STUDY AIMING TO DEFINE AND SPECIFY THE BCR-ABL TRANSCRIPT TYPES IN MOROCCAN CML PATIENTS (ABOUT 110 CASES)

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The main product of the translocation t (9, 22) (q34, q11) is the hybrid gene BCR-ABL, located in the first chromosomal abnormality associated with a specific malignant disease in humans, the Philadelphia chromosome (Ph), characteristic of chronic myeloid leukemia (CML).

For fifteen years, the diagnostic and therapeutic management of CML has been rattled, molecular understanding of leukemia and the possibility of having targeted therapies that affect the molecular dysfunction of this disease have improved patient outcomes, and despite the fact that the WHO estimates leukemia at 250,000 cases a year worldwide, considers that these cancers have high cure rates if treated correctly.

Multiplex PCR is a simple, inexpensive and rapid technique that allows the specific and simultaneous detection of different BCR-ABL variants, the presence of these transcripts associated with CML can help in the prognosis and treatment of the disease.

In this context, we conducted a molecular study of this pathology through the analysis of variants of the BCR-ABL fusion gene in 110 patients followed in the pediatric and internal medicine departments of the CHU HASSAN II in Fez, and also in the service of hematology, CHR of Fez, this study confirmed the diagnosis of CML as well as the data of the literature, by showing b3a2 type fusion rate (59%) higher than b2a2 type (41%). This proves the need to make systematic, qualitative research of BCR-ABL transcripts by multiplex RT-PCR, in order to have sufficiently informative data for variant transcripts thus making it possible to choose the specific primers for the subsequent follow-up of the molecular response under treatments. From a practical point of view, this technique has enormous advantages over conventional RT-PCR especially in terms of realization time saving.

Key words: Chronic myeloid leukemia, BCR-ABL fusion gene, multiplex RT-PCR.