SUMMARY AND CONCLUSION

Acute Lymphoblastic Leukemia (ALL) is one of the most important and frequent pediatric cancers. Its exact cause is still unknown, however the genetic factors were found to play an important role in it. The t(1;19)(q23;p13.3) that results in formation of a fusion gene called PBX1/TCF3 [PBX1/E2A] is one of the chromosomal abnormalities associated with B-ALL.

The current study aimed to detect the prevalence of t(1;19) among pediatric cases of ALL and to assess its clinic-pathological significance on patients positive for it.

The study was performed on 26 newly diagnosed B-ALL patients; 13 males and13 females; all of them were children aged from 1.5 to 18 years.

All patients were subjected to: full history taking, complete clinical examination and laboratory investigations including: Complete blood picture (CBC), serum LDH and ESR, Bone marrow aspiration for morphological classification, Immunephenotyping and cell culture for cytogenetic studies for t(9;22) and t(1;19) using FISH technique.

The study revealed that B-ALL patients characterized by high total leukocytic count but not more than $50x10^3$/µL and low platelets count between 50 and $100x10^3$/µl that helped in the diagnosis.

Also, the study revealed that the presence of t(1;19) among B-ALL patients was 23.1% and the presence of t(1;19) is correlated with the increase in blast cell count both in peripheral blood and bone marrow.

Also, the occurrence of t(1;19) with ALL is a sign of bad prognosis as its presence decrease the overall survival of the studied patients. However, the presence of both t(1;19) and t(9;22) in ALL patients showed more bad prognostic sign unless intensive induction therapy is used.

In summary, with our small group of patients we found high degree of bad prognosis and unfavorable outcome in B-ALL patient with t(1;19).

These data show that the detection of t(1;19) in B-ALL patients is important as a prognostic predictor for the disease outcome and in choosing the best line of treatment as intensive therapy was found by other studies to improve its outcome.

Although the detection of chromosome abnormalities by conventional cytogenetics is an important tool in assessing risk stratification of ALL, banding cytogenetics alone may fail to detect a number of patients' abnormalities with clinical relevance.

Thus, the development of fluorescence in situ hybridization (FISH) has allowed the identification of cryptic abnormalities and the detection of alterations in patients with normal, complex, or ill-defined chromosomes under conventional cytogenetics.