment for TEL/AML1(ETV6/RUNX1) fusion enables proper treatment strategies in a given population. Review of online hospital-based reports, international projects, multicenter studies, and review articles demonstrated a wide variation in global incidence, with incidence in west being ~25% and lesser in India (Table S1 and S2-supplementary material). However, the initial observation of very less number of prognostically favorable TEL/AML1 rearranged B-ALL patients from our tertiary care cancer center in south India prompted focus on evaluating the prevalence of this abnormality. The aim and objectives of the study were to see the prevalence of TEL/AML1 gene fusion in newly diagnosed B-ALL patients, compare with the global distribution of the fusion gene, and evaluate the clinical, pathological, molecular, and cytogenetic features where available in TEL/AML1 positive patients.

Materials and Methods

A retrospective study of all cases, previously diagnosed as B-ALL during the period January 2009 to November 2020, at a tertiary care cancer center from South India, was undertaken. Data on demographic, clinical, hematological, interphase FISH, cytogenetics, reverse transcription polymerase chain reaction (RT-PCR) findings, treatment protocol, and follow-up details were collected from the case files in a format. All the newly diagnosed cases for which ALL prognostic panel (BCR-ABL, TEL-AML1, MLL) was performed and TEL AML result was available were included in the study. All cases where adequate blasts counts were not evident and also relapsed ALL cases were excluded from the study. Primary outcome provides information on the prevalence of TEL/AML1 gene fusion positivity in patients diagnosed with B-ALL from this region and for understanding how the prevalence compares with the global incidence for managing the patients. Secondary outcome includes defining the clinicopathologic features, cytogenetics and FISH findings, baseline lab values and overall survival in the TEL AML1 positive patients that were analyzed.

FISH: Interphase FISH studies were performed till November 2019, on heparinized bone marrow/peripheral blood fixed samples in 178 patients. LSI ETV6/TEL/RUNX1(AML1) extra signal dual color translocation probe set and ZytoLight-ETV6/RUNX1(TEL/AML1) dual color dual fusion probe were used for testing in 81 and 97 samples, respectively. The probe details, typical signal patterns and interpretation are provided in Table S3 (Supplementary material). The denaturation and hybridization procedures were performed according to the manufacturer’s instructions and counterstained with 4,6-diamino-2-phenyl-indole stain. Fluorescent signals were visualized at 1250 magnification. The cutoff for TEL/AML1 positivity was 5%. For each case, 200 interphase cells were evaluated by two analysts.

The status of BCR ABL fusion and MLL gene rearrangement was also evaluated using appropriate probes (Table S3).

RT-PCR: TEL/AML1 mutation was assessed by RT-PCR in 36 patient samples from December 2019 onward. RNA was extracted from bone marrow/peripheral blood samples in ethylenediaminetetraacetic acid, using Qiagen RNA blood mini kit and, c-DNA synthesis and real time PCR was performed using TRU-PCR ALL Panel Kit Version 2.1 (3B Black Biotech India Ltd, Bhopal, India).

Data on karyotype was available in 92 ALL cases. Twenty-four or forty-eight-hour unstimulated heparinized bone marrow/peripheral blood cultures had been set up as per standard protocol. Twenty metaphases were evaluated, and karyotype reported as per International System for Human Cytogenomic Nomenclature (2016). Correlation with cytogenetics was done where available.

Statistical Analysis

Since the number of TEL/AML1 positive cases were few, simple statistical measure, percentage was used to express the prevalence and other data.

Ethics

The procedures followed were in accordance with the ethical standards of the responsible committee on human experimentation and with the Helsinki Declaration of 1964, as revised in 2013. Patient consent was taken prior to the enrolment of participants in the study. Approval of the study was obtained from Basavatarakam Indo American cancer Hospital & Research Institute’s ethical committee. (EC Reference study code: 96, dated 27 May 2021).

Results

The patient cohort consisted of 214 B-ALL patients, at diagnosis, both adults and children. Data on demographic, clinical hematological, FISH, and karyotype findings are presented in Tables 1, 2, and 3. A total of 8.4% (18/214) patients harbored the TEL/AML1 gene rearrangement. The
| Table 1 Clinical, pathological data, FISH, RT-PCR, and karyotype findings in B-ALL patients positive for TEL/AML1 gene rearrangement. |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| **Case no**     | 1   | 2   | 3   | 4   | 5   | 6   | 7   | 8   | 9   | 10  | 11  | 12  | 13  | 14  | 15  | 16  | 17  | 18  |
| **Age**         | 5M  | 3M  | 4M  | 4M  | 2M  | 4M  | 4F  | 18M | 5M  | 2M  | 8M  | 4M  | 13M | 5M  | 3M  | 8M  | 6M  | 7M  |
| **Clinical presentation and history** | Fever and weakness—2 months | Fever and weakness—1 week | Fever—2 weeks and multiple petechial rashes | Fever—2 weeks and multiple joint pains | Fever—1 month, bilateral cervical LN, S+ | Fever—1 month, cough cold, petechial rash—1 day, H+5+ | Fever and AD | Fever and weakness—1 week | Fever—2 weeks and multiple petechial rashes | Fever—1 month, cough cold, petechial rash—1 day, H+5+ | Fever and AD | Fever and weakness—1 week | Fever—2 weeks and multiple petechial rashes | Fever—1 month, cough cold, petechial rash—1 day, H+5+ | Fever and AD | Fever and weakness—1 week | Fever—2 weeks and multiple petechial rashes |
| **Hb g/L**      | 73  | 62  | 89  | 35  | 69  | 48  | 97  | 85  | 34  | 91  | 116 | 89  | 77  | 74  | 69  | 88  | 76  | 7 |
| **WBC×10^3/L**  | 9.7 | 110 | 3.2 | 36.7| 5.92| 4.5 | 6.8 | 17.95| 4.59| 151 | 6.32| 3.66| 8.9 | 1.01| 50.31| 17.5| 11.22| 23.62|
| **Platelet x10^9/L** | 100 | 10  | 46  | 12  | 86  | 17  | 65  | 89  | 22  | 74  | 115 | 24  | 15  | 62  | 18  | 50  | 39  | 45 |
| **PS minor blasts (%)** | 25  | 95  | 10  | 90  | 18  | 6  | 50  | 46  | 0  | 30  | 36  | 65  | 4  | 98  | 70  | 56  | 80 |
| **BM blast (%)** | 85  | 90  | 77  | 88  | 95  | 60  | 95  | 58  | 80  | 88  | 40  | 69  | 77  | 3  | 55  |
| **TLE, AMEJ**   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   | —   |
| **Signal pattern** | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  | AT  |
| **FISH signal pattern** | 1G;19F | 1G;19F | 3G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F | 2G;19F |
| **Interpretation** | 1  | 2  | 3  | 3 + 4 (2) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) | 3 + 4 (1) |
| **Clone no and size (%)** | 39  | 61  | 10  | 89  | 38  | 20  | 47  | 42  | 83  | 95  | 64  | 91  | 11  | 8.9 | 5  | 16  | N  |
| **BCR/ABL, E2A-PBX** | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  | N  |
| **Karyotype** | NK  | NK  | NK  | NK  | NK  | NK  | NK  | NK  | NK  | NK  | NK  | NK  | NK  | NK  | AK  | NM  | AK  | N  |

Abbreviations: #, TEL AMEI/BCR-ABL(p210,p190)-RT-PCR; +/G, +, block/granular positive; AD, abdominal distension; B-ALL, B-acute lymphoblastic leukemia; FISH, fluorescence in situ hybridization; H+S+, hepatosplenomegaly; LN, lymphadenopathy; N, negative; NC, noncontributory; ND, not done; P, positive; RT-PCR, reverse transcription polymerase chain reaction; S+, splenomegaly.

Table 2 Data of demographic and TEL/AML1 results in 214 B-ALL patients

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Group 1: 1–18 years</th>
<th>Group 2: 19–39 years</th>
<th>Group 3: &gt;40 years</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall, no of patients (%)</td>
<td>125(58.41)</td>
<td>63(29.43)</td>
<td>26(12.14)</td>
</tr>
<tr>
<td>Median age of presentation (y)</td>
<td>5</td>
<td>26</td>
<td>46.5</td>
</tr>
<tr>
<td>No of males</td>
<td>77</td>
<td>45</td>
<td>15</td>
</tr>
<tr>
<td>No of females</td>
<td>47</td>
<td>18</td>
<td>11</td>
</tr>
<tr>
<td>Gender of baby not disclosed</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Male female ratio</td>
<td>1.6:1</td>
<td>2.5:1.0</td>
<td>1.3:1</td>
</tr>
<tr>
<td><strong>TEL AML1 fusion positive cases</strong></td>
<td>Total:18/214 (8.41%)</td>
<td>FISH:15/178 (8.6%) / RT-PCR:3/36 (8.3%)</td>
<td></td>
</tr>
<tr>
<td>TEL AML1 fusion positive cases as per age group by both technologies: No (%)</td>
<td>17/125 (13.6%)</td>
<td>1/63 (1.58%)</td>
<td>–</td>
</tr>
<tr>
<td>TEL AML1 negative cases:196/214 (91.58%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Types of additional abnormalities in negative group No of patients (%) &amp;% cells with abnormal findings in different patients.</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Additional copies of AML1—21(12.8%) 24–92% cells</td>
<td>2 patients:1 copy 4 patients:2 copies 1 patient:1–2 copies 2 patients:3 copies 3 patients:3–4 copies 4 patients:4 copies 5 patients:5 copies</td>
<td>Additional copies of TEL gene—2 patients (1.2%) 43–63% cells—3 copies in each patient</td>
<td>Additional copies of TEL and AML1 genes—8 (4.9%) Patient: 2 clones seen: Clone 1—44% cells had 4 copies of only AML1. Another clone—34% cells had 3 copies of TEL &amp; 4 copies of AML1 Patient: 2 clones seen. Clone 1: 42.3% cells had 3–4 copies of AML1 only. Clone 2: 28.46% cells had 3 copies of TEL &amp; 3–4 copies of AML1 genes Patient: 3–4 copies AML1&amp;TEL genes seen in 81% cells Patient: Clone1—50% cells had 4 copies of AML1 &amp; 3 copies of TEL gene 2nd clone—34% had 3 copies of TEL gene Patient: 83% cells had 3 copies TEL gene &amp; 77% cells had 3–7 copies of AML1 Patient: 65% cells had 5 copies TEL &amp; 4–5 copies AML1 gene Patient: 40% cells had (2 copies) AML1 gene &amp; 1 copy of TEL gene Patient: 18% cells had 1 copy of TEL gene and 2 copies of AML1 gene</td>
</tr>
<tr>
<td>Deletion of TEL gene and amplification of AML12(1.2%) Patient: Loss of TEL gene in all cells and 40% cells—3 copies of AML1 Patient: Loss of TEL gene and 4 copies AML1—59% cells Del of TEL gene6(3.7%) 14.5–86.8% cells</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Abbreviations:** B-ALL, B-acute lymphoblastic leukemia; FISH, fluorescence in situ hybridization; RT-PCR, reverse transcription polymerase chain reaction.
fus on was detected by FISH in 15/178 (8.4%) patients and by RT-PCR in 3/36 (8.3%) patients. The clone size or positivity rate varied from 8.9 to 95%. The fusion was frequent in 17/125 (13.6%) children, aged between 2 and 13 years (median: 4 years), and an 18-year-old young adult. Fusion was noted in 94.4% males. Additional genetic abnormalities characterized 14/15 (93.3%) patients, reflected as atypical signal patterns on FISH suggestive of various abnormalities. TEL/AML1 fusion was absent in 91.58% cases. Additional genetic abnormalities were also noted in 23.9% of these patients, with amplification of AML1, seen more often. Cytogenetic analysis in 92 B-ALL patients revealed the karyotype was normal in 57 (61.95%) and abnormal in 35/92 (38.04%) patients. It is important to note that 14 patients with normal karyotype and cases 16 and 18 with abnormal complex cytogenetic had TEL/AML1 rearrangement/mutation. Case 18 showed evidence of del(12)(p13) in 60% metaphases.

Table 3 Correlation of FISH and cytogenetic results of 6 cases lacking TEL/AML1 gene rearrangement

<table>
<thead>
<tr>
<th>Case no</th>
<th>Cytogenetic findings</th>
<th>TEL/AML1 findings</th>
<th>Correlation of karyotype and FISH findings</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>47,XX,+8[14],46XX[2]</td>
<td>TEL/AML1 negative, with amplification of the AML1 gene—2 copies in 45% cells</td>
<td>Cryptic amplification of AML1 gene</td>
</tr>
<tr>
<td>2</td>
<td>50–57,XX/XXX,+X[11],+4[10],+5 [6],+6[13],+8[6],+9[7],+10 [6],+11[8],+12[3]t(1;12)(q24.11) [5],+14[4],+15[2],+16[3],+17 [12],+18[6],−9[11],+20[3],+21 [10] [cp16]/46,XX[4]</td>
<td>TEL/AML1 negative, amplification of AML1 gene (1 copy)</td>
<td>Karyotype demonstrating a +21 corroborating with FISH amplification.</td>
</tr>
<tr>
<td>3</td>
<td>46,XY,dup(9)(q34.1q34.1)[4]/47, XY,+mar[2]/46,XY[9]</td>
<td>TEL/AML1 negative, amplification of AML1 gene—2 copies—33%</td>
<td>Cryptic amplification of AML1 seen.</td>
</tr>
<tr>
<td>4</td>
<td>46,XY,del(8)[p22][8]/46,XY[6]</td>
<td>TEL/AML1 negative, Amplification of Tel and AML1 genes</td>
<td>Cryptic amplification of TEL and AML1 genes</td>
</tr>
<tr>
<td>5</td>
<td>50–53,XX/XY,+X,+4,+6,+8,+10,+14,+17,+18,+21,+22[cp15]/46,XY[5]</td>
<td>TEL/AML1 negative, amplification of AML1 gene—2 copies</td>
<td>Karyotype shows gain of chromosome 21 (only 1 copy) and the other copy of AML1 is cryptic.</td>
</tr>
<tr>
<td>6</td>
<td>54–55,XY,+4[4],+6[2],+8[3],+10 [3],+16[1],+17[3],+17×2[1],+18 [3],+21[2],+21×2[2],+22[3] [cp4]/46,XY[16]13</td>
<td>TEL/AML1 negative, amplification of AML1 gene—2 copies—58%</td>
<td>Karyotype and FISH demonstrate gain of 2 copies of chromosome 21 and 2 copies of AML1 gene</td>
</tr>
</tbody>
</table>

Abbreviation: FISH, fluorescence in situ hybridization.

Discussion

ALL is the most frequent malignancy accounting for 85% of all childhood leukaemia.32–36 B-ALL constituted 76% of all ALL that
The World Health Organization classification of hematopoietic and lymphoid tissue (2017) defines B lymphoblastic leukemia/lymphoma into various sub-types including “B lymphoblastic leukemia/lymphoma with 7 recurrent genetic abnormalities.” Conventional cytogenetics, interphase FISH, RT-PCR find application in the detection of recurrent genetic abnormalities as they play a pivotal role in prognostication, selection of therapy, and response to treatment. Translocation t(12;21)(p13;q22), a somatically acquired early lesion, results in the critical TEL/AML1 fusion on chromosome 21, and AML1/TEL fusion on derivative 12p that can be lost. TEL allele is often deleted the fusion protein acts in a dominant negative fashion inhibiting the normal function of transcription factor AML1. The abnormality can occur as a sole abnormality or within the context of a complex karyotype characterized by three or more chromosomal abnormalities. Conventional cytogenetics is the gold standard to detect both known and unknown genomic abnormalities in the genome; however, poor chromosome morphology, few malignant metaphases encountered in ALL, and inherent cytogenetic invisibility of the abnormality limit the detection of t(12;21) to 0.05% of patients. Cryptic and subtle abnormalities, below 7 to 8 MB resolution, can be missed on karyotyping. FISH and RT-PCR enable detection of TEL/AML1 in 20 to 25% of precursor B ALL. Translocation t(12;21) has a favorable outcome and useful for the prediction of outcome in childhood ALL. Coexistence of the same,
with other gene rearrangements and in complex setting, favors poorer clinical outcome.

B-ALL patients with t(12;21) abnormality are younger, \(~3–5~\) years, blasts have B precursor phenotype, and are CD19, CD10 and CD34 positive with expression of myeloid antigens CD13, sensitive to chemotherapy and associated with favorable prognosis and late relapse.\(^1,3,3^3\) TEL/AML1 fusion is seen rarely in adults (1–4%);\(^2,3\) however, increased numbers of adults diagnosed with B-ALL, prompted assessment for the same. In the present study, under-representation of the cryptic TEL/AML1 rearrangement overall (8.4%) and in children (13.6%) is low contrary to the expected high prevalence of 25% in western countries.\(^4\) Hospital-based reports,\(^5,7,9,12–30\) international projects,\(^1,10,24\) multicenter

Fig. 3 Immunophenotyping in a prototype case showing aberrant expression of CD13 and CD33.
Frequency of TEL/AML1(ETV6/RUNX1) in B-ALL  Devi G et al.

studies,11,24 and review articles8,15 indicated existence of geographical differences in distribution of TEL/AML1 worldwide, including India (►Table S1 and S2). Global studies indicated the incidence of TEL/AML1 positive B-ALL was high ranging from 17% in Spain,16,44 18.9% in Brazil,17 28% in Tunisia,2 31% in United States,5 37.5% in Egypt,14 to 40% in Israel.18 Exception was Turkey (8.5%).16 The incidence was low in Asian countries, 14.1 to 17.9% in China and Korea,13–15 5 to 10.6% in Pakistan,10–12 and 0 to 19.8% in north and western India.19–26 8.3% in Chennai,27 4% in Karnatak28 4.8% in Kerala,29 and 13.64% in Hyderabad.30 The low prevalence of TEL/AML1 positivity is 13.6% children with B-ALL, which resonates with previous studies from this region.27,30 Variation in the incidence of TEL/AML1 positivity may be dependent on the technology used. When conventional cytogenetics and FISH were used for testing, the global incidence varied from 8.3 to 19.8%13,17,25–27 however, when only FISH was used it varied from 8.5 to 40%,5,7,9,14,16,18,28,30 and 4.3 to 13.64% in south India.28,30 RT-PCR enabled detection of patients with the abnormality in 7.4 to 10.8% in developing countries like Pakistan10–12 and in 0 to 16.2% in India.19–22,24,29 Preselection of precursor B ALL enabled increased detection of the TEL/AML1 rearranged cases. Affordability for the test is an important factor. In the present study, both technologies enabled detection of the fusion gene at the same rate of 8.3 to 8.4%. The population studied, sample size, patient selection, technology(s) used for testing affect the detection rate. If FISH is the modality, the probes used in house/commercial, company, design of the probe, size, validation, cutoff value set, and interpretation are important for defining the status of the abnormality. For RT-PCR, the primers were used.

It is well known that reciprocal translocation t(12;21) (p13;q22) results in the pathogenic TEL/AML1 fusion on chromosome 21, and AML1/TEL fusion on derivative 12p. The latter may be lost sometimes. Deletion of TEL allele on the normal chromosome as a consequence of del(12)(p12) and duplication of der(21)t(12;21) that looks like a +21 hyperdiploid karyotype with <5 AML1 and rarely gene amplification with cluster of >5 or intra-chromosomal amplification of AML1 is also encountered. Interphase FISH enabled the detection of not only TEL/AML1 fusion but also associated additional genetic abnormalities in 93% of these cases and in the negative group too. The reported loss of the untranslocated TEL,5,7,9,14,16,25,27 duplication of TEL/AML1 fusion (der 21t(12;21)) were seen infrequently in our study as compared with 35 and 17%, respectively, reported previously.25 An unusual finding was the occurrence of cryptic loss of the reciprocal AML1-TEL fusion on der12p in 66.5% of our patients. This appears to be rare8 and has not been reported earlier from this region. Loss of derivative 12p was also associated with extra copy(s) of AML1 in 40%, with amplification of TEL gene (33.3%). These findings were consistent with the previous reports.5–8,13,14,16–18 TEL/AML1 rearrangement with one or more copies of der 21t(12;21) has been reported in 42 to 50% with additional abnormalities,5,6,8,13,17,18,38 including additional AML1 in 6 to 23.8% patients,5–7,14,16,25 and clones with loss of TEL gene and an extra AML1 in 9.5%.6 Duplication of the fusion gene is rare and may occur in the form of duplication of der 21t (12;21) or ider 21(q10)t(12;21). TEL gene functions as a tumor suppressor gene, and its function may be inhibited when in combination with TEL/AML1 fusion in a dominant negative fashion. Alternatively, TEL gene may inactivate the fusion protein necessitating the deletion of the TEL gene for leukemogenesis. Submicroscopic deletions and point mutations of TEL homologue may contribute to inactivation of TEL.25 Additional genetic abnormalities in relation to the cryptic t(12;21) translocation are envisaged to be secondary events critical to leukemogenesis and not disease progression. The significance of additional genetic changes with respect to clinical features and outcome between presence or absence is debatable.14

The observation of TEL/AML1 rearrangement and additional genetic abnormalities detected by FISH in patients having normal cytogenetics in 14/18 (77%) patients, complex karyotype in 2 (11.1%), one with 12p deletion in 80% metaphases connoting loss of AML1/TEL fusion, and the other case with nonrandom chromosomal abnormalities indicate (1) TEL/AML1 rearrangement is the sole, cryptic abnormality; (2) additional mutational events were submicroscopic too, and (3) the normal karyotype is actually a pseudodiploid karyotype.

Evaluation of clinical and pathological features demonstrated occurrence of TEL/AML1 positivity mainly in children (94.4%), aged 2 to 13 years (median: 4 years) predominantly among males (94.1%). The fusion was absent in all adults tested. The patients had classic CD34 and CD10 positive phenotype (CALLA positive B-ALL) with aberrant expression of cross lineage antigens, CD13 and CD33,2,33 WBC counts were high in 44.4% patients, low in 22.2%, and rest within normal range. Another study demonstrated significant association of TEL/AML1 positive group with lower age group > 1 to 5 years (median: 5 years), WBC counts of 10–20 × 10⁹/L (median: WBC count of 11.2 × 10⁹/L), CD34 negative phenotype, and absence of CD13/33 myeloid marker expression and low relapse rate.25

Our hospital is a regional tertiary care cancer center for cancer treatment in a metropolitan city. The possibility of geographic variation in presentation of the disease cannot be ruled out. India is genetically and ethnically a diverse country. Genetic propensity for TEL/AML1 fusion in childhood ALL has been described.31 Regional, population based, biological differences, gene–environment interactions, are critical in leukemogenesis and may differentially contribute to the prevalence of TEL/AML1 fusion occurrence.

This study revealed additional genetic abnormalities in 23.9% TEL/AML1 negative patients lacking the BCR-ABL and MLL gene rearrangement. These include extra AML1 copies, extra AML1, alone or in combination with TEL aberrations (amplification or deletion) and abnormalities of TEL gene (►Table 2). Extra AML1 was cryptic or corroborated by cytogenetics (►Table 2). One study reported no loss of TEL homologue, extra copies of AML1 in 37%. The authors cited that AML1 may be the current target of genetic abnormalities in ALL and acute myeloid leukemia, which probably induces...
the transcriptional defect in $AML_1$ in the process of leukemogenesis, and showed abnormalities. These occur as a consequence of “tri/tetra/polysomy 21, high degree of amplification, and jumping translocations/insertions.” The biological significance of the observed anomalies is not known. Although we have not analyzed these cases for clincopathological correlations, $TEL/AML1$ negative cases with extra $AML1$/trisomy 21 were reported to be associated with CD13/33-negative and CD34-positive phenotype, low LDH value, low WBC counts, age ranging from 1 to 5 years, high hyperploidy.25 B-ALL with iAMP211 has been defined as the presence of 3 or more RUNX1 signals on one marker chromosome or a total of five or more RUNX1 signals per cell. Metaphase FISH with Vysis $TEL/AML1$ dual color dual fusion probes display one signal connoting a normal chromosome 21, and several red signals along an abnormal chromosome 21 as tandem duplication, while interphase FISH displays a cluster of red signals ($AML1$) and one separate red signal representing the normal chromosome 21.1,13,18,29 To the best of our knowledge, interphase FISH showed distinct well separated signals of $AML1$, and no localized clusters in all with multiple copies of $AML1$. However as per the definition, three patients with five or more $AML1$ signals per cell can be construed as having an iAMP amplification. It is important to identify patients with iAMP who have a poor prognosis.

Each technology has its advantages and limitations. Prevalence of good prognostic $TEL/AML1$ positive patients was found to be low at this center. Multicenter studies should be undertaken to understand this genetic subtype of B-ALL better in larger sample volume and prognostic implications.

The recurrent genetic abnormalities tested in B-ALL patients have revealed large number of patients lacking these abnormalities and need further interrogation. Comprehensive emerging technologies have identified several genetic determinants. Next-generation sequencing and other evolving technologies will address these genetic abnormalities. Hence, use of orthogonal testing and algorithmic approach will propel identification of new entities in our population.

**Conclusion**

This is the first hospital-based large study from south India demonstrating low prevalence of cryptic $TEL/AML1$ in 13.6% children with BALL, lower than western data but comparable with south Indian studies. FISH was useful in identifying unique additional genetic abnormalities in $TEL/AML1$ positive and negative cases. Clinico-pathologic associations were classic. The study adds to the Indian data. The detection of relevant specific abnormalities in B-ALL patients is of fundamental importance.

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Nil.

**Presentation at a Meeting**

None.

**Conflict of Interest**

None.

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