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**Novel genomic aberrations detected with customised DNA microarray in Acute Myeloid Leukaemia (AML) patients that could be related to patient’s survival status**

Angeli Ambayya\*1, Chang Kian Meng1, Jameela Sathar1, Subramanian Yegappan1

*1Department of Haematology, Hospital Ampang, Malaysia*

**ABSTRACT**

Insights into DNA microarray has led to elucidation of acquired copy number variations (CNVs) and copy neutral loss of heterozygosity (CN-LOH) in AML. In our study, we delineated genomic aberrations that could predict survival status of AML patients. Fifty three genomes of AML patients were studied using customised CGH+SNP DNA microarray. We compared patients with complete remission (CR) following induction therapy and those who expired either before or just after induction chemotherapy. A total of 449 somatic aberrations in patients in CR group [ranging from 0.23 kb to 138.20 Mb] were identified and 530 aberrations [range 1.58 kb to 147.67 Mb] were seen in the expired patient group. Statistical analysis revealed 4 significant novel regions of losses seen exclusively in the expired patients that could be related to their poor OS (P < 0.01 by Fisher’s exact test): 10q11.22, 8p23.1, 22q11.21 and 8p11.22. On the other hand, recurrent gains seen in 19q13.2, 10q24.32 and 1q43 showed significant association with patients in CR suggesting a predictor of better OS in AML patients (P < 0.01 by Fisher’s exact test). We identified 29 losses and 58 gains which involved 28 genes that have customised probes for every exon. We found mutually exclusive exonic CNVs in the genes between the two groups (7 genes in the CR group and 11 genes in the expired group). Recurrent CNVs observed on the exons of TP53 gene in the expired patients and TET2 in patients in CR. With the use of our customised DNA microarray, we have discovered cryptic genomic aberrations and novel regions of genomic aberrations that could point to CR and poor OS among AML patients in Malaysia.