ELSEVIER

Blood 142 (2023) 6421

The 65th ASH Annual Meeting Abstracts

ONLINE PUBLICATION ONLY

634.MYELOPROLIFERATIVE SYNDROMES: CLINICAL AND EPIDEMIOLOGICAL

Analysis of Methylation Level and Clinical Characteristics of Juvenile Myelomonocytic Leukemia

Wenyu Yang[1], *Yunlong Chen*[1], *Jingliao Zhang, MD*[1], *Xiaofan Zhu*[2]

[1] Pediatric Blood Diseases Center, State Key Laboratory of Experimental Hematology, National Clinical Research Center for Blood Diseases, Haihe Laboratory of Cell Ecosystem, Institute of Hematology & Blood Diseases Hospital, Chinese Academy of Medical Sciences, Tianjin, China
[2] Pediatric Blood Diseases Center, State Key Laboratory of Experimental Hematology, National Clinical Research Center for Blood Diseases, Haihe Laboratory of Cell Ecosystem, Institute of Hematology & Blood Diseases Hospital, Chinese Academy of Medical Sciences & Peking Union Medical Colleg, Tianjin, China

Objective: juvenile myelomonocytic leukemia (Juvenile myelomonocytic leukemia JMML) is a rare clonal disease of hematopoietic stem cells in young children. The response to chemotherapy is poor, the prognosis is poor, and a few patients can be relieved spontaneously. The level of methylation is closely related to the prognosis of JMML. In this study, the distribution characteristics and clinical indexes of JMML methylation were analyzed retrospectively. Methods: the newly diagnosed JMML from 2008.1 to 2022.11 in our center was selected as the research object. The samples were detected for DNA methylation and the clinical characteristics were analyzed. Results: methylation level was detected in 35 of 96 children with newly diagnosed JMML. The median age of onset was 27 months (3-82 months). There were 27 males and 8 females. The median platelet count was 70.6 × 109 × 10˜9 × 10˜9 × 10˜9 / L, and the median absolute value of monocytes was 5.0 × 10˜9 × 10˜9 × 10˜9 × 10˜9 ml. All patients underwent JMML mutation and oral mucosal verification, including PTPN11 somatic mutation in 18 cases (51.4%), NRAS mutation in 10 cases (28.6%), KRAS mutation in 4 cases (11.4%), NF1 mutation in 7 cases (20%) and CBL mutation in 1 case (2.9%). Among them, 9 cases (25.7%) were compound mutations and 5 cases were recurrent mutations of PTPN11 and NF1. The DNA methylation level was divided into three subgroups: 4 cases (11.4%) hypomethylation (LM) group and 14 cases (40%) methylation group (IM) 17 cases (48.6%) hypermethylation (HM) group. Among the 17 patients in HM group, there were 7 cases of PTPN11 single mutation (41.2%) and 9 cases of compound mutation (52.9%), which were significantly higher than 3 cases of PTPN11 in IM group (21.4%). In IM group, simple NRAS or KRAS mutations accounted for 50%. The mutation distribution in LM group was 1 case of KRAS mutation, 2 cases of RANSBP2-ALK fusion gene and 1 case of no mutation. There were significant differences in age, platelet, fetal hemoglobin (HbF), PTPN11 mutation and ≥ 2 somatic mutation among different methylation subgroups ($P < 0.05$). The correlation analysis showed that methylation was positively correlated with 24 months of age, ≥ 33 × 10 9 mmol L, HbF, PTPN11 mutation and ≥ 2 somatic mutation ($P < 0.05$). Conclusion: high risk factors such as age at first diagnosis, PTPN11 mutation and compound mutation are significantly correlated with methylation in patients.

Disclosures No relevant conflicts of interest to declare.

https://doi.org/10.1182/blood-2023-184670