Global Promoter Methylation Analysis Reveals Novel Candidate Tumor Suppressor Genes in Natural Killer Cell Lymphoma

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Abstract

**Purpose:** To identify tumor suppressor genes epigenetically silenced by promoter hypermethylation in extranodal natural killer cell lymphoma (NKCL).

**Experimental Design:** Promoter methylation was analyzed with global and locus-specific methylation assays in NKCL cases and NK cell lines. Gene expression profiles were used to identify genes for which aberrant promoter methylation was associated with transcriptional silencing. Selected DNA methylations were validated by RRBS, pyrosequencing, or q-MSP. Decitabine treatment was performed to evaluate reactivation of methylated genes. The tumor suppressor effect of silenced genes was evaluated functionally by reintroducing them into NK cell lines.

**Results:** We observed significant promoter hypermethylation in most NKCL samples compared with normal NK cells. Correlation of global promoter methylation with gene expression profiles identified 95 genes with strong evidence for being silenced because of promoter methylation, including BCL2L11 (BIM), DAPK1, PTPN6 (SHP1), TET2, SOCS6, and ASNS. Known tumor suppressor genes were significantly overrepresented in this set of genes. Decitabine treatment of NK cell lines was associated with reexpression of all 10 selected methylated and silenced genes. Ectopic expression of frequently silenced BIM in two BIM-nonexpressing NK cell lines led to increased apoptosis and eventual elimination of BIM-transduced cells. It also sensitized these cell lines to chemotherapy-induced apoptosis. Similarly, reintroduction of SOCS6 significantly inhibited growth in SOCS6-nonexpressing NK cell lines. NK cell lines lacking ASNS expression showed increased sensitivity to treatment with l-asparaginase. Reintroduction of ASNS reduced drug sensitivity.

**Conclusion:** Promoter region hypermethylation is frequent in NKCL, and aberrantly methylated genes are pathologically and clinically significant. Clin Cancer Res; 21(7); 1699–711. © 2015 AACR.

Introduction

Natural killer (NK) cell malignancies are aggressive neoplasms and represent 1% to 2% of all non-Hodgkin lymphomas (NHL; ref. 1). They are divided into 2 clinic subtypes based on the WHO classification: aggressive NK cell leukemia (ANKL) and extranodal NK cell lymphoma (NKCL) of nasal type (2). NKCL prevalence is higher in Central and South America and East Asia than in other regions (1). NKCLs are associated with Epstein–Barr virus (EBV) infections (3), and patients with localized nasal or paranasal disease respond significantly to combined radiotherapy and chemotherapy (4); however, NKCLs are resistant to chemotherapy in advanced stages and when the disease is extranasal. An l-asparaginase–containing multiagent chemotherapeutic regimen containing steroid (dexamethasone), methotrexate, ifosfamide, and etoposide (SMILE) is currently the best option for refractory NKCLs and has shown promising clinical response in patients with advanced disease (5, 6). Recently, the combination of genomic and functional analysis has identified PRDM1 as a candidate tumor suppressor gene (TSG) in NKCLs (7–9). However, few aberrant genes that contribute to NKCL pathogenesis and can potentially serve as therapeutic targets have been identified and characterized.

Aberrant promoter methylation is a major mechanism contributing to neoplastic transformation by deregulating expression of oncogenes and TSGs (10). Transcriptional repression mediated by CpG island/promoter hypermethylation has been detected for PRDM1 (7, 9), SHP1 (PTPN6; ref. 11), DAPK1 (12), and HACE1 (13) in NKCL, suggesting that aberrant promoter methylation is an important mechanism of TSG silencing in NKCL in other malignancies (14, 15). However, only locus-specific assays were used for the assessment of promoter hypermethylation in NKCL samples, and the global promoter
methylation changes have not been reported. To more comprehensively evaluate the inactivation of potential TSGs in NKCLs, we applied genetic, epigenetic, and functional approaches to study a series of NKCL cases and cell lines and have detected promoter hypermethylation and transcriptional silencing of SHIP1, BIM, SOCS6, TET2 and other novel candidate TSGs that may serve as therapeutic targets in NKCLs. In addition, we showed frequent silencing of asparagine synthetase (ASNS) and an association between L-asparaginase-based regimens. Asparaginase-related side effects may be reduced by decreasing the dosage of asparaginase administered to patients with NKCL with high levels of ASNS hypermethylation.

**Materials and Methods**

**Cell lines and tumor specimens**

Twelve NKCL cases and 7 NK cell lines (NK92, KHYG1, YT, SNK1, SNK6, NKYS, and KAI3) were used in this study. The characteristics of NK cell tumor cases and NK cell lines have been described previously (3) and are summarized in Supplementary Table S1. KHYG1 and KAI3 cell lines were obtained from ATCC. All cell lines were expanded, frozen, and used for the NCBI reference hg19. The basic MSCC statistics are shown in Supplementary Table S2. The sequencing data was submitted to SRA database of PubMed (http://www.ncbi.nlm.nih.gov/sra/).

**Decitabine treatment**

Decitabine (5-aza-2'-deoxycytidine) treatment was performed as previously described (7). Briefly, 4 x 10^5 cells from KHYG1, NK92, or SNK6 cell lines were seeded in 2 mL in 6-well plates in the presence of 0.25, 0.5, or 0.75 μmol/L of decitabine (Sigma-Aldrich). After 2 days, cells were spun down at 300 x g for 10 minutes, and fresh culture medium including the same decitabine concentrations was added. Cells were harvested for qRT-PCR after 4 total days of treatment.

**L-Asparaginase treatment of NK cell lines and cell survival assay**

A total of 5 x 10^4 cells from NK cell lines (n = 6) in 1 mL medium were seeded into 24-well plates in duplicates. Cells were treated with 0, 0.01, 0.05, 0.075, 0.1, or 0.5 IU of l-asparaginase (Sigma-Aldrich) for 24 or 48 hours. Cell survival was determined after the treatment using Cell Titer Glo Luminescent Cell Viability Assay (Promega Inc.) or Vi-CELL XR Cell Viability Analyzer (Beckman Coulter Inc.) according to the manufacturers’ recommendations.

**Statistical and computational analysis of epigenetically silenced genes**

R language scripts (http://www.R-project.org) were used for statistical analysis of genome-wide methylation data and to identify genes showing concurrent promoter methylation and transcriptional repression.

Additional experimental methods of (j) sample isolation and NK cell activation, (ii) GEI, (iii) pyrosequencing, (iv) Western blotting, (v) RRBs, (vi) q-MSI, (vii) qRT-PCR, (viii) expression of BIM-EL, SOCS6, and ASNS in NK cell lines, (ix) apoptosis assay, (x) transfection of 293T cells with BIM, and (xi) additional statistical methods are described in the Supplementary Methods.
Global Methylation Analysis in Natural Killer Cell Lymphoma

Results

Most NKCL samples have global promoter hypermethylation compared with normal NK cells

We compared global DNA methylation in malignant NK samples (12 NKCL cases and 2 NK cell lines) with normal NK cells and normal tonsil. Each mappable HpaII site was uniquely assigned to the closest TSS. We calculated the number of HpaII cuts per site for each sample, arbitrarily treating the promoter as the region within 1 kb of the TSS. The overall distribution of HpaII sites and of MScC reads in normal NK cells is shown in Supplementary Fig. S1. MScC reads are strongly associated with CpG islands (CGIs) and most promoters overlap with CGIs. Consistent with the normal absence of methylation at most promoter-associated CGIs (18), the average number of cuts per site was higher in CGI-associated promoters than elsewhere in both normal and malignant NK samples (mean, 13.97 vs. 3.58) and the number of cuts per site varied little among CGI-associated promoters in normal NK cells (3.76 mean log2 cuts per site, 0.70 SD for promoters with at least 5 sites). However, the corresponding mean value was lower and the SD higher, for all malignant NK samples (range, 3.09–3.69; mean, 0.75–1.34; SD), consistent with frequent aberrant promoter methylation in malignant samples. Graphing the average number of cuts per site at various distances from the TSS revealed a clear global pattern of promoter hypermethylation, hypomethylation distal to the promoter, or usually both in 11 of the 14 malignant samples (Fig. 1A), which suggests widespread dysregulation of DNA methylation in malignant NK samples. The 3 exceptional cases (#3, 9, and 12) likely either have low tumor content or more normal regulation of DNA methylation; they were therefore not included in additional analyses.

Previous analysis showed that genes hypermethylated in cancer frequently have a “poised” promoter as in embryonic stem cells (ESC; refs. 19, 20); that is, one with histone marks of both activation (H3K4me3) and repression (H3K27me3), the latter associated with Polycomb complexes. Strikingly, most malignant NK samples show a much more prominent pattern of hypermethylation at poised genes than at other promoters (Fig. 1B).

Cut site reads were summed for each gene after assigning sites to various categories. Log2 values were compared between 11 malignant samples (9 tumors and 2 cell lines) and the 2 normal samples (NK cells and tonsil) using 2-sided t tests. A large fraction of promoters were significantly hypermethylated in malignant samples (Fig. 1C); most categories of CGIs were hypermethylated as well. In contrast, distal gene bodies and extragenic regions, which are highly methylated in normal NK cells, tend to be relatively hypomethylated in malignant samples. Comparing normal and malignant samples after summing cut site reads based on the pattern of chromatin modification in human embryonic stem cells (hESCs; refs. 21) demonstrated that a much larger fraction of “poised” promoters (Polycomb-repressed in hESCs) were significantly hypermethylated compared with other promoters (Fig. 1D).

In contrast, distal transcribed regions, heterochromatin, and Polycomb-repressed regions not associated with promoters are highly methylated in normal samples (Supplementary Fig. S1B) and frequently are relatively hypomethylated in malignant samples.

Relationship between promoter methylation and gene expression

Because the transcriptional effects of altered DNA methylation at distal sites are hard to predict and are likely variable, further analysis centered on promoter methylation. We compared methylation and gene expression for the 10,912 genes that had both gene expression data and at least one mappable HpaII site ± 1 kb of the TSS. Most malignant samples display globally increased promoter methylation (Fig. 1). In general, genes with low expression were more hypermethylated than those with high expression (Supplementary Results). Because promoter methylation generally silences gene expression, there will be selection for methylation of tumor suppressor genes but negative selection against methylation at genes required for survival and proliferation such as housekeeping genes. No selection for or against hypermethylation is expected for genes not expressed in NK cells because they are functionally silent. Indeed, genes with little or no expression in normal NK cells are significantly more likely than other genes to be hypermethylated in tumors as a manifestation of the abnormal methylation; their gene bodies are also more likely to be hypomethylated as often seen in cancer although the detailed pattern varies among the malignant samples (Supplementary Fig. S2).

Part of the explanation for the tendency of promoters poised in hESCs to become hypermethylated is that such genes are especially likely to have low or no expression in NK cells; however, this is unlikely to be a full explanation because even when the analyzed genes are in the top half of mean normal expression, “poised” genes are more frequently hypermethylated (for genes with at least 5 promoter cut sites, a mean of 2.17 samples per gene with significantly decreased cut counts compared with 1.55 for the remaining genes; Wilcoxon test, P = 1.1 × 10–7).

For the 9 malignant samples (7 tumors and 2 cell lines) with both MScC and GEP data, the Pearson correlation coefficient (R_MScC-GEP) was calculated for each gene, using log2 MScC and GEP values. The median R_MScC-GEP was 0.146 for all evaluable genes; this value is low partly due to the inclusion of genes that are either not expressed in NK cells or are never hypermethylated; variation in their apparent expression, MScC values, or both would result from experimental noise, yielding no true correlation.

To narrow our further analysis to genes with the strongest evidence for silencing due to promoter hypermethylation, we devised 6 weak filters (Fig. 2), described in more detail in Supplementary Methods, which together yield a small tractable list of genes (Table 1 and Supplementary Table S3). (i) The gene must be expressed in NK cells. (ii) Cut counts and (iii) expression must vary among the samples. Three or more samples show evidence for a decrease in (iv) cut counts or (v) expression compared with normal NK cells. (vi) R_MScC-GEP must be at least 0.5 or 0.65, yielding 174 or 95 genes, respectively (Fig. 2). Each successive filter increased the mean R_MScC-GEP among the remaining genes (Fig. 2). We developed a linear predictor to prioritize additional genes that barely failed one or more filters, as described in Supplementary Methods. Table 1 and Supplementary Table S3 show the genes with the best evidence for being recurrently silenced in NKCL due to promoter methylation. In addition, Table 1 shows the pattern of hypermethylation of the 95 genes among 11 malignant samples. Supplementary Figure S3 illustrates examples of the strong negative correlation between promoter methylation and mRNA expression of the genes on the short list.

To validate our approach here to identify methylated genes using MScC data, we performed reduced representation bisulfite sequencing (RRBS) on 2 NK cell lines with MScC data (NK92 and KHYG1) and 3-day IL2-activated normal NK cells. Side-by-side
comparison of the MSCC and RRBS data for the promoters of 95 methylated genes showed high concordance between these 2 methodologies (Table 1). In addition, a global comparison of pairwise (NK cell line vs. normal NK) methylation differences (Supplementary Fig. S4) showed high ($R > 0.7$) correlations between MSCC and RRBS results.

The 174-gene list was evaluated by Ingenuity Pathway Analysis (IPA; Table 2 and Supplementary Table S4). The genes were very significantly enriched in several functional groups of interest that involve cell death, cell activation, homeostasis and differentiation, proliferation and cancer, motility, and regulation of transcription. "Cellular homeostasis" and "cell death of immune cells" showed the greatest significance, at $5.7 \times 10^{-3}$ and $1.4 \times 10^{-8}$, respectively. Of note, many known tumor suppressor genes were enriched in our list (Supplementary Results).

Methylated candidate tumor suppressor genes are silenced in NK cell lines

We performed qRT-PCR on NK cell lines to determine whether the expression of methylated candidate tumor suppressor genes was silenced. mRNA expression of 2 proapoptotic genes, **BIM** and **DAPK1**, was low in NK-cell lines compared with normal NK cells (Supplementary Fig. S5A). Similarly, we observed silencing of regulators of the JAK-STAT pathway, **SOCS6**, **IL12RB2**, and **ZFHX3** (ATBF1), in NK cell lines compared with normal NK cells (Supplementary Fig. S5B). The expression of 2 other candidate genes, **TET2** and **TLE1**, was in general low in NK cell lines compared with activated NK cells (Supplementary Fig. S5C). We observed low expression of **ASNS** in 5 of 6 NK cell lines compared with normal NK cells (Supplementary Fig. SSD, left); however, the KHYG1 cell line showed unusually high mRNA expression based on qRT-PCR, an observation consistent with MSCC and GEP results. Finally, we observed silencing of **CD300A**, which encodes an inhibitory NK cell receptor, in NK cell lines (Supplementary Fig. SSD, right). In general, the 2 NK cell lines found to be hypermethylated by MSCC showed low gene expression for candidate TSGs assayed with qRT-PCR. qMSP was performed on NK cell lines (n = 6) for the genes with qRT-PCR data available using unmethylated (DAPK1, ZFHX3, TLE1, SOCS6) or methylated (IL12RB2, TET2 and CD300A) DNA-specific primers and cell lines with low expression of these genes showed promoter hypermethylation compared with normal NK cells (Supplementary Fig. S5F). For **BIM** and **ASNS** qMSP experiments in NK cell lines, both methylated and unmethylated DNA-specific primers were used as described below.

**Figure 1.**
Compared with normal cells, most malignant NK samples show promoter hypermethylation, which affects a large fraction of genes. A, average MSCC counts were calculated for each of 12 NKCL cases, 2 NK cell lines, normal NK cells (average of 5 technical replicates), and tonsil (average of 5 technical replicates) and plotted against the relative distance to the TSS at 0.1-kb intervals using a 0.5-kb sliding window. B, average MSCC counts at poised genes for normal NK cells (average of 3 technical replicates), and tonsil (average of 5 technical replicates) and plotted against the relative distance to the TSS at 0.1-kb intervals using a 0.5-kb sliding window. C, a t test was used to compare the 2 normal samples (tonsil and NK cells) to 9 cases and 2 cell lines with clear aberrant methylation. Cut sites for each gene were clustered into categories as shown (sites ≥ 1x4 of the TSS are considered promoter sites). Only genes with ≥ 3 cut sites for a given category were included, yielding 2,343, 15,842, 2,202, 1,774, 1,669, 17,627, and 14,994 genes in the order shown. The fractions of hypermethylated and hypomethylated gene regions at various levels of significance are shown. D, as in C, except that sites were annotated based on the chromatin assignments in hESCs (available at www.genome.ucsc.edu; ref. 21).
Finally, we evaluated BIM expression in NK cell lines by Western blotting and detected very low or no BIM protein in accordance with the qRT-PCR result (Supplementary Fig. S6).

Locus-specific validation of BIM, ASNS, and DAPK1 promoter methylation with pyrosequencing and qMSP

We evaluated the validity of the MSCC technique by comparing the promoter methylation profile of the NKCL cases with previously published Biotage pyrosequencing results (9) for the HpaII site at 747-bp upstream of the PRDM1a TSS. MSCC and pyrosequencing results were both available for this site in 13 malignant NK samples and 2 (resting and IL2-activated NK cells for Biotage pyrosequencing) or 3 (technical triplicate of IL2-activated NK cells for MSCC) normal NK samples. Comparison of the methylation difference between normal and malignant NK samples revealed a high inverse correlation (R = −0.75) between MSCC and pyrosequencing results (Supplementary Fig. S7B).

Next, we screened 2 separate regions in each of BIM, ASNS, or DAPK1 promoters within ±1 kb of the TSSs in 2 NK cell lines and normal NK cells using pyrosequencing. Side-by-side comparison of the 8 CpG sites with both MSCC and pyrosequencing data available showed a high inverse Pearson correlation between MSCC cut counts and pyrosequencing (R = −0.81 and −0.97 for BIM; R = −0.72, −0.53 and −1.00 for ASNS; R = −1.00, −1.00, −1.00 for DAPK1; Supplementary Figs. S7C and S8). No promoter methylation was detected in normal NK cells, whereas NK92 cells showed promoter hypermethylation in all 3 genes (Supplementary Fig. S8A–S8C). KHYG1 cells showed hypermethylation in the promoter of DAPK1 (Supplementary Fig. S9C). We then screened the BIM promoter (−510 to −360 bp of the TSS) with qMSP in NK cell lines (n = 7) using primers specific for methylated (M) or unmethylated (U) DNA (Supplementary Fig. S9A, left). We observed hypermethylation in 6 of 7 NK cell lines (Supplementary Fig. S9B, left). Screening the same BIM promoter region in 8 NKCL cases with qMSP using methylaton-specific primers revealed increased BIM methylation in all NKCL cases compared with normal NK cells, suggesting that the BIM promoter is frequently hypermethylated in NKCL (Supplementary Figs. S9B, middle). Next, we applied the qMSP methodology on 7 malignant NK cell lines to examine methylation between 305 and 16 bp of the ASNS TSS (Supplementary Fig. S9A, right). We detected promoter hypermethylation in 6 of 7 (86%) NK cell lines (Supplementary Fig. S9C, left) and in 5 of 8 (62.5%) NKCL cases (Supplementary Fig. S9C, middle). As a control, we observed amplification of enzymatically methylated DNA only with BIM or ASNS methylation–specific qMSP primers but not with primers specific for unmethylated DNA (Supplementary Fig. S9D).

Table 1. Promoter methylation pattern of 95 epigenetically silenced genes detected by MSCC in NKCL samples

Table 2. Selected functional groups for 174 recurrently hypermethylated genes in IPA

NOTE: The name of the genes in these groups is indicated in Supplementary Table S4.
Figure 3. Decitabine treatment reactivates expression of hypermethylated genes. A–C, BIM, DAPK1, SOCS6, ZFHX3, PTPN6, TET2, CD300A, TLE1, LEF1, and ASNS expression was determined by qRT-PCR in NK cell lines treated with decitabine for 4 days. D, GAPDH, IL12RB2, ASNS, or CD300A mRNA expression was determined by qRT-PCR in decitabine-treated NK92 or KHYG1 cells as negative controls. The mRNA levels of decitabine-treated NK cell lines were normalized to that of the untreated cells. Data are shown as mean ± SD. The data are representative of 2 biological replicates, each with 2 technical replicates ($n = 4$).
**Figure 4.** Ectopic expression of BIM or SOCS6 in methylated NK cell lines results in apoptosis, and reintroduction of BIM sensitizes malignant NK cells to asparaginase-induced apoptosis. A, quantification of the percentage of GFP+ cells 2 and 3 days after transduction of NKYS cells with empty vector or BIM-EL (left). The percentage of GFP+ cells in empty vector or BIM-EL-transduced NKYS cells 3 days after transduction were normalized to the percentage of GFP+ cells 2 days after transduction. Data are mean ± SD of 2 independent experiments with 2 biologic replicates (n = 4). *, P = 0.0075 versus percent GFP+ at day 2.

Quantiﬁcation of the rate of apoptosis in empty vector or BIM-EL-transduced NKYS cells by determining the percentage of Annexin-V/GFP double-positive NKYS cells (left). The percentage of apoptotic cells for each sample was calculated as follows: (% Annexin-V/GFP double-positive cells)/(Total % GFP-positive cells). Data are mean ± SD of 2 independent experiments with 2 biological replicates (n = 4). *, P = 0.037 versus vector-only. (Continued on the following page.)

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Decitabine treatment is associated with reexpression of silenced candidate TSGs in NK cell lines

Next, we wanted to test whether silenced tumor suppressor gene candidates could be reactivated using decitabine, a DNA methyltransferase inhibitor commonly used to evaluate the association between methylation and gene expression (7). NK cell lines with MSCC (i.e., NK92 and KHYG1) or qMSP data (i.e., SNK6) on promoter hypermethylation of the candidate tumor suppressor gene were treated for 4 days with Decitabine. We observed 2-fold upregulation of BIM mRNA expression in decitabine-treated NK92 and SNK6 cells, in which the BIM promoter is methylated (Fig. 3A, left). Consistent with qRT-PCR, we observed induction of BIM protein expression by Western blotting in NK92 cells (Supplementary Fig. S10). Similarly, DAPK1 was induced in response to decitabine in DAPK1-null NK92 and KHYG1 cells (Fig. 3A, right). A robust and decitabine dose-dependent increase in mRNA expression was observed for SOCS6, ZFXHS, SHP1, and TET2 in KHYG1 and NK92 cell lines (Fig. 3B). CD3300A showed more than 200-fold increase of gene expression in all doses of decitabine tested in NK92 cells (Fig. 3C, left). TLE1, LEF1, and ASNS similarly showed more than 2-fold upregulation of mRNA expression in NK92 cells (Fig. 3C). Finally, we evaluated GAPDH and IL12RB2 expression in decitabine-treated NK92 cell line and ASNS and CD3300A expression in decitabine-treated KHYG1 cells as negative controls and observed no significant changes in gene expression, as expected (Fig. 3D).

Reintroduction of BIM leads to negative selection pressure and causes apoptosis in BIM-null NK cell lines

To address whether decreased BIM expression contributes to enhanced survival of malignant NK cells, we reintroduced BIM-EL into 2 BIM-null NK cell lines, NKYS and KAI3, using the retrovirus murine stem cell virus (MSCV)-GFP (pMIG). GFP+ cells represented the transduced population, and tracking the changes in the percentage of GFP+ cells over time was used to evaluate whether there is any selection pressure on transduced cells. We observed a significant decrease in the percentage of GFP+ NKYS cells between 2 and 3 days after transduction (Fig. 4A, left). Similarly, we observed a significant decrease in the percentage of GFP+ KAI3 cells 3 days after transduction compared with the percentage 2 days after transduction (Fig. 4A, right), suggesting that there is selection against NK cell lines with ectopic BIM expression. Ectopic expression of BIM was confirmed in BIM-EL–transduced NKYS cells by Western blotting (Supplementary Fig. S11).

Next, we stained BIM-EL–transduced NKYS cells with Annexin V to determine whether reintroduction of BIM-EL increases the rate of apoptosis. We observed a significant increase in Annexin V staining in the GFP-gated cellular population 2 days post-transduction (Fig. 4A, left). Similarly, we observed a significant increase in Annexin V staining in BIM-EL–transduced KAI3 cells 2 days after transduction (Fig. 4A, right) suggesting that methylation-mediated silencing of BIM enhances survival of malignant NK cells.

Reintroduction of BIM increases the sensitivity of malignant NK cells to asparaginase-induced apoptosis

We treated empty vector (EV) or BIM-EL–transduced BIM-null NK cell lines with l-asparaginase to test whether there is an increase in sensitivity in induction of apoptosis. BIM-transduced NKYS cells treated with 0.01 or 0.05 IU of l-asparaginase showed a higher percentage of Annexin+ cells compared with cells transduced with BIM-EL but not treated with l-asparaginase or empty vector–transduced, l-asparaginase–treated cells (Fig. 4B, left). Next, we treated another BIM-transduced BIM-null NK cell line, KAI3, with 0.1 or 0.5 IU of l-asparaginase and observed an increase in induction of apoptosis in l-asparaginase–treated, BIM-transduced KAI3 cells compared with l-asparaginase–treated, vector-only transduced cells (Fig. 4B, right).

Ectopic expression of SOCS6 in NK cell lines leads to negative selection pressure and induces apoptosis under limiting IL2 concentrations

To address whether epigenetic silencing of SOCS6 contributes to the neoplastic transformation of NK cells through more sustained activation of the JAK/STAT pathway, we transduced the SOCS6-null NKYS cell line with a SOCS6 expression vector or with empty vector. We then quantified the percentage of GFP+ cells at regular time intervals to assess whether SOCS6-transduced NKYS cells are negatively selected. IL2 is known to activate STAT3 and STAT5 (22). Therefore, IL2 was removed from the cell culture medium of transduced cells 6 days after transduction. The percentage of GFP+ cells declined about 30% in the SOCS6-transduced population between 3 and 12 days after transduction, whereas empty vector transduced cells did not show any decrease (Fig. 4C, left). We repeated the experiment with the SOCS6-null YT cell line and again observed a significant reduction in GFP+ cells between 4 and 8 days after transduction in SOCS6-transduced YT cells but not those transduced with empty vector (Fig. 4C, middle). SOCS6-transduced DHL16 cell line, which is a...
germinal center B-cell–like diffuse large B-cell lymphoma (GCB-DLBCL) cell line with no JAK-STAT3 pathway activation, was not negatively selected (Fig. 4C, right). Ectopic expression of SOCS6 was confirmed in SOCS6-transduced NKYS and YT cells by qRT-PCR (Supplementary Fig. S12B and S12C).

To address whether the negative selection observed in SOCS6-transduced NK cell lines is due to increased apoptosis, we transduced YT cells with the SOCS6 expression vector or empty vector and observed a significantly higher percentage of Annexin-V+/GFP+ cells in SOCS6-transduced YT cells than in empty vector–transduced cells (Fig. 4D, left). In addition, we observed moderately lower levels of phospho-STAT3 (Tyr705) expression in SOCS6-transduced NKYS cells than in empty vector–transduced cells (Fig. 4D, middle and right), suggesting that SOCS6-mediated inhibition of NK cell growth may be due to JAK/STAT3 pathway inhibition.

**NK cell lines with low ASNS expression are more sensitive to L-asparaginase treatment**

To address whether the effectiveness of L-asparaginase treatment correlated with the ASNS mRNA levels in the malignant NK cells, we treated NK cell lines (n = 6) with progressively increasing doses of L-asparaginase. Initially, we treated KHYG1, SNK6, NKYS, and YT cells with 0.1 or 0.5 IU of asparaginase and observed greater asparaginase sensitivity in SNK6, NKYS, and YT cells than in KHYG1 cells (Fig. 5A). In the second experiment, we treated KHYG1, KAI3, NK92, and YT cell lines with lower concentrations (0.01, 0.05, or 0.075 IU) of asparaginase and observed high sensitivity in KAI3, NK92, and YT cell lines, which have low ASNS mRNA expression due to promoter methylation (Fig. 5B). As expected, the KHYG1 cell line, with no promoter methylation and high ASNS expression, was least sensitive to asparaginase treatment (Fig. 5B, left). In fact, ASNS mRNA expression was highly correlated with normalized cell survival in response to 0.01, 0.05, and 0.075 IU asparaginase (R = 0.77, 0.84, and 0.88, respectively; Fig. 5C).

Next, we asked whether ASNS reexpression can reduce cell death after asparaginase treatment or not. To address this question, we transduced ASNS-nonexpressing NKYS cell line with an empty vector or ASNS expression vector. Then, we sorted GFP+ cells and treated empty vector or ASNS-transduced NKYS cells with 0, 0.01, 0.05, or 0.075 IU asparaginase for 48 hours. Ectopic expression of ASNS in ASNS-transduced NKYS cells was demonstrated by qRT-PCR (Fig. 5D, right). There was marked reduction in cell viability in empty vector–transduced cells for all tested concentrations, and no cytotoxicity was observed in ASNS-transduced cells (Fig. 5D, left). However, there was significantly more normalized cell survival after asparaginase treatment in ASNS-transduced cells compared with empty vector–transduced cells, which supports the idea that epigenetic silencing of ASNS in NKCLs increases asparaginase sensitivity (Fig. 5D, middle).

**Discussion**

Using the MSCC technique to analyze DNA methylation throughout the genome revealed that promoter hypermethylation and distal DNA hypomethylation were widespread in most malignant NK samples. Selection for inactivation at individual loci cannot entirely explain this hypermethylation because it was also frequent at promoters of genes with little or no expression in normal NK cells. Several categories of genes appear to be prone to hypermethylation in malignant NK samples including the category of genes “poised” in hESCs and genes expressed but functionless in NK cells (e.g., CD3D). We therefore used a number of strategies to filter out noise and to identify a set of genes that are most likely to be functionally significant. Known TSGs and genes important in normal NK function are enriched among these hypermethylated genes. We also determined the profile of promoter methylation in 2 cell lines using another global technique, RRBS, which yielded very comparable results. This increased our confidence in our previous analysis and the set of recurrently hypermethylated and silenced genes, many of which likely function as TSGs in these NK cell tumors.

Inactivation of TSGs through genetic or epigenetic mechanisms is a critical mediator of the neoplastic transformation of normal cells. Hypermethylation of the promoters of TSGs has commonly been observed in a variety of lymphoid malignancies (14) including NKCLs (9, 11). Epigenetic silencing of multiple TSGs may have additive or synergistic effects leading to the evasion of normal growth control mechanisms.

The genes found to be silenced through promoter methylation in malignant NK cells can limit the growth and survival of NK cells through regulation of multiple pathways (Table 2). Silencing of BIM may enhance NK cell survival by conferring resistance to proapoptotic signals, as observed in Burkitt lymphoma cells (14). EBV infection may contribute to BIM promoter methylation and silencing (23), and interestingly, NKCL is almost invariably EBV infected. Downregulation of DAPK1, a serine/threonine kinase known to activate a p19ARF/p53-dependent apoptotic checkpoint (24), was observed in chronic lymphocytic leukemia (25) in addition to NKCLs (12).

SOC56 and ZNF3 transduced cells are less sensitive to the JAK/STAT pathway (26, 27) and are downregulated in a variety of solid tumors including gastric, pancreatic, and lung cancers (28–31). As previously observed (11), we found SHP1 (PTPN6) promoter methylation in NKCL cases (Table 1 and Supplementary Table S3) and now showed its reactivation after decitabine treatment (Fig. 3B, right). Interestingly, aside from its role as a negative regulator of signaling through activating NK-cell receptors, SHP1 has been shown to inactivate STAT3 through dephosphorylation of tyrosine-705 (32), which suggests that epigenetic silencing of SHP1 may promote activation of the JAK/STAT3 pathway. Epigenetic silencing of the negative regulators of this pathway may be associated with the neoplastic transformation of NK cells as constitutive activation of the JAK/STAT pathway is observed in NKCLs (33).

Alterations in epigenetic regulators are frequent in lymphomas and likely of importance in NKCL. TET2 loss-of-function mutations are frequent in myelodysplastic syndrome (MDS; ref. 34) and T-cell lymphoma (35). Silencing of TET2 may contribute to aberrant promoter methylation of genes that contribute to the development of NKCL (36). In fact, early epigenetic inactivation of TET2 may contribute to the establishment of global promoter hypermethylation observed in NKCL samples.

TLE1 is a groucho homolog, and its epigenetic inactivation was observed in hematologic malignancies (37) including acute myelogenous leukemia (38). IL12RB2 is a TSG in B-cell malignancies (39, 40). The consequences of silencing of IL12RB2 in NK cells are less clear; however, a recent study showed induction of cell death during prolonged IL12 receptor signaling in NK cells (41), suggesting that silencing of IL12RB2 may contribute to NK cell survival in the presence of prolonged IL12 stimulation from the microenvironment.
Figure 5.

NK cell lines with silenced ASNS expression are more sensitive to L-asparaginase treatment, and reintroduction of ASNS reduces drug sensitivity. NK cell lines were treated with L-asparaginase for 24 hours using 0.1 or 0.5 IU (A) or 0.01, 0.05, 0.075 IU (B) of L-asparaginase, and cell survival was determined as a percentage of the untreated control for each cell line. KHYG1 cells, which do not have promoter methylation and high ASNS expression, were used as the control during asparaginase treatment of NK cell lines. Relative ASNS mRNA expression based on qRT-PCR is shown below each panel. The numeric values below each panel represent the ASNS expression fold difference relative to resting NK cells. ASNS promoter methylation is shown for each NK cell line based on the qMSP Ct value difference between each malignant NK cell line and 3-day IL2-activated NK cells, as shown in Supplementary Figs. S5 and S9 C. No, no hypermethylation; ++, highly hypermethylated, using the cutoff values described in Supplementary Fig. S5. C, Pearson correlation coefficient (R) between mRNA expression based on qRT-PCR, and percent normalized cell survival was determined for NK cell lines (n = 4) treated with 0.01, 0.05, or 0.075 IU of L-asparaginase (left). Tables show normalized ASNS mRNA expression and percentage (%) survival in NK cell lines (n = 4) after 0.01, 0.05, or 0.075 IU of asparaginase treatment (right). Data are mean ± SD of 2 independent experiments. D, absolute (left) or normalized (middle) cell numbers of empty vector (EV) or ASNS-transduced NKYS cells treated with the indicated concentrations of asparaginase concentrations are shown. GFP+ cells were sorted 8 days after transduction. Three days later, sorted cells were seeded for asparaginase treatment, and 48 hours after treatment, viable cell number was determined as described in Materials and Methods. Each column shows mean ± SD of 3 biological replicates. Ectopic ASNS expression is shown by qRT-PCR 2 days after transduction of NKYS cells (right). Each data point shows mean ± SD of triplicate of ASNS calibrated to RPL13A (housekeeping gene). ASNS levels in ASNS-transduced cells normalized to empty vector–transduced cells are shown. *, P < 0.01 versus vector only.
PRDM1 was not in our list because the available HpaII sites around the TSS (−747 and +99 bp) are not in the critical hypermethylated genomic locus of PRDM1 (9) we previously identified in NKCLs. The lists failed to include HACE1 only because the SD for gene expression fell below the threshold, which may reflect suboptimal microarray probe sets. Methylolation-mediated silencing of ASNS in malignant NK samples is a significant observation from the clinical point of view; a similar observation was made in acute lymphoblastic leukemia (42). The mechanism responsible for the apparent selection for loss of ASNS expression. In addition, L-asparaginase treatment–associated side effects (44, 45) may be minimized by using lower concentrations of L-asparaginase for treating patients with NKCL with low ASNS expression.

In summary, we integrated global promoter methylation and gene expression profiling data to identify candidate TSGs silenced because of promoter hypermethylation. Selected candidates were validated by functional assays. Our findings improve our understanding of the pathogenesis of NKCL and may suggest novel potential therapeutic targets.

Disclosure of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

References

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Global Methylation Analysis in Natural Killer Cell Lymphoma


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