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Congenital B-lymphoblastic leukemia with a cryptic MLL rearrangement and post-treatment evolution to mixed phenotype acute leukemia

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ABSTRACT

Congenital leukemia is a rare event with a poor prognosis. We report a case of congenital leukemia with a cryptic rearrangement of MLL demonstrable only with RT-PCR. Interestingly, with treatment, the patient showed lineage plasticity of the leukemia with the development of monocytic lineage blasts after presenting with B-cell lineage blasts. This was heralded by the development of a new clonal cytogenetic abnormality. This case highlights the primitive nature of the leukemic cells in congenital leukemia, and emphasizes that RT-PCR for MLL rearrangements may identify a subset of cases which are otherwise negative by karyotyping, FISH, and chromosomal microarrays.

1. Introduction

Leukemia which occurs in the first month of life (congenital leukemia) is a rare event, with an estimated incidence of 1 in 5 million births [1]. Congenital leukemias constitute a subset of infant leukemia where a significant percentage of cases show rearrangements involving the MLL (KMT2A) oncogene [2]. These rearrangements presumably arise in utero, and this leukemia subtype is notable for having the lowest somatic mutation burden of any human malignancy measured thus far [3]. Despite this, outcomes remain poor, and novel approaches to the treatment of this leukemia are needed. We describe an unusual case of congenital leukemia with lineage switch following treatment, CNS involvement, and a cryptic MLL rearrangement detectable only by RT-PCR.

2. Case study

A full term male was born to a 29-year-old G2P2 mother with an unremarkable prenatal course. He was 7 pounds 14 ounces at birth with normal APGAR scores at 1 and 5 min. On physical exam, he was noted to have nodular purpuric lesions on his trunk and face, despite a non-traumatic delivery, and marked hepatosplenomegaly. A complete blood count showed a white blood cell count (WBC) of 126 K/μL, hemoglobin of 16.7 g/dL, platelet count of 23 K/μL, and 47% circulating lymphoblasts (Fig. 1A).

Flow cytometric immunophenotyping showed the circulating blasts expressed CD19, CD20, CD22, CD24 partial, HLA -DR, CD34, and TdT. There was variable expression of the myeloid markers CD15 and CD33. The blasts were negative for CD3, CD10, MPO, and all other T-cell, myeloid, and monocytic markers evaluated, including CD14, CD64, and CD7 (Fig. 1**C**). A diagnosis of B-lymphoblastic leukemia was made. Cytogenetics testing did not reveal any karyotypic abnormalities, and FISH studies were negative for MLL rearrangement (break apart probes), BCR-ABL fusion, ETV6-RUNX1 fusion, and showed disomy for chromosomes 4, 10 and 17. A cerebrospinal fluid sample taken at diagnosis was positive for lymphoblasts (700 WBC/mm3, 39% blasts; 64,000 RBC/mm3). Because the lumber puncture was traumatic, the patient did not meet criteria for CNS3 disease based on the Steinherz/Bleyer algorithm where the CSF WBC/RBC needs to be greater than 2 times blood WBC/RBC. Therefore, the patient was classified as CNS2c.

The patient received induction chemotherapy per modified Children's Oncology Group (COG) infant ALL protocol AALL01P1 with dexamethasone, vincristine, and daunomycin at 50% of age-adjusted infant doses; PEG-asparaginase, and intrathecal methotrexate.

While induction chemotherapy resulted in clearance of the peripheral lymphoblasts, a post-induction bone marrow evaluation showed only a partial response with 15% residual

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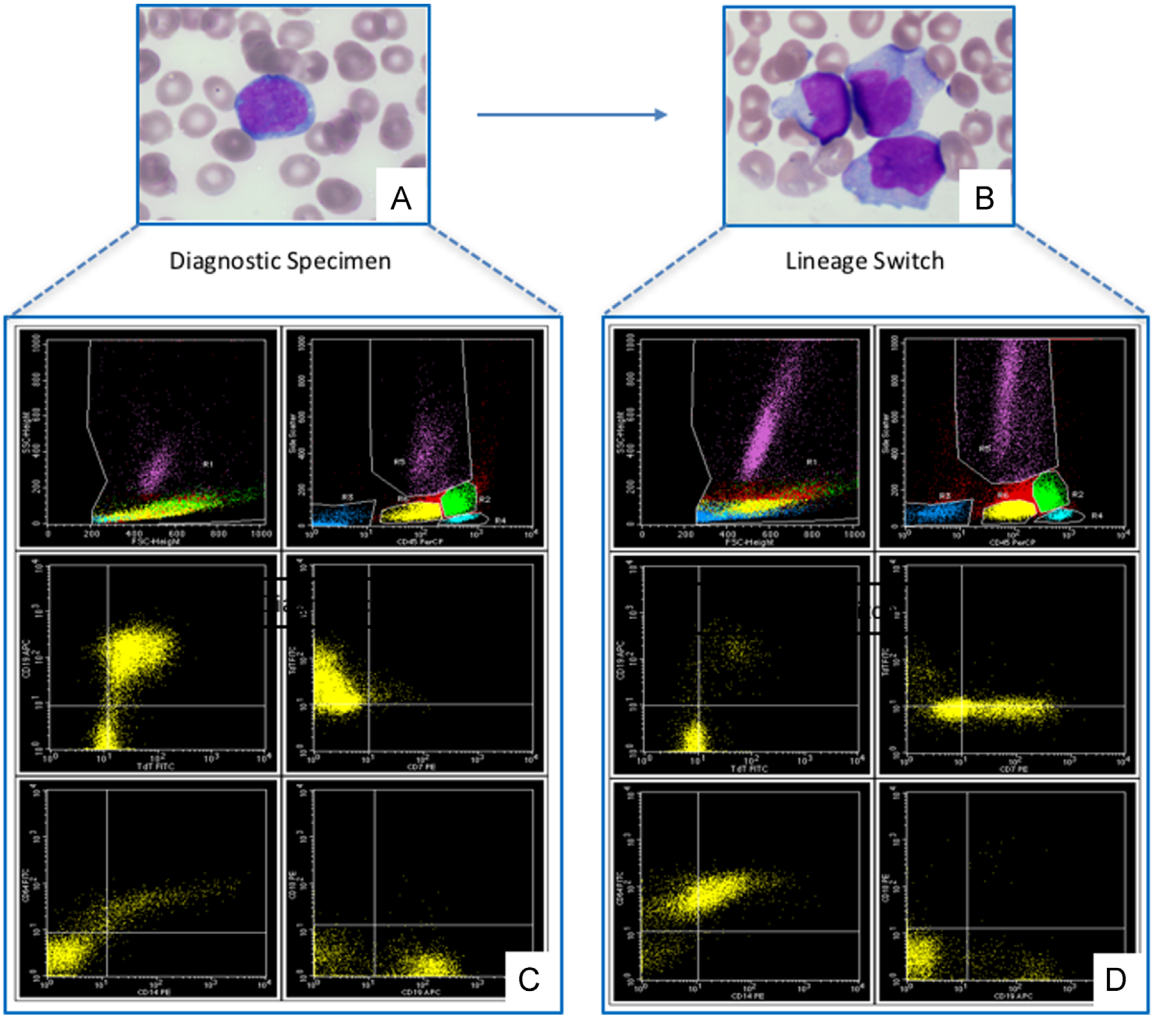

Fig. 1. A. Photomicrograph showing diagnostic specimen with lymphoblast morphology (Giemsa stain, 600X). **B.** Photomicrograph showing lineage switch specimen with monoblast morphology (Giemsa stain, 600X). **C.** At diagnosis, the CD45 dim blasts (yellow) were CD19+(shown), CD22+, CD34+, CD10- (shown), CD14- (shown), CD64- (shown), CD7- (shown) and TdT+(shown). **D.** With lineage shift, the blasts were CD19- (shown), CD34-, CD14+(shown), CD64+(shown), TdT- (shown), and CD7 partial (shown; see text for details).

lymphoblasts (day +35). Extended induction chemotherapy was given for an additional month (per St. Jude Infant Total XVI) which included cyclophosphamide, cytarabine, and oral mercaptopurine.

The post-extended induction bone marrow evaluation still showed 12% residual lymphoblasts (day +66). Evaluation of the blasts by flow cytometry at both time points (+35 and +66) showed an immunophenotype that was unchanged from the original diagnostic specimen.

Due to the suggestive immunophenotype and presentation, the bone marrow was sent at the day +66 time point for RT-PCR evaluation of various MLL fusion transcripts. A positive result was obtained for the presence of a MLL-MLLT1 t(11;19)(q23;q13) fusion transcript. Despite the negative karyotyping and FISH results for MLL rearrangements, the RT-PCR results suggested that a cryptic MLL rearrangement was a driver in this neoplastic process.

He was then started on consolidation therapy per modified St. Jude Infant Total XVI with vincristine, high dose methotrexate (MTX) IV, and IT triples (MTX/ara-C/Hydrocortisone) with oral 6MP.

One month later the patient developed leukocytosis (WBC 46 K/μL) with 70% blasts and was re-induced to treat the persistent B-lymphoblastic leukemia. A post re-induction bone marrow performed at day +130 found 6% lymphoblasts with the same flow cytometric immunophenotype found at diagnosis. However, karyotyping demonstrated a subset of cells with clonal evolution: 46, XY,+6[2]/46, XY[18].

The chemotherapy was then modified to a regimen of vinorelbine, mitoxanthrone, dexamethasone and Bortezomib[4]. A bone marrow evaluation following re-induction with the modified regimen (day +180) revealed 33% blasts, this time with monocytic features by morphology (Fig. 1**B**). Rare lymphoblasts were also present; cytochemical staining for MPO was negative in all blasts. A repeat RT-PCR for t(11;19)(q23;p13) was again positive.

Flow cytometric immunophenotyping confirmed the morphologic impression of blast monocytic lineage; there was a small subset of blasts with an immunophenotype consistent with the original B-ALL, and a much larger subset of blasts expressing CD2 dim, CD4 partial, CD7, CD56, CD22 dim, CD13 partial, CD15, CD33, CD117 partial, CD14, CD64, and CD38 bright. These blasts were negative for CD19, CD10, CD24, and TdT, and expressed dim MPO, an immunophenotype consistent with monocytic blasts (Fig. 1**D**). A subsequent cerebrospinal fluid (CSF) specimen demonstrated significant leukocytosis (36 WBC/mm^3; 1 RBC/mm^3) with 96% promonocytes with atypical morphologic features, suggesting CNS involvement by the lineage switched leukemia.

We performed chromosomal microarray analysis (CMA) analysis using CytoScan HD arrays from Affymetrics (Affymetrics, Santa Clara, CA) on the patient's sample obtained at the time of

relapse, (day +180) to interrogate the MLL and MLLT1 loci for deletions and duplications that may have arisen during the rearrangement which created the MLL-MLLT1 fusion detected by RT-PCR. This analysis revealed a copy number gain (duplication), involving the entire chromosome 6, which was consistent with the presence of the clone with trisomy 6 observed by karyotyping. No deletions or duplications were observed at the MLL and MLLT1 loci. Similarly, CMA analysis did not reveal any pathogenic, disease associated copy number abnormalities (CNA) at other genomic regions, consistent with the previously reported low CNA burden in MLL-rearranged ALL in infants [5].

The patient was able to attain a MRD negative remission, as determined by flow cytometric immunophenotyping, following an experimental infant relapse protocol at an outside facility. However, his chemotherapy course overall was marked by multiple bacterial and fungal infections, and despite all therapeutic efforts, the patient succumbed to infection at day +320 of life and passed away. He received a total anthracycline dose of 100 mg/m^2 daunomycin and 20 mg/m^2 mitoxanthrone.

3. Discussion

Congenital B-ALL is a rare disease with a poor prognosis, a high rate of MLL rearrangements, and has a variable rate of CNS involvement. In one recent study, there was only a 17% survival rate, with 93% of patients having a detectable MLL rearrangement by FISH or RT-PCR, and just 10% having CNS involvement [2]. Just a handful of previous case reports and small case series have described lineage switch in cases of congenital leukemia [6–12]. Interestingly, one case described a congenital leukemia with t(11;19), with a lineage switch from lymphoid to monocytoid heralded by the acquisition of trisomy 6, as in the current case [9].

In the largest published case series, Rossi et al. identified seven cases of infant B-ALL, including three cases of congenital leukemia, with lineage switch from B-lymphoid to myelomonocytic leukemia [12]. An additional two cases were described with a switch from AML M5 to B-ALL. Of the nine described cases with lineage switch, seven had detectable MLL rearrangements. These cases were identified from 1482 cases of pediatric leukemia in the authors' institution, which suggested an incidence of 0.6%. A recent meta-analysis of lineage switched pediatric leukemias identified 18 such cases reported, of which five were congenital acute leukemia; all five had MLL rearrangements detectable [13].

RT-PCR positive, FISH negative MLL rearrangements have been described previously [14]. Large scale recombinome studies of MLL rearranged leukemia has identified a mechanism for such cases which involves either a fragment of the MLL gene being inserted elsewhere in the genome, or a fragment of a locus being inserted proximally to the MLL gene [15]. Both circumstances would create a copy-neutral MLL-fusion oncogene that would not be detectable with break apart FISH testing or chromosomal microarrays.

Given the frequency of lineage switch association with MLL rearrangements in congenital leukemia, every effort should be made to thoroughly evaluate the MLL locus. In the present case, MLL rearrangement was only detectable by RT-PCR. Because of this, we would recommend RT-PCR for MLL rearrangements for all cases of congenital acute leukemia which have normal karyotypes and FISH results.

Submicroscopic deletions and duplications have been detected by FISH and CMA analysis at breakpoints of apparently balanced rearrangements that gave rise to abnormal gene fusions in leukemia. Investigation of such submicroscopic CNAs can provide insights into the nature and mechanisms of chromosomal rearrangements resulting in abnormal gene fusions. In addition, CMA analysis allows genome-wide screening for acquired genomic alterations (CNAs and loss of heterozygosity) contributing to leukemogenesis. In the current case, CMA did not detect alterations at the MLL locus suggesting any changes at the locus were balanced copy-neutral changes.

Mechanisms that would explain lineage switch have been proposed and include a bipotential progenitor, de-differentiation, and preferential proliferation of a minor clone not detectable at diagnosis [12]. An interesting recent case of lineage switch involving a MLL rearranged infant leukemia, occurred following treatment with CD19 directed chimeric antigen receptor T-cells [16]. In this case, an IgH rearrangement present in the original leukemia was not present in the relapsed myeloid blasts despite an identical MLL rearrangement found in both. This suggests that a bipotential progenitor with a germline IgH locus was the founder clone.

Outcomes are usually poor in congenital leukemia, and the present case was no exception. New therapeutic efforts may provide increased efficacy if targeted to the MLL rearranged oncogene given the frequency of MLL rearrangements in congenital leukemia. We speculate that the frequency of MLL rearrangements in congenital leukemia may be higher than previously estimated due to cryptic MLL rearrangements. In any case, the finding of lineage plasticity in congenital leukemia predicts the presence of MLL rearrangements.

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