Comprehensive Methylation Analysis in Pediatric Patients with Acute Myeloid Leukemia

Summary

DNA methylation patterns have been associated with molecular subtypes, chromosomal abnormalities, and gene fusions and useful to predict the appropriate risk of pediatric AML.

Introduction

The definition of DNA methylation patterns is expected to reveal clinical and molecular features and survival in patients with AML.

Patients and Methods

We performed comprehensive DNA methylation analysis using Infinium MethylationEPIC BeadChip (Illumina) in 64 patients with AML who were enrolled in Japanese AML-05 clinical trial (2006-2010).

Associations between DNA methylation and genetic aberrations.

Unsupervised hierarchical clustering based on methylation values of the 567 CpG sites.

- Cluster 1: Mainly RUNX1-RUNX1T1 and KMT2A (MLL)-rearrangement with low MECOM expression.
- Cluster 2 and 4: Molecular features of adverse outcome such as FLT3-ITD, FUS-ERG and high PRDM16 expression.
- Cluster 3: CEBPA mutated patients with normal karyotype.

Result-1

We focused on FLT3-ITD for Clustering of DNA methylation pattern to uncover the patients with dismal genetic aberrations.

We would like to revise the risk stratification using genetic alterations, comprehensive gene expression and DNA methylation patterns, and to identify the new druggable targets!