High expression of transcription factor 4 (TCF4) is an independent adverse prognostic factor in acute myeloid leukemia that could guide treatment decisions

Mutations in transcription factor 4 (TCF4) have recently been described in myeloid dysplastic syndromes (MDS) and acute myeloid leukemia (AML). We analyzed the impact of TCF4 mRNA expression on clinical outcome in AML patients (n=525). Patients with high TCF4 expression (TCF4-high, defined as the 25% highest TCF4 expressors) had a significantly worse overall survival (OS) and event-free survival (EFS) than patients with lower TCF4 expression (TCF4-low) (5-year OS 18% vs. 44%, P<0.0001; 5-year EFS 15% vs. 34%, P<0.0001, respectively). This was confirmed in an independent cohort (n=436). Multivariate analysis showed that TCF4-high is an independent prognostic factor for OS and EFS in the whole cohort and in patients carrying a normal karyotype.

Importantly, TCF4-high patients benefited most from an allogeneic hematopoietic cell transplantation (HCT), compared to an autologous HCT or additional chemotherapy (CT) (5-year OS 39%, 8%, P<0.0001; 5-year EFS 31%, 0%, 10%, P<0.001, respectively), while TCF4-low patients seemed to benefit most from an autologous HCT, compared to allogeneic HCT or additional CT (5-year OS: 61%, 45%, 39% P=0.002; 5-year EFS: 42%, 32%, 34%, P=0.102, respectively).

We demonstrate that high expression of TCF4 is an independent adverse prognostic factor in AML that could guide treatment decisions.

TCF4 plays a role in a variety of developmental processes, including hematopoiesis. TCF4 is part of the basic helix-loop-helix (bHLH) class 1 family, also called E-proteins. These E-proteins recognize an E-box DNA binding site (CANNTG), which are present in a variety of tissue-specific enhancers.1,2 Recently, Papaemmanuil and colleagues reported mutations in TCF4 in MDS patients.1 A total of 9 mutations were found in 7 of the 738 (0.9%) sequenced MDS patients. The TCF4 mutations were found in various MDS subclasses. Mutations in TCF4 have also been reported for AML cases (0.5%)3 and were associated with a poor prognosis,4 suggesting a potential role of TCF4 in the pathogenesis of these myeloid malignancies. Here we report that TCF4 mRNA expression levels are an independent prognostic factor in AML patients.

TCF4 expression values measured using Affymetrix HGU133 plus 2.0 arrays were derived from a database which contains a cohort of 525 AML patients treated according to HOVON protocols (AML-04, -04A, -29, -32, -42, -43; available at http://www.hovon.nl).5 Both bone marrow aspirates or peripheral-blood samples (at the time of diagnosis) have been analyzed. Blasts and mononuclear cells were purified by Ficoll–Hypaque (Nygaard) centrifugation and cryopreserved. The AML samples contained 80-100% blast cells after thawing, regardless of the blast count at diagnosis. To determine the TCF4 expression, an average of 5 probe sets (which bind at different locations of the gene) were used. The microarray expression data were confirmed by qPCR (Online Supplementary Figure S1). In addition, the TCF4 expression levels of healthy CD34+ control cells (hCD34+; n=11) and mononuclear cell fractions derived from normal bone marrow (NBM; n=5) were available. A second, independent cohort of 436 AML patients was used for validation.7 Patients were divided into genetic risk groups according to the European LeukemiaNet (ELN) guidelines.8

In the studied cohort of 525 AML patients, TCF4 is differentially expressed in AML blasts compared to NBM and hCD34+ (Figure 1A). To study the impact of TCF4 expression levels on survival, the cohort was divided on the basis of differences in expression levels; expression below or above the median, tertiles, quintiles, sextiles and septiles. In all these cohorts, univariate analysis showed that high expression of TCF4 was associated with poor outcome. The highest expressors of TCF4 showed a more than 2-fold shorter 5-year OS than the lowest expressors (Online Supplementary Figure S2). Since we found that TCF4 expression is not normally distributed and because approximately 25% of the patients showed a much higher expression (Figure 1B), a distribution of the cohort based on the highest 25% (TCF4-high) and the lowest 75% TCF4 expression (TCF4-low) was used for further analysis. Characteristics of the patients in the TCF4-high and TCF4-low groups are described in Online Supplementary Table S1. TCF4-expressing patients more often had high-risk cytogenetic abnormalities (P<0.001), FLT3-ITD (P<0.001) and their morphology more frequently corresponded with M0 or M1 FAB-subgroups (P<0.001). TCF4+ patients were more likely to have biallelic CEBPA mutations (P=0.011). No associations between TCF4 expression and age, sex, white blood cell (WBC) count, or other cytogenetic or molecular abnormalities could be identified.

Survival analysis according to the Kaplan-Meier method showed that TCF4-high patients had a worse survival than patients classified as TCF4-high (5-year OS 18% vs. 44%, P<0.0001; 5-year EFS 15% vs. 34%, P<0.0001, respectively) (Figure 1C and D). We confirmed the impact of TCF4 expression using the OS and EFS variables of interest, the whole cohort and patients carrying normal karyotype (Online Supplementary Figure S3). In the multivariate Cox regression survival analysis, TCF4-expression was an independent adverse prognostic factor for OS and EFS (Online Supplementary Table S2). Since we found that TCF4 expression is not normally distributed and because approximately 25% of the patients showed a much higher expression (Figure 1B), a distribution of the cohort based on the highest 25% (TCF4-high) and the lowest 75% TCF4 expression (TCF4-low) was used for further analysis. Characteristics of the patients in the TCF4-high and TCF4-low groups are described in Online Supplementary Table S1. TCF4-expressing patients more often had high-risk cytogenetic abnormalities (P<0.001), FLT3-ITD (P<0.001) and their morphology more frequently corresponded with M0 or M1 FAB-subgroups (P<0.001). TCF4+ patients were more likely to have biallelic CEBPA mutations (P=0.011). No associations between TCF4 expression and age, sex, white blood cell (WBC) count, or other cytogenetic or molecular abnormalities could be identified.

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Table 1. Multivariate Cox’s regression survival analysis. Factors predicting overall survival and event-free survival in acute myeloid leukemia patients of the first cohort with available complete data of all cytogenetic and molecular parameters (n=506).

<table>
<thead>
<tr>
<th>Variable</th>
<th>Overall survival (n=506)</th>
<th>Event-free survival (n=506)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>CH2 (Wald)</td>
<td>DF</td>
</tr>
<tr>
<td>Favorable ELN risk group†</td>
<td>40.11</td>
<td>3</td>
</tr>
<tr>
<td>Intermediate-I ELN risk group</td>
<td>16.55</td>
<td>1</td>
</tr>
<tr>
<td>Intermediate-II ELN risk group</td>
<td>9.36</td>
<td>1</td>
</tr>
<tr>
<td>Adverse ELN risk group</td>
<td>39.36</td>
<td>1</td>
</tr>
<tr>
<td>Age (&gt;60 years)</td>
<td>18.06</td>
<td>1</td>
</tr>
<tr>
<td>WBC (&gt;100 *10^9)</td>
<td>11.02</td>
<td>1</td>
</tr>
</tbody>
</table>

OS: overall survival; EFS: event-free survival; ELN: European LeukemiaNet; DF: degrees of freedom; HR: Hazard Ratio; CI: Confidence Interval; WBC: white blood cell count.

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expression levels on survival in the second cohort of 436 AML patients (OS: \( P = 0.001 \); EFS: \( P < 0.0001 \)) (Online Supplementary Figure S3). In the multivariate Cox regression analysis, patients classified as \( TCF4^{\text{low}} \) had a significantly higher risk of death (HR 1.7, CI: 1.3–2.1; \( P < 0.0001 \)), relapse or not obtaining a CR than \( TCF4^{\text{high}} \) patients (HR 1.6, CI: 1.3–2.0; \( P < 0.0001 \)) (Table 1A). In addition, multivariate Cox regression analysis revealed \( TCF4 \) expression, as a continuous variable per 100 arbitrary units (AU), was a significant predictor of OS and EFS (HR 1.04, CI: 1.01-1.07, \( P = 0.024 \); HR 1.05, CI: 1.02-1.08, \( P = 0.002 \), respectively) (Online Supplementary Table S2A). When selecting for AML patients with a normal karyotype, \( TCF4^{\text{high}} \) patients again showed a worse OS and EFS than \( TCF4^{\text{low}} \) patients (5-year OS 21% vs. 41%, \( P = 0.0001 \); 5-year EFS 18% vs. 33%, \( P < 0.0001 \), respectively) (Online Supplementary Figure S4). In the multivariate Cox regression analysis of normal karyotype AML patients, \( TCF4 \) expression is also an independent predictor of survival (OS: HR 1.7, CI: 1.2-2.5, \( P = 0.003 \); EFS: HR 1.7, CI: 1.2-2.4, \( P = 0.005 \)) (Online Supplementary Table S2B). Also as a continuous variable, \( TCF4 \) expression remained an independent prognostic factor in this cohort (OS: HR 1.07 (per 100 AU), CI: 1.02-1.13, \( P = 0.003 \); EFS: HR 1.08 (per 100 AU), CI: 1.03-1.13, \( P = 0.003 \)) (Online Supplementary Table S2C).

Interestingly, survival analysis according to the Kaplan-Meier method showed that \( TCF4^{\text{low}} \) and \( TCF4^{\text{high}} \) patients of the first cohort demonstrated a different survival benefit depending on the consolidation treatment they received, i.e., an additional cycle of chemotherapy (CT), autologous or allogeneic hematopoietic cell transplantation (autoHCT, alloHCT, respectively) (OS: Figure 1E and F; EFS: Online Supplementary Figure S5). \( TCF4^{\text{low}} \) patients who received alloHCT showed a superior survival compared to \( TCF4^{\text{high}} \) patients who received autoHCT or who received additional CT (5-year OS 39%, 8%, 10%, \( P = 0.0001 \); 5-year EFS 31%, 10%, 12%, respectively) (Online Supplementary Figure S5).
In addition, the additional information in the response to treatment. Before the prognostic factor in OS and EFS; nevertheless, high p15 also remains an independent prognostic factor (shown and aberrant expression of Tcf4 appeared increased in rat-E1A-immortalized RK3E cells following p15 and p16, suggesting that these bHLH proteins act as negative regulators of cell growth. In contrast, Tcf4 expression increased in rat-E1A-immortalized RK3E cells following β-catenin induced neoplastic transformation and aberrant expression of Tcf4 promoted neoplastic transformation of RK3E cells. These different observations might be explained by differences in cellular context, or by the different transcript variants of TCF4, which could affect the function of the protein. Possibly, TCF4 can either stimulate or inhibit cell growth, depending on its environment, which might indicate that an aberrant expression is not only a prognostic marker, but also a pathological feature. This would be in line with the report of mutations in TCF4 in MDS and AML.

Tcf4 has also been reported to be highly expressed in hematopoietic stem cells (HSC) and to show a decreased expression in committed progenitors. Since the frequency of TCF4 mutations is relatively low (0.5% in AML), obviously not all patients with high expression of TCF4 can have mutated TCF4. Interestingly, in MLL-AF9-mediated transformation of progenitor cells, TCF4 has been shown to be up-regulated. In the first cohort, patients with high TCF4 expression are significantly more classified in the M0 or M1 FAB-subgroups than TCF4-patients, suggesting that the leukemic cells of the TCF4-patients derive from more immature cells. In addition, TCF4 expression of patients in the TCF4 group is comparable to the level of TCF4 expression of hCD34+ cells. Furthermore, when looking at the CD34 mRNA expression in the first cohort, 73.3% of the TCF4 patients show a high CD34 expression (above the median), compared to 42.1% of the TCF4 patients. When including CD34 expression in the multivariate Cox regression analysis, CD34 expression is an independent prognostic factor in OS and EFS; nevertheless TCF4 expression also remains an independent prognostic factor (data not shown).

Our observations report on the prognostic relevance of the level of TCF4 expression in AML and demonstrate that high TCF4 expression is associated with a worse survival. In addition, the TCF4 expression levels seem to provide additional information in the response to treatment. Before considering TCF4 expression levels in clinical decision-making, additional validation studies, also to define optimal cut-off levels, are needed. Further mechanistic studies are warranted on the role of TCF4 in myeloid diseases.

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