Philadelphia chromosome-like B-cell Acute Lymphoblastic Leukaemia in adults: A single centre experience

Siew Lian Chong[1], Asral Wirda Ahmad Asnawi[1,2], Pek Kuen Liew[1], Sharifah Shahnaz Syed Abd Kadir[1], Tee Chuan Ong[1], Jerome Tan[1], Ngee Siang Lau[1], Yee Yee Yap[1], Veena Selvaratnam[1], Subramanian Yegappan[1], Sen Mui Tan[1]

[1]Department of haemodiaylisis, Hospital Ampang, Selangor, Malaysia, [2]Faculty of Medicine and Health Sciences, Universiti Sains Islam Malaysia, Negeri Sembilan, Malaysia.

ABSTRACT

Introduction: Acute Lymphoblastic Leukaemia (ALL) is an aggressive form of haematological malignancy. Unlike B-ALL in children where cure rate is around 80-90% via intensive chemotherapy, adults with B-ALL suffer from relapse with poor overall survival in up to 40% of patients. In order to effectively risk-stratify patients for prognostication, all adult ALL patients were screened for the presence of the recurrent translocation known as Philadelphia (Ph) chromosome where targeted therapy is administered in combination with chemotherapy to improve their outcome. However, this strategy does not account for the poor outcomes seen in Ph-negative ALL patients. Within Ph-negative patients is a newly identified high-risk entity called Ph-like B-ALL. To date, there are no studies actively investigating the genomic landscape of Ph-like B-ALL in the Malaysian population. The genomics of Ph-like B-ALL is largely unknown with a significant lack in information on the human transcriptome related to its overall risk and prognosis. There is a need to improve our understanding of the biology of this disease in order to support or recommend any management options. Hence, for this study, we aimed to determine the molecular landscape in adult Ph-like B-ALL patients and to determine the known reported genetic variants in the CRLF2, ABL1-class and JAK2 genes in adult Ph-negative B-ALL patients using sanger sequencing. **Materials and Methods:** A preliminary analysis of 46 diagnostic samples of Ph-negative B-ALL using multiplex PCR of the common genetic aberrations involving the CRLF2, ABL1 and JAK2 rearrangements were performed. **Results:** Three patients (3/46) expressed the CRLF2 rearrangements. These 3 samples were further analysed by PCR/gel purification and Sanger sequencing for confirmation. **Conclusion:** Findings from this research would be the foundation towards the development of a customised mutational analysis panel to be used at diagnosis.