

In most situations, the course of the pregnancy does not seem to be affected by the presence of leukemia and the course of the malignancy does not seem to be affected by the pregnancy. Most leukemias don't seem to behave differently during pregnancy. **Aims.** The aim of this report is to summarize the type and treatment outcome of 9 consecutive cases of pregnant patients with Leukemia who were referred and evaluated at our Prince Sultan Hematology & Oncology Center (PSHOC) at King Fahd Medical City (KFMC) within a short period of 9 months. **Design and Methods.** Between May 2007 till January 2008 a total of 9 consecutive cases of leukemia were referred, diagnosed and treated in our institution of PSHOC at KFMC, Riyadh, Saudi Arabia. The clinical, laboratory, and treatment outcome information of these cases were summarized and analyzed along with addressing the legal and religious issues related to these cases. **Results:** In the specified period a total of 9 consecutive pregnant women with suspected hematological malignancies were referred to our center over a short period of 9 months. 8 cases were diagnosed as AML (2 cases AML-M5, 2 cases AML-M2, 1 case AML-M0, and 1 case as AML-NOS but patient was Philadelphia negative for BCR-ABL p210; Blast crisis of CML) and 5 cases as Ph+ve CML. The median age was 27 year. High WBC was the main laboratory presentation in all of these cases. Our approach for AML management during pregnancy consisted of; first trimester AML to terminate the pregnancy due to high teratogenic effect of chemo in this period (in one case of AML M0 who died later because of disease & sepsis) and early delivery and symptomatic management during the third trimester using leukopheresis and hydroxyurea (in one case who had AML M2 with t(8;21) but CD56+ she received 3+7 followed by one HiDAC then alloeneic BMT from MRD at KFSHRC in Riyadh). We had 3 cases of AML during second trimesters and our approach to use 3+7 as induction followed by 2+5 as a consolidation. The last patient was diagnosed in the post partum period and she received the standard treatment protocols. **Conclusions.** Leukemia complicating pregnancy is not uncommon medical problem in our society where there is a high fertility rate and large number of young age population. The management of leukemia during pregnancy is challenging but is achievable. Using our approach in AML pregnant patients we were able to achieve a high remission rate 83% (3/6 patients) with an acceptable mortality and morbidity of 17% (1/6 patients). 50% (3/6 patients) underwent Allogeneic HSCT.

Reference

James O. Armitage. Lymphoma and Leukemia in Pregnancy. Educational book of American Society of Hematology, 1999.

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THE ROLE OF CYTOGENETICS AND MOLECULAR GENETICS IN THE MANAGEMENT OF ACUTE MYELOID LEUKEMIA. THE EXPERIENCE FROM THE HEMATOLOGY CLINIC CLUJ-NAPOCA, ROMANIA

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Background. The overall prognosis of acute myeloid leukemias (AML) remains poor despite progress achieved over the past decade. Cytogenetics define three risk groups (good, intermediate and poor), based on the presence or absence of certain chromosomal abnormalities. Molecular genetics may further subdivide the group of patients with normal karyotype. **Aims.** Between October 2007 and October 2008, thanks to a collaboration between our institution and the University of Ulm, Germany, funded by the German José Carreras Leukemia Foundation, we analyzed systematically from a cytogenetic and molecular genetic point of view our adult AML patient population. **Design and Methods.** There were 40 patients (23 men, 17 women) aged 21-79 years (median 48 years). Besides the routine cytological, cytochemical and immunophenotypical analysis, karyotyping was applied in all cases and in those cases with normal karyotype the mutational status of the NPM1 and FLT3 genes was assessed. **Results.** Four cases (10%) were in the cytogenetically defined good-risk group (1 case with t(15;17), 2 cases with t(8;21), 1 case with inv(16)). Twenty cases (50%) were in the intermediate-risk group (2 cases with trisomy 8, 2 cases with trisomy 22, 16 cases with normal karyotype). Sixteen patients (40%) were included in the poor-risk group (15 cases with multiple abnormalities, 1 case with -5, 1 case with -7, 1 case with inv(3)). The molecular analysis in patients with normal karyotype revealed the presence of the NPM1 mutation alone in 10 patients, the association of NPM1 and FLT3 mutation in one patient

and the presence of mutated FLT3 alone in another 4 patients. Out of the 40 patients, 34 were treated with curative intent. In 3 patients with NPM1 mutation as sole abnormality, all-trans retinoic acid (ATRA) was added to chemotherapy. In 17 patients (50% of those treated with curative intent) complete remission (CR) was achieved. Based on cytogenetic and molecular data, we divided the patients into 2 broad prognostic groups: favorable cytogenetic/molecular profile, comprising patients with low-risk cytogenetics as well as those with normal karyotype and the NPM1 mutation as sole molecular abnormality and a second group of unfavorable cytogenetic/molecular profile, comprising patients with poor-risk cytogenetics, as well as those with intermediate-risk cytogenetics except those with NPM1 mutation as sole abnormality. When comparing the treatment outcome between these two groups, there was a significantly better response and survival in the favorable cytogenetic/molecular profile group. Three out of four patients harboring mutated NPM1 and treated with chemotherapy + ATRA achieved a complete remission. None of the patient with a mutated FLT3 gene entered complete remission. **Conclusions.** This study represents the first attempt in our center towards a modern, systematic categorization of AML cases. Our results emphasize the bad prognosis of cases with unfavorable cytogenetics and the presence of the FLT3 mutation as well as the favorable prognosis of patients with good-risk cytogenetics and the NPM1 mutation. Complex, cytogenetic and molecular diagnosis is essential in the 21st century, considering the fact that targeted small molecules against several mutated sites may soon become available.

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EXPLORING WILMS TUMOR GENE (WT1) IN ACUTE MYELOID LEUKEMIA - INITIAL EXPERIENCES

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Background. The Wilms tumor gene (WT1) that is normally expressed only in podocytes, is expressed in peripheral blood of at least 75-80% of acute leukemia patients. It may contribute to the development of acute leukemia. There are some suggestions in the literature, that the higher the WT1 expression, the less likely to achieve complete haematological remission (CHR), therefore the prognosis is worse. Patients showing WT1 expression at diagnosis can turn into WT1 negative at CHR. After the reappearance of WT1 transcripts, relapse is expected, which makes detection of WT1 transcripts eligible for testing minimal residual disease (MRD). **Aims.** We aim to demonstrate the potential usefulness of WT1 to establish the quality of remission in AML patients and for the early identification of patients at high risk of relapse. **Design and Methods.** Peripheral blood (PB) samples were collected at diagnoses, after induction and consolidation chemotherapy (1-5 days after the achievement of a neutrophil count $0.5 \times 10^9/l$) from 26 AML patients. The median follow-up was 6 month (mean 7.4, range 0.1-24). We measured AML patients' WT1 expression with Applied Biosystems 7500 Real Time PCR. The assay of the gene is based on TaqMan reaction, using the Applied Biosystems Hs00240913-m1 assay. The expression of WT1 was normalized with that of the housekeeping gene GAPDH. No WT1 expression was detected in healthy controls. **Results.** There was no correlation between WT1 expression and WBC count at diagnoses. We did not find correlation between the amount of WT1 transcript at diagnoses and survival time, FAB and cytogenetic risk subgroups or FLT3 mutations. The worst survival time was found, when the degree of WT1 expression did not fall after chemotherapy. (The median survival time was 5 month, range 1-14). Better survival time was observed (median 8.5 month, range 6-13), when the amount of WT1 transcripts substantially decreased after chemotherapy. The disappearance of WT1 transcripts was detected only in one patient. This patient is in complete remission (CR) since 11 month. In all of the patients, who reached a favorable WT1 value after chemotherapy and achieved CR and later relapsed, increased WT1 expression was detected well before the signs of relapse was observed. **Conclusions.** Our results show that detection of WT1 expression is a possibility to estimate the prognosis and to follow up AML patients more accurately. Consistent and repeated quantitative analysis of WT1 expression may provide prognostic information and early identification of patients at highest risk of relapse.