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Research Article

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Loss of nuclear pro-IL-16 facilitates cell cycle progression in human cutaneous T cell lymphoma

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Cutaneous T cell lymphomas (CTCLs) represent a heterogeneous group of non-Hodgkin lymphomas that affect the skin. The pathogenesis of these conditions is poorly understood. For example, the signaling mechanisms contributing to the dysregulated growth of the neoplastic T cells are not well defined. Here, we demonstrate that loss of nuclear localization of pro-IL-16 facilitates CTCL cell proliferation by causing a decrease in expression of the cyclin dependent-kinase inhibitor p27Kip1. The decrease in p27Kip1 expression was directly attributable to an increase in expression of S-phase kinase-associated protein 2 (Skp2). Regulation of Skp2 is in part attributed to the nuclear presence of the scaffold protein pro-IL-16. T cells isolated from 11 patients with advanced CTCL, but not those from healthy controls or patients with T cell acute lymphocytic leukemia (T-ALL), demonstrated reduction in nuclear pro-IL-16 levels. Sequence analysis identified the presence of mutations in the 5' end of the PDZ1 region of pro-IL-16, a domain required for association of pro-IL-16 with the nuclear chaperone HSC70 (also known as HSPA8). HSC70 knockdown led to loss of nuclear translocation by pro-IL-16 and subsequent increases in Skp2 levels and decreases in p27Kip1 levels, which ultimately enhanced T cell proliferation. Thus, our data indicate that advanced CTCL cell growth is facilitated, at least in part, by mutations in the scaffold protein pro-IL-16, which directly regulates Skp2 synthesis.

Introduction

Primary cutaneous T cell lymphomas (CTCLs) represent a heterogeneous group of extranodal non-Hodgkin lymphomas whose pathogenesis is poorly understood. The most frequent forms of CTCL are mycosis fungoides and Sezary syndrome. In vivo expansion of CTCL cells is thought to be attributable to an increased proliferative response in combination with greater resistance to apoptotic stimulation (1–4). In CTCL T cells, apoptosis resistance appears to be related to the lack of T receptor-induced Fas (CD95) expression as well as loss of TRAIL-2 receptor expression (5–7); however, specific signaling pathway mechanisms that result in hyperproliferation of the malignant cells are only partially understood. Several T cell growth factors have been investigated in the setting of CTCL, including IL-2, IL-7, IL-15, IL-16, and IL-18 (8–14), although not all have demonstrated growth potential in CTCL cell lines or primary T cells from patients with CTCL. The mechanism by which these cytokines contribute to CTCL proliferative responses continues to be an area of active research. Proliferative responses are also likely influenced by matrix protein contact during the earlier stages of the disease when the neoplastic cells are primarily restricted to the skin, suggesting a dependence on the specific cutaneous microenvironment (15). As the disease progresses, the cells become independent of this microenvironment; this is most likely achieved through modulation of cell adhesion molecules and the acquisition of self-sustaining growth factors, particularly those with cell cycle regulatory functions.

Along those lines, we have recently identified an intracellular protein that is involved in regulating T lymphocyte proliferation. The protein, pro-IL-16, is derived from the precursor protein (IL-16), comprised of 631 amino acids, and is present at very high levels in approximately 90%–97% of all T cells (16). After cell activation via the T cell receptor, precursor IL-16 is cleaved by caspase-3, which produces mature IL-16 (derived from the C-terminal 121 AA) and pro-IL-16 (17–20). Mature IL-16 is well characterized as a CD4 ligand that induces chemotaxis and CD25 expression in CD4⁺ T cells (21–23). While IL-16 can function as a competence growth factor for normal primary T cells, it has been shown to function as a complete growth factor for T cell lines (24).

Conversely, the fate and biologic activity of pro-IL-16 has only recently been investigated. Zhang and colleagues have identified that in primary T cells nuclear presence of pro-IL-16 results in a resting state, while loss of nuclear expression is associated with cell cycle progression (18, 20, 25). This is accomplished by virtue of a classical bipartite nuclear localization sequence as well as differential phosphorylation of a CKII and cdc2 kinase substrate site; all 3 components comprising a CeN motif. In H9 cells, a cell line derived from a patient with Sezary syndrome, pro-IL-16 was detected only in the cytoplasm, and the lack of nuclear expression was attributed to sequence mutations in the nuclear localization sequence (18, 20, 25). Functionally, there are a number of potential regulatory domains within pro-IL-16. Pro-IL-16 has been shown to function as a scaffold protein that directly associates with GABPβ, histone deacetylase 3 (HDAC-3), and heat shock cognate protein 70 (HSC70) and binds directly to

Conflict of interest: The authors have declared that no conflict of interest exists.

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Table 1
Clinical characteristics, laboratory data, and treatment modalities of patients with CTCL

Case no.	Gender	Age	Stage	Yr/Dx	CD4/CD8	CD4 Ab	%CD4+/CD7-	Large cell	LDH	Therapeutics interventions
1	F	71	III	0.2	8.12 ± 0.8	2,243 ± 403	28.4 ± 26.2	18%	549	ECP, topical corticosteroid+ protopic
2	M	76	IIIB	3.3	1.4 ± 0.6	66.7 ± 36.2	7.6 ± 2.1	60%	826	ECP, prednisone, IFN
3	F	95	IV	2	76.2 ± 32.18	673 ± 189.3	47	92%	942	ECP, IFN, Targretin
4	F	81	III	4	29.6 ± 32.5	1,451 ± 621.2	36.8 ± 28.8	91%	635	ECP, IFN
5†	F	78	IV	0.3	20.25 ± 3	2,312 ± 67	63	43%	901	ECP, IFN
6	M	61	IIIA	2.2	0.76 ± 0.075	380.5 ± 87.5	54 ± 55.2	51%	693	ECP, IFN
7	F	63	IIIA	0.2	14.86 ± 7.88	2,426 ± 122	NA	28%	750	MTX, ECP
8	F	90	IV	0.1	31.1 ± 11.9	6,577.3 ± 3,215	7.6 ± 3.5	30%	1211	ECP
9	F	78	IV	1	86 ± 2	3,874 ± 228.7	14 ± 1	84%	965	ECP, IFN, Ontak
10	M	63	IVA	9	11.5 ± 0.5	1,838 ± 110	83	24%	540	ECP
11	F	71	IVA	4	12.67 ± 1.1	1,558 ± 221	Pending	NA	672	ECP, Targretin, IFN, Zolinza
12	M	73	IV	1	5.67 ± 2	1,204	NA	195%	NA	Fluocinonide
13	F	63	IV	2	1.94 ± 4	NA	NA	NA	208	NA

†Patient 5 died after 6 months participation. ECP, extracorporeal photopheresis; IFN, IFN- α ; MTX, methotrexate. NA, not available; Yr/Dx, years from diagnosis to entry into the study. The patients were clinically staged preceding the 2007 ISCL/EORTC classification. LDH units are LDH-U/L. CD4 abs units are cell number per microliter.

the core promoter region of S-phase kinase-associated protein 2 (Skp2) through interaction of promoter-associated GABP β (26). Skp2 is a key component of the SCFSkp2 ubiquitin E3 ligase complex that regulates protein degradation of the cyclin-dependent protein kinase inhibitor p27Kip1 (27, 28). Therefore, nuclear presence of pro-IL-16 prevents Skp2 translation, allowing for elevated expression levels of p27Kip1, resulting in T cell quiescence. Loss of nuclear pro-IL-16 prevents HDAC-3 association with the Skp2 promoter, resulting in elevated Skp2 levels, lower p27Kip1 levels, and cell cycle progression.

The expression of IL-16 in patients with CTCL has been reported (13, 29). Both studies demonstrate an increased expression of *IL16* mRNA in skin biopsies obtained from patients with CTCL mycosis fungoides. Furthermore, the magnitude of increase for IL-16 correlated with disease severity. Protein expression was evaluated by immunohistochemistry analysis and also shown to correlate with disease progression, and, recently, it has been shown that serum IL-16 levels may represent a biomarker for disease severity (30). Assessment of IL-16 protein levels was determined using antibodies targeting the IL-16 C-terminal domain, and, therefore, the regulatory function of pro-IL 16, Skp2, and p27Kip1 in this group of patients was not explored.

In this study, we investigated the potential changes in Skp2, p27Kip1, and pro-IL-16 expression levels in advanced CTCL circulating T cells to determine their potential role in the dysregulated T cell growth observed in this group of patients.

Results

Demographics and clinical characteristics of the patients with CTCL participating in the study. The clinical characteristics of the patients are summarized in Table 1. Patient age at the time of the study ranged from 61 to 95 years, with a median age of 75.1 ± 8.8 years (stage III, mean 70.4 ± 8.47 years; stage IV, mean 79.2 ± 11.8 years). The female-to-male ratio was 8:3. All patients were of mixed European descent. The average time from diagnosis with CTCL to par-

ticipation in the study was 2.2 ± 1.9 years. Peripheral lymphocyte immunophenotyping was performed at least twice on each patient during the 19 months of sample acquisition. All patients had an elevated CD4/CD8 ratio and absolute CD4 levels, with the exception of case no. 2 and no. 6. These 2 subjects have previously demonstrated a classical immunophenotype, but over time a marked drop in the number of peripheral circulating lymphocytes, below normal levels, was observed with disease progression. The LDH value was elevated in all patients participating in the study. The following treatment modalities were used during the 2 years of blood sample acquisition: extracorporeal photopheresis (11 out of 11), IFN- α 2B (7 out of 11), prednisone (1 out of 11), methotrexate (1 out of 11), oral Targretin (2 out of 11), Ontak (1 out of 11), and vorinostat (1 out of 11).

The presence of p27Kip1 inhibition and Skp2 overexpression in CTCL T cells. While levels of the cyclin kinase-dependent inhibitor p27Kip1 have been reported to be altered in several hematological cancers (31, 32), this type of assessment has not been reported in CTCL. Therefore, we investigated whether cell cycle dysregulation in patients with advanced CTCL is associated with alterations in the levels of the CDK inhibitor p27Kip1. Eleven patients with advanced CTCL, 2 patients with T cell acute lymphocytic leukemia (T-ALL), and 10 healthy controls were included in the study. As shown in Figure 1, a marked reduction in the expression of p27Kip1 was observed for all examined patients with CTCL as compared with that in normal controls or cells from 2 patients with T-ALL. All 10 normal subjects demonstrated elevated levels of p27Kip1 similar to those of the 2 subjects shown in the figure. Loss of regulation of p27Kip1 expression would suggest a hyperproliferative state. In normal T lymphocytes, the primary mechanism for regulating p27Kip1 protein expression is independent of transcription but accomplished through an ubiquitin-mediated degradation, facilitated by Skp2 (33). To confirm this process in CTCL peripheral cells, we investigated whether decreased levels of p27Kip1 correlated with increased levels of Skp2. As anticipated, Skp2 protein

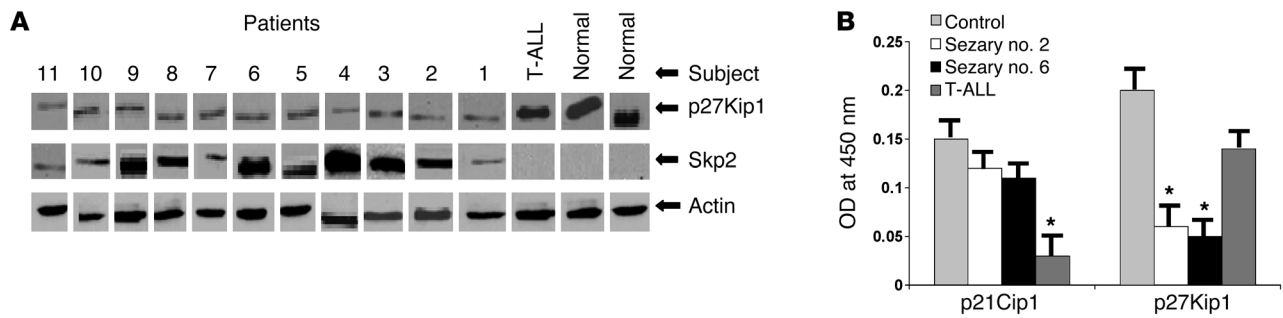


Figure 1 Detection of Skp2, p27Kip1, and p21Cip1 in primary CD4⁺ T cells from individuals with advanced CTCL and T-ALL and normal individuals. (A) Cell lysates from 7 × 10⁶ cells from each sample were run on SDS-PAGE prior to probing with antibodies to p27Kip1 or Skp2. β-Actin was used for protein normalization. Due to the timing for patient recruitment, the gels were run at separate times, and the lanes were compiled for the figure. (B) P21Cip1 levels from 2 patients with CTCL (no. 2 and no. 6) and from both patients with T-ALL were detected by ELISA and compared with levels from control individuals (n = 8). *P < 0.03, compared with control cells. The error bars represent standard deviation.

was detected at very low to undetectable levels in normal resting T cells (Figure 1). In T cells from advanced CTCL subjects, Skp2 levels were elevated. Using β-actin protein for normalization, p27Kip1 levels decreased on average by 5.6 fold as compared with those of normal controls, and Skp2 levels increased from undetectable in normal cells to detectable in all Sezary samples. As an additional control for these findings, T cells from 2 individuals with T-ALL were also investigated. Cell cycle regulation in primary T-ALL cells has been shown to be more dependent on cyclin-dependent kinase inhibitor p21Cip rather than on p27Kip1 levels (34, 35). As shown in Figure 1, there were no detectable alterations in expression levels of either p27Kip1 or Skp2, indicating a fundamental difference in the mechanism for dysregulated T cell growth in these 2 diseases. Results from only 1 patient with T-ALL are shown, but similar results were obtained for both patients. To determine whether loss of p27Kip1 was specific in advanced CTCL, levels of p21Cip1 were also assessed. Quantification of p21Cip1 levels in advanced CTCL cells indicated a slight decrease as compared with that in normal T cells; however, the loss was not as pronounced as that for p27Kip1 (Figure 1). As expected from previous studies (34, 35), the p21Cip1 levels in T cells obtained from the individuals with T-ALL were significantly lower than levels found in normal T cells. These data indicate that there is not a general loss of cyclin kinase-dependent inhibitors but suggest some specificity for p27Kip1.

Circulating T lymphocytes from patients with CTCL express decreased levels of pro-IL-16. Skp2 protein synthesis has recently been shown to be regulated transcriptionally through the interaction of its core promoter region with HDAC-3 in the context of the scaffold protein pro-IL-16 (26). The absence or presence of nuclear pro-IL-16 determines binding efficiency of HDAC-3 to the core promoter region. As such, intracellular pro-IL-16 levels should positively cor-

relate with p27Kip levels and negatively correlate with Skp2 levels. As previously published (16), assessment of intracellular pro-IL-16 expression in normal T lymphocytes demonstrated a homogeneous expression level for all cells, with 95%–98% of the cells positive for pro-IL-16, with a mean fluorescence index of 206.89 ± 50.1 (Figure 2). This has been consistent for all normal samples (n = 10) investigated thus far. When CD4⁺ T cells from the patients with advanced CTCL were investigated, there was a distribution in expression level, with a decrease in total pro-IL-16 levels ranging from more than 1% to more than 81%, with a range of expression patterns (Figure 2). Most patients demonstrated a homogeneous loss of total intracellular IL-16; however, the profile for patients no. 2, no. 6, and no. 8 depicted bimodal or multimodal loss, suggesting the potential preferential loss of pro-IL-16 in selected T cell subsets. The homogeneous loss of IL-16 indicates that all T cells have been affected, independent of subset selectivity or changes in surface phenotype, such as CD25 expression. Assessment of T-ALL cells for intracellular pro-IL-16 indicated normal expression levels of 98% (Figure 2). This was consistent for both patients investigated.

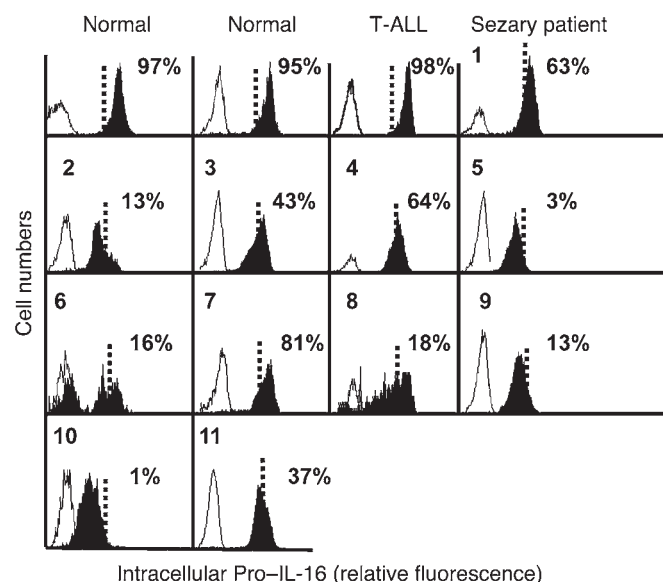


Figure 2 Intracellular detection of pro-IL-16. Primary CD4⁺ T cells obtained from normal controls, patients with T-ALL, or patients with advanced CTCL were isolated and intracellularly labeled for pro-IL-16 protein by antibody staining. Isotype control staining is shown in the open curves, while IL-16 detection is shown in the filled curves. Numbers represent the percentage of pro-IL-16⁺ cells based on the gating strategy, as indicated by the dashed lines. The patient numbers are shown in the top left corners and match patient numbers as identified in Figure 1.

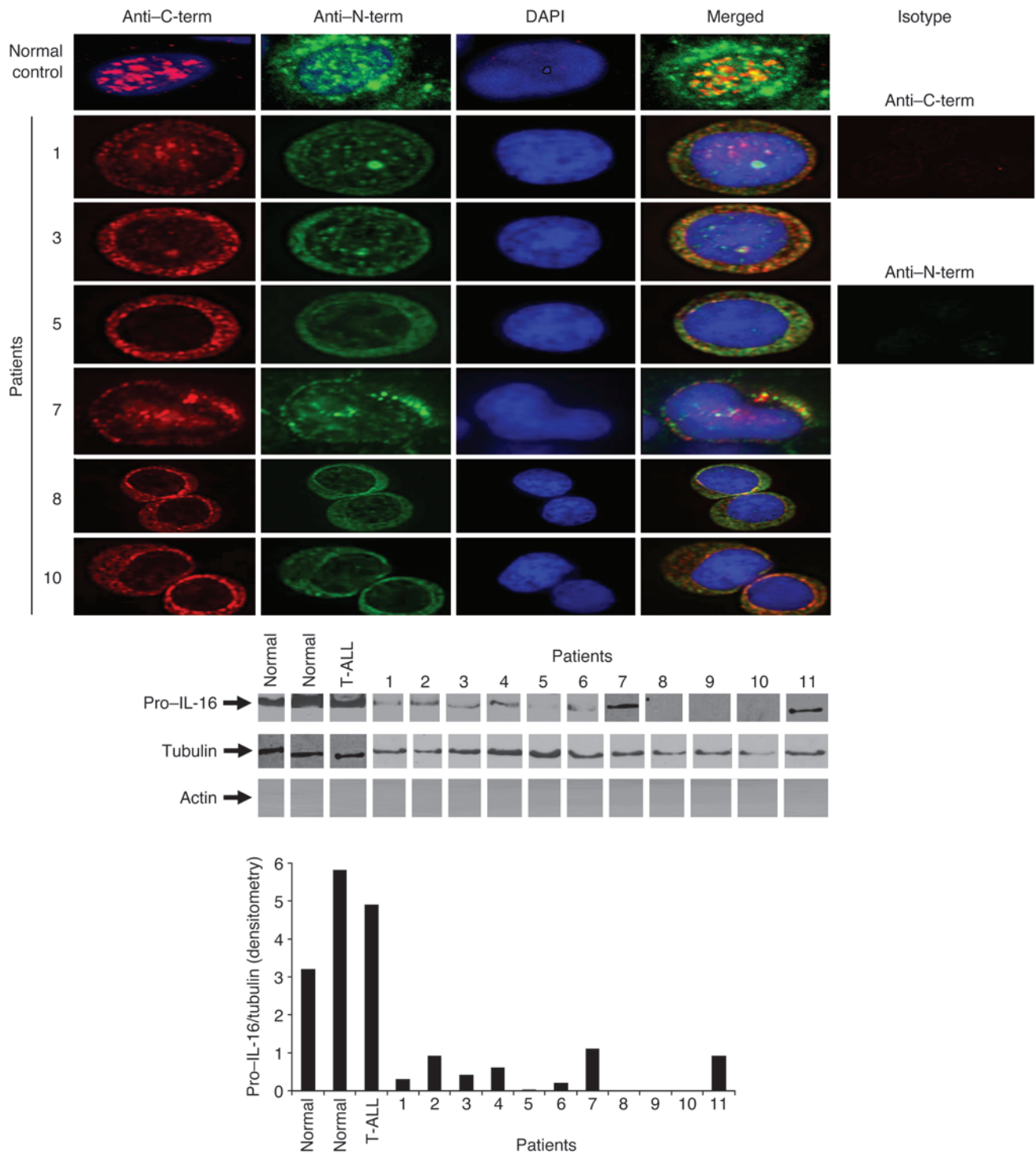


Figure 3

Detection of nuclear pro-IL-16 protein by confocal microscopy and Western blotting. T cells from a normal control and selected patients with CTCL were isolated and intracellularly labeled using anti-C-terminal (anti-C-term) and anti-N-terminal (anti-N-term) antibodies to pro-IL-16. Images were taken at a depth of 5 μ m. Nuclei were identified using DAPI staining (top panel). Nuclear fractions from normal, T-ALL, and CTCL CD4⁺ T cells were used for Western blotting for pro-IL-16 (N-term). Due to timing of patient recruitment, the samples were run on separate gels and compiled for the figure (middle panel). The bottom panel depicts the ratio of pro-IL-16/tubulin for each of the Western samples.

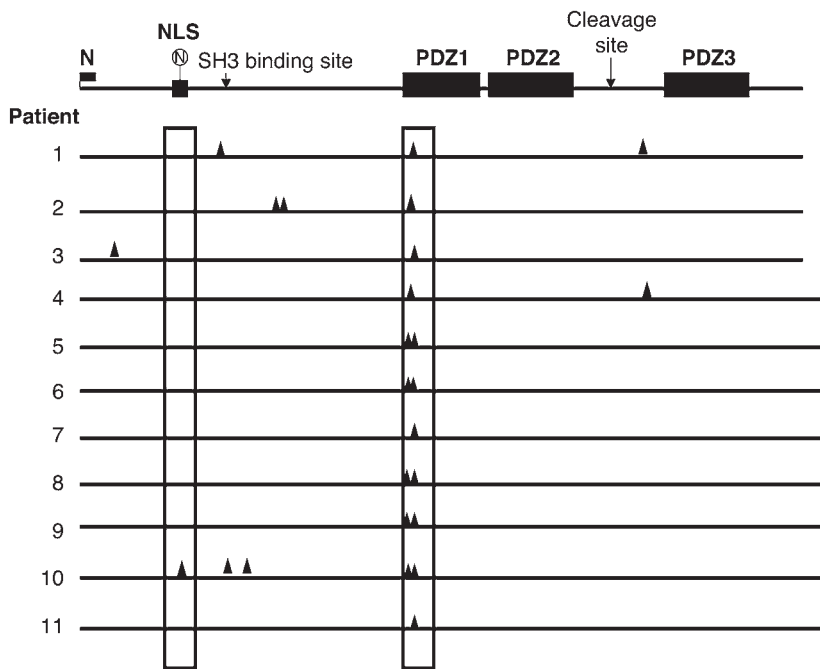


Figure 4

Schematic representation of detected mutations in the protein sequences of pro-IL-16 from CD4⁺ T cells from patients with CTCL as compared with a consensus sequence. The triangles depict where the mutations were detected. The vertical boxes outline regions for the nuclear localization sequences (NLSs) and the 5' region of PDZ1, respectively. N, N terminal start site.

Lower expression of total pro-IL-16 correlates with loss of nuclear pro-IL-16 protein. Pro-IL-16 in normal T cells is present in both the cytoplasmic and nuclear compartments; however, its role in regulating T cell proliferation is dependent on nuclear expression (20, 26, 36). To determine whether loss of total pro-IL-16 reflected a change in nuclear levels, T cells from selected samples were analyzed for pro-IL-16 intracellular distribution by confocal microscopy. Samples were selected based on total intracellular levels and were classified as near-normal pro-IL-16 expression (patient no. 7, 19% loss), substantial loss of pro-IL-16 (patients no. 1 and 3, 36% and 57% loss, respectively), and almost complete loss of pro-IL-16 (patients no. 5, 8, and 10, with 97%, 82%, and 99% loss, respectively). As indicated in Figure 3, patients no. 1, 3, and 7 had detectable pro-IL-16, based on both the N- and C-terminal antibodies, in the nucleus. This level, however, appeared to be less than that detected in normal T cells (normal control). Detection levels were further reduced in patients no. 5, 8, and 10, for which pro-IL-16 protein was not evident by confocal microscopy. To quantify the decrease of pro-IL-16, T cells from all patients were subjected to nuclear fractionation, and nuclear pro-IL-16 levels were assessed by Western blotting. As shown in Figure 3, all patients expressed lower detectable levels of pro-IL-16 than either normal control cells or cells obtained from a patient with T-ALL. For patients no. 5, 8, 9, and 10 pro-IL-16 was not detectable, confirming the images obtained by confocal microscopy. Densitometric analysis based on tubulin expression indicated that nuclear pro-IL-16 levels were reduced in all patients by 6 to 10 fold compared with those in normal control cells (Figure 3). As the starting cell population was not

fractionated, based on phenotypic subsets, the complete loss of nuclear pro-IL-16, in several of the patients' T cells by Western blot analysis, further suggests that this aberration is not clonally restricted but present in the majority of the T cell population.

Loss of pro-IL-16 nuclear translocation is not related to mutations in the nuclear localization sequence. In previous studies using transfected T cell lines, nuclear translocation of pro-IL-16 was dependent on an intact consensus nuclear local sequence (NLS) (19, 20). Loss of nuclear pro-IL-16 in the CTCL-derived (Sezary-derived) H9 cells was also attributed to an identified sequence mutation in the NLS (20). To determine whether a similar mutation in the NLS was present in the primary T cells, mRNA was obtained, cloned, and expressed for each patient, and the resultant cDNA was assessed for predicted protein sequence. A comparison map of the total IL-16 sequence for each patient is shown in Figure 4. As depicted, only 1 patient demonstrated a sequence mutation in the NLS region, patient no. 10. All other patients exhibited normal sequence in that region. Consistent mutations were, however, detected in a region that corresponds to the N-terminal region of PDZ1 (37, 38). Further analysis indicates that a consistent sequence mutation from G-S-A to W-N-G or W-N-S was detected in all patients investigated thus far (Figure 5). PDZ1 is of

particular interest, as this region has been shown to facilitate binding to the transcription factor GABP β as well as the nuclear chaperone HSC70 (26).

Chaperone effect of HSC70 for pro-IL-16. While HSC70 has been shown to be a chaperone protein for nuclear transport of other proteins, this has not been demonstrated for pro-IL-16. To address this potential, Jurkat cells, which do not express IL-16 protein, were infected with lentivirus to stably express a GFP-pro-IL-16 fusion protein. Using siRNA technology, HSC70 protein synthesis was then inhibited, and loss of HSC70 protein was confirmed by Western blot analysis (Figure 6). Two different primer sets were used, and the primer set exhibiting greatest efficiency for loss of HSC70 protein was used for intracellular distribution analysis. The cells were then assessed for intracellular distribution of pro-IL-16 by confocal microscopy. As shown in Figure 6, cells infected with siRNA for HSC70 demonstrated a lack of nuclear pro-IL-16, while cells infected with either an empty vector (data not shown) or a control (nontargeting) vector demonstrated both nuclear and cytoplasmic pro-IL-16. To confirm the direct relationship between pro-IL-16 and p27Kip1, Western blot analysis was performed for both p27Kip1 and Skp2 after siRNA treatment. As shown in Figure 7, the ratio, as determined by densitometric analysis, for the loss of nuclear pro-IL-16 correlates with elevated Skp2 synthesis and reduction in levels of p27Kip1, consistent with what was observed in the primary Sezary T cells. Expression of GFP-pro-IL-16 was also associated with a significant reduction of Jurkat cell proliferation (Figure 7), as has been previously reported (20). After siRNA treatment, proliferative responses

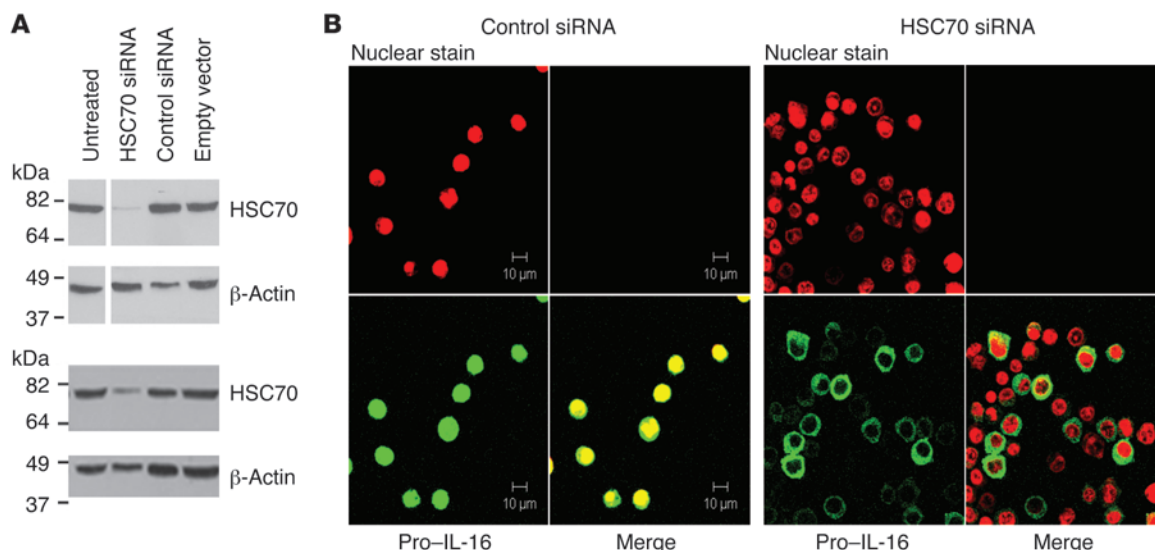


Figure 6 Effect of HSC70 deletion on nuclear pro-IL-16. IL-16-expressing Jurkat cells were transfected with HSC70 siRNA, control siRNA, or empty vector. The effect of siRNA treatment on HSC70 protein expression is shown in **A**, using 2 different siRNA constructs (1 and 2, respectively). Distribution of pro-IL-16, as compared with nuclear staining, after siRNA treatment is shown in **B**. Original magnification, $\times 400$.

Discussion

The increase in the number of skin-associated and circulating malignant T cells in advanced CTCL is likely a combination of both dysregulated T cell proliferation as well as a decrease in the apoptotic response. Resistance to apoptosis has been shown to relate to defective T receptor signaling pathways, resulting in either loss of Fas (CD95) or TRAIL-2 (DR5) expression (5-7, 40). In addition, overexpression of the apoptosis inhibitor cFLIP (7) or the inability to upregulate CD95L expression (5) further support a defect in apoptosis. The mechanisms related to dysregulated growth, however, have been less well defined. Changes in the proliferative state of CTCL T cells have thus far been attributed to inactivation or loss of translation resulting from methylation of the tumor suppressors BCL7a (41), p15, and p16INK4 (42, 43), which inhibit the retinoblastoma protein via interaction with cyclin D. However, deactivation of p16INK4 by bim-1 and ras oncogenes appears to occur primarily during latter stages of disease. In an attempt to further identify alterations in the regulation of CTCL neoplastic cell growth, we investigated potential changes in expression levels of another cyclin kinase-dependent inhibitor, p27Kip1 (44, 45). Our studies indicate that in 11 out of 11 primary T cell samples obtained from patients with CTCL there was a reduction in p27Kip1 levels, consistent with a hyperproliferative state. The loss of p27Kip1 was not detected in cells obtained from patients with T-ALL, and therefore the reduction in nuclear p27Kip1 levels in CTCL T cells suggests a potential difference between this disease and T-ALL for regulation of T cell proliferation.

P27Kip1 is regulated through a degradative process mediated by the SCFSkp2 ubiquitin E3 ligase complex (46-48). The complex-associated protein Skp2 has been shown to be required for ubiquitination and subsequent degradation of p27Kip1 both in vivo and in vitro. Elevated levels of Skp2 expression, with subsequent decreases in p27Kip1, are required for G₁-S transition in most cell types and in particular have been shown to have a critical

participation in cell cycle regulation in lymphomas (31, 46, 49). This is particularly evident in the setting of diffuse cutaneous B cell lymphomas, in which Skp2 serves as an independent marker in predicting clinical outcome (50). In T cell lymphomas, loss of CBP and p27Kip1 insufficiency has been associated with fatal T cell lymphomas in CBP conditional knockout mice (51), which may also relate to the ability of Skp2 to enzymatically degrade other tumor suppressors, such as FoxO1A and FoxO3 (52, 53). Due to the importance of Skp2-mediated degradation on p27Kip1 for regulation of cell growth, determination of intracellular Skp2 levels along with factors that can regulate Skp2 synthesis are of particular interest for the understanding of pathogenesis and progression of hematological malignancies.

Assessment of Skp2 levels in the T cells from our cohort of patients with advanced CTCL indicated that in all cases Skp2 levels were elevated as compared with those in normal controls. Despite the importance of both p27Kip1 and Skp2 for regulating T cell growth, sequence mutations in either of these proteins have not been reported in association with any T cell cancer. This suggests that alterations in either p27Kip1 or Skp2 activity can be attributable to other proteins involved in regulating their activity. Regulation of Skp2 expression has recently been reported to be mediated by a protein complex comprised of the transcription factor GABP β , HDAC-3, and a scaffold protein, pro-IL-16. Pro-IL-16 contains 2 PDZ domains whereby PDZ1 interacts selectively with GABP β , while the PDZ2 domain interacts with HDAC-3. As a scaffold protein, pro-IL-16 facilitates GABP β and HSC70 binding to the core promoter region of Skp2 in association with a GABP β binding site on the Skp2 promoter. Loss of nuclear pro-IL-16 prevents HDAC-3 interaction with the Skp2 promoter and allows for active transcription. Dependence on nuclear pro-IL-16 to maintain quiescent T cells has been demonstrated in both T cell lines as well as primary T cells (34). When CTCL peripheral T cells were analyzed

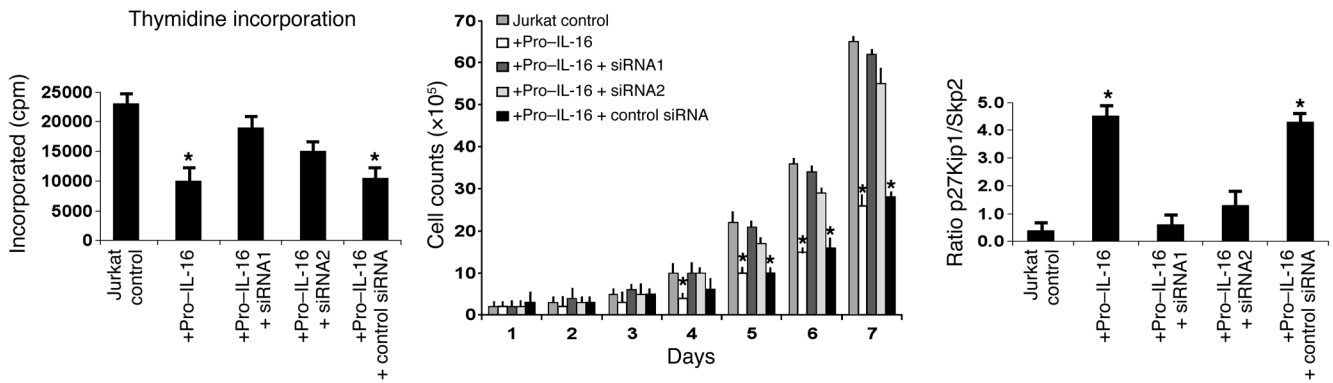


Figure 7 Effect of siRNA treatment on thymidine incorporation, total cell numbers, and ratio of p27Kip1/Skp2 levels, as determined by densitometry of Western blots ($n > 4$). * $P < 0.05$, compared with values obtained from Jurkat cell alone. The error bars represent standard deviation.

for the presence of intracellular pro-IL-16, all patients demonstrated reduced total levels, as determined by FACS analysis. Using Western blotting, 4 out of the 11 patients demonstrated a total loss of intracellular IL-16 greater than 85% (patients no. 5, 8, 9, and 10).

The mechanism for loss of IL-16 protein has not been identified; however, loss of mRNA was also detected (data not shown) and may suggest that epigenetic factors, such as methylation, or microRNA regulation may account for a reduction in pro-IL-16 protein synthesis. Studies are underway to address this hypothesis. Even in patients for which intracellular IL-16 was detected, the presence of nuclear pro-IL-16 was either completely absent or significantly reduced, as indicated by both confocal microscopy and Western blot analysis of nuclear fractions. Previous reports identified that nuclear translocation of pro-IL-16 was facilitated by a nuclear localization sequence (20). However, predicted amino acid sequencing of pro-IL-16 from the patients with Sezary syndrome indicated that all but 1 patient had a normal NLS sequence. Further sequence analysis did indicate the presence of mutations in the 5' region of PDZ domain 1, distant from the binding pocket defined by the D-T-G-F sequence. In addition to binding GABP β , PDZ1 was also shown to associate with the HSC70 (26). HSC70, unlike GABP β , does not contain the consensus C-terminal sequence required to bind to the D-T-G-F pocket. This indicates that HSC70 binds to a different region of PDZ1 than GABP β and further suggested that HSC70 binding to pro-IL-16 in CTCL peripheral T cells may be

affected by the predicted sequence mutations. Mutational studies that inserted the predominant W-N-G sequence into the 5' end of wild-type pro-IL-16, the region in which mutations were present in patients with Sezary syndrome, resulted in marked reductions in HSC70 binding. This identifies the importance of the G-S-A sequence in pro-IL-16 for HSC70 binding. This concept was confirmed, as all patients demonstrated either a lack of HSC70 binding to pro-IL-16 or a substantial reduction. The extent of loss of HSC70 binding to pro-IL-16 correlated with the extent of loss of nuclear pro-IL-16, indicating a nuclear chaperone role for HSC70 (54). To investigate this further, we

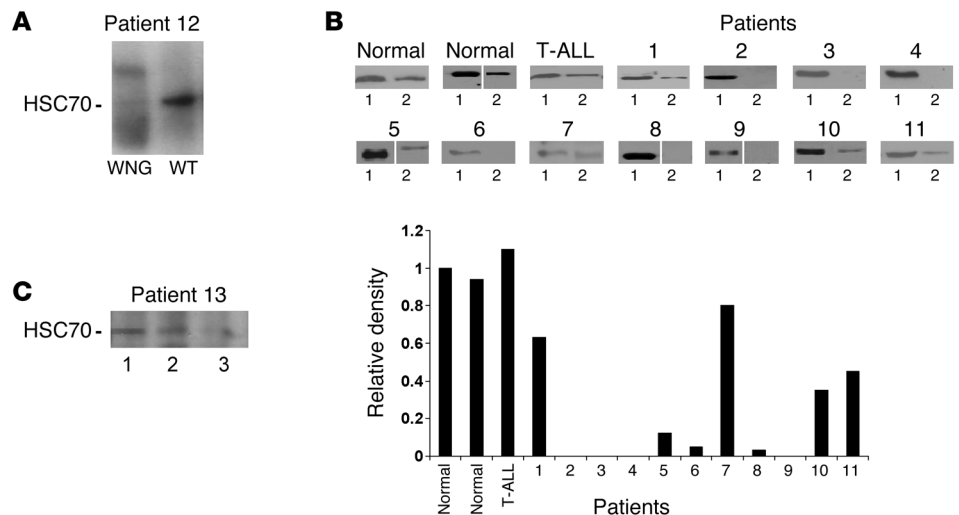
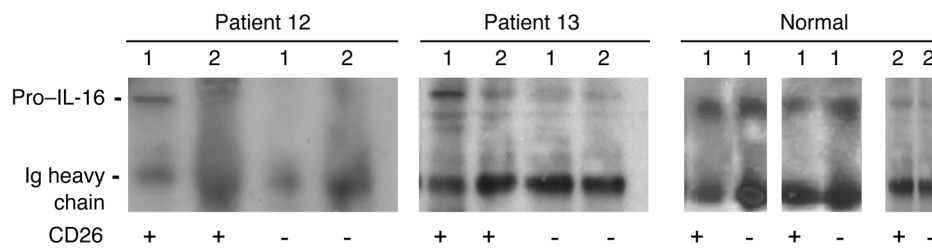


Figure 8 Association of pro-IL-16 with HSC70. (A) Pro-IL-16 protein was expressed with either the wild-type G-S-A or mutated W-N-G sequence in Jurkat cells and then immunoprecipitated with anti-pro-IL-16 and probed on a Western blot with anti-HSC70 antibody. (B) Primary T cells from normal controls or subjects with T-ALL or CTCL were lysed and immunoprecipitated with anti-HSC70 antibody for total protein (lane 1) or with anti-pro-IL-16 antibody (lane 2). All lanes were probed with anti-HSC70 antibody for protein presence (top panel). The ratio of total HSC70 protein to pro-IL-16-associated HSC70 protein is depicted in the bottom panel. (C) Patient no. 13 was included to demonstrate total HSC70 protein immunoprecipitated with anti-HSC70 antibody (lane 1), HSC70 protein immunoprecipitated with anti-pro-IL-16 antibody (lane 2), and HSC70 protein immunoprecipitated with control rabbit antibody (lane 3).

**Figure 9**

Association of pro-IL-16 with HSC70. Primary CD4⁺ T cells from patients with Sezary syndrome (patients no. 12 and no. 13) and 2 normal controls were sorted into CD26⁺ and CD26⁻ subsets, lysed, and immunoprecipitated with anti-HSC70 antibody (lane 1) or isotype control antibody (lane 2). All lanes were probed with anti-pro-IL-16 antibody for Western blotting.

performed siRNA HSC70 studies in which HSC70 knockdown resulted in loss of nuclear pro-IL-16 with associated increases in Skp2 protein, decreases in p27Kip1, and significant increases in proliferative responses as indicated by thymidine uptake and absolute cell numbers.

Over the past decade, several studies have analyzed genetic aberrations in CTCL at the level of chromosomal alterations, candidate regions, and gene mutations (55–58). As compared with most hematological malignancies, the information on genetic aberrations in CTCL is still limited, and a consistent pattern has not been identified, most likely as a result of the phenotypic variety among patients and rarity of the disease. However, recent studies suggest higher levels of chromosomal imbalances (CI ≥ 5), as those observed with advanced CTCL are associated with decreased survival (59). Of interest, abnormalities on the long arm of chromosome 15, in which pro-IL-16 is encoded (60), have been observed in patients with stage III and IV disease (59).

These data indicate that dysregulated growth in Sezary T cells results in part from the lack of the nuclear presence of a scaffold protein, pro-IL-16, which functions to regulate Skp2 transcription. The lack of nuclear expression of pro-IL-16 is related to sequence mutations in PDZ1, which prevent binding of a functional chaperone protein, HSC70. These studies begin to identify, for what we believe to be the first time, a novel mechanism for dysregulated T cell growth in patients with advanced CTCL and suggest that reconstitution of wild-type intracellular pro-IL-16 may facilitate T cell quiescence.

Methods

Blood samples (patient population)

Peripheral blood samples were obtained from patients diagnosed with stage III and IV CTCL. Once patients provided written consent, blood samples were drawn at the time of follow-up diagnostic laboratory evaluations or immediately preceding extracorporeal photopheresis treatment. A total of 11 patients were initially enrolled, 3 males and 8 females. Patients were classified as stage III CTCL (5 patients) and stage IV CTCL (6 patients), according to the TNM staging system and recommended guidelines by the International Society for Cutaneous Lymphomas (61). Control samples were obtained from 10 healthy volunteers (normal controls) and 2 T-ALL patients. To complete some studies, an additional 2 patients with CTCL (1 male and 1 female, both stage IV) as well as 2 additional control subjects were added. All protocols and procedures have been approved by the IRB committees at Boston Medical Center (Boston, Massachusetts, USA), Arizona Medical Center (Tucson, Arizona, USA), and Dana-Farber Cancer Institute (Boston, Massachusetts, USA).

Flow cytometry analysis and antibodies

Peripheral lymphocytes from patients and controls were isolated from blood samples by Ficoll (Pharmacia) gradient centrifugation. CD4⁺ T cells were enriched by magnetic bead separation using positive selection with anti-CD4 antibodies (R&D Systems) as reported previously (62, 63). The resultant cell population was routinely greater than 90% CD4⁺ T cells. Subsequently, the CD4⁺ cells were evaluated for expression of pro-IL-16 using the monoclonal antibody (clone 14.1) as previously described (64). Briefly, 1×10^6 CD4⁺ cells were permeabilized using 0.1% Triton X 100 for 15 minutes, prior to adding 10 ng anti-IL-16 antibody for 30 minutes at 4°C. After extensive washing with PBS, a FITC-conjugated rabbit anti-mouse IgG (5 µg) was then added to the cells for 30 minutes at 4°C. The cells were washed 3 times with PBS with 0.1% azide, and then IL-16 expression was assessed by flow cytometry.

Western blot

Primary tumor cells (7×10^6 cells/sample) were harvested by centrifugation, washed twice with cold PBS, and lysed in 50 mM Tris-HCl (pH 7.4), 150 mM NaCl, 1.5 mM EDTA, and 0.5% Nonidet P-40, plus a mixture of proteinase inhibitors (protein lysis buffer). Protein concentrations were determined by the Bradford assay, and equal amounts of protein were used for each experiment. Proteins were subjected to electrophoresis through a 12% SDS-PAGE gel, electrophoretically transferred to nitrocellulose membrane, and probed with various antibodies as indicated in each experiment (Skp2, p27Kip1, and pro-IL-16). The secondary antibodies labeled with HRP (Santa Cruz Biotechnology Inc.) were used at a dilution of 1:5,000. Protein bands were visualized by ECL (Pierce). Densitometry was used for quantifying Western blots with NIH ImageJ 1.63 software (<http://rsbweb.nih.gov/ij/>).

Cell fractionation

Primary circulating CD4⁺ lymphocytes isolated from CTCL and control samples were harvested as described above and washed twice with cold PBS before incubation with buffer I (see below) on ice for 15 minutes. Twenty microliters of 10% Nonidet P-40 were added to the 400-µl cell suspension, hand mixed for 10 seconds, and then centrifuged at 16,110 g for 5 minutes at 4°C using a desk-top microcentrifuge to pellet the nuclei. The supernatants were further fractionated by centrifugation at 32,200 g for 20 minutes at 4°C. The supernatant fraction of this centrifugation was collected and classified as the cytoplasmic fraction. The nuclear pellet was washed twice with ice-cold PBS before adding 50 µl buffer II (see below) to lyse the nuclei. After 15 minutes on ice, nuclear lysates were centrifuged at 32,200 g for 10 minutes at 4°C, and this supernatant fraction was classified as nuclear. The protein concentration in each fraction was determined using Bio-Rad bovine γ-globulin as standard protein and Bio-Rad protein assay reagent (buffer I, 20 mM



Tris-HCl, 0.5 mM DTT, 10 mM β -glycerol-phosphate, 300 mM sucrose, 0.2 mM EGTA, 5 mM MgCl₂, and 10 mM KCl; buffer II, 10 mM Tris-HCl, 0.5 mM DTT, 10 mM β -glycerol-phosphate, 0.2 mM EGTA, 5 mM MgCl₂, 350 mM KCl, and 25% glycerol; both buffers contain the protease inhibitors aprotinin, chymostatin, antipain, and pepstatin at 10 μ g/ml and PMSF at 1 mM).

ELISA

Quantitation of IL-16 protein in the serum of patients and controls as well as supernatant from CD3-stimulated and nonstimulated cultures of peripheral lymphocytes was accomplished by ELISA as previously described (64). Briefly, anti-IL-16 monoclonal antibody was coated directly onto 96-well ELISA plates (Costar) at a concentration of 1 μ g/ml in coating buffer (0.1 M sodium bicarbonate, pH 8.8) and incubated overnight at 4°C. To eliminate nonspecific binding by the primary antibody, the plates were blocked with 300 μ l blocking buffer (PBS containing 10% FBS and 0.05% NaN₃) for 2 hours at ambient temperature. The plates were then washed twice with PBS Tween (PBS containing 0.05% Tween 20). A standard curve was generated using serial dilutions of recombinant IL-16. Samples (100 μ l) were incubated in duplicate in the 96-well plates (Nunc) at 37°C for 1 hour. After the 1-hour incubation, the protein was removed, and the wells were washed with PBS containing 0.1% Tween 20. Nonspecific binding was reduced by blocking with 1% bovine serum albumin for 1 hour. After washing, 100 μ l rabbit polyclonal anti-IL-16 antibody (10 μ g/ml) diluted in PBS containing 0.05% Tween 20 was added to each well. The presence of IL-16 was then detected by incubating for 1 hour with biotinylated goat anti-rabbit IgG diluted 1:500 in PBS. The lower limit of detection for the ELISA is routinely 10–15 pg/ml. Linearity was in the range of 12–500 pg/ml (coefficient of 0.993 in that range).

P21 ELISAs were conducted on isolated peripheral T cells from patients with advanced CTCL and normal controls after cell lysis using 1% N-P40. P21 levels were determined using an ELISA Kit (Invitrogen) and conducted according to the manufacturer's instructions.

Pro-IL16 mRNA sequencing

Total RNA was isolated from 3×10^6 CD4⁺ T cells from either patients with advanced CTCL or normal controls using the RNA Miniprep Kit (Stratagene) as detailed by the manufacturer. The RNA was quantified (Bioate, Thermo Electron Corporation), and RT-PCR was generated using the OneStep RT-PCR Kit (Qiagen). Briefly, RT-PCR reactions were composed of 1 μ g cDNA template, 100 ng each of sense (5'-CGGGGTACCAAGAG-GCAGGCTCGGATG-3') and antisense (5'-CCGGAATCTTGGCTTCAG-CATGTCCT-3') oligonucleotide primers, and Qiagene OneStep RT-PCR reagents. The primers were designed to cover 18 nucleotides upstream of the translational start codon and 18 nucleotides downstream of the translational stop codon, producing a predicted 1.9-KB product. PCR products were separated by electrophoresis (1% agarose gel) and were detected by ethidium bromide staining, and expected PCR products were verified by reference to a 1.9-kilobase DNA ladder.

Cloning of the RT-PCR products. The RT-PCR products were digested with KpnI and EcoRI, separated on 0.8% agarose gel, excised, purified (Qiagene, MinElute Gel Extraction Kit, catalog no. 28604), and ligated into pcDNA 3.1(+) (Invitrogen) vector using the Stratagene DNA Ligation Kit.

E. coli transformation. The vectors were transformed into a competent *E. coli* strain, DH5 α TM (Life Technologies), and transformants were selected on LB plates containing 100 μ g/ml ampicillin. DNA was purified from selected clones (Promega Wizard Plus Minipreps DNA Purification System) and sequenced. Correct orientation of the gene was confirmed using T7 and BGH reverse primers (Invitrogen).

HSC70 siRNA

Stealth siRNA duplexes for silencing of human HSC70 were designed by Block-it RNAi designer (Invitrogen) and purchased from Invitrogen. The sense sequence used was 5'-UAAUUCUAAAGUACAUUGAGACCAGC-3'. Stably transfected IL-16-expressing cells were transiently transfected using oligofectamine (Invitrogen), with or without a final concentration of 100 nM for the siRNAs. Forty-eight to seventy-two hours after transfection, when protein levels of HSC70 decreased to 10% to 20% of those in control cells, cells were subjected to immunofluorescence studies. Nontargeting siRNA duplexes were also obtained from Invitrogen (Stealth RNAi Negative Control Med GC, catalog no. 12935-300). Confirmation for selective HSC70 targeting was achieved using a second siRNA primer pair, for which the sense sequence was 5'-UCCUACCAAGCAGACACAGACC-3' (Invitrogen). Jurkat cell transfections were conducted in a similar fashion as described above.

Confocal microscopy

Primary lymphocytes were isolated and then fixed and permeabilized using a methanol fix solution (Sigma-Aldrich) as previously described (36). The cells were then incubated with fluorescently labeled anti-IL-16 antibodies; FITC-conjugated mouse monoclonal antibody (clone 14.1) directed to the C-terminal, and PE-conjugated rabbit polyclonal antibody directed to the N-terminal region. Intracellular IL-16 protein was visualized using a Nikon deconvolution wide-field Epifluorescence confocal microscope.

Generation of HSC70 mutant constructs for in vitro expression

A 1.24-kb segment of human N-terminal pro-IL-16 that includes the PDZ1 domain, with the 3-amino acid wild-type HSC70 binding site covering 18 nucleotides of the 5' end to PDZ1 core DTGF motif, was cloned into the pXM vector. Using site-directed mutagenesis (QuikChange II, Stratagene), according to manufacturer's instructions, the HSC70 binding site was mutated to WNG using the following primers (mutated nucleotides are shown in brackets): forward, 5' GACTCAGCTGCAAAT[**TGGAACGGC**]GAAACATC TGCCCTTGG; reverse, 5' CCAAGGCAGATGTTTC[**GCCGTTCCA**]ATTTCAGCTGAGTC. Mutated plasmids were expanded and purified by standard techniques (Qiagen), and the success of mutation confirmed by sequencing prior to transfection. To confirm success of mutagenesis, wild-type and WNG mutant constructs of N-terminal IL-16 were sequenced at the Boston University Molecular Genetics Core Facility prior to transfection.

Transfection. Jurkat cells from ATCC were transfected with 4 μ g of the construct using the TransIT-Jurkat Reagent (Mirus Bio) per the manufacturer's protocol. Cells were harvested 24–48 hours after transfection for use in immunoprecipitation assays.

Immunoprecipitation and Western blotting. Five to eight million transfected or control cells were lysed with buffer (Cell Signaling Technology) containing RNase A (Sigma-Aldrich) and protease inhibitors (Roche). Lysates were precleared by incubating with 3 μ g rabbit isotype antibody (Invitrogen) and 40 μ g Protein A-agarose beads (Sigma-Aldrich) for 2 hours at 4°C on a rotator. Samples were centrifuged at 3,000 g for 1 minute at 4°C, and supernatants were collected into new tubes. These precleared supernatants were then incubated with 1.5 μ g rabbit anti-N-terminal IL-16 antibody (in-house reagent) or control rabbit antibody, or for some studies with 1.5 μ g mouse anti-HSC70 antibody or isotype control antibody, for 2 hours before 40 μ g Protein A-agarose beads were added and incubated overnight at 4°C. The beads were washed 3 times with equal volumes of complete lysis buffer, and pellets were resuspended in SDS Sample buffer with reducing agent (Invitrogen). Samples were boiled and run on a 4%–12% Bis-Tris gel (Invitrogen) and transferred to PVDF membranes (Millipore). Membranes were blocked with 4% milk in Tris-buffered saline with 0.1% Tween 20 and probed with mouse anti-HSC70 antibody (Thermo Scientific, clone 13D3) and goat anti-mouse HRP conjugated secondary antibody (Cell Signaling Technology). Detection was per-



formed with an ECL Reagent Kit (GE Healthcare), and films were scanned for densitometry analysis with ImageJ Software (<http://rsbweb.nih.gov/ij/>).

Statistics

All statistics were conducted using a Student's *t* test analysis, with significant differences established at a 5% confidence level. *P* values of less than 0.05 were considered significant.

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