Cluster of differentiation 96 as a leukemia stem cell-specific marker and a factor for prognosis evaluation in leukemia

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Abstract. Resistance to chemotherapy is a major challenge for leukemia treatment. It has been suggested that leukemia stem cells (LSCs), a small pool of self-renewing leukemic cells, play important roles in development of chemotherapy resistance. The expression of cluster of differentiation 96 (CD96), a potential marker for LSCs, was investigated in CD34+CD38- cells of 105 acute leukemia (AL) patients by flow cytometry. The data showed that all the CD34+, CD34+CD38+ and CD34+CD38-CD96+ proportions were much higher in AL compared to the normal control (P<0.01), while a clear difference was identified in the CD34+CD38- and CD34+CD38-CD96+ proportions between acute lymphoid leukemia and acute myeloid leukemia (AML). However, all the AML patients with >15% CD34+CD38+ cells achieved complete remission (CR), suggesting that as an LSC-rich population, the amount of CD34+CD38- cells may not be positively associated with the proportion of refractory LSCs. The mean percentage of the co-presence of CD96 expression itself was similar in AML patients with CR and non-CR (P>0.05). However, the CR rate was significantly higher in the AML population with <10% CD96 expressed, which indicated that a distinct sub-group of CD34+CD38-CD96+ cells may still contribute to the drug resistance or poor prognosis.

Introduction

According to the cancer stem cell model, the small pool of self-renewing cancer stem cells must be eliminated in order to eradicate the tumor (1-4). Acute myeloid leukemia (AML) is a developmental disease characterized by clonal growth and subsequent accumulation of myeloid blasts in the bone marrow (BM), which is initiated and maintained by a subset of self-renewing leukemia stem cells (LSCs). Thus far, human AML stem cells are the most extensively characterized cancer stem cell population. LSCs share numerous properties with hematopoietic stem cells (HSC) with the ability of self-renewal. Thus, it has been suggested that the clonal progression of preleukemia may occur in a succession of HSC subclones until augmented or poorly regulated self-renewal pathways are activated, leading to the emergence of final stage LSCs usually at the level of a downstream progenitor (5).

A number of studies have shown that LSC-enriched populations are resistant to various chemotherapy agents and are therefore possibly responsible for the outgrowth of minimal residual disease, which in turn is believed to cause relapse (6,7). Thus, the expression profile of LSC specific cell surface markers may be used as a prognosis factor to predict the drug response in AML patients. Similar to the normal HSCs, AML-LSC are enriched in the CD34+CD38+ population (8). However, AML-LSCs also express certain unique cell surface marker combinations, such as CD123+CD117+, CD90+, CD47+ and intermediate aldehyde dehydrogenase activity (9-13). CD96 (T cell-activated increased late expression) is a transmembrane glycoprotein possessing three extracellular immunoglobulin-like domains (14), which is expressed by T and NK cells but not the majority of B cells, monocytes and granulocytes in human peripheral blood cells (15). Notably however, CD96 has been identified as an LSC-specific marker in human AML (16,17). Although, the functions and prognosis value of CD96 expression in human AML remains unclear.

The present study investigated the potential co-association between CD96 expression and chemotherapy response in AML, acute lymphoid leukemia (ALL) and mixed lineage acute leukemia (MAL) patients, to increase the understanding of the role of CD96 in leukemia diagnosis and prognosis.

Materials and methods

Patient samples. BM samples of 105 acute leukemia (AL) patients presenting with AML, ALL and MAL at the Union...
Hospital Center for Stem Cell Research and Application (Wuhan, China) were obtained following informed consent at diagnosis and following chemotherapeutic treatment. A total of 15 normal BM samples were collected as control. The mean age was 48 years and ranged from 2 month to 82 years. The study was approved by the Research Ethics Committee at the Union Hospital. Patient distributions are shown in Table I. Diagnosis and identification of subtypes for the patients was based on morphology using the French-American-British classification, immune-phenotyping, molecular genetics and cytogenetics, and fluorescence in situ hybridization (FISH). All the AML patients were induced by a dose-adjusted regimen, except AML-M3. The complete remission (CR) group was defined as first CR. When the patient could not achieve the first CR within two induction treatments, or relapsed in 6 months after the first CR, they were classified into the non-CR (NCR) group.

Flow cytometry. The majority of the samples were analyzed freshly. Red blood cells (RBCs) were lysed using a 10 min lysing procedure on ice with 10 ml lysis buffer [155 mmol/l NH₄Cl, 10 mmol/l KHCO₃, 0.1 mmol/l Na₂ and ethylenediaminetetraacetic acid (pH 7.4)] and washed with phosphate-buffered agar (PBA) [phosphate-buffered saline (PBS) containing 0.1% bovine serum albumin]. The monoclonal antibodies (10 µl; BD Biosciences, Franklin Lakes, NJ, USA) CD38 fluorescein isothiocyanate, CD34 phycoerythrin and CD96 were added respectively to a certain volume of whole BM according to the cell counts (~5x10⁶ cells/tube). Subsequently the samples were maintained in the dark at 4°C for 30 min. The samples were lysed with fluorescence-activated cell sorting (FACS) lysing solution (BD Biosciences) for 10 min, followed by washing with PBA once at ~1,000 x g at 4°C for 5 min. Finally, the cell pellets were resuspended in 300 µl PBS and the data was collected by FACS Calibur™ (BD Biosciences).

Statistical analysis. The data were analyzed using the SPSS software package (version 16.0 for Windows; SPSS, Inc., Chicago, IL, USA) in the study. All the variables were presented as mean values and standard error (SE) or median and interquartile range with the independent samples group t-test or χ² test. Analysis of the prognosis was performed using the Wilcoxon signed ranks. All the statistical tests were two-sided and P<0.05 was considered to indicate a statistically significant difference.

Results

CD34/CD38/CD96 expression in AL patients. The frequencies of CD34⁺, CD34⁻CD38⁻ and CD34⁻CD38⁺CD96⁺ populations were analyzed in BM nucleated cells from a cohort of 105 AL and 15 healthy volunteers. The information of the patients and healthy volunteers as normal controls is summarized in the Table I. A total of 20,000 nucleated cells were analyzed for each specimen to evaluate the expression of CD34 and 2,000 gated-CD34⁺ cells were collected when analyzing with CD38 and CD96.

As expected, the frequency of the CD34⁺ population in nucleated cells was low (<4.6%) in all the healthy volunteers with the mean of 2.07%. However, its expression varied significantly in AL patients, with the mean value of 35.20% (median 30.26%, SE 0.27%), which was much higher in comparison to the normal controls (P<0.01). Similarly, as shown in Figs. 1 and 2, the proportion of the CD34⁺CD38⁻ population in nucleated cells was <0.6% (mean 0.10%, median 0.03%, SE 0.01%) in all the healthy volunteers, which was 9.22% (median 2.36%, SE 0.14%) in AL patients, indicating the significant difference between them (P<0.01). Subsequently, the CD96 expression in CD34⁺CD38⁻ cells was examined. As shown in Figs. 1 and 3, the CD34⁺CD38⁻ cells from healthy volunteers had less expression of CD96, with the mean of 7.78% (median 4.00%, SE 0.99%), while the proportion was as high as 29.36% (median 7.32%, SE 0.40%) in the 105 AL patients. The difference had clear significance (P<0.01).

The CD34 expression also varied significantly in AML patients, with the mean value of 35.12% (median 27.80%, SE 0.32%), which was significantly higher compared to the healthy controls (P<0.01), but was close to the total AL samples. Similarly, the proportion of the CD34⁺CD38⁻ population in nucleated cells in healthy volunteers was much lower compared to the AML patients (P<0.01), which was at the mean of 6.91% (median 1.25%, SE 0.15%). In addition, CD96 expression on CD34⁺CD38⁻ cells in AML patients (mean 26.71%, median 5.57%, SE 0.33%) was also significantly higher compared to the normal control (P<0.01).

The CD34 expression in ALL patients was at the mean value of 39.15% (median 30.26%, SE 0.27%), which was significantly higher compared to the healthy controls (P<0.01), but there was no difference when comparing with the AML patients (P>0.05). The CD34⁺CD38⁻ cells in the ALL patients was at the mean value of 24.48% (median 23.22%, SE 1.44%), which was significantly higher compared to the healthy controls (P<0.01), but still much lower than the AML patients (P<0.01). The CD96 expression in the CD34⁺CD38⁻ cells in the ALL patients (mean 11.34%, median 0.74%, SE 1.86%)

<table>
<thead>
<tr>
<th>Classification</th>
<th>No.</th>
<th>Gender, M/F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal</td>
<td>15</td>
<td>6/9</td>
</tr>
<tr>
<td>AL</td>
<td>105</td>
<td>59/46</td>
</tr>
<tr>
<td>AML</td>
<td>87</td>
<td>49/38</td>
</tr>
<tr>
<td>M0</td>
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<td>5/2</td>
</tr>
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</tr>
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<td>2/1</td>
</tr>
</tbody>
</table>

M, male; F, female; AL, acute leukemia; AML, acute myeloid leukemia; ALL, acute lymphoid leukemia; MAL, mixed lineage acute leukemia.
was similar to the normal controls (P>0.05) and lower than the AML patients (P<0.05). With regards to MAL, further analysis or comparisons were not performed due to the limited cases.

**CD34/CD38/CD96 expression in the AML subtypes.** The differences between 3 subtypes of AML (M1, M2, and M4) were considered, which had ≥10 samples in each group. Only the CD34 expression in M2 and M4 patients had a statistical difference (P<0.05). None of the other indices, including CD34+ cell percentages in the M1 and M2 or M1 and M4 groups, CD34+CD38− proportions and CD96 expression in the 3 subtypes, were identified as significantly different (P>0.05).

**Association of CD34+CD38− and CD96+ expression with the chemotherapy response in AML patients.** The presence of LSCs has been proposed to be an important reason for drug
Table II. CD34+CD38+ proportions and the chemotherapy response of AML patients.

<table>
<thead>
<tr>
<th>CD34+CD38+ cells in CD34+ cells</th>
<th>NCR cases</th>
<th>CR cases</th>
<th>Subtotal</th>
</tr>
</thead>
<tbody>
<tr>
<td>≥15%</td>
<td>0</td>
<td>10</td>
<td>10</td>
</tr>
<tr>
<td>&lt;15%</td>
<td>17</td>
<td>28</td>
<td>45</td>
</tr>
<tr>
<td>Subtotal</td>
<td>17</td>
<td>38</td>
<td>55</td>
</tr>
</tbody>
</table>

CD, cluster of differentiation; AML, acute myeloid leukemia; CR, complete remission; NCR, non CR.

Table III. CD96 expression in CD34+CD38+ cells and the response for chemotherapy of AML patients.

<table>
<thead>
<tr>
<th>CD34+CD38+CD96+ cells in CD34+CD38+ cells</th>
<th>NCR cases</th>
<th>CR cases</th>
<th>Subtotal</th>
</tr>
</thead>
<tbody>
<tr>
<td>≥10%</td>
<td>11</td>
<td>12</td>
<td>23</td>
</tr>
<tr>
<td>&lt;10%</td>
<td>6</td>
<td>26</td>
<td>32</td>
</tr>
<tr>
<td>Subtotal</td>
<td>17</td>
<td>38</td>
<td>55</td>
</tr>
</tbody>
</table>

CD, cluster of differentiation; AML, acute myeloid leukemia; CR, complete remission; NCR, non CR.

CD96 had previously been reported to express on T and NK cells, but not on B cells, granulocytes, monocytes or RBCs (17,19). However, recent studies suggested that CD96 was a putative maker expressed by LSCs in AML patients. Although the physiological functions of CD96 on AML-LSCs are unknown, it may contribute to their adhesion to the BM compartment. To increase the understanding of the association of CD96 expression and CD34+CD38+ stem cell markers and subsequently to reveal the role of CD96 in leukemia, the CD34+CD38+CD96+ population and the clinical characteristics in 105 AL patients, including 87 AML, 15 ALL and 3 MAL, and 15 healthy volunteers as normal controls were examined.

As expected, the frequency of the CD34+ population in nucleated cells was much lower than that in the AL patients (P<0.01), which was in the same situation as CD34+CD38+ and CD34+CD38+CD96+ expression (P<0.01), as shown in Figs. 1-3. Advanced analysis also showed that AML and ALL had higher CD34+ and CD34+CD38+ cells compared to the normal controls (P<0.01). These results were consistent with previous studies (13,20,21). However, the present data also showed that although there were high frequencies and no difference in CD34+ expression between AML and ALL (P>0.05), the CD34+CD38+ cells in ALL patients was significantly lower than that in the AML patients (P<0.01). In addition, there were still evident differences of CD96 expression on CD34+CD38+ cells in ALL patients with that in AML; the former was similar to the normal controls (P>0.05) and lower than the AML patients (P<0.05). The results suggested that, regardless of the several studies indicating a population of LSC exhibiting a CD34+CD38+ phenotype in ALL and AML (22,23), the proportions were different. CD96 may not appear to be a potential distinguished LSCs marker in ALL. However, except for the statistical difference of CD34
expression in the M2 and M4 patients (P<0.05), none of the other indices, including the CD34+ cell percentages in the M1 and M2 or M1 and M4 groups, CD34+CD38+ proportions and CD96 expression in the 3 subtypes of AML (M1, M2 and M4), were identified as different (P>0.05). Sufficient cases may be studied to evaluate the diversity.

Numerous studies were performed to reveal the characteristics and function of leukemia stem cells. One of the most prevalent aims focused on the CD34+CD38− LSC-enriched cells, which had been proposed as an important factor in drug resistance. Certain studies described that the fraction of CD34+CD38− cells at the time of diagnosis exhibited a significant correlation with poor prognosis in childhood ALL of B-cell lineage and AML (20,21). Of note, the present results showed that in 17 NCR patients out of 55 AML cases, the mean of CD34+CD38− proportion in CD34+ cells at the new diagnosis time was lower compared to the 38 CR AML patients (P<0.05). Furthermore, all 10 cases of AML patients with >15% CD34+CD38− cells achieved CR, while 17 out of 45 patients (38%) who had <15% CD34+CD38− cells remained NCR (P<0.01), as shown in Fig. 4 and Table II. In summary, all 17 NCR patients had <15% CD34+CD38− cells in nucleated cells. However, conflicting results were not identified between our and the previous study. The previous studies analyzed the fraction of CD34+CD38− cells based on total abnormal cells, which may or may not include a significant number of CD34+ cells. The CD34+CD38− cells were counted based on pure CD34+ cells, which varied significantly in all the AL patients even in a similar proportion of abnormal cells, but may be more comparable. This type of percentage was selected as it may avoid the inaccuracy of too few CD34+CD38− cells for the rare CD34+ cells, and waive the difference resulting from the unbalance of various amounts of CD34+ cells in the abnormal cells. The frequencies should not simply be compared. The CD34+CD38− proportion in the CD34+ cells could also provide a significant explanation for the prognosis of AL. In addition, the results verified that only the CD34+CD38− cells were an enriched marker of LSCs. The amount of LSCs may not be positively correlated with the prognosis of AL. In addition, the results verified that only 19% (P<0.01). The results strongly indicated that a higher expression of CD96 (>10%) may promote a poor response for chemotherapy, which may be closely associated with primary resistant. Of note, CD96 was proved to be an efficient identical marker of LSCs in CD34+CD38− groups, which was consistent with previous studies (16,17). For the limit of adherence and follow-up of the patients, only the outcomes in 55 AML patients with completed clinical data were analyzed, however, it may have a certain association with other types or subtypes of leukemia that require further research.

CD96 expression was also evaluated in CD34+CD38− cells in 14 high-risk MDS BM samples. Although CD96 expression was much higher compared to the normal control, no evidence showed that the CD34+CD38− or CD34+CD38+ CD96+ proportion was associated with MDS chemotherapy efficacy or the prognosis. However, MDS stem cells exhibit a deranged phenotype that is different from normal and AML stem cells, and this may cause them to be particularly difficult to eradicate by therapies targeted against surface antigens.

In conclusion, CD96 was frequently expressed in the CD34+CD38− LSC population in AL patients. CD96 is significantly associated with the response for chemotherapy in AML patients, which strongly suggested that CD96 may be a marker of LSCs, candidate therapeutic target and prediction factor in AL patients.

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References


