### Impact of CD133 (AC133) and CD90 expression analysis for acute leukemia immunophenotyping

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Background and Objectives. AC133 is a novel monoclonal antibody (Moab) reacting with a population of immature/primitive or granulo-monocytic committed CD34<sup>+ve</sup> cells. Up to now, only few studies with small numbers of cases have examined AC133 (recently designated CD133) expression in acute leukemia. To determine the value of this Moab for acute leukemia immunophenotyping, we investigated a large series of leukemic cell samples for their reactivity with Moab AC133.

Design and Methods. A total of 298 cell samples from patients with *de novo* acute myeloid leukemia (AML) (n=142), acute lymphoblastic leukemia (ALL) (n=119), CD34<sup>+ve</sup> biphenotypic acute leukemia (n=13), and CD34<sup>+ve</sup> CML blast crisis (=BC; 21 myeloid BC/3 lymphoid BC) were investigated by flow cytometry for Moab AC133 reactivity. CD133 expression was compared with CD90(Thy-1) expression, another CD34-associated antigen.

*Results.* Fifteen (5%) samples expressed CD90, whereas 114 (38%) samples were positive for Moab AC133 (20% cut-off level). No significant differences in CD133 and CD90 expression levels between AML and ALL were observed. In AML, but not ALL, CD133 was more often expressed in CD34<sup>+ve</sup> cases than in CD34<sup>-ve</sup> ones (p<0.00001). However, CD133 expression was not restricted to CD34<sup>+ve</sup> leukemic cells in individual cell samples. All 8 pro-B-ALL cell samples with 11q23-anomalies and MLL (*mixed lineage leukemia*) gene translocations were positive for CD133, whereas only 2 of 9 pro-B-ALL without MLL gene translocations expressed CD133 (p<0.002). In contrast, none of the 5 AML cell samples with a t(9;11) and MLL gene translocation reacted with Moab AC133. CD34<sup>+ve</sup> CML cells in myeloid BC were less often positive for CD133 than CD34<sup>+ve</sup> de novo AML cells (p<0.0001).

Interpretation and Conclusions. CD133 and CD90 expression analysis is not helpful for lineage determination in acute leukemia immunophenotyping. However, Moab AC133 may be an informative marker for the detection and further characterization of immature AML cells, as well as pro-B-ALL cells with MLL gene translocations, by flow cytometry. © 2001, Ferrata Storti Foundation

Key words: acute leukemia, CD133 (AC133), CD90, flow cytometry, immunophenotyping

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cute leukemias derive from either malignant, transformed, uncommitted multipotent stem cells or lineage-restricted progenitor cells.<sup>1-3</sup> So far, CD34 is the most commonly used antigen to define immature hematopoietic progenitor cells.<sup>4</sup> In acute leukemia immunophenotyping, CD34 is not lineagerestricted and thus not useful for distinguishing acute myeloid leukemia (AML) from acute lymphoblastic leukemia (ALL).<sup>5</sup> Therefore, new Moabs, recognizing subsets of CD34 leukemic cells with the potential to distinguish uncommitted multipotential stem cells from lineage-restricted progenitor cells are of special interest for acute leukemia immunophenotyping. Moab AC133 reacts with a population of non-committed or granulomonocytic (GM)-committed CD34+ve cells in normal hematopoiesis.<sup>6,7</sup> Recently it was shown that among the CD34-veCD38-veLin-ve subset of human cord blood an extremely rare population of AC133+veCD7-ve cells is highly enriched for progenitor activity and capable of differentiation into CD34+ve cells.8 So far, it is not clear which molecule is detected by Moab AC133, recently designated CD133 by the 7th Workshop and Conference on Human Leukocyte Differentiation (June 2000). The AC133-antigen may be the human homolog of the mouse kidney prominin, which is preferentially found on the apical surface of various murine embryonic and adult epithelia.9-11 Recent data suggest that CD133 expression also defines a subset of circulating endothelial cells that may play a role in neoangiogenesis.<sup>12</sup>

Up to now, only a few studies with small numbers of cases have examined CD133 expression in acute leukemia: in one study, CD133 expression was mainly restricted to immature AML FAB subtypes.<sup>13</sup> However, in another study the highest CD133 expression levels were found in myelomonocytic differentiated AML FAB M4/M5 cases.<sup>6</sup> Two other studies revealed no correlation between CD133 expression, FAB subtypes and cytogenetics in AML.<sup>14,15</sup> AC133 reactivity was observed in 56-67% of ALL cell samples examined.<sup>6,15,16</sup> In contrast, another study could not detect CD133 expression in any of 17 ALL samples tested.<sup>13</sup> In AML, some stud-

ies have found that Moab AC133 reacts preferentially with CD34<sup>+ve</sup> leukemic cells,<sup>13,14,17</sup> although another study found no clear difference in CD133 expression levels between CD34<sup>+ve</sup> and CD34<sup>-ve</sup> AML.<sup>15</sup> A recent study revealed disconcordant CD133 expression in patients with AML or myelodysplastic syndrome (MDS) compared with precursor cells from normal marrow or peripheral blood stem cells.<sup>18</sup>

To determine the value of CD133 expression analysis for acute leukemia immunophenotyping on a large number of acute leukemia samples, we investigated 298 cell samples from children and adults with acute leukemia for their reactivity with Moab AC133 by flow cytometry. Furthermore, CD133 expression was compared with CD90(Thy-1) expression, an epitope found on approximately 25% of CD34<sup>+ve</sup> cells with enhanced proliferative and self-renewal capabilities.<sup>19</sup> Finally, we correlated CD133 and CD90 expression with immunophenotypic features, FAB morphology and cyto-/molecular genetic data of the examined patients.

#### **Design and Methods**

#### Patients and cell samples

We examined either freshly obtained or cryopreserved bone marrow or peripheral blood samples from 298 patients with acute leukemia for their reactivity with Moab AC133<sup>6</sup> and anti-CD90 Moab 5E10.<sup>19</sup> In our series, 110 children with ALL (90 B-lineage ALL, 20 T-lineage ALL), 38 children and 104 adults with *de novo* AML, and 9 adults with ALL (8 B-lineage ALL, 1 T-lineage ALL) were included. Moreover, cell samples from 13 patients (2 adults, 11 children) with biphenotypic acute leukemia (=BAL), and 24 adults with CD34+ve CML blast crisis (=BC; 21 myeloid BC/3 B-lymphoid BC) were examined in this study. The age of the patients examined ranged between 10 months and 78 years (median 51 years) for those with *de novo* AML, between 1 month and 59 years (median 5 years) for those with ALL, between 1 year and 70 years (median 12 years) for BAL, and between 32 years and 83 years (median 53 years) for those in CML blast crisis. Diagnosis of acute leukemia was based on immunologic criteria according to EGIL recommendations<sup>5</sup> and morphologically in accordance with FAB criteria.<sup>20</sup> B-lineage ALL cases were subgrouped into pro-B-ALL, common-ALL, pre-B-ALL, and mature B-ALL, and T-lineage ALL cases into pro-/pre-T-ALL, cortical T-ALL, and mature T-ALL.<sup>5</sup> The diagnosis of BAL was based on the EGIL scoring system.<sup>5</sup>

#### Leukemia immunophenotyping

Leukemic cells from heparinized bone marrow or peripheral blood samples were isolated by Ficoll-Hypaque (Pharmacia, Freiburg, Germany) density gradient centrifugation, and leukemia-associated antigens were detected by a panel of Moabs either by a direct or indirect immunofluorescence assay as previously described.<sup>21,22</sup> Cell samples were analyzed by flow cytometry (FACScan; Becton Dickinson, San Diego, USA) using the Cell-Quest-software program (Becton Dickinson). Cell samples were considered positive for a specific antigen if the antigen was expressed on at least 20% of the leukemic cells/sample (= 20 % cut-off level).<sup>5,22</sup>

# Detection of CD133 and CD90 expression in acute leukemia by flow cytometry

Cells were stained by direct immunofluorescence using the phycoerythrin (PE)-conjugated Moab AC1336 (IgG1; Miltenyi Biotech, Auburn, CA, USA) and the FITCconjugated anti-CD90 Moab 5E1019 (IgG1; PharMingen, San Diego, CA, USA) as recommended by the manufacturers. Non-specific binding of Fcy-receptors was blocked by pre-incubation of the cells with a polyclonal rabbit serum (Gibco BRL, Paisley, UK). At least 10,000 cells per sample were acquired and analyzed by flow cytometry as described above. Freshly obtained cell samples were analyzed by three-color immunophenotyping, using CD90-FITC, CD133-PE and CD34-PECy5 (clone QBend10; Beckman Coulter, Marseille, France). Nonviable cells were excluded by scatter gating. Previously cryopreserved cell samples were analyzed by two-color immunophenotyping using the combinations CD90-FITC/CD34-PE, CD34-FITC/CD133-PE, and CD90/CD133-PE. In each of these samples, non-viable cells were excluded from analysis by propidium iodide co-staining (0.3 µg/mL; Sigma, Deisenhofen, Germany). No differences in CD133 and CD90 expression patterns between freshly obtained and previously cryopreserved cell samples were observed. Cell samples were considered positive for CD90 or CD133 if at least 20% of the leukemic cells/sample specifically stained with Moabs 5E10 or AC133 revealed a higher fluorescence intensity than cells stained with the isotype-matched control antibody (=20% cut-off level).5,22

#### **Cytogenetics**

Chromosome analyses were performed on metaphases from short-term (24h, 48h) cultures of pretreatment bone marrow and/or peripheral blood cells. Cell cultivation and chromosome preparation were carried out according to standard protocols. G-banding was used and the chromosomes interpreted according to ISCN (1995) nomenclature.<sup>23</sup> Patients with adult AML were grouped into three different risk categories: good: t(8;21), inv(16)/t(16;16), t(15;17); intermediate: normal karyotype, other abnormalities; poor: -5/5q-, -7/7q-, 11q23-abnormalities, inv(3)/t(3;3), t(9;22), t(6;9), 17pabnormalities, complex aberrant karyotype (three or more numerical or structural abnormalities).

# Reverse transcriptase polymerase chain reaction (RT-PCR)

RT-PCR was performed as previously described.<sup>24,25</sup> Primer sequences used for the detection of specific leukemic fusion transcripts have been described elsewhere (MLL ("mixed lineage leukemia") gene rearrangements,<sup>26</sup> PML/RAR $\alpha$ ,<sup>27</sup> AML1/ETO,<sup>27</sup> BCR/ABL,<sup>28</sup> TEL/AML1<sup>25</sup>).

#### Statistical analysis

Differences in the immunophenotypic expression patterns, cyto-/molecular genetic groups and FAB morphology between CD133 and/or CD90 positive and negative cell samples were analyzed using the Chi-squared test (Pearson coefficient). The Kruskal-Wallis test was used to determine differences in CD133 or CD90 expression for the immunophenotypic subtypes in ALL, morphologic FAB subtypes in AML as well as the different CD34<sup>+ve</sup> acute leukemia subtypes. In individual cases, CD133 and CD90 expression was correlated with the age of the patient examined using bivariate correlation (Spearman coefficient rs). *p* values < 0.05 were considered statistically significant. All statistical analyses were done with the SPSS software program (version 9.0).

#### Results

# CD133 and CD90 expression on CD34<sup>+ve</sup> and CD34<sup>-ve</sup> acute leukemia cells (Table 1)

In *de novo* AML, 44 (65%) of 68 CD34<sup>+ve</sup> acute leukemia cell samples expressed CD133, whereas only 9 (12%) of 74 CD34<sup>-ve</sup> acute leukemia cell samples were CD133 positive (p < 0.00001). In ALL, 38 (42%) of 91 CD34<sup>+ve</sup> acute leukemia cell samples expressed CD133 and 9 (32%) of 28 CD34<sup>-ve</sup> acute leukemia cell samples were CD133 positive (not significant).

In *de novo* AML, 6 (9%) of 70 CD34<sup>+ve</sup> acute leukemia cell samples expressed CD90 and 3 (4%) of 78 CD34<sup>-ve</sup> AML cell samples were CD90 positive (not significant). In ALL, 2 (2%) of 91 CD34<sup>+ve</sup> ALL cell samples expressed CD90 and none of 28 CD34<sup>-ve</sup> acute leukemia cell samples were CD90 positive (not significant).

Cell samples of CD34<sup>+ve</sup> CML in myeloid BC were less often positive for CD133 than were CD34<sup>+ve</sup> *de novo* AML cell samples [5/21 (24%) CD133 positive cell samples vs. 44/68 (65%); *p* <0.001]. In contrast, CD90 expression differed, but not significantly, within these two subtypes [4/21 (19%) CD90 positive cell samples vs. 6/68 (9%); not significant]. The percentage of CD34<sup>+ve</sup> cells/sample of the examined CD34<sup>+ve</sup> CML and CD34<sup>+ve</sup> *de novo* AML cell samples did not differ significantly within the two subgroups (CD34<sup>+ve</sup> CML: 70±22% CD34<sup>+ve</sup> cells/sample). CD34<sup>+ve</sup> *de novo* AML: 76±18% CD34<sup>+ve</sup> cells/sample). CD34<sup>+ve</sup> BAL cases revealed no specific CD133 and CD90 expression pattern compared with CD34<sup>+ve</sup> AML or CD34<sup>+ve</sup> ALL cases (Table 1).

Figure 1 shows representative examples of CD133 and CD90 expression in acute leukemia.

#### CD133 and CD90 expression in acute leukemia: correlation with immunophenotype, FAB morphology, and age of the patients examined

There was no significant difference in CD133 expression between AML and ALL cell samples using the 20% cut-off level [53/142 (37%) CD133 positive cell samples vs. 47/119 (39%); not significant]. Within ALL, B-lineage ALL cell samples were more often positive for Moab AC133 than were the T-ALL cell samples (Table 2; p <0.01). Neither in B-lineage nor in T-lineage ALL was a correlation between immunophenotypic subtypes and CD133 expression observed (Table 2). In AML, CD133 positive cell samples

| Table 1. | CD133     | and C    | D90 exp  | pression | in   | CD34 <sup>+ve</sup> | and |
|----------|-----------|----------|----------|----------|------|---------------------|-----|
| CD34-ve  | (20% cut- | off leve | I) acute | leukemia | i su | ibtypes.            |     |

|                              | CD34 <sup>+ve</sup><br>de novo AML<br>(n=68) | CD34 <sup>.ve</sup><br>. de novo AN<br>(n=74) | CD34 <sup>+ve</sup><br>AL ALL<br>(n=91) | CD34 <sup>.ve</sup><br>ALL<br>(n=28) | CD34+ve<br>BAL<br>(n=13) | CD34 <sup>∞</sup><br>blast crisis<br>(n=24) |
|------------------------------|--|---|---|--------------------------------------|--------------------------|---|
| ≥ 20% CD133+<br>cells/sample | 44 (65%)*                                    | 9 (12%)                                       | 38 (42%)                                | 9 (32%)                              | 6 (46%)                  | 8 (33%)                                     |
| <20% CD133+<br>cells/sample  | 24 (35%)                                     | 65 (88%)                                      | 53 (58%)                                | 19 (68%)                             | 7 (54%)                  | 16 (67%)                                    |
| ≥ 20% CD90+<br>cells/sample  | 6 (9%)                                       | 3 (4%)  | 2 (2%)                                  | 0 (0%)                               | 1 (8%)                   | 3 (13%)                                     |
| <20% CD90+<br>cells/sample   | 62 (91%)                                     | 71 (96%)                                      | 89 (98%)                                | 28 (100%)                            | 12 (92%)                 | 21 (87%)                                    |

\*Number of cell samples (% of cell samples within the specific leukemia subtype). Abbreviations: BAL, biphenotypic acute leukemia.



Figure 1. Representative examples of CD133 and CD90 expression analysis in acute leukemia by flow cytometry as described in Design and Methods. a) AML FAB M1 (CD34 95%/CD133 91%/CD90 0%); b) Pro-B-ALL with t(4;11) CD34 2%/CD133 93%/CD90 0%) c) CML in myeloid blast crisis (CD34 90%/CD133 0%/CD90 27%).

|                        | CD133 positive           | p     | CD90 positive | р  |
|------------------------|--------------------------|-------|---------------|----|
| B-lineage ALL          | 44/98 (45%) <sup>a</sup> | <0.01 | 1/98 (1%)     | ns |
| T-lineage ALL          | 3/21 (14%)               |       | 1/21 (5%)     |    |
| B-lineage ALL subtypes |                          |       |               |    |
| pro-B-ALL              | 10/17                    | ns    | 0/17          | ns |
| c-ALL                  | 26/54                    |       | 1/54          |    |
| pre-B-ALL              | 8/26                     |       | 0/26          |    |
| mature B-ALL           | 0/1                      |       | 0/1           |    |
| T-lineage ALL subtypes |                          |       |               |    |
| pro-/pre-T-ALL         | 1/8                      | ns    | 1/8           | ns |
| cortical T-ALL         | 2/9                      |       | 0/9           |    |
| mature T-ALL           | 0/4                      |       | 0/4           |    |
| My positive ALL        | 24/56 (43%)              | ns    | 2/56 (4%)     | ns |
| My negative ALL        | 23/63 (37%)              |       | 0/63 (0%)     |    |

Table 2. CD133 and CD90 expression (20% cut-off level) inALL: correlation with immunophenotypic subtypes.

Table 4. FAB morphology of CD133 and/or CD90 positive AML cases (20%-cut-off level) compared with CD133 and/or CD90 negative AML cases.

|           | CD133<br>positive AML | CD133<br>negative Al | р<br>ML | CD90<br>positive AN | CD90<br>IL negative AN | p<br>1L |
|-----------|-----------------------|----------------------|---------|---------------------|------------------------|---------|
| FAB total | 41 (36%)*             | 72 (64%)             | -0.005  | 6 (5%)              | 107 (95%)              | nc      |
| FAB M1-7  | 35 (33%)              | 71 (67%)             | <0.005  | 5 (5%)              | 101 (95%)              | 115     |
| FAB MO    | 6                     | 1                    | <0.002  | 1                   | 6                      | ns      |
| FAB M1    | 12                    | 13                   |         | 3                   | 22                     |         |
| FAB M2    | 15                    | 17                   |         | 0                   | 32                     |         |
| FAB M3    | 0                     | 8                    |         | 1                   | 7                      |         |
| FAB M4    | 7                     | 14                   |         | 1                   | 20                     |         |
| FAB M5    | 1                     | 16                   |         | 0                   | 17                     |         |
| FAB M6    | 0                     | 2                    |         | 0                   | 2                      |         |
| FAB M7    | 0                     | 1                    |         | 0                   | 1                      |         |

\*Positive cell samples/cell samples examined (positive cell samples in %). Abbreviation: ns, not significant.

Abbreviations: ns, not significant; My, co-expression of at least one myeloid antigen (CD13, CD15, CD33, CD65s); \*positive cell samples/cell samples examined (positive cell samples in %).

| Table 3.Immunophenotype of CD133 and/or CD90 positive de novo A | AML cases. |
|---|------------|
|---|------------|

| CD antigen | CD133<br>positive AML | CD133<br>negative AML | p        | CD90<br>positive AML   | CD90<br>negative AML | р       |
|------------|-----------------------|-----------------------|----------|------------------------|----------------------|---------|
| 0024       | AA/E2 (020/)2         | 24/00 (27%)           | .0.00001 |                        | (1)(1)) (170/)       | 20      |
| CD34       | 44/53 (83%)"          | 24/89 (21%)           | <0.00001 | 0/9 (0/%)              | 02/133 (4/%)         | 115     |
|            | 50/53 (94%)           | 51/88 (58%)           | <0.00001 | 979 (100%)             | 92/132 (70%)         | =0.05   |
|            | 20/53 (38%)           | 5/89 (0%)             | <0.0001  | 3/9 (33%)              | 22/133 (17%)         | ns      |
| HLA-DR     | 47/53 (89%)           | 59/89 (66%)           | <0.004   | 6/9 (6/%)              | 100/133 (75%)        | ns      |
| CD7        | 23/53 (43%)           | 21/89 (24%)           | <0.02    | 3/9 (33%)              | 41/133 (31%)         | ns      |
| CD2        | 10/51 (20%)           | 9/87 (10%)            | ns       | 2/9 (22%)              | 17/129 (13%)         | ns      |
| CD19       | 5/52 (10%)            | 9/88 (10%)            | ns       | 0/9 (0%)               | 14/131 (11%)         | ns      |
| CD13       | 50/53 (94%)           | 70/89 (79%)           | <0.02    | 6/9 (67%)              | 114/133 (86%)        | ns      |
| CD33       | 43/53 (81%)           | 87/89 (98%)           | <0.0006  | 7/9 (78%)              | 123/133 (92%)        | ns      |
| MPO        | 34/53 (64%)           | 65/89 (73%)           | ns       | 4/9 (44%)              | 95/133 (71%)         | ns      |
| CD65s      | 25/53 (47%)           | 56/89 (63%)           | ns       | 2/9 (22%)              | 79/133 (59%)         | < 0.03  |
| CD15       | 22/52 (42%)           | 50/89 (56%)           | ns       | 0/9 (0%)               | 72/132 (55%)         | < 0.002 |
| CD64       | 29/52 (56%)           | 67/89 (75%)           | <0.02    | 3/9 (33%)              | 93/132 (70%)         | < 0.03  |
| CD14       | 2/52 (4%)             | 19/89 (21%)           | <0.005   | 0/9 (0%)               | 21/132 (16%)         | ns      |
| CD4        | 9/50 (18%)            | 32/89 (36%)           | < 0.03   | 3/8 (38%)              | 38/131 (29%)         | ns      |
| CD36       | 11/48 (23%)           | 33/87 (38%)           | ns       | 2/9 (22%)              | 42/126 (33%)         | ns      |
| IF         | 13/52 (25%)           | 30/87 (34%)           | ns       | 2/9 (22%)              | 41/130 (32%)         | ns      |
| CD56       | 10/51 (20%)           | 32/88 (36%)           | <0.04    | 4/9 (44%)              | 38/130 (29%)         | ns      |
| CD41       | 3/52 (6%)             | 8/89 (9%)             | ns       | 3/9 (33%)              | 8/132 (6%)           | <0.004  |
| CD61       | 4/52 (8%)             | 8/87 (9%)             | ns       | 3/9 (33%)              | 9/132 (0%)           | <0.001  |
| CD01       | 4/ 52 (0/0)           | 0/07 (7/0)            | 115      | 5/7 (55%)<br>6/9 (67%) | /7/130 (7/0)         | <0.007  |
| CD00       | 6/52 (11%)            | 3/80 (3%)             | nc       | 0/ 7 (0/ %)            | 1/100 (00/0)         | 115     |
| 6070       | 0/33 (11/0)           | 3/07 (3/0)            | 113      | _                      | -                    | —       |

<sup>a</sup> positive cell samples/cell samples examined (positive cell samples in %). Abbreviations: MPO, myeloperoxidase ; LF, lactoferrin ; ns, not significant.

showed a more immature immunophenotype (Table 3) and were more often of the immature FAB MO subtype (Table 4) compared with CD133 negative AML cell samples. In individual ALL cases, there was a weak inverse correlation between CD133 expression (% of positive cells) and the age of the patient ( $r_s = -0.29$ ; p < 0.002; n=119), whereas in *de novo* AML, no significant correlation between CD133 expression and the age of the patients was observed (data not shown). The increased number of TdT positive AML and rather low number of myeloperoxidase (MPO) positive AML cases in this study (Table 3) is most likely due to the flow-cytometric based detection of these antigens in our laboratory compared to the previously used conventional fluorescence light microscopy technique.

CD90 expression differed, but not significantly, between AML and ALL cell samples [9/142 (6%) CD90 positive cell samples vs. 2/119 (2%)]. There was also no significant difference in CD90 expression between B-lineage ALL and T-ALL cell samples (Table 2). Neither in B-lineage nor in T-lineage ALL was a correlation between immunophenotypic subtypes and CD90 expression observed (Table 2). In AML, CD90 positive cell samples showed an immunophenotype with partial mega-karyocytic differentiation (CD41, CD61) (Table 3). No significant differences in CD90 expression between the morphologic FAB subtypes were observed (Table 4). Neither in *de novo* AML nor in ALL was any significant correlation between CD90 expression and the age of the patients observed.

# Correlation of CD133 and CD90 expression with cyto-/molecular genetic data

All 8 pro-B-ALL cell samples with 11g23-anomalies and MLL (mixed lineage leukemia) gene translocations [t(4;11) n=7, t(11;19) n=1] were positive for CD133, whereas only 2 of 9 pro-B-ALL without MLL gene translocations expressed CD133 (p < 0.002). In contrast, none of the 5 AML cell samples with a t(9:11) and MLL gene translocation reacted with Moab AC133. In B-lineage ALL, CD133 expression did not distinguish leukemic cells with t(12;21) and TEL/AML1 fusion transcript (n=9) or leukemic cells with t(9;22) and BCR/ABL fusion transcript (n=7) from the respective negative cases (data not shown). In AML, none of 7 leukemic cell samples with t(15;17) and PML/RAR $\alpha$  fusion transcript reacted with Moab AC133, whereas 36 (41%) of 88 AML cases with normal karyotypes or other abnormalities were CD133 positive (p < 0.04). AML cells with t(8;21) and AML1/ETO fusion transcript (n=3) showed no special CD133 expression pattern (data not shown). In adult de novo AML, CD133 expression did not differ significantly between cytogenetic risk groups (good: n=6, intermediate: n=46, high: n=18; cytogenetic risk groups were defined as shown in Design and Methods) (data not shown). For CD90 expression, no significant correlations with specific cyto-/molecular genetic anomalies were observed, either in AML or in ALL (data not shown).

#### Discussion

In this study, we investigated the expression of the stem cell-related markers CD133 (AC133) and CD90 on leukemic cell samples from 298 children and adults with acute leukemia and determined its diagnostic value for acute leukemia immunophenotyping. In normal hematopoiesis, CD133 expression is thought to be restricted to CD34+ve progenitor cells.<sup>6,7</sup> However, our study demonstrates, in line with previous studies, that CD133 expression is not restricted to CD34<sup>+ve</sup> leukemia cells within individual cell samples in our series, neither in AML nor in ALL.13-17 Recently, it was shown that among the CD34-ve CD38-veLin-ve subset of human cord blood an extremely rare population of AC133+veCD7-ve cells is highly enriched for progenitor activity and capable of differentiation into CD34<sup>+ve</sup> cells.<sup>8</sup> The observed CD34-independent CD133 expression of leukemic cells might represent the malignant counterpart of this very small physiologic subset rather than an aberrant CD133 expression on more mature CD34-ve leukemic cells. Thus, a CD133 positive phenotype in CD34-ve acute leukemia should be considered with caution as a possible aberrant phenotype for minimal residual disease (MRD) monitoring by flow cytometry, both in AML and ALL.

In AML but not ALL, Moab AC133 reacted preferentially with CD34\*\*\* leukemic cells. Moreover, CD133 expression was correlated with an immature immunophenotype and an immature FAB subtype in AML. As previously described by Yin *et al.*<sup>7</sup> for GM-committed normal progenitor cells, we also observed a decreasing reactivity of Moab AC133 with increasing levels of CD64 in individual AML cell samples ( $r_{S}$ = -0.4 (n=141), *p* <0.001), indicating a downregulation of CD133 with monocytic differentiation. Thus, Moab AC133 may be an informative marker for the detection and further characterization of immature AML cells by flow cytometry.

In colony assays *in vitro*, normal CD133 positive CD34 cells predominantly showed differentiation along the granulomonocytic differentiation pathway, suggesting that AC133 positivity defines a subset of GM-committed progenitor cells.<sup>6,7</sup> It was, therefore, intriguing to speculate that Moab AC133 reactivity may be helpful in distinguishing between immature AML and ALL cells, as was shown for CD117 expression analysis.<sup>29</sup> However, in line with previous studies, neither CD133 nor CD90 expression was restricted to AML samples in this series.<sup>15,17</sup> Our results clearly underline that neither CD133 nor CD90 expression analysis is feasible for lineage distinction between AML and ALL cell samples.

In our series, CD90 was significantly less often expressed on acute leukemia cells than was CD133 (p<0.001). In previous studies, 2-42% of AML cell samples examined had at least 5% CD90 positive cells/sample.<sup>30-33</sup> We observed 16 (11%) of 142 AML cell samples with  $\geq$ 5% CD90 positive cells/sample. In one study, CD90 expression was restricted to CD34<sup>+ve</sup> AML cells,<sup>31</sup> however, in other studies CD90 expression levels were similar in CD34<sup>+ve</sup> and CD34<sup>-ve</sup> AML samples.<sup>30,32</sup> We found a preferential expression of CD90 in immature AML, although this difference in CD90 expression between CD34<sup>+ve</sup> and CD34<sup>-ve</sup> AML was less marked than the observed difference in CD133 expression. In previous studies, 0-26% of ALL cell samples examined revealed ≥5% CD90 positive cells/sample.<sup>30,33</sup> We observed 13 (11%) of 119 ALL cell samples with  $\geq$ 5% CD90 positive cells/sample. In one study, 32 (97%) of 33 CD34+ve ALL were dimly positive for CD90, whereas all 10 CD34-ve ALL cases were negative for CD90.34 However, in accordance with Campos et al., we could not detect any correlation between CD34 and CD90 expression in ALL.<sup>32</sup> Thus, CD90 expression in *de novo* acute leukemia is generally low and not restricted to CD34<sup>+ve</sup> leukemic cells. Higher CD90 expression levels, as detected by Moab 5E10, may be observed by using the PE- instead of FITCconjugated antibody.<sup>19</sup> However, a study investigating CD90 expression levels in 52 AML cases using the PEconjugated Moab 5E10 found only one patient with more than 5% CD90 positive leukemic cells.<sup>30</sup>

CD133 expression differed markedly between AML and ALL cells with 11q23-anomalies and MLL gene translocations. All 8 pro-B-ALL cases with MLL gene translocations were positive for CD133, whereas all 5 AML FAB M4/5 cases with t(9;11) were negative for CD133. The MLL gene on chromosome 11, band g23, is usually disrupted in 11g23 translocations and is thought to play an important role in leukemogenesis as it has been implicated in fusions with more than 25 other genes in both ALL and AML.<sup>35-37</sup> Our findings indicate that in AML cells with MLL gene translocations, CD133 expression is downregulated during monocytic differentiation, whereas CD133 expression in pro-B-ALL cells with MLL gene translocations might reflect the rather immature stem cell-related phenotype of these ALL cell samples with 11q23-anomalies.<sup>36</sup> However, Moab AC133 is not useful for the specific detection of leukemic cells with MLL gene translocations in ALL, as CD133 was also expressed in common-/pre-B-ALL cases without 11q23-anomalies.

A previous study observed a significantly higher CD90 expression in B-lineage ALL cases with cytogenetic anomalies compared with in those with a normal karyo-type.<sup>38</sup> In contrast, we could not detect any correlation between cyto-/molecular genetic aberrations and CD90 expression in our series, either in ALL or in AML.

Biphenotypic acute leukemias (BAL) are a relatively newly defined leukemia entity characterized by the coexpression of differentiation markers of different lineages.<sup>5,39</sup> So far, only a few features of the cell biology of this possibly heterogenous leukemia subgroup have been described: BAL more often express CD34 as well as the multidrug-resistance (MDR)-related P-glycoprotein than do AML and ALL.<sup>40</sup> BAL often reveal a t(9;22) in cytogenetic studies<sup>41</sup> and seem to be associated with a poor prognosis.<sup>42</sup> It is unclear whether these leukemias arise from an immature multipotent stem cell with the potential to differentiate into several lineages.<sup>41,42</sup> Our results show that the expression analysis of CD133 and CD90 in BAL cell samples does not further distinguish this entity from other leukemia subtypes. It is assumed that CD34<sup>+ve</sup> blast crisis (BC) in CML arises from an immature malignant cell clone with multipotent stem cell characteristics.<sup>43</sup> In our series, cell samples of CD34<sup>+ve</sup> CML with myeloid BC expressed CD133 less often than did cell samples of CD34<sup>+ve</sup> *de novo* AML. Therefore, the expression pattern of CD133 may further define the phenotype of the malignant transformed CML origin cells as CD133<sup>low</sup> compared with the higher CD133 expression in the malignant transformed *de novo* AML cells. However, CD133 expression in CML can not distinguish leukemic cells with or without the t(9;22), as this cytogenetic anomaly was detected in both CD133 positive and negative CML cells.<sup>44</sup>

We conclude that CD133 and CD90 expression in acute leukemia is neither lineage-specific nor restricted to CD34<sup>+ve</sup> leukemic cells. Therefore, these markers are not useful for lineage determination in acute leukemia immunophenotyping.<sup>45</sup> However, Moab AC133 might be an informative antibody for the detection and further characterization of immature AML cells as well as pro-B-ALL cells with MLL gene translocations by flow cytometry.

#### **Contributions and Acknowledgments**

*CW, LK and WDL were responsible for the design of this study and for the interpretation as well as publication of the experimental data. RR, GS and CS did the immuno-phenotypic characterization of the examined AML and ALL cases and participated in the statistical analysis of the experimental findings. CS and SS performed the cyto-genetic and molecular studies in AML and JH in ALL. TH and UC were responsible for the classification of the examined AML cases according to morphologic FAB sub-types. All above mentioned contributors were involved in the revision of the manuscript and approved the final version to be submitted.* 

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#### Disclosures

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#### Manuscript processing

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#### Potential implications for clinical practice

AC133-antigen and CD90 expression analysis is not helpful in distinguishing acute myeloid and lymphoblastic leukemias by flow cytometry. AC133-antigen expression analysis might be useful in further characterization of immature AML cells and pro-B-ALL with 11q23-gene rearrangements.

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