Clinical Implications of Phosphorylated STAT3 Expression in De Novo Diffuse Large B-cell Lymphoma

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Introduction

Diffuse large B-cell lymphoma (DLBCL) is the most common type of lymphoma and encompasses a heterogeneous group of tumors with several variants, subgroups, and subtypes or entities (1). With the current standard treatment introduction of rituximab in the past decade has improved the survival of patients with DLBCL (4), but patients with ABC-like DLBCL still display a worse outcome (5).

Gene expression profiling (GEP) has identified distinct molecular subtypes, in particular the germinal center B-cell–like (GCB) and activated B-cell–like (ABC) DLBCL (3). The introduction of rituximab in the past decade has improved the survival of patients with DLBCL (4), but patients with ABC-like DLBCL still display a worse outcome (5).

Signal transducer and activator of transcription 3 (STAT3) is a member of the STAT family of transcription factors. In

Purpose: Activated signal transducer and activator of transcription 3 (STAT3) regulates tumor growth, invasion, cell proliferation, angiogenesis, immune response, and survival. Data regarding expression of phosphorylated (activated) STAT3 in diffuse large B-cell lymphoma (DLBCL) and the impact of phosphorylated STAT3 (pSTAT3) on prognosis are limited.

Experimental Design: We evaluated expression of pSTAT3 in de novo DLBCL using immunohistochemistry, gene expression profiling (GEP), and gene set enrichment analysis (GSEA). Results were analyzed in correlation with cell-of-origin (COO), critical lymphoma biomarkers, and genetic translocations.

Results: pSTAT3 expression was observed in 16% of DLBCL and was associated with advanced stage, multiple extranodal sites of involvement, activated B-cell–like (ABC) subtype, MYC expression, and MYC/BCL2 expression. Expression of pSTAT3 predicted inferior overall survival (OS) and progression-free survival (PFS) in patients with de novo DLBCL. When DLBCL cases were stratified according to COO or MYC expression, pSTAT3 expression did not predict inferior outcome, respectively. Multivariate analysis showed that the prognostic predictability of pSTAT3 expression was due to its association with the ABC subtype, MYC expression, and adverse clinical features. GEP demonstrated upregulation of genes, which can potentiate function of STAT3. GSEA showed the JAK–STAT pathway to be enriched in pSTAT3+ DLBCL.

Conclusions: The results of this study provide a rationale for the ongoing successful clinical trials targeting the JAK–STAT pathway in DLBCL. Clin Cancer Res; 20(19); 5113–23. ©2014 AACR.
Translational Relevance

Activated signal transducer and activator of transcription 3 (STAT3) plays a role in tumor invasion, cell proliferation, angiogenesis, and immune response. Enhanced STAT3 activity has been found in many cancers, but its role in diffuse large B-cell lymphoma (DLBCL) has not been well studied. In this study, we showed that expression of phosphorylated STAT3 (pSTAT3) was seen in 16% of de novo DLBCL and was associated with advanced stage, multiple extranodal sites of involvement, activated B-cell–like (ABC) subtype, MYC expression, and MYC/BCL2 expression. Although multivariate analysis did not show expression of pSTAT3 as an independent prognostic marker, the expression of pSTAT3 showed inferior overall survival and progression-free survival in patients with de novo DLBCL treated with R-CHOP. pSTAT3 in DLBCL upregulates genes potentiating function of STAT3, which has been found to be an attractive therapeutic target.

Patient selection

A cohort of 443 patients with de novo DLBCL treated with the standard R-CHOP regimen was collected as part of The International DLBCL. Rituximab-CHOP Consortium Pro-gram Study (25). All cases were centrally reviewed by a group of hematopathologists and classified according to the World Health Organization classification criteria (1). Cases that were excluded from this study included: large cell transformation of low-grade B-cell lymphoma, immunodeficiency-associated lymphoproliferative disorders (especially human immunodeficiency virus infection), primary mediastinal large B-cell lymphoma, primary cutaneous B-cell lymphoma, and primary central nervous system DLBCL. All patients had sufficient clinical and follow-up data. This study was conducted in accord with the Declaration of Helsinki. Utilization of archived diagnostic tissue samples, therapy and outcome data procurement were approved by the Institutional Review Boards (IRB) of all participating collaborative institutions. The overall study was approved by the IRB at The University of Texas MD Anderson Cancer Center (Houston, TX).

Tissue microarray immunohistochemical studies

Representative areas with the highest percentage of tumor cells were selected for tissue microarray (TMA) construction as described previously (5). Immunohistochemical (IHC) studies for various markers were performed: B-cell lymphoma 2 (BCL2), B-cell lymphoma 6 (BCL6), cyclin D1, CD10, CD30, Forkhead box protein P1 (FOXP1), GCB-expressed Transcript-1 (GCET1), multiple myeloma oncogene 1 (MUM1), MYC, nuclear factor-kB (NF-kB) components (p50, p52, p65, and c-Rel), p53, phosphorylated protein kinase B (pAKT), and phosphorylated STAT3 (pSTAT3). Receiver–operating characteristic (ROC) curves and X-tile analyses were used to assess adequate cutoff (5). When an optimal cutoff could not be determined by ROC curve and X-tile analyses, a conventional cutoff value for individual markers was decided on the basis of previous reports in the literature. The cutoff scores for these markers were as follows: 10% for cyclin D1, 20% for CD30 and p53, 30% for CD10 and BCL6, 40% for MYC, 50% for pSTAT3, 60% for GCET1, MUM1, and FOXP1, and 70% for AKT and BCL2. All markers except cyclin D1 were determined by ROC curve. Any nuclear expression of each NF-kB component was considered positive.

Fluorescence in situ hybridization and TP53 sequencing

Fluorescence in situ hybridization (FISH) analysis was performed on formalin-fixed, paraffin-embedded tissue sections using BCL2 and BCL6 dual-color break-apart probes (Vysis), locus-specific IGH/MYC/CEP8 tricolor dual-fusion probes (Vysis) and a locus-specific MYC dual-color break-apart probe (Vysis) as reported previously (26). TP53 exon sequencing was performed as described previously (27). Sequencing data were compared with the TP53 reference sequence (NC_000017.10) in the Genbank database for data analysis.

GEP and gene set enrichment analysis

Total RNA was extracted from formalin-fixed, paraffin-embedded tissue samples using the HighPure RNA Extraction...
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Kit (Roche Applied Science) and subjected to GEP as described previously (5). The robust multivariate analysis (RMA) algorithm was used for background correction (28), and then quantile normalization was conducted (29). Cell-of-origin (COO) classification was determined primarily based on GEP data and secondarily on immunohistochemical results using the Visco-Young algorithm as described previously (5).

Gene set enrichment analysis (GSEA) was performed with GSEA application (Broad Institute at MIT, Cambridge, MA) using Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway gene sets (186 gene sets). GSEA results with false discovery rate (FDR) < 0.3 were considered to be statistically significant.

Statistical analysis

Comparison among categorical variables and numerical variables was carried out by using the Fisher exact test and Kruskal–Wallis test, respectively. OS and progression-free survival (PFS) were defined from the date of diagnosis to the date of last follow-up or death and from the date of diagnosis to the date of progression or death, respectively. Survival probability was determined using the Kaplan–Meier method, with difference compared by the log-rank test. A Cox proportional-hazards model was used for univariate and multivariate analysis. All variables with P < 0.05 were considered to be statistically significant. SPSS Statistics V21 (IBM), GraphPad Prism V5 (GraphPad software), and X-Tile version 3.6.1 (Yale University, New Haven, CT) were used for statistical analyses.

Results

pSTAT3 expression is associated with poor outcome

The clinical features of the patient cohort are similar to that of our prior studies (30). Nuclear expression with or without cytoplasmic expression of pSTAT3 in large atypical lymphoid cells was regarded as positive in association with intensity (Supplementary Fig. S1). Expression of pSTAT3 in small, mature lymphocytes was disregarded. Clinical characteristics of patients with pSTAT3+ versus pSTAT3− DLBCL are summarized in Table 1. pSTAT3 was positive in 72 (16%) patients, of which 49 were men and 23 were women. pSTAT3+ DLBCL did not show distinct morphologic features compared with pSTAT3− DLBCL, having predominantly centroblastic morphology. Advanced stage (66% vs. 52%; P = 0.036), involvement of multiple extranodal sites (33% vs. 20%; P = 0.026) and the ABC subtype (67% vs. 45%; P = 0.001) were more commonly observed in pSTAT3+ DLBCL compared with pSTAT3− DLBCL. Significant differences with respect to pSTAT3 expression were not observed for gender, age, B symptoms, Eastern Cooperative Oncology Group (ECOG) score, serum lactic dehydrogenase (LDH), International Prognostic Index (IPI), tumor size, and treatment response (P > 0.05).

Patients with pSTAT3+ DLBCL had significantly worse OS and PFS compared with patients with pSTAT3− DLBCL (Fig. 1A and B). The 5-year OS was 48.8% for pSTAT3+ DLBCL and 64.7% for patients with pSTAT3− DLBCL (P = 0.016). The 5-year PFS was 39.9% for pSTAT3+ DLBCL and 64.7% for patients with pSTAT3− DLBCL (P = 0.016). The median OS was 56.9 months [95% confidence interval (CI), 18.1–95.7] for patients with pSTAT3+ DLBCL and was not reached for patients with pSTAT3− DLBCL. The median PFS was 43.5 months (95% CI, 21.1–65.8) for pSTAT3+ DLBCL and 78.7 months (95% CI, 61.9–95.5) for patients with pSTAT3− DLBCL.

When stratified into GCB and ABC subtypes, patients with pSTAT3+ DLBCL showed a trend suggestive of inferior OS compared with patients with pSTAT3− DLBCL.
DLBCL in the GCB subgroup ($P = 0.189$) and the ABC subgroup ($P = 0.089$), respectively (Fig. 1C and E). Patients with pSTAT3+ DLBCL had worse PFS in the GCB subgroup ($P = 0.044$), but showed no significant difference of survival in the ABC subgroup ($P = 0.089$). Separating stage I–II vs. III–IV, pSTAT3 retained prognostic value in the lower stage subgroup ($P = 0.008$ for OS and $P = 0.021$ for PFS), but not in the advanced-stage subgroup ($P = 0.591$ for OS and $P = 0.441$ for PFS). In the patient subgroup with less than two extranodal sites of involvement, pSTAT3 predicted poorer prognosis ($P = 0.029$ for OS and $P = 0.028$ for PFS), but not in patients with two or more extranodal sites ($P = 0.958$ for OS and $P = 0.881$ for PFS, Supplemental Table S6).
We also measured STAT3 mRNA levels and evaluated whether STAT3 mRNA level correlated with pSTAT3 expression. To measure mRNA expression of the STAT3 gene, from the GEP dataset, we retrieved the intensity of four STAT3 probe-sets and used the average value as STAT3 expression at the mRNA level. Patients were divided into three groups for survival analysis according to the mean values of mRNA expression: low STAT3 mRNA (< mean – one standard deviation), high STAT3 mRNA (> mean + 1 standard deviation), and intermediate STAT3 mRNA levels (the remaining cases). The mean values of pSTAT3 expression in cases with low, intermediate, and high STAT3 mRNA were 12%, 22%, and 36%, respectively, showing correlation between STAT3 mRNA and pSTAT3 expression (P = 0.0002; Supplementary Fig. S2). However, STAT3 mRNA did not show significant difference with respect to OS in all cases (P = 0.1487) and ABC DLBCL (P = 0.6183). Although significant stratification was seen in GCB DLBCL, cases with high STAT3 mRNA and low mRNA showed the best and worst survival, respectively. Seven cases with high STAT3 mRNA in GCB DLBCL is insufficient number to achieve statistical power and could be an random event. The worse prognosis in cases with low STAT3 mRNA could be due to contamination from background inflammatory cells.

**pSTAT3 expression is associated with MYC and MYC/BCL2 expression**

Immunohistochemical and genetic characteristics of pSTAT3+ and pSTAT3− DLBCL are summarized in Table 2. An association between STAT3 and the MYC and BCL2 genes has been reported previously by other investigators in limited patient series (31, 32). Therefore, in this study, we comprehensively assessed MYC and BCL2 expression with respect to pSTAT3, in association with genetic aberrations. MYC and MYC/BCL2 double expression were more commonly observed in pSTAT3+ DLBCL cases (P < 0.001 and P = 0.001, respectively). However, BCL2 expression was not significantly different in DLBCL cases positive or negative for pSTAT3 expression (P = 0.420). Rearrangements of BCL2, BCL6, or MYC detected by FISH did not show any significant differences between pSTAT3+ DLBCL and pSTAT3− DLBCL (P > 0.05). One pSTAT3+ case (2%) showed rearrangements of both MYC and BCL6 genes, and no case had coexistent MYC and BCL2 rearrangements. Regarding TP53 exon mutations detected by sequencing, TP53 gene deletions detected by

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aDouble hit, MYC and BCL2 or BCL6 rearrangements.
bSummation of the classical and alternative NF-κB pathway expression.
FISH, or p53 expression, there were no significant differences between pSTAT3+ and pSTAT3− DLBCL cases (P > 0.05). Stratifying our cohort according to p53 expression, pSTAT3+ DLBCL showed a significant worse outcome in OS (P = 0.016) and PFS (P = 0.024) in the p53-negative group (Fig. 2A and B). A total of 13 (19%) DLBCLs harbored TP53 mutations. All of the TP53 mutations were confined to exons 4 to 8, which are the most critical sites.
for DNA binding (33). Eleven cases were missense mutations and two cases were nonsense mutations.

**Association of pSTAT3 expression with NF-κB components, cyclin D1 or pAKT**

Cooperation of STAT3 and NF-κB is well known (21, 34). However, few studies have correlated expression of individual NF-κB components (p50, p52, p65, and cRel) with pSTAT3 expression. In this study, a significant trend that p52 single component and p52/p65 dimer were more commonly observed in pSTAT3+ DLBCL compared with pSTAT3− DLBCL (P = 0.05 and 0.081, respectively). Other NF-κB single components or combinations of NF-κB dimers (p50/p65, p50/cRel, and p52/cRel) were not more commonly expressed in pSTAT3+ DLBCL (P > 0.05). Neither the classical NF-κB pathway (p50/p65 or p50/cRel), nor the alternative NF-κB pathway (p52/p65 or p52/cRel), nor both showed significant association with pSTAT3 expression (P > 0.05).

**Cyclin D1** is a known downstream target of pSTAT3 (35) and protein kinase B (AKT) can be activated via the JAK–STAT pathway (36). Therefore, we assessed protein expression of cyclin D1 and pAKT in this study. Neither cyclin D1 nor pAKT protein expression was significantly different between pSTAT3+ DLBCL and pSTAT3− DLBCL (P > 0.05).

**Multivariate analysis of prognostic parameters**

Stratified according to MYC expression, the prognostic effect of pSTAT3 was abrogated in patients with MYC+ DLBCL (P = 0.966 for OS and P = 0.818 for PFS; Fig. 2C and D). Survival analysis was not performed in MYC− group because only 4 MYC−/pSTAT3+ cases were present. Stratifying DLBCL cases into MYC/BCL2 protein double-positive (DP) and non–double-positive (non-DP) groups, pSTAT3 showed no effect on survival in the DP (P = 0.745 for OS and P = 0.592 for PFS) as well as the non-DP patient subgroups (P = 0.388 for OS and P = 0.281 for PFS; Fig. 2E–H). When stratifying DP and non-DP subgroups into COO classification, no effect on survival was seen (Supplementary Fig. S3 and Supplementary Table S1).

Univariate analysis identified advanced age, multiple extranodal sites of involvement, ABC subtype, pSTAT3 expression, and MYC expression increased hazard in patients with *de novo* DLBCL (P < 0.05 in all variables). Multivariate analysis using these five variables demonstrated that pSTAT3 is not an independent variable (P = 0.460 for OS and P = 0.523 for PFS). All the other variables were significant (Table 3).

**GEP and GSEA of pSTAT3+ DLBCL**

To further characterize pSTAT3+ DLBCL, we compared the GEP signatures of pSTAT3+ and pSTAT3− DLBCL using the Affymetrix HuG133plus2 platform (Affymetrix; Fig. 3A). With a FDR threshold of 0.3, a total of 26 genes were differentially expressed between the two groups, including 15 upregulated genes and 11 downregulated genes in pSTAT3+ DLBCL. Among the upregulated genes in pSTAT3+ DLBCL, STAT3, IL2RA, CD44, EPHA4, and CDK5R1 were significant. Upregulation of the IL2RA gene suggests a positive feedback mechanism of pSTAT3 because IL2 activates STAT3 via activating Janus-activated kinase (JAK). CD44 can acetylate and dimerize STAT3 in a growth factor- and cytokine-independent manner and has been shown to be involved in cell migration, tumor invasion, and metastasis, potentiating STAT3 function and partially explaining the adverse outcome in pSTAT3+ DLBCL (37). EPHA4 encodes ephrin receptor A4, which has receptor tyrosine kinase activity. CDK5R1 encodes CDK5/p35, which is a downstream target molecule of ephrin receptor A4 and its expression has been shown to predict inferior survival in patients with non–small cell lung cancer (38). Many of the downregulated genes encode proteins of unknown function. Huang and colleagues (24) proposed a prognostically valuable 11-gene signature in pSTAT3+ DLBCLs. The 11 genes were HSD17B4, MT1X, NAT8L, PCNX, RHEB, RNF149, SLA, SLC2A13, ZNF805, C15orf29, and ZNF420. However, few of these genes (RHEB, PCNX, and ZNF420) were expressed with marginal significance for survival in our cohort and combination of the 11 genes showed overall significant trend (P = 0.07). GSEA analysis showed trends for several gene sets, including the JAK–STAT pathway gene set, being enriched in pSTAT3+ DLBCL (Fig. 3B).

**Discussion**

In this study, 16% of *de novo* DLBCL cases expressed pSTAT3. The prevalence of pSTAT3 expression in DLBCL is lower than that reported in earlier studies, in which 30%...
to 40% of DLBCL expressed pSTAT3 (22, 24, 39, 40). Of note, pSTAT3 expression are 67%, 51%, 34%, 23%, 16%, and 11% if the pSTAT3 cutoffs are 10%, 20%, 30%, 40%, 50%, and 60%, respectively (Supplementary Table S2). With 30% cutoff, the prevalence of pSTAT3 expression is in similar range to prior data. However, our cutoff value for pSTAT3 was determined on the basis of a ROC curve to achieve optimal sensitivity and specificity. Compared with survival analysis using 50% cutoff (Fig. 1), 30% cutoff does not show any significant differences between pSTAT3+ DLBCL and pSTAT3- DLBCL (Supplementary Fig. S4). Furthermore, no clinical differences are observed between the two groups using 30% cutoff except COO classification (Supplementary Table S3). We additionally conducted survival analysis in four separate quartile groups (Q1: <30%; Q2: ≥30% and <50%; Q3: ≥50% and <70%; and Q4: ≥70%; Supplementary Table S4). Although overall quartile analysis showed significant stratification, Q3 and Q4 did not show significant difference (Supplementary Fig. S5, bottom row). Merging Q3 and Q4, we conducted survival analysis in three groups (T1: <30%; T2: ≥30% and <50%; and T3: ≥50%; Supplementary Table S5). T2 and T3 showed significant difference, whereas T1 and T2 did not (Supplementary Fig. S5, top row). On the basis of our analysis, we chose 50% as an optimal cutoff for pSTAT3 expression. With 50% cutoff, we could minimize possible contamination of pSTAT3 expression in non-lymphoma cells. As has also been shown by others (22–24, 39), pSTAT3 was more commonly expressed in ABC-DLBCL. Such a finding can be explained by Ding and colleagues (20) who showed that STAT3 gene transcription was negatively regulated by BCL6, hence providing a basis for STAT3 activation in ABC-DLBCL. We also showed that STAT3 mRNA level is quantitatively correlated with pSTAT3 expression. (Supplementary Fig. S2)

We showed that pSTAT3 expression in de novo DLBCL is associated with adverse outcome, confirming a similar observation by Huang and colleagues and Meier and colleagues (24, 40). We could not, however, show that pSTAT3 expression is an independent prognostic factor in patients with DLBCL in multivariate analysis (Table 3). Furthermore, pSTAT3 expression is associated with MYC expression and MYC/BCL2 double expression. However, when MYC expression was controlled, pSTAT3 did not significantly predict prognosis (Fig. 2). In cases with MYC/BCL2 DP or non-DP, significant difference was not observed, either. No survival difference was seen after stratified into GCB/ABC in DP and non-DP groups (Supplementary Fig. S4). Furthermore, multivariate analysis did not identify pSTAT3 as an independent hazard. Instead, other variables, such as stage, COO classification, and MYC expression, were shown to be independent prognosticators (Table 3). We additionally conducted bivariate analyses including each variable in the multivariate analysis and pSTAT3 expression to see if increased hazardous effect of pSTAT3 is observed (Supplementary Table S6). pSTAT3 did not show increased hazard except when pSTAT3 coanalyzed with ABC phenotype. Therefore, inferior outcome of patients with pSTAT3+ DLBCL appeared to be a result of the associated poor prognostic indicators such as advanced-stage disease and multiple extranodal sites of involvement. Interestingly, in patients with less aggressive or advanced disease, such as limited stage (stage I or II), involvement of less than 2 extranodal sites, absence of p53 expression, or GCB-type...
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pSTAT3 expression showed a worse outcome. Our data therefore suggest that pSTAT3 expression predicts poor outcome in less aggressive/advanced DLBCL, but it does not provide additional survival impact in patients with advanced disease or with already known poor prognostic factors, including MYC expression or BCL2/MYC coexpression (23, 30, 41).

The results of GEP analysis in this study showed that pSTAT3+ DLBCL is distinct from pSTAT3− DLBCL. Many of the upregulated genes, such as STAT3, IL2RA, IL1B, EPHA4, and CDK5R1 in pSTAT3+ DLBCL contain several binding sites for STAT3 in their promoters and some of the upregulated genes have been reported to correlate with aggressive features in carcinomas (37, 38). The results of GSEA also provide evidence that the JAK–STAT pathway is enriched in pSTAT3+ DLBCL, although the statistical significance is marginal. In a recent study by Huang and colleagues (24), the authors suggested that an 11-gene signature was associated with poor OS in patients with STAT3+ DLBCL, treated with CHOP and R-CHOP, respectively, without achieving statistical significance. Some of these genes were marginally upregulated in pSTAT3+ DLBCL by GEP in our study, partially in agreement with Huang and colleagues (24).

Although our GEP results did not show that MYC was significantly upregulated in pSTAT3+ DLBCL, it is not surprising to observe the correlation between MYC expression and pSTAT3 in this study because MYC is a known target of STAT3 (31, 42, 43). Kikuchi and colleagues (31) demonstrated that STAT3 was essential for MYC mRNA expression in a proB cell line (BAF/B03). Barre and colleagues (42) showed that STAT3 was recruited to the MYC promoters upon IL6 stimulation of glioblastoma cells using chromatin immunoprecipitation (ChIP). Bowman and colleagues (43) reported that MYC expression was induced by STAT3 in fibroblasts. In primary DLBCL patient samples, Gupta and colleagues (23) showed a trend between pSTAT3 and MYC expression in a small study of 23 patients.

NF-κB and pSTAT3 are known to cooperate and four different modes of reciprocal interaction in transcriptional control have been suggested (34). (i) STAT3/p65 in the nucleus can recruit p300 histone acetyltransferase, which acetylates histone as well as p65. Acetylated p65 is less prone to nuclear export, hence persists longer in the nucleus where it is transcriptionally active. (ii) In the nucleus, NF-κB/STAT3 can bind to particular DNA target sequences at sites where neither can bind alone. (iii) Unphosphorylated STAT3 can bind with and displace IκB so that NF-κB can be activated without any upstream signals. (iv) IκBζ, which is induced by NF-κB, can bind to STAT3 and inhibit STAT3-DNA binding. We showed a significant trend that p52 single expression and p52/p65 dimer expression were more commonly seen in pSTAT3+ DLBCL, supporting a cross-talk between STAT3 and NF-κB (44, 45). Lam and colleagues (21) showed the induction of IL6 and IL10 by the NF-κB pathway in ABC-DLBCL cell lines. Considering constitutive activation of NF-κB and common pSTAT3 expression in ABC DLBCL, targeting either or both of them appears to be an attractive addition to the current R-CHOP regimen especially in this subtype.

Recently, STAT3 was found to be a substrate of histone deacetylase 3 (HDAC3) in ABC-DLBCL (46). Although the primary substrates of HDACs are histones, nonhistone proteins, including NF-κB transcription factors, could also be targeted by HDACs (47). In the context of cross-talk between NF-κB and STAT3, targeting HDAC seems to be a reasonable approach. Gupta and colleagues (46) demonstrated that a HDAC inhibitor panobinostat (also known as LBH589) could dephosphorylate STAT3 in an ABC-DLBCL cell line, (Ly3), as well as DLBCL patient samples, in a dose-dependent manner. However, a recent phase I study using panobinostat with everolimus in patients with relapsed and refractory lymphoma did not show a response in patients with DLBCL (48). Lam and colleagues (21) also showed that blocking JAK/STAT3 activation using a JAK inhibitor in ABC-DLBCL cell lines reduces cell proliferation and survival. They also demonstrated a synergistic effect on tumor cell death by combining JAK/STAT3 and NF-κB inactivation in ABC-DLBCL cell lines. A phase II clinical trial using an oral JAK inhibitor (INCB18424) is in progress in patients with relapsed or refractory DLBCL or peripheral T-cell lymphoma (NCT01431209).

Scuto and colleagues (49) demonstrated that inhibition of STAT3 with short hairpin RNA was associated with apoptosis in a human ABC-like DLBCL cell line (Ly3), as well as tumor regression in nonobese diabetic/severe combined immunodeficient (NOD/SCID) mice injected by Ly3 cells. In their study, direct STAT3 inhibition reduced significant reduction of STAT3 targets such as MYC and survivin at the protein level. Survivin is an antiapoptotic protein and has been shown to be unfavorable prognostic marker in DLBCL (50). Furthermore, Scuto and colleagues also showed that inhibition of STAT3 thwarted IL10-dependent STAT3 activation, proving that STAT3 can be an attractive therapeutic target. Currently, a multi-institution phase I/II clinical trial using an antisense oligonucleotide inhibitor targeting STAT3 in patients with DLBCL is in progress (NCT01563302).

In summary, pSTAT3 expression is more commonly seen in ABC-DLBCL and is associated with advanced-stage, multiple extranodal sites of involvement, MYC expression, and MYC/BCL2 double expression. Although pSTAT3 is not an independent prognostic marker, pSTAT3 expression in DLBCL predicts an unfavorable outcome. GEP suggests that pSTAT3+ DLBCL is molecularly distinct from pSTAT3− DLBCL with a unique oncogenic pathway activation signature, which identify a group of patients who might benefit from the use of molecularly targeted therapies. Ongoing successful clinical trials targeting the STAT3 pathway may shed new light on the significance of STAT3 expression, particularly in refractory/resistant DLBCL.

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

Conception and design: C.Y. Ok, Z.Y. Xu-Monette, J.H. van Krieken, K.H. Young
Development of methodology: J. Chen, Z.Y. Xu-Monette, K.H. Young
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): C.Y. Ok, J. Chen, L. Li, A. Chiu, Y. Zu, A.J.M. Ferrori, M.B. Müller, L.J. Medeiros, K.H. Young
Study supervision: K.H. Young
Other (provision of case material and clinical data): A. Orazi
Other (approval of final article): A.J.M. Ferrori

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References


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Clinical Implications of Phosphorylated STAT3 Expression in De Novo Diffuse Large B-cell Lymphoma

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