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J Women's Health Care 2018, Volume 7
DOI: 10.4172/2167-0420-C2-012

10th World Congress On
PRECISION & PERSONALIZED MEDICINE
October 05-06, 2018 Osaka, Japan

Clinical correlation between translocation variant and outcome in Philadelphia chromosome-positive chronic myeloid leukemia and acute lymphoblastic leukemia patients

Zeeshan Ansar Ahmed, Ahsan Uddin, Sony Siddique, Nawal Roy, Zubaida Khattak, Muneeba Shareef, Zeba Aziz and Tariq Moatter
Aga Khan University Hospital, Pakistan

Background: BCR/ABL fusion gene usually occurs as a result of Philadelphia (Ph) translocation between chromosomes 9 and 22 in Chronic Myeloid leukemia (CML) as well as in Acute Lymphoblastic Leukemia (ALL). This rearrangement results in the formation a chimeric BCR/ABL fusion gene on the derivative chromosome 22. Fluorescence *in situ* Hybridization (FISH) analysis using dual color BCR/ABL translocation probes allows the visualization of BCR/ABL rearrangements in both interphase and metaphase cell and the presence of the BCR/ABL fusion gene on chromosomes 22 have been reported in substantial subset of these patients. The pattern of rearrangement may be classical, variable or mixed. Only classical pattern has been reported to have good prognosis with lesser disease progression and good response to tyrosine kinase inhibitors.

Method: The incidence of both classical and variable BCR/ABL gene rearrangement was determined in all the patients suspected of CML and ALL using dual fusion Fluorescence In Situ Hybridization (D-FISH) probes. A minimum of 200 nuclei scored were possible.

Result: This study investigated 860 patients of CML and ALL between January 2016 and September 2016 at the Aga Khan University Hospital. Out of 860 patients 775 (90%) were diagnosed as CML and 85 cases (10%) were diagnosed as ALL. About 659 cases (76%) of both CML and ALL patients displayed the classical DF-FISH signal pattern and 201(24%) of CML and ALL showed variable DF-FISH signal pattern. In variable DF-FISH signal, various different patterns were analyzed 1F1G1R is 31%, 1F2G1R is 27%, 1F2G2R is 26% and 1F1G2R is 14% were observed in both CML (22%) and ALL (2%). The rare combination of classical and variable was observed in around 2% cases with CML.

Conclusion: The classical pattern was the commonest pattern identified in both CML and ALL, predicting a good prognosis. Variable patterns were identified in equal proportion except for 1F1G2R which was the least common.

Zeeshan.ansar@aku.edu

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