**Molecular Pathways**

**TLX1-Induced T-cell Acute Lymphoblastic Leukemia**

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**Abstract**

The TLX1 transcription factor oncogene is frequently activated by chromosomal translocations in T-cell acute lymphoblastic leukemia (T-ALL) and defines a distinct molecular group of tumors characterized by differentiation arrest at the early cortical stage of thymocyte differentiation and excellent response to therapy. Recent developments from the analysis of genomic data on TLX1-specific transcriptional targets and analysis of the molecular mechanisms of TLX1 transformation in human- and mouse-induced leukemias have shown novel insight into the activity of this transcription factor oncogene. Aberrant expression of TLX1 in T-cell progenitors disrupts normal T-cell development and triggers the development of aneuploidy during T-cell transformation. Importantly, the disruption of the mitotic checkpoint in TLX1-induced tumors may be linked not only to the acquisition of secondary genetic alterations in T-ALL but also to increased sensitivity of these tumors to chemotherapy with drugs targeting the formation of the mitotic spindle. *Clin Cancer Res;* 17(20); 6381–6. ©2011 AACR.

**Background**

T-cell acute lymphoblastic leukemia (T-ALL) is an aggressive hematologic cancer caused by malignant transformation of developing T cells. The TLX1 transcription factor oncogene is the target of translocation t(10;14)(q24;q11) in 5% to 10% of pediatric and up to 30% of adult T-ALL cases (1–4). This translocation juxtaposes an intact oncogene to the very strong enhancer elements of the T-cell receptor loci, resulting in aberrantly high TLX1 expression levels.

TLX1 (also known as HOX11) is the founding member of a family of orphan HOX genes, encoded in loci located outside the A, B, C, and D paralog groups. In addition to TLX1, the TLX family of transcription regulators includes TLX2 and TLX3 (5) and is characterized by the presence of a threonine in the third helix of the homeodomain, which confers specific DNA-binding properties. Like other HOX genes, TLX factors play important roles during development. Under normal conditions, TLX1 expression is only detected during embryonic life in the mouse and is restricted to the branchial arches, the hindbrain, and the splenic primordium (6, 7). Moreover, TLX1 plays a critical role for spleen development, and Tlx1 knockout mice show complete agenesis of the spleen in the absence of developmental alterations (8, 9).

Among T-ALL patients, TLX1-expressing tumors constitute a distinct molecular group, characterized by a block in T-cell differentiation at the early cortical stage of T-cell development (2) and by a favorable prognosis (1, 2, 10). Moreover, TLX1-induced leukemias represent a distinct oncogenic group with specific genetic alterations rarely found in non–TLX1-induced T-ALLs, including the rearrangement of the NUP214-ABL1 oncogene (11), deletion of the PTPN2 phosphatase (12), and mutations in the WT1 (13) and PHF6 (14) tumor suppressor genes. However, until recently, very little was known about the specific mechanisms that mediate T-cell transformation downstream of TLX1. Moreover, the generation of a mouse model of TLX1-induced T-ALL eluded the efforts of several groups over the past decade (15, 16). In this context, the generation of an LCK-TLX1 transgenic mouse model that recapitulates the histologic, transcriptional, and genetic features of TLX1-induced T-ALL has provided a much-needed tool for the analysis of the molecular and cellular mechanisms of TLX1-induced transformation (16). In these studies, LCK-TLX1 transgenic mice showed accelerated mortality owing to the development of clonal T-ALL tumors, occurring with an average latency of 6 months and a penetrance of more than 90% (16). Notably, almost identical phenotypes were observed in 3 different founder lines, ruling out a role for insertion mutations introduced during the generation of the transgene in the oncogenic process. TLX1-induced mouse leukemias showed clonal rearrangements of the TCRB locus (16) and were transplantable, although with a low leukemia-initiating cell content (A.A. Ferrando and K. De Keersmaeker, unpublished results).

Mouse models of cancer have been instrumental in the analysis of genetic interactions between oncogenes and tumor suppressors and are increasingly being recognized as invaluable tools for the analysis of the basic mechanisms...
mediating oncogenic transformation, particularly with regard to tumor initiation and disease progression. Notably, analysis of T-cell differentiation in 3- to 6-week-old TLX1 transgenic mice showed that tumor development in these animals is preceded by a severe defect in thymocyte development, characterized by a reduced thymus size, weight, and cellularity. This T-cell development defect is mediated by increased apoptosis and a differentiation block at the earliest stages of thymocyte differentiation. Notably, gene expression profiling with oligonucleotide microarrays of TLX1-induced mouse T-ALL compared with other genetic mouse models of T-ALL showed that TLX1 tumors have a distinct gene expression signature dominated by the downregulation of numerous transcripts. Cross-species comparison of this TLX1-associated mouse gene expression signature in human T-ALLs showed a marked overlap of this transcriptional program with that of human tumors that express TLX1 or the closely related TLX3 transcription factor oncogene. These results suggest that TLX1 may be primarily working as a transcriptional repressor in T-ALL and that TLX1 and TLX3 may share a common gene expression program driving T-cell transformation. Moreover, the close relationship between the transcriptional programs of mouse and human TLX-induced T-ALLs underscores the relevance of TLX1-transgenic mice for the study of the basic mechanisms of TLX-induced transformation.

The 6-month latency before the development of leukemia in LCK-TLX1 transgenic mice (15, 16) and the observation that these tumors show clonal expression of the T-cell receptor β suggest that TLX1 overexpression may not be sufficient for T-cell transformation and that full leukemia development may depend on the acquisition of secondary cooperating mutations. The NOTCH1 signaling pathway plays a prominent role in T-ALL pathogenesis, and more than 50% of the patients harboring activating NOTCH1 mutations (17). Consistently, about 12% of TLX1-induced tumors in mice showed activating mutations in the Notch1 gene (16). Extensive analysis of secondary chromosomal amplifications and deletions by array comparative genomic hybridization (aCGH) showed focal deletions involving known T-ALL tumor suppressor genes such as Pten, Trp53, and Cdkn2a/Cdkn2b, in TLX1-induced mouse tumors. In addition, the presence of a recurrent heterozygous deletion in mouse chromosome 12, encompassing the Bcl11b gene in 3 mouse TLX1 tumors, strongly suggested that Bcl11b could play a tumor suppressor role in T-ALL. The Bcl11b gene encodes a Kruppel-like zinc finger transcription factor with a critical role in the differentiation and survival of T-cell progenitors in the thymus (18, 19). BCL11B associates with the SIRT1 deacetylase (20) and has been implicated in transcriptional repression via its association with the NuRD nucleosome-remodeling and histone-deacetylase complex (21). Consistently, mutation analysis of Bcl11b in mouse TLX1-induced tumors showed the presence of inactivating, heterozygous mutations in an additional 27% of the mouse tumors. In total, 47% of mouse TLX1 tumors analyzed showed heterozygous deletions or mutations targeting Bcl11b. Similarly, aCGH analysis of a panel of 69 human T-ALL patients identified 2 cases carrying focal heterozygous deletions targeting the BCL11B gene. In addition, 13% of T-ALL patient samples showed heterozygous BCL11B mutations. Overall, these results identified the BCL11B gene as a novel tumor suppressor gene recurrently deleted and mutated in T-ALL.

Analysis of Bcl11b knockout mice shows that this transcription factor is strictly required for early T-cell development (18). Thus, Bcl11b homozygous knockout mice show a block in thymocyte development without defects in other blood lineages (18). Bcl11b seems to be critical for maintenance of T-cell identity, so that loss of Bcl11b results in loss of T-cell lineage commitment and expression of transcriptional programs characteristic of non–T-cell hematopoietic lineages. Moreover, Bcl11b haploinsufficiency results in a marked decrease in thymocyte numbers and overt predisposition to lymphoma development (22). Notably, and of particular relevance for TLX1-induced transformation, TLX1 binds the promoter of the BCL11B gene and downregulates BCL11B expression (16). The model that emerges from these results is that aberrant expression of TLX1 partially down-regulates BCL11B during T-cell transformation and that this negative transcriptional regulatory axis is fixed and reinforced by secondary genetic alterations in the BCL11B locus, acquired during tumor progression (Fig. 1). Strikingly, PHF6 and WTI, 2 additional tumor suppressors that are frequently mutated in TLX1-induced T-ALL (13, 14), are also TLX1 direct target genes (16), suggesting that this model may also apply to additional TLX1-target tumor suppressor genes (Fig. 1).

However, besides identifying focal areas of amplification and deletion, perhaps the most prominent cytogenetic alteration identified in TLX1-induced leukemias in mice is the presence of chromosomal gains and losses. Indeed, 78% of mouse TLX1 tumors were aneuploid and showed a particularly high prevalence of trisomy 15. This intriguing observation suggested a close relationship between TLX1 overexpression and defects in the checkpoint machinery responsible for proper chromosome segregation during mitosis.

Early work on TLX1 showed that this transcription factor oncoprotein can interact with protein serine–threonine phosphatase 2A catalytic subunit (PP2AC) and protein phosphatase 1 (PP1C). Notably, inhibition of PP2A can regulate the cell cycle, and TLX1 expression promoted progression to the M-phase (23). Moreover, TLX1-expressing B cells from IgHmu-HOX11Tg mice exhibited increased incidences of chromosome missegregation upon treatment with aneugenic agents and showed aberrant bypass of spindle checkpoint arrest (24). In agreement with these results, tumor cell lines derived from TLX1-positive mouse T-ALLs showed a defective mitotic checkpoint (16). This defect in the control of progression through mitosis could be attributed to a direct effect of
TLX1 on the mitotic machinery or, alternatively, result from secondary genetic alterations present in TLX1-induced tumors. Importantly, analysis of polyclonal thymocytes from preleukemic TLX1-transgenic mice showed the presence of impaired mitotic checkpoints, linking the expression of TLX1 with the induction of aneuploidy at the earliest stages of T-cell transformation. Finally, integrative analysis of gene expression signatures with chromatin immunoprecipitation (ChIP)-chip data on direct TLX1 targets showed a marked enrichment of mitotic genes directly controlled by TLX1 among the genes downregulated in preleukemic TLX1-expressing thymocytes compared with cells from normal littermate controls (Fig. 1; ref. 16). One of these genes was CHEK1, a crucial player in proper function of the cell-cycle machinery and the mitotic checkpoint (16).

These results reveal a previously unrecognized role for an oncogenic transcription factor in mitotic checkpoint deregulation in T-ALL pathogenesis. It remains to be determined whether other oncogenes and tumor suppressors in T-ALL are cooperating with TLX1 in deregulation of cellular checkpoints. MYC, an important downstream player of NOTCH1 in T-ALL (25), has been shown to directly regulate crucial factors in the mitotic checkpoint machinery (26). In addition, the PTEN tumor suppressor gene is inactivated in 17% of T-ALL cases (27), and PTEN loss induces defects in multiple cell-cycle checkpoints, including the mitotic spindle checkpoint (28, 29). Still, it remains to be determined whether oncogenic transcription factors in other cancer types are stressing the cellular mitotic checkpoint machinery by mechanisms similar to TLX1 in the context of T-ALL.

Clinical–Translational Advances

T-ALL patients often have a large tumor burden with mediastinal masses, very high circulating blast cell counts, and infiltration of the central nervous system at the time of diagnosis (30). In the early days of combination chemotherapy for ALL, T-ALL was associated with very poor prognosis, with remission durations of only 10 months or less, and cure rates lower than 10% (31). However, after the introduction of intensified chemotherapy schemes, a remarkable improvement was observed in the prognosis of children and adolescents with this disease, so that 5-year relapse-free survival rates are now more than 75% (32). Similarly, wider use of intensified therapy has resulted in advances in the treatment of adults with T-ALL, with cure rates now exceeding 50% (33). Our current understanding of the molecular basis of T-cell malignancies has...
emerged largely from analysis of recurrent chromosomal translocations, which typically juxtapose strong promoter elements to developmentally important transcription factor genes (34, 35). These translocations induce aberrant expression of oncogenic transcriptional regulators in developing T cells. This group of transcription factors includes the following: (i) basic helix-loop-helix (bHLH) proteins encoded by TAL1, TAL2, LYL1, and BHLHB1 (36–40, 41); (ii) LIM-only domain (LMO) proteins encoded by LMO1 and LMO2 (42–45); (iii) products of the orphan homeobox genes TLX1 (46–49) and TLX3 (2, 50); and (iv) mutated or truncated forms of NOTCH1, encoding constitutively activated forms of the NOTCH1 receptor (17, 51). In addition, rare cases show rearrangements and mutations generating oncogenic tyrosine kinases, such as NUP214-ABL1 and JAK1 (11, 52). From a therapeutic point of view, administration of small molecule kinase inhibitors may offer an opportunity for molecularly tailored therapies for cases expressing oncogenic kinases.

In addition, γ-secretase inhibitors that block NOTCH1 signaling looked very promising to treat T-ALL. However, the first clinical trials testing γ-secretase inhibitor monotherapy showed serious toxicity and inefficacy of such treatment for T-ALL, and evidence has been collected that combining γ-secretase inhibitors with glucocorticoids might increase the therapeutic potential of γ-secretase inhibitors in T-ALL (53).

Over the past decade, several laboratories have characterized the mechanisms that mediate the transforming effects of activated NOTCH receptors and bHLH factors (54–57); however, much less is known about the genetic programs operating downstream of TLX1. This TLX family member yields leukemias with a good prognostic outcome (1, 2, 10). After the discovery that TLX1 induces malfunction of the cellular mitotic checkpoint (16), it is tempting to speculate that this defective mitotic checkpoint in TLX1 tumors could indeed be related to increased sensitivity to chemotherapy drugs, inducing DNA damage and/or targeting the mitotic spindle.

The absence of a role for TLX1 during adult life and its restricted expression in thymocytes carrying t(10;14)(q24;q11) suggest that TLX1 might be an attractive target for molecularly tailored therapy. Transcription factors function in multiprotein complexes dependent on extended protein–protein interactions and have been traditionally considered poor targets for drug development. However, detailed structural data, improvements in small molecule design, and peptide engineering have facilitated the development of specific inhibitors of the BCL6 and NOTCH1 transcription factor oncoproteins (58–61). Identification of the protein complex mediating TLX1 function in T-ALL and resolving the crystal structure of this homeobox gene in complex with DNA and essential coregulatory proteins may eventually facilitate the generation of specific TLX1 inhibitors for the treatment of T-ALL. Finally, the implementation of short hairpin RNA screens directed to identify genes and pathways whose inactivation results in specific ablation of TLX1-expressing cells may uncover new targets for the treatment of TLX1-induced leukemias. In this context, mouse models of TLX1-induced T-ALL will be instrumental for the validation and preclinical testing of anti-TLX1 therapies in their translation to the clinic.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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