INTRODUCTION

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The acute leukemia are heterogenous group of neoplasm arising from transformation of uncommitted or partially committed hamatopoietic stem cells & rapidly progressive fatal course if untreated ***(Grimwade,et al, 2001)*** .Proliferating leukaemic blasts replace normal bone marrow cells and subsequently enter into the peripheral blood.

Approximately 50% of adult & 80% of childhood acute myeloblastic leukemia (AMLs) harbor nonrandom karyotype abnormalities that define subentities with unique biological and clinical feature ***(Raimondi et al, 1999)***.The detection of non random chromosmal translocations is essential for the diagnosis and characterization of leukemia, which in turn influences prognosis & choice of therapy. Several cytogenetic abnormalities, t(8;21), inv (16) /t (16;16), t(15;17) and abn (11q23), are considered in the recent world Health organization classification of AML ***(Vardiman, et al, 2002)*** . Recognition of patients with the abnormalities t(8;21), t(15;17) and inv(16) is of particular interest in AML prognostication because these abnormalities are associated with a relatirely favorable prognosis ***(Grimwade,et al, 2001; Byrd, et al, 2002).***

The current pathological approach to the diagnosis of acute leukemia is a multifaceted one involving morphology, cytochemistry immunophenotyping, cytogenetic and molecular diagnostic studies. The standard method of detection of chromosomal translocation is karyotype analysis which requires considerable technical expertise & requires more than one week to produce results. Importantly, considerable percentage of

bone marrow (BM) samples from leukemia patients show insufficient metaphases, submicroscopic or masked translocations.

Although conventional cytogenetic studies remain the cornerstone of genetic testing, molecular-based technologies have emerged as a most useful tool for the detection of disease -defining genetic lesions. Since most patients with acute leukemia generate fusion genes/ transcripts, reverse transcripitase-polymerase chain reaction (RT-PCR) and fluorescence in situ hybridization (FISH) are powerful tool for the detection of the translocations. Multiplex RT-PCR screening for translocation is independent on dividing cells, has a high level of sensitivity and may identify translocations that are not detected by conventional karyotyping. PCR and FISH have several advantages over karyotype analysis. These methods require neither much material from patient nor specialized techniques, and produce data relatively quickly.