CDKN2A/B, PAX5 Deletion in Paediatric B-ALL Patients in Malaysia

Jeyanthy Eswaran^{1,3}*, Jia Yee Ho¹, Amanda Anne Lavinya¹, Nor Soleha Mohd Dali², Nursaedah Abdullah Aziz², Yuslina Mat Yusoff², Min Yee Chow¹, Ezalia Esa², Matthew Bashton³, Nor Rizan Kamaluddin², Christine J. Harrison³, Zubaidah Zakaria²

¹Translational & Clinical Research Institute, Newcastle University, Level 6, Herschel Building, Brewery Lane, Newcastle-upon-Tyne, NE1 7RU

In B-cell precursor acute lymphoblastic leukaemia (BCP-ALL), B-cell development is arrested at the precursor B cell receptor (pre-BCR) checkpoint and malignant blasts avoid clonal extinction by hijacking pre-BCR signalling in favour of the development of BCP-ALL. These genetic changes found in key BCP-ALL signalling pathways have been utilised in risk stratification for treatment in a large number of protocols worldwide. The most common secondary alterations in genes involved in B-cell differentiation (PAX5, IKZF1, EBF1), RAS signalling, JAK/STAT signalling, cell cycle regulation and tumour suppression (RB1, CDKN2A/B, TP53) can contribute to the leukemogenesis and linked to BCP-ALL stratification. In addition, few recent meta-analyses studies indicate adverse impact of CDKN2A/B deletions possibly being more prominent in Asian patients. Here, we studied the prevalence of CDKN2A/B and PAX5 deletions and their implications with co-operating genetic abnormalities in paediatric BCP-ALL patients using SNP6 copy number array and multiplex ligation-dependent probe amplification. Deletions in the genes CDKN2A/B and PAX5 were the most common focal changes observed in this Malaysian BCP-ALL cohort. There are a total of 25 patients (45%) detected with CDKN2A/B or PAX5 focal deletion; their primary abnormalities are BCR-ABL1, ETV6-RUNX1, FUS-ERG, TCF3-PBX1, high hyperdiploidy and B-other ALL. Eighteen patients (32%) harboured the CDKN2A/B and/or PAX5 focal deletions. Further correlation with the BCP-ALL treatment outcome data for these patients will reveal the prognostic implications of these markers in this cohort. Overall, our data agree with the previous studies and conform CDKN2A/B and/or PAX5 deletion as the highly prevalent copy number alteration in Malaysian pilot childhood BCP-ALL cohort.

Keywords: single-cell, mRNA-seq, functional studies, Fluidigm, Polaris

Acknowledgements

We would like to thank the Director of Institute for Medical Research for the support, Prem Govind and Sophie Aldred for their help on the project. This research was funded by the Ministry of Health Malaysia [NMRR-16-1468-32122 (IIR)].

*Correspondence: Dr. Jeyanthy Eswaran

Telephone/fax number: +607-5553800 (Ext: 3957)

Email address: Jeyanthy.Eswaran@newcastle.ac.uk; Jeyanthy.Eswaran@newcastle.edu.my