Rapid dlagnostic molecular screening of most frequent acute myeloid leukemia assoclaed fusion transcripts by multipcr

Ahmed Adei Mohmed Al-Ghonmy

Modern therapy for AML is based on the principle of risk stratification. Previously, universally accepted stratified classification included age, WBC count at diagnosis and response to therapy and later on other predictive factors are included. One of the most important laboratory features used nowadays to accurately risk stratify patients is the presence of chromosomal translocation within the leukemic blasts.Molecular detection of chromosomal translocations depends mainly on PCR based techniques due to its higher specifity and sensitivity over conventional cytogenetics. However, individual detection of each chromosomal aberration is time consuming, costly, requires large patient sample and increases the risk of contamination.This study aimed to establish simple one step multiplex RT-PCR assay for detection of three prognostically significant translocations in AML: t(8;21) with AML1-ETO fusion transcript, t(15;17) with PML-RARa fusion and Inv (16) with CBFII-MYH11 fusion.Peripheral blood sample and bone marrow aspirate were obtained from 40 de novo cases with AML before starting induction therapy.Among the 40 analyzed cases, 12.5% were found to be positive for t(8;21) with AMLI-ETO fusion transcript. The fording confirmed that t(8;21) positive AML is characterized by male predominance, lower Hb & TLC count at diagnosis & a favorable prognosis.t(15;17) with PML-RARa fusion transcripts was detected in 10% of cases. The finding confirmed that t(15;17) positive AML is characterized by male predominance, favorable prognostic outcome compared to those without the translocation. Moreover Hb, TLC and blast percentages did C 04LLISurnmary & Conclusionnot reveal any significance difference between positive & negative t(15;17) cases.Inv (16) with CBFII-MYH11 fusion transcript was detected in 5% of cases. The finding confirmed that inv(16) positive AML is characterized by male predominance, favorable prognostic outcome compared to thosewithout the fusion gene. Hb, TLC and blast percentages did not reveal any significance difference between positive & negative inv(16) cases.There was a complete agreement between multiplex RT-PCR results and that of the FISH method. So it is concluded that multiplex RT-PCR is areliable and sensitive ”Screening” method for detection of therapy relevant chromosomal translocations in short time and it is recommended to applymultiplex RT-PCR techniques in clinical laboratories in order to risk stratify AML patients at diagnosis.