

DOWN SYNDROME AND LEUKEMIA – AN OVERVIEW OF CYTOGENETIC AND MOLECULAR EVENTS*

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Down syndrome (DS) is the most common trisomic disorder seen in humans with an incidence of 1/700-1/1000 live births. In addition to its characteristic phenotypic features, heart defects, gastrointestinal system abnormalities, premature aging, and hematological disorders, including an increased risk of leukemia, are associated with DS. The relation between DS and leukemia has been known for many years and has continued to be a focus of interest not only for the probable role of trisomy 21 in the development of leukemia at the molecular level but also for the unique features of the leukemia. These include the predominance of acute myeloid leukemia (AML) in younger children with the megakaryoblastic subtype and spontaneous regression of myeloproliferation in newborns.

Acute Leukemia

Down syndrome patients have a 10-to 20-fold increased risk of developing both acute lymphoblastic leukemia (ALL) and AML compared to non-DS children; one percent of DS individuals will develop leukemia during their lifetime¹. Although most cases of leukemia in DS individuals occur early in childhood, the risk spans into adulthood². AML predominates in DS patients under three years of age, while the relative proportions of ALL and AML are the same in older children with or without DS³⁻⁴. A large proportion of AML cases in DS children have been classified as "megakaryoblastic" (AML-M7) by positive electron microscopic detection of platelet peroxidases and/or staining with monoclonal antibodies against platelet antigens⁵. In DS patients, the incidence of AML-M7 is approximately 600 times higher than that in non-DS children with AML⁶. AML-M7 is usually associated with a myelodysplastic phase either in the neonatal period or immediately preceding the development of AML, and myelofibrosis is common in patients with DS³. Although extramedullary involvement, especially bone infiltration, is relatively common in non-DS patients with AML-M7, the development of granulocytic sarcoma is very rare in DS patients with AML-M7⁷.

A significant number of AML patients with DS have additional cytogenetic changes similar to the cytogenetic abnormalities of de novo cases of AML in non-DS patients^{4, 8-9}. Trisomies of chromosomes 1q, 8, and monosomy 7 are the most

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common numerical abnormalities, while tetrasomy 21 is the most frequent quantitative microscopic abnormality in AML-M7 in DS⁸⁻¹⁰. Non-DS AML-M7 is associated with t (1;22) (p13;q13), while this is not seen in DS cases¹¹⁻¹². However, numerical abnormalities of chromosome 21 have been demonstrated in AML-M7 patients without Down syndrome as either primary or nonrandom secondary changes. Favorable treatment outcomes have been reported in DS patients with ALL using intensive regimens which were associated with excessive methotrexate toxicity¹³. DS patients with AML have a superior response rate to intensive chemotherapy with high dose cytosine arabinoside (AraC) containing regimens compared to non-DS patients⁹. Low dose AraC therapy has also been reported to be effective in some DS patients with myelodysplastic syndrome or AML-M7^{6, 14}.

Transient Myeloproliferative Disorder

Transient myeloproliferative disorder (TMD), also known as transient leukemia, transient leukemoid reaction, or transient abnormal myelopoiesis, occurs in neonates with DS. Cases of TMD may not be recognized due to its mild symptoms, uncomplicated course and self-limiting nature; some cases may even resolve in utero. For these reasons, it is very hard to estimate the true incidence of this disorder in the DS population. It is usually recognized during the first month of life; prenatal diagnosis has also been reported^{3, 15}. The most fascinating characteristic of this disorder is that spontaneous regression occurs within several months with supportive care alone, which may include red cell and platelet transfusions. TMD is frequently suspected when a high white blood cell (WBC) count with blasts are observed on the peripheral blood smear. The bone marrow findings of TMD show increased blasts without evidence of myelofibrosis, while the ratio of the blasts in the bone marrow is lower compared to that in the peripheral blood. Skin involvement which occurs frequently in neonatal AML, does not occur in TMD.

Although TMD is a self-limiting disorder, infants can have life-threatening complications, including hyperviscosity secondary to hyperleukocytosis, disseminated intravascular coagulation and pericardial tamponade, which all require rapid intervention such as exchange transfusions^{4, 16-17}. Hepatofibrosis, a rare complication, has been the leading cause of death in TMD¹⁸⁻¹⁹. Hydrops observed in some DS fetuses is hypothesized to be due to hepatofibrosis associated with TMD³. The majority of DS neonates with TMD do not have clonal chromosomal abnormalities which is the opposite of DS patients with AML⁸⁻²⁰. The most frequent cytogenetic abnormality observed in infant leukemias, 11q23 rearrangement, has not been reported in TMD. Cases of TMD have also been reported in phenotypically normal infants with trisomy 21 mosaicism and in neonates without any constitutional cytogenetic abnormalities^{17, 21-23}. Interestingly, in the latter

cases, trisomy 21 has been identified in the blast cells alone while following resolution of TMD, trisomy 21 is no longer identified in either peripheral or bone marrow cells. These findings strongly suggest a relationship between TMD and trisomy 21. Although spontaneous resolution of the hematological abnormalities occurs in DS patients with TMD, about one-fourth of these patients later develop AML. There is no clear-cut evidence of clonal evolution of TMD to AML, though it may be likely in view of the increased risk of developing particularly AML-M7.

The blast cells of TMD morphologically resemble AML-M7 cells with cytoplasmic projections and bluish staining of the cytoplasm with the Giemsa stain. These cells have been shown to express some platelet antigens and contain platelet associated enzymes. Erythroid antigens are expressed in some cases and, recently, the same expression pattern of the transcription factors GATA-1 and GATA-2 in normal erythroid precursors has been reported in blasts of TMD and AML-M7 patients with DS²⁴. These findings suggest that TMD and AML-M7 arise from a common megakaryocytic-erythroid progenitor or from a myeloid progenitor with the capacity to differentiate into erythroid and megakaryocytic lineages. Studies with fluorescence in situ hybridization in MDS patients with DS further support the erythroid origin of malignant cells by showing the trisomy 8 in blasts and normoblasts but not in myeloid and lymphoid cells²⁵. Leukemic blasts from DS patients with AML-M7 produce both megakaryocyte and basophil/mast cell precursors in culture²⁶. The observation of scattered hemopoietic cells in fibrous tissues, including pleomorphic megakaryocytes in the livers of patients with liver fibrosis, provided evidence of a mechanisms to explain hepatic fibrosis seen in some DS patients with TMD. Japanese investigators proposed that liver fibrosis in TMD results from the secretion of the cytokines platelet-derived growth factor (PDGF), transforming growth factor- β (TGF- β), and platelet factor 4, which stimulate collagen synthesis, by abnormal hemopoietic cells in the liver and may be analogous to myelofibrosis in AML-M7²⁷. Recently, slight fibrotic changes in the bone marrow of two DS patients with TMD and hepatic fibrosis have been reported²⁸.

Is TMD a true neoplastic process? Despite the monoclonal nature of TMD in DS which has been shown by analysis of the methylation patterns of the X chromosomes using restriction fragment length polymorphisms in female patients, Miyauchi et al.²⁷ proposed that TMD was not a true malignancy based on the following observations: i) TMD undergoes spontaneous regression in most cases without chemotherapy, ii) trisomy 21 is the only chromosomal abnormality in most TMD cases, while DS patients with either MDS or AML often have additional chromosomal abnormalities, iii) extramedullary hematopoiesis consists of both blast cells and mature trilineage hematopoietic cells as opposed to a homogenous blast infiltration in AML cases, and iv) mature hematopoietic colonies with normal features which are usually absent in acute leukemia grow

in conjunction with the abnormal blast colonies in vitro²⁹⁻³⁰. As a result, TMD can be defined as a self-limited, monoclonal proliferation of hematopoietic progenitors with trisomy 21 which undergoes spontaneous maturation in tissues.

Hematological Abnormalities in Down Syndrome

Newborn infants with DS frequently have hematological abnormalities besides TMD including polycythemia, macrocytosis, and thrombocytosis. Polycythemia is common soon after birth, while macrocytosis and thrombocytosis may develop later in infancy³¹. Thrombocytosis usually subsides by the end of the first year of life, while DS individuals continue to have higher red cell mean corpuscular volumes (MCV) throughout their lives³¹⁻³². Increased red blood cell (RBC) turnover secondary to accelerated cell membrane aging or other unexplained intrinsic defects giving rise to a younger red cell population has been proposed as a mechanism to explain high MCV in DS patients. A recent study suggests that DS patients with high MCV have a normal RBC life span as RBC hexokinase activity and creatine levels were normal³³. It has also been speculated that alterations in the folate remethylation pathway secondary to increased cystathionine β -synthase (CBS) activity (localized to 21q22.3) may play a part. These hematological changes suggest that trisomy 21 has an effect on hematopoiesis, particularly the erythroid and megakaryocytic lineages, especially during the perinatal period.

Leukemogenesis and Trisomy 21

How does trisomy 21 contribute to the development of neoplasia? It is known that patients with constitutional trisomies of chromosomes 8, 9, 13, 18, and 21 are at an increased risk of developing various hematological malignancies and solid tumors compared to the general population³⁴. This suggests a relationship between the underlying mechanism giving rise to trisomy and the development of the neoplastic process. This may not be true based on the following arguments. A high percentage of patients with constitutional trisomies do not develop cancer; this may be because additional mutational events (hits) must occur for the neoplasia to develop. The types of tumors observed in constitutional trisomies more frequently affect certain organs (leukemia and cutaneous syringoma in trisomy 21, kidney and liver tumors in trisomy 18, kidney tumors and neuroblastoma in trisomy 13). This suggests that an increased gene dosage of genes located on a particular trisomic chromosome may play a central role in the development of neoplasia rather than the underlying mechanisms leading to trisomy itself. This is further supported by the fact that acquired trisomies of the same chromosomes are occasionally detected in patients with the same types of tumors without constitutional abnormalities. But it must be kept in mind that there may be significant differences in the contribution to the development of neoplasia by the trisomic chromosome in a constitutionally trisomic cell and in a cell with an acquired trisomy.

Oncogenes and Chromosome 21

The oncogenes AML1, ERG and ETS-2 have been localized to chromosome 21 and play an important role in the neoplastic processes. The AML1 gene is associated with AML-M2 with the t(8;21) (q22;q22) cytogenetic abnormality and with the cryptic TEL-AML1 chimeric transcript, which has been identified in 25 percent of cases of pediatric B-precursor ALL³⁵⁻³⁷. These observations suggest that the AML1 gene may be involved in both TMD and leukemia in DS patients. AML1 is a transcription factor which binds to the enhancer core motif in the transcriptional regulatory region of the granulocyte-macrophage colony-stimulating factor (GM-CSF), interleukin-3 (IL-3), and the colony stimulating factor 1 (CSF-1) receptor. The 8;21 translocation of AML-M2 results in the fusion of the AML1 gene to the transcription factor ETO gene, located on chromosome 8, and production of the AML-ETO chimeric protein. This protein interacts with the enhancer core DNA sequence and can alter the transcriptional regulation of AML1 target genes via interference with AML1-dependent transactivation, leading to leukemogenesis.

AML1-deficient mice (generated through gene knock-out targeting in embryonal stem cells), have complete absence of fetal liver derived hematopoiesis³⁸. This finding strongly suggests that the AML1 gene plays an essential role in definitive hematopoiesis along with the other transcription factors³⁹. Linkage analysis studies have identified that the gene of a familial platelet disorder (FPD), characterized by both quantitative and qualitative platelet abnormalities with a propensity to develop myeloid malignancies, is localized to 21q22⁴⁰. This gene lies in close proximity to the AML1 gene on chromosome 21 and the hematological abnormalities observed in FPD resemble the clinical picture of DS patients with TMD in several aspects.

Genomic Imprinting, Chromosome 21 and Cancer

Since a large proportion of patients with DS or other constitutional trisomies do not develop cancer, it can be postulated that additional mutational steps are required for the multistep process of carcinogenesis. This hypothesis raises the following question. what are those additional hits? Studies have focused on the characteristics of the extra copy of chromosome 21 in cases of DS with leukemia. The increased incidence of TMD or leukemia in DS is not associated with increasing maternal age. "Atypical" constitutional karyotypes, including isochromosome 21, double-ring 21, and mosaic trisomy, each of which generates identical copies of the entire long arm of chromosome, have been reported with increased frequency in DS patients with TMD and AML-M7⁴¹. This condition, known as "disomic homozygosity", in which two identical copies of a single allele are inherited, may have some important implications in the development of the neoplastic process.

The parental origin of the extra chromosome in trisomy 21 is similar in patients with or without leukemia⁴⁵⁻⁴⁶. Maternal and paternal uniparental disomies for chromosome 21 result in normal phenotype, providing evidence that genomic imprinting on chromosome 21 does not occur⁴⁷⁻⁴⁸. These two lines of evidence argue against genomic imprinting as a possible mechanism contributing to the development of neoplasia in DS.

Alternatively, the significance of the disomic homozygosity can be based on the genomic imprinting mechanism giving rise to inactivation of several critical genes with identical base-pair sequences located on chromosome 21. This would lead to decreased expression of these genes while leaving a possibly defective allele on the third copy of chromosome 21 dominant (Fig. 2). Evidence against this assumption is that meiosis II and mitotic nondisjunctions ending in identical or near-identical copies of chromosome 21 are known to occur in both parents of infants with TMD and also AML patients with DS⁴³⁻⁴⁴.

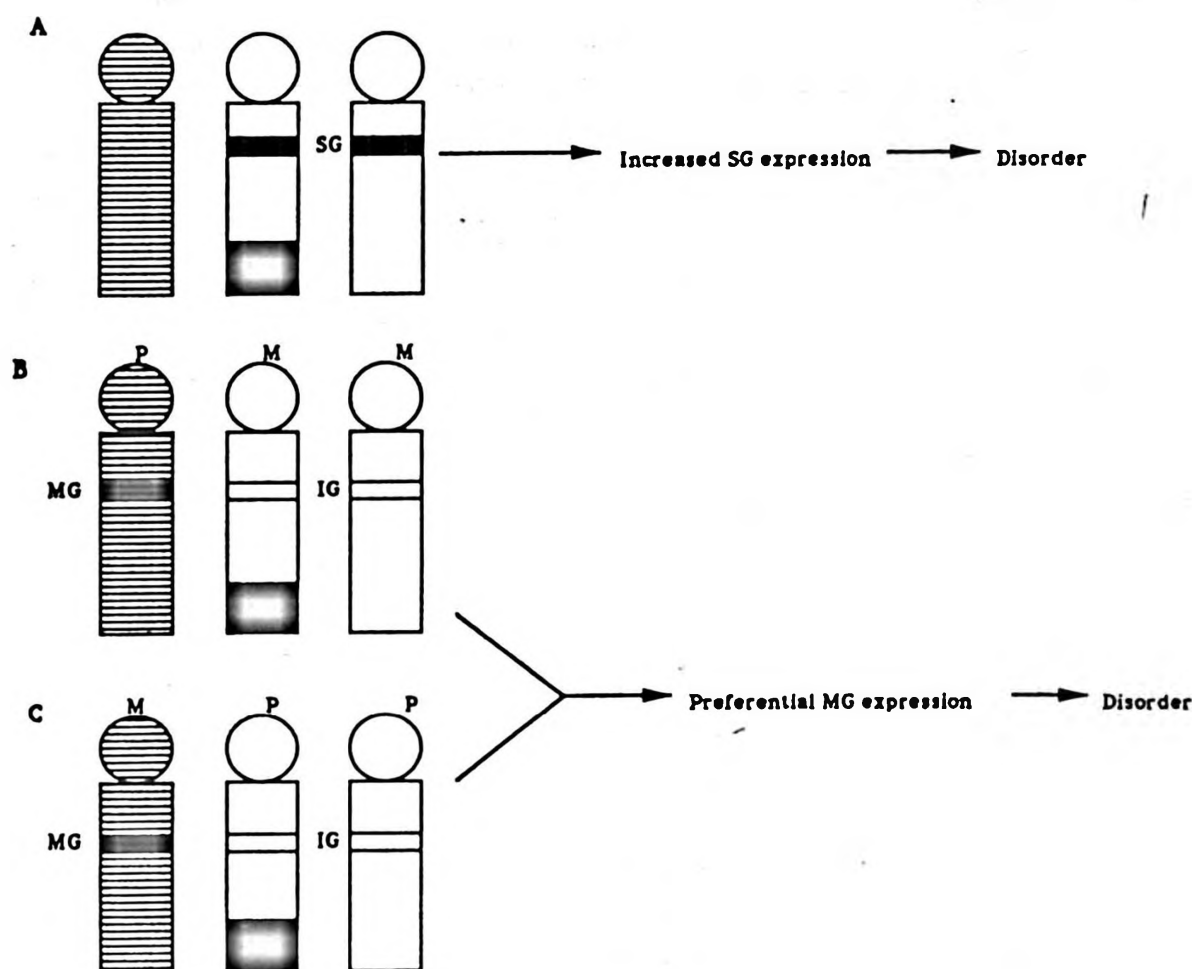


Fig. 2: Different pathophysiologic pathways for the contribution of uniparental disomy to the development of myeloproliferation. Abbreviations: SG: susceptibility gene; MG: mutated gene; IG: imprinted gene; P: paternal; M: maternal.

TMD, AML and Neonatal Tumors

Miyauchi et al.²⁷ proposed that abnormal blasts seen in TMD may originate from the fetal liver due to the frequent finding of a higher percentage of blast cells in the peripheral blood compared to bone marrow. AML1 appears to be a crucial transcription factor in fetal liver hematopoiesis³⁸. Carolyn et al.⁴⁰ hypothesized that patients with a certain subtype of familial platelet disorder may have a defective AML1 gene which results in qualitative and quantitative platelet abnormalities and may lead to the development of AML after additional genetic defects are acquired. This suggests that an increased gene dosage of genes such as AML1 plays an important role in the development of TMD. In contrast to FPD, increased expression of the AML1 gene in TMD may lead to overstimulated proliferation of critical progenitor cells in the presence of additional submicroscopic abnormalities involving genes regulating erythromegakaryocytopoiesis, without affecting their capacity to differentiate into mature blood cells. The expression of these genes with hematopoiesis-controlling properties may be regulated in an age-dependent manner. This can explain the "transient" nature of TMD, the responsible gene(s) being expressed late in fetal life or through the early months of the postnatal period.

Spontaneous regression of neonatal tumors is not confined to trisomy 21-carrying neoplasias and has been reported in neonatal fibrosarcoma, congenital myofibromatosis, and stage IV-S neuroblastoma patients without constitutional genetic abnormalities⁴⁹⁻⁵¹. A striking, common pattern has been observed in patients with certain types of neonatal tumors, particularly in patients with constitutional trisomies. As pointed out by Satge and Van den Berghe³⁴, spontaneous resolving tumors are characteristic of the perinatal period in which the tumors are either in situ or incompletely developed; spontaneous resolution of well-developed tumors does not occur in children and adults as seen in the case of TMD and AML-M7 in DS in which overproduction of immature fetal tissues is due to a dysregulation of normal embryological development. A similar scenario was proposed to explain intratubular germ cell neoplasia seen in trisomy 21 fetuses and the excess of testicular tumors seen in DS children or adults⁵²⁻⁵³. The influence of the intrauterine milieu and qualitative and quantitative changes of the developing immune system following birth must be taken into consideration in the development and the regression of these tumors. This theory may be very relevant in the case of DS. Down syndrome patients have immunological abnormalities and the interferon α , β , and γ receptor genes are located on chromosome 21. Several hypotheses have been proposed to illuminate the relation between immune dysfunction and trisomy 21⁵⁴⁻⁵⁵. The observation of lymphoid depletion in two fatal cases of DS with TMD and visceral fibrosis further supports the role of an antileukemic mechanism of the immune system in TMD¹⁸.

In other words, in some DS patients with TMD, a severely disturbed immune system may not be able to control the proliferation of clonal cells causing fibrosis of visceral organs. A hypothetical schema of development of clonal proliferative disorders in DS is summarized in Figure 3.

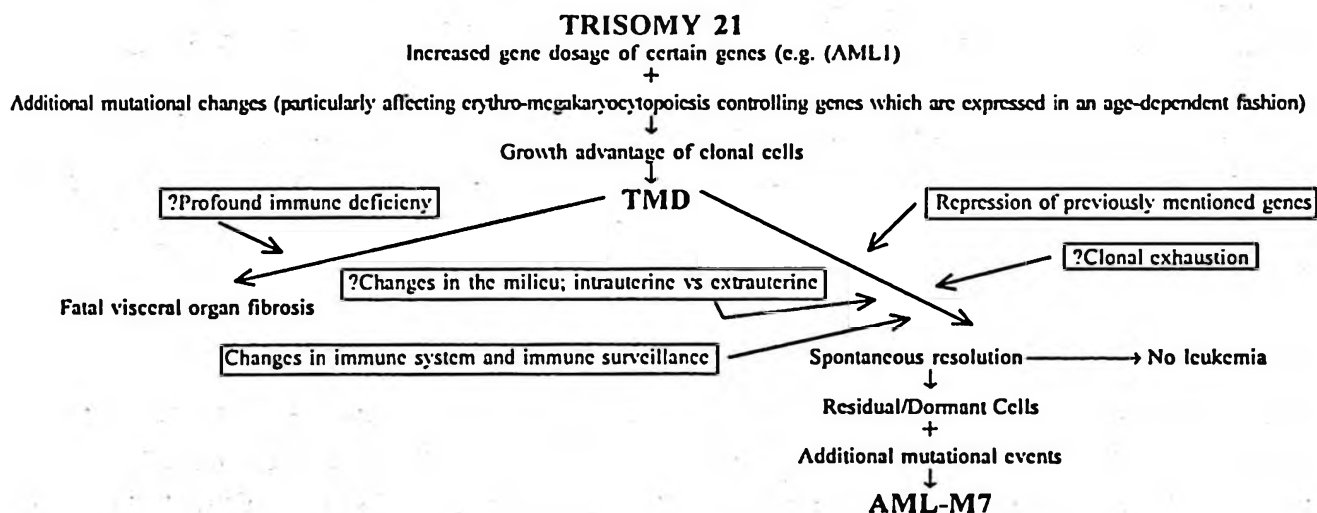


Fig. 3: Hypothetical steps in the development of TMD and AML-M7 in Down syndrome.

Recent Developments

The development of AML-M7 in 20 to 25 percent of TMD patients with DS may support the hypothesis that some residual cells may progress into a true malignant neoplasm by gaining new genetic abnormalities. Development of AML-M7 following TMD in a patient without Down syndrome can be explained by the same mechanism⁵⁶. It is impossible to refute the central role played by different cytogenetic abnormalities in the development and progression of particular cancer, though the relative significance and contribution of each mutation can be questioned, especially in the temporal relationship to the cancer. The persistence of multipotent progenitors expressing AML1/ETO transcripts in long-term remission patients with t(8;21) AML; spontaneous regression of congenital acute monoblastic leukemia with t(8;16) (p11;p13), which is associated with a poor prognosis; detection of t(14;18) (characteristic cytogenetic abnormality in follicular lymphomas); and expression of BCR-ABL (hallmark of chronic myeloid leukemia) in some healthy adults support the above concept⁵⁷⁻⁶⁰.

Recent progress in the field of molecular genetics and molecular biology has prompted investigators to take advantage of these leukemogenic mutations as targets for therapy. All-trans retinoic acid has been used successfully for induction therapy of patients with acute promyelocytic leukemia characterized by the 15;17 translocation, which involves the retinoic acid receptor- α gene on chromosome 15⁶¹. Favorable results have been achieved with anti-sense oligonucleotide therapy directed to specific gene sequences involved in that particular cancer⁶². This

approach is based on the genetic abnormalities associated with the oncogenic mutation. It has been shown that patients with AML-M4 with inversion of chromosome 16 have a better prognosis if the multi drug resistance associated protein gene (MRP), localized to chromosome 16p13, was deleted during the process of chromosomal inversion⁶³. The favorable response to intensive regimens and the moderate-to-severe methotrexate toxicity in ALL patients with DS have prompted investigators to study drug metabolism in AML patients with DS. Recently Taub et al.⁶⁴ showed that enhanced metabolism of AraC in DS cells is a contributing factor in the superior outcome of AML patients with DS. The gene dosage effect of genes localized to chromosome 21, such as cystathionine β -synthase, was hypothesized to be a mechanism which leads to altered drug metabolism.

Conclusion

The field of oncogenesis has expanded tremendously in the last decade, yet there are still several unanswered questions. Recent molecular oncologic inventions not only shed light on the pathogenesis of the neoplastic disorders but also contribute to the treatment of these disorders. The development of TMD and AML in patients with DS (characterized by trisomy 21) is an interesting model for studying the relationship between molecular changes and leukemogenesis. Despite the significant progress in the field of oncology, the treatment of non-DS AML patients remains a challenge⁶⁵. Solutions may arise from observations which initially appear straightforward.

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