Abstract B86: Circulating cytokines, chemokines, and small molecules follow distinct expression patterns in acute myeloid leukemia

Mirazul Islam, Elsa Haniffah Mohamed, Ezalia Esa, Nor Rizan Kamaluddin, Shamsul Mohd Zain, Yuslina Yusoff, Yassen Assenov, Zahurin Mohamed, and Zubaidah Zakaria

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Abstract

Acute myeloid leukemia (AML) is a heterogeneous disease with a complex interplay of genetic and/or cytogenetic alterations in hematopoietic progenitors, together with aberrant cytokines, chemokines, and small molecules (analytes) expression in the tumor microenvironment, contribute to AML pathogenesis. Although deregulated analytes are well documented in AML, their co-expression patterns are not yet identified. The baseline of circulating analytes in AML is found to be significantly variable between studies. Also, plasma baselines for some analytes that are biomarkers for other cancers have not been previously reported in AML. We hypothesized that comprehensive profiling of plasma analytes would provide greater insight of baselines variability and co-expression signature compared with individual analyses, potentially leading to the identification of novel diagnostic biomarkers and therapeutic targets in AML. Two sets of analytes were selected for this study: (i) 22 reported-analytes (baselines have been previously reported in AML) and (ii) 10 novel-analytes (baselines have not been previously reported in AML). We used multiplex array technology to simultaneously detect and quantify 32 plasma analytes levels in 38 patients (cases= 19, controls=19). We observed that baseline expression ranges are higher for three analytes (FGF2, MPO, and sFas) and lower for two analytes (SCF and sFasL) compared to previously published reports. In our study, 16 analytes are found to be significantly deregulated (13 higher, 3 lower, Mann-Whitney U-test, p-value <0.005) where 5 of them have never been reported before in AML. We predicted a 7-analytes containing multiplex
panel (Cathepsin D, Ferritin, MIF, Galectin-3, HGF, MPO, and IL8) for diagnosis of AML, among them, MIF could be a possible therapeutic target. In addition, we observed that circulating analytes show co-expression signatures, that lead us to speculate that expression signatures have the potential to be used for subclassification of AML, complementing cytogenetic, genetic, and epigenetic information. In conclusion, circulating analytes expression in AML differs from normal, and follow distinct expression patterns.

**Note:** This abstract was not presented at the conference.


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