A Descriptive Study of Flow Cytometric Analysis of 159 Acute Leukemia Patients: A Single Institute Experience in Egypt

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Background

This study was carried out to analyze the proportion of acute myeloid leukemia (AML), acute lymphoblastic leukemia (T / Pro and Pre B-ALL), biphenotypic lineage and Undifferentiated acute leukaemia among 159 acute leukemia(AL) patients .We also analyzed the coexpression of AML with lymphoid cell surface markers (T / B) and ALL with myeloid cell surface markers. By this method more than 98% of acute leukemia cases can now be precisely allocated to their respective lineages (**Channa J et al. 2000**).

Aim

To determine the proportions of each lineage and the coexpression of myeloid and lymphoid cell surface markers for later detection of their prognostic impact.

Patients and Methods

Data of **159** consecutive cases of AL were analyzed in our study from Jan 2005 through March 2009. Thirty four were Children (12 AML; 12 B-ALL; 8 T-ALL and 2 biphenotypic), 125 adults (79 AML; 27 B-ALL; 16 T-ALL; 1 biphenotypic and 2 undifferentiated). Ninghty one patients were males and 68 were females. Flow cytometry was performed for all AL cases using the standard protocols. Myeloid associated markers included (MPO, CD 13, CD33, CD117, CD15, CD14 and CD64); T-lymphoid associated markers (Tdt, CD2, CD3, CD5 and CD7); B-lymphoid associated markers (Tdt, CD10, CD19, CD20 and CD22); Lineages non specific markers (CD34, HLADR) and Panleucocytic marker (CD45). Florescence labeled antibodies were obtained from (Becton Dickinson, U.S.A) and run on FACSCALIBER using CELLQUEST software.

Results

Ninghty one patients were AML, 63 were ALL, 3 biphenotypic and 2 undifferentiated AL. Six (6.6%) out of 91 AML patients showed CD19 coexpression; 7(7.7 %) with CD7, 3(3.3%) with CD15. Three (4.7%) out of 63 ALL patients with CD 13 coexpression and 3(4.7%) with CD 33 coexpression.

Conclusion

Flow cytometry enabled us to determine the proportions of each lineage of acute leukaemia as well as the coexpression of cell surface markers between different lineages. Follow up of the prognostic impact of this coexpression on our patients is still in progress.