C-type Lectin-like Molecule-1 as a Potential Biomarker for Diagnosis and Prognosis in Acute Myeloid Leukemia

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Abstract

Background Cytogenetic and molecular genetic abnormalities are now considered to be important factors affecting the prognosis of acute myeloid leukemia (AML), while variable outcomes may appear in the same risk group. Immunophenotyping has been the core in AML diagnosis, which is simple and universal application. The aim of this study was to explore and identify new immunophenotypic markers that related to the diagnosis and prognosis of AML.

Methods The expression of C type lectin like molecule 1 (CLL-1) in AML blasts were examined in 52 patients with newly diagnosed or relapsed/refractory AML, and was compared with other classic markers in AML, in order to assess the value of CLL-1 as an independent biomarker or in combination with other markers for diagnosis in AML. Subsequently, we assessed the value of CLL-1 as a biomarker for prognosis in this malignant tumor.

Results The results showed that CLL 1 was expressed on the cell surface of the majority of AML blasts (78.8%), and also expressed on leukemic stem cells in varying degree but absent on normal hematopoietic stem cells. Notably, CLL 1 was able to complement the classic markers CD33 or CD34. After dividing the cases into CLL-1high and CLL-1low groups according to cutoff 59.0%, we discovered that event free survival and overall survival (OS) of the CLL-1low group were significantly lower than the CLL-1high group, and low CLL 1 expression seems to be independently associated with shorter OS.

Conclusions These data identified CLL 1 as a potential biomarker for diagnosis and prognosis of AML.

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Figures

Figure 1

Expression of CLL 1 on AML and stem cells. (a) Variant CLL 1 expression levels among primary AML samples. CLL 1 staining from ten representative samples is shown. (b) Distribution of CLL 1+, CD33+, and CD34+ cells in primary AML samples. (c) CLL 1 expression on CD34+CD38 stem cells in AML and NBM. (d) Expression profile of CLL 1 in normal tissue at protein level was assessed by utilizing publicly

available databases for mass spectrometry proteomic analysis (Human Proteome Map: CLL 1). AML: acute myeloid leukemia, NBM: normal bone marrow, NS: not significant

Figure 2

Patient survival. Probability of EFS (a) and OS (b) in AML patients according to CLL 1 expression (entire cohort). EFS (c) and OS (d) in AML patients with poor outcome according to CLL 1 expression. EFS (e) and OS (f) in AML patients according to treatment response. EFS and OS were estimated using the

Kaplan Meier method and the log rank test was used for comparison of the survival curves. EFS: event-free survival, OS: overall survival, AML: acute myeloid leukemia, CR: complete response

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