Interleukin-6/STAT3 Pathway Signaling Drives an Inflammatory Phenotype in Group A Ependymoma

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Abstract

Ependymoma (EPN) in childhood is a brain tumor with substantial mortality. Inflammatory response has been identified as a molecular signature of high-risk Group A EPN. To better understand the biology of this phenotype and aid therapeutic development, transcriptomic data from Group A and B EPN patient tumor samples, and additional malignant and normal brain data, were analyzed to identify the mechanism underlying EPN Group A inflammation. Enrichment of IL6 and STAT3 pathway genes were found to distinguish Group A EPN from Group B EPN and other brain tumors, implicating an IL6 activation of STAT3 mechanism. EPN tumor cell growth was shown to be dependent on STAT3 activity, as demonstrated using shRNA knockdown and pharmacologic inhibition of STAT3. EPN tumor cell growth was shown to be dependent on STAT3 activity, as demonstrated using shRNA knockdown and pharmacologic inhibition of STAT3 mechanism. EPN tumor cell growth was shown to be dependent on STAT3 activity, as demonstrated using shRNA knockdown and pharmacologic inhibition of STAT3. The inflammatory factors secreted by EPN tumor cells were shown to reprogram myeloid cells, and this paracrine effect was characterized by a significant increase in pSTAT3 and IL-8 secretion. Myeloid polarization was shown to be dependent on tumor secretion of IL6, and these effects could be reversed using IL6-neutralizing antibody or IL6 receptor–targeted therapeutic antibody tocilizumab. Polarized myeloid cell production of IL8 drove unpolarized myeloid cells to upregulate CD163 and to produce a number of proinflammatory cytokines. Collectively, these findings indicate that constitutive IL6/STAT3 pathway activation is important in driving tumor growth and inflammatory cross-talk with myeloid cells within the Group A EPN microenvironment. Effective design of Group A–targeted therapy for children with EPN may require reversal of this potentially immunosuppressive and protumor pathway.

Introduction

Molecular subgroups of primary ependymoma (EPN) have recently been defined, including two main EPN subgroups arising in the posterior fossa, termed Groups A and B, that confer different biologic phenotypes and clinical courses (1–3). Phenotypically, Group A tumors occur in younger children and are characterized by upregulation of a variety of pathways, including angiogenesis, mesenchymal cell differentiation, cell proliferation, and inflammatory response, that are hallmarks of aggressive tumor biology.

Note: Supplementary data for this article are available at Cancer Immunology Research Online (http://cancerimmunolres.aacrjournals.org/).

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Normal brain samples (grade gliomas (HGG); 8 sonic hedgehog, 5 Group 3 and 7 Group teratoid/rhabdoid tumors (AT/RT); 14 pediatric and 7 adult high-pediatric and adult brain tumors. This consisted of 17 atypical EPN. A broader transcriptomic analyses utilized EPN samples

Transcriptomic analysis
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ncbi.nlm.nih.gov/geo/query/acc.cgi?acc

sion Omnibus (GEO) database (8) and are publicly accessible

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values (7). To reduce error associated with multiple testing, a

broadinstitute.org/gsea/msigdb; ref. 10).

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ref. 9).

Broad Institute Gene Pattern platform (Supplementary Fig. S1; nonnegative matrix factorization (NMF) available through the

EPN were assigned to consensus molecular subgroups using

DNA ampli-

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from patient surgical samples by tissue disaggregation and flow
cytometric sorting as described previously (3). Briefly, resected
tumor was finely minced with a razor and further triturated by vigorous pipetting. A single-cell suspension was obtained by

passing the sample through a 70-μm cell strainer (Becton Dickinson) of sufficiently large pore size to permit passage of all

immune and tumor cells but not clumped tumor cells. Disag-
gregated cells were viably frozen in standard freezing media

containing 10% DMSO and stored in liquid nitrogen for subse-
quently. Isolation of tumor and myeloid subpopulations

was performed by staining disaggregated samples with anti-

CD45-FITC and anti–CD11b-APC antibodies (Becton Dickinson

clones 2D1 and ICRF44, respectively) followed by flow sorting

using a Beckman-Coulter MoFlo XDP-100. RNA was isolated

from sorted cells using a microRNeasy kit (Qiagen). Extracted RNA

was amplified using the Nuge WT-Ovation One-Direct System

(NuGEN Technologies) that reverse transcribes RNA to cDNA,

which is amplified during SPIA amplification, a linear isothermal

DNA amplification process resulting in end-products of single-

strand DNA. Amplified RNA was labeled (NuGEN Encore Biotin

Module) and hybridized to Affymetrix Human Genome U133plus2 chips. Microarray. CEL file data were normalized as
described above.

Cytokine release assay

Viably frozen disaggregated tumor samples were thawed and

flow sorted to separate immune cells from tumor cells as previ-

ously described (3). Tumor cells were cultured in 1 ml. optimem

media supplemented with 15% FBS (O15) for 96 hours on ultra-

low attachment plates. Media were harvest and immediately

frozen at −80°C for later use. A high sensitivity Milliplex Map

kit (Millipore) was used to measure the concentration of 13

common cytokines [GM-CSF, IFNγ, IL1β, IL2, IL4, IL5, IL6, IL7,

IL8, IL10, IL12 (p70), IL13, and TNFα] as per the manufacturer’s

instructions. IL6 secretion in media from cell lines was also

measured using Quantikine ELISA human IL6 (R&D Systems)

according to the manufacturer’s instructions.

Western immunobLOTS

Primary antibodies used were pSTAT3 (Tyr-705; cat# 9145
cloned D3A7), STAT3 (cat# 9139 clone 124H6), suppressor

of cytokine signaling 3 (SOCS3; cat# 2923), myeloid cell leukemia

sequence 1 (BCL2-related; MCL1; cat# 5453 clone D35A5; Cell

Signaling Technologies). Anti–β-actin (cat# 12262 clone

8H10D10; Cell Signaling Technologies) was used as the protein

loading control. Membranes were blocked in TBS-Tween 5% milk

or BSA depending on the manufacturer’s recommendation. Bands

were visualized with Immobilon Western Chemiluminescent

HRP substrate (Millipore) on X-ray film, and densitometry mea-

surements were performed. All experiments were performed three
times, and representative blots are shown.

Cell lines

EPN cell line 811 was established from the fourth recurrence in

a patient with metastatic anaplastic EPN that exhibited a Group A

phenotype. This unique cell line is positive for chromosome 1q

gain (1q+) as was the tumor. 1q+ is known to be a poor risk factor

for EPN. This cell line was maintained under normal culture

conditions in Optimem media supplemented with 15% FBS

(O15; Invitrogen). Patient samples were obtained with consent

(COMIRB#95-500). Glioblastoma (GBM) cell line U87, obtained

Materials and Methods

Transcriptomic analysis

The primary EPN study cohort consisted of 21 primary Group A

and 20 primary Group B posterior fossa EPN and 9 supratentorial

EPN. A broader transcriptomic analyses utilized EPN samples

obtained at relapse (8 Group A and 6 Group B) and other

pediatric and adult brain tumors. This consisted of 17 atypical
teratoid/rhabdoid tumors (AT/RT); 14 pediatric and 7 adult high-

grade gliomas (HGG); 8 sonic hedgehog, 5 Group 3 and 7 Group

4 medulloblastomas (MED); and 15 pilocytic astrocytoma (PA).

Normal brain samples (n = 13) were also included in this analysis,

obtained from autopsy and epilepsy surgery from both infra- and

supratentorial anatomic sites. All patient samples were obtained

with consent (COMIRB 95-500). Tumor samples were processed

identically at our institution and analyzed using the Human

Genome U133plus2 Array (Affymetrix) platform as described

previously (3). Microarray. CEL datafiles were background cor-

corrected and normalized using the guanine cytosine robust multi

array average (gcRNA) algorithm resulting in log2 expression

values (7). To reduce error associated with multiple testing, a

filtered list was created containing the highest expressed probe

across all samples for each gene that possessed multiple probe

sets. This list was further filtered to remove probe sets that were

expressed below a threshold level that denoted absence of expres-

sion in any sample. These microarray data have been deposited in

the National Center for Biotechnology Information Gene Expres-

sion Omnibus (GEO) database (8) and are publicly accessible

through GEO Series accession number GSE66354 (http://www.


EPN were assigned to consensus molecular subgroups using

nonnegative matrix factorization (NMF) available through the

Broad Institute Gene Pattern platform (Supplementary Fig. S1; ref. 9).

Geneset enrichment analysis (GSEA) was used to examine enrichment of genes in predefined reference sets that are based

on biologic knowledge using tools available from the Broad

Institute Molecular Signatures Database (MSigDB; http://www.
broadinstitute.org/gsea/msigdb; ref. 10).

Tumor versus myeloid cell transcriptome analysis

to determine the distribution of transcripts of interest between
tumor cells and tumor-associated myeloid cells, we performed

transcriptomic analysis on populations that had been isolated

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from ATCC, was cultured in MEM supplemented with 10% FBS, nonessential amino acids, sodium pyruvate, and sodium bicarbonate. Conditioned media (CM) from cell lines, as used for characterization of cytokine release and monocyte polarization, were obtained by harvesting media from a known number of cells after 24-hour incubation. Cell line authentication was performed using short tandem repeat profiling and comparison with known cell line DNA profiles.

**shRNA transfection**

A pLKO system (Sigma-Aldrich) was utilized for lentiviral RNAi-mediated STAT3 protein knockdown. TRC numbers for shRNAs used STAT3 TRCN0000002839, STAT3 TRCN0000002840, STAT3 TRCN0000002842 or pLKO.1 nontargeting (SHC016).

**Monocyte polarization assays**

CD14⁺ monocytes were isolated from HLA-matched donor peripheral blood by flow sorting using CD14-FITC (Becton Dickinson) and MoFlo Astrios EQ flow cytometry sorter. Post-sorted cells were incubated in various conditions for 96 hours on ultra-low attachment plates (Corning). 811-conditioned media (811 CM) were collected off 90% confluent 811 cell line and immediately frozen at −80°C for later use. IL6-neutralizing antibody (R&D Systems) was used at concentration of 50 μg/mL, and tocilizumab (Genentech) was used at concentration of 1 mg/mL. Media were harvested from cells after 96 hours, and cytokine concentrations were measured by multiplex bead cytokine analysis as described above. Cells were stained with pSTAT3-PE (BD) according to the manufacturer’s instructions and run on Beckman Coulter Gallios 561; analysis was done using FlowJo v10.0.7 (FlowJo).

**IL8 functional assay**

Media were harvested from 811-polarized monocytes (MonoCM) or nonpolarized monocytes (MonoO15) as described above. Fresh CD14⁺ monocytes were then incubated in MonoCM or MonoO15 for 96 hours. IL8-neutralizing antibody (R&D Systems) was added to MonoCM at 5 μg/mL. Cells were collected and stained with CD14-FITC (Becton Dickinson) and MoCD45-PE (BD) according to the manufacturer’s instructions and run on a FACSCanto II flow cytometry sorter. Post-sorted cells were incubated in various conditions for 96 hours, and cytokine concentrations were measured as described above. Cytokine concentrations from primed media were subtracted to assess additional secretion.

**Statistical analyses**

Statistical analyses were performed using R bioinformatics, Prism (GraphPad), and Excel (Microsoft) software. For all tests, statistical significance was defined as P < 0.05.

**Results**

**STAT3-upregulated genes and IL6 signaling pathway genesets are significantly enriched in Group A EPN**

We used nonbiased GSEA analysis to identify transcription factor activity that might mechanistically underlie the Group A inflammatory response phenotype. Primary EPN Group A (n = 21) and B (n = 20) transcriptomic profiles were screened for enrichment of transcriptional programs using MSigDB C3 TFT (transcription factor targets) v.4 motif genesets (n = 615) containing genes that share a transcription factor–binding site motif defined in the TRANSFAC database (version 7.4, http://www.gene-regulation.com/). In Group A EPN, transcription factor target genes of leading cancer inflammatory mediator STAT3 (MSigDB: V5STAT3_01) were the second most enriched of 615 TFT genesets (NES = 2.07; FDR q < 0.0001; Table 1; Supplementary Fig. S2A). Specific STAT3 TFT motif–containing genes highly upregulated (fold change, FC > 10) in Group A include chemokine (C-C motif) ligand 2 (CCL2) and v-raf murine sarcoma virus oncoprotein homolog F (MAFF; Table 2).
We further characterized the involvement of STAT3 in Group A EPN by using GSEA to measure enrichment of experimentally determined STAT3-upregulated geneset (n = 36), created from a review of the role of STAT3 in cancer inflammation and immunity (ref. 13; Supplementary Table S1). This geneset was enriched in Group A to a greater extent (NES = 2.33; FDR q < 0.001) than the STAT3 TTF geneset (Table 1; Supplementary Fig. S2B). Experimentally determined STAT3-upregulated genes in Group A (Table 2) were largely discrete from those identified as STAT3 TTFs with the exception of CCL2 and ICAM1. Notable STAT3-upregulated genes (FC > 10) in Group A include chitinase 3-like 1 (CHI3L1, AKA YKL-40), IL8, CCL2, SOCS3, IL6, and prostaglandin-endoperoxide synthase 2 (PTGS2, AKA COX-2). Collectively, these data suggest activation of the STAT3 signaling pathway in Group A EPN.

It is known that IL6 drives oncogenic activation of STAT3, increasing cell proliferation, survival, and invasion while suppressing antitumor immunity (13). Persistent IL6/STAT3 pathway activation is involved in various inflammation-associated cancers, most notably colorectal (14), gastric (15), and liver (16) cancers. Given the high level of IL6 gene expression, we hypothesized that IL6 may be driving activation of STAT3 in Group A EPN. Enrichment of MSigDB C2 BioCarta pathway v.4–curated genesets (n = 217; http://www.biocarta.com/genes/index.asp) was assessed using GSEA and showed that, in agreement with our hypothesis, the BioCarta IL6 pathway geneset was among the 10 highest enriched pathways in Group A (NES = 1.81; FDR q = 0.015; Tables 1 and 2; Supplementary Fig. S2B). Of note, the BioCarta cytokines and inflammatory response geneset (BIOCARTA_INFLAM_PATHWAY) was the second most enriched BioCarta pathway geneset (NES = 1.95; FDR q = 0.0034; Supplementary Fig. S2D).

A broader examination of Group A EPN–associated IL6/STAT3 pathway genes identified by GSEA gene expression was next performed in EPN from recurrences and supratentorial sites, as well as other common pediatric and adult brain tumors and normal brain. Recurrent Group A EPN showed reduced expression of IL6, consistent with the decreased inflammatory phenotype observed at recurrence that was previously identified (3). IL6 expression was significantly higher in primary Group A EPN than in all other brain tumor types (Fig. 1A). IL6 expression was higher in Group A EPN than in both adult GBM (FC = 7.0; P = 0.039) and MED (FC = 16.5; P = 2.5 × 10⁻⁶), which is notable as constitutive IL6/STAT3 activation has been identified in these tumor types (17, 18).

Similar to IL6, IL8 was significantly overexpressed compared with recurrent Group A EPN (FC = 7.6; P = 0.0016), with all other brain tumor types (FC = 22-fold higher than all other tumor samples combined; P = 4.3 × 10⁻⁴), and with normal brain ([NB] FC = 104; P = 1.4 × 10⁻¹⁶; Fig. 1B). Thus, overexpression of key inflammatory mediator IL6 and IL8 appears to be hallmarks of the Group A EPN transcriptome in the context of not only EPNs as a whole, but of all brain tumors. The apparent restriction of IL6 and IL8 gene expression to Group A EPN in this broad transcriptomic analysis provides further evidence that an IL6/STAT3 signaling pathway underlies the inflammatory signaling pathway present in Group A EPN.

Key Group A EPN IL6/STAT3 inflammation signature genes are differentially distributed between tumor and tumor-infiltrating myeloid cells

Prior studies of EPN immunobiology have identified that tumor-infiltrating immune cells can significantly contribute to the overall gene expression profiles of surgical tumor samples (19). A subset of genes associated with longer progression-free survival in EPN were found to be restricted to tumor-infiltrating myeloid cells that contribute up to 25% of the cellular content of surgical tumor specimens (12). The contribution of tumor-infiltrating myeloid cells to the inflammatory TME, through the IL6/STAT3 activation, is well established (13, 20). We, therefore, sought to determine the contribution of tumor-infiltrating myeloid cells to the inflammatory TME. We, therefore, sought to determine the contribution of tumor-infiltrating myeloid cells to the inflammatory TME.
myeloid cells to the Group A EPN IL6/STAT3 gene expression signature. Surgical samples from two postoperative fossa EPNs were disaggregated and flow-sorted to isolate myeloid cells (CD45" and CD11b") and tumor cells (CD45+). Transcriptomic analysis was performed, and the relative expression of Group A IL6/STAT3 inflammation signature genes between these TME cellular compartments was measured (Supplementary Fig. S3). Of the 34 genes identified by GSEA as enriched in the STAT3 TST, STAT3-upregulated and IL6 pathway genesets (Table 2), IL8, ICAM1, PTGS2, and IL1B were on average more than 10-fold higher in the myeloid than in the tumor cell compartments. Conversely, CHI3L1 gene expression was 67-fold higher in the tumor compartment. CHI3L1 has a proposed role in driving the Group A EPN–specific mesenchymal phenotype (2). Thus, tumor-infiltrating myeloid cells contribute to the IL6/STAT3 inflammatory gene expression signature in the Group A EPN.

Tumor cell secretion of IL6 is associated with STAT3 phosphorylation in Group A EPN

We isolated viable tumor cells, excluding other cells in the TME, from EPN clinical samples (7 Group A; 8 Group B) by tissue disaggregation and flow sorting to remove all immune cell types as described above. Tumor cells were cultured in 1 mL serum-supplemented media (O15) for 96 hours. Multiplexed cytokine profiling revealed that IL6 was the only cytokine that was significantly higher in Group A than in Group B with a trend toward significance (P = 0.031; Fig. 2A). Of the remaining cytokines, only IL10 was >2-fold higher in Group A than in Group B with a trend toward significance (P = 0.12; Supplementary Fig. S4).

Presence of significantly higher STAT3 transcripts and STAT3-regulated transcripts is evidence of STAT3 activity; hence, we evaluated STAT3 phosphorylation as a more direct indicator of STAT3 activity in EPN patient samples. Phosphorylation of STAT3-Tyr705 by upstream signaling results in dimerization and translocation to the nucleus, resulting in transcription of STAT3-target genes. The ratio of tyrosine 705-phosphorylated (pSTAT3) to total STAT3 protein, as measured by Western blot analysis, was used as a measure of STAT3 activity in patient tumor samples (12 Group A; 12 Group B; Fig. 2B shows a representative blot). Densitometric quantification of pSTAT3 and total STAT3 revealed a significantly higher ratio of phosphorylation in Group A (FC = 1.84; P = 0.011; Fig. 2C).

Table 2. Significantly upregulated genes in Group A EPN from enriched STAT3 and IL6 pathway genesets

<table>
<thead>
<tr>
<th>Gene symbol</th>
<th>Gene title</th>
<th>FC</th>
<th>P</th>
<th>q</th>
</tr>
</thead>
<tbody>
<tr>
<td>IL8</td>
<td>Interleukin 8</td>
<td>24.13</td>
<td>5.22E-09</td>
<td>2.17E-06</td>
</tr>
<tr>
<td>CCL2</td>
<td>Chemokine (C-C motif) ligand 2</td>
<td>21.62</td>
<td>1.39E-08</td>
<td>3.67E-06</td>
</tr>
<tr>
<td>IRF1</td>
<td>Interferon regulatory factor 1</td>
<td>8.66</td>
<td>8.48E-08</td>
<td>1.17E-05</td>
</tr>
<tr>
<td>ICAM1</td>
<td>Intercellular adhesion molecule 1</td>
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<td>2.70E-07</td>
<td>0.20E-05</td>
</tr>
<tr>
<td>MAPK1</td>
<td>v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)</td>
<td>15.87</td>
<td>7.73E-07</td>
<td>5.19E-05</td>
</tr>
<tr>
<td>SERPING1</td>
<td>Serpin peptidase inhibitor, clade G (C1 inhibitor), member 1</td>
<td>3.11</td>
<td>6.45E-06</td>
<td>0.000264</td>
</tr>
<tr>
<td>CISH</td>
<td>Cytokine inducible SH2-containing protein</td>
<td>2.24</td>
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<td>0.000737</td>
</tr>
<tr>
<td>ABPA1</td>
<td>Amyloid beta (A4) precursor protein-binding, family A, member 1</td>
<td>1.93</td>
<td>0.000496</td>
<td>0.0393</td>
</tr>
</tbody>
</table>

Experimentally determined STAT3-upregulated genes (Yu et al., ref. 13)
Constitutively activated STAT3 in EPN has pro-proliferative and antiapoptotic roles

Having identified a potentially critical role for constitutively activated STAT3 in EPN, we examined proliferation and survival of EPN cells after loss of STAT3. Functional studies were performed using an EPN cell line that was recently established from the fourth recurrence in a child with metastatic posterior fossa anaplastic EPN that exhibited a Group A phenotype. This cell line (811) was validated by karyotype analysis and was shown to harbor chromosome 1q-gain (1q+), a known poor risk factor for EPN (21). Characterization of these EPN cells demonstrated that 811 secreted comparable amounts of IL6 as secreted by GBM cell line U87, in which aberrant IL6/STAT3 pathway activation had previously been identified and associated with invasiveness (ref. 22; Fig. 3A).

Loss of STAT3 through shRNA knockdown (Fig. 3B) resulted in significant reduction in proliferation of 811 cells than NT control shRNA (shNT) as measured by both cell-viability measurement (MTS) and DNA synthesis (3H-thymidine; Fig. 3C and D). Pharmacologic STAT3 inhibition (S3I-201) showed that 811 cells were more sensitive (viability IC50 = 108 μmol/L; DNA synthesis IC50 = 86 μmol/L) than U87 cells (viability IC50 = 140 μmol/L; DNA synthesis IC50 = 225 μmol/L; Supplementary Fig. S5A and S5B). The clinical relevance of these S3I-201 IC50 values is unknown, as S3I-201 has not yet been tested in a clinical trial, rather this inhibitor provides proof-of-principle for therapeutic targeting of STAT3. STAT3 inhibition did not affect cell cycle in 811 cells (Supplementary Fig. S5C). However, shRNA knockdown of STAT3 resulted in activation of apoptosis, with significant increase of cleaved caspase 3/7 compared with shNT (Fig. 3E), and significant apoptosis was demonstrated using S3I-201 at >IC50 concentration (Supplementary Fig. S5D). Collectively, these data support the hypothesis that, in EPN with constitutively activated STAT3, this transcription factor has both prosurvival and anti-apoptotic roles.

We observed an S3I-201 dose-dependent reduction of pSTAT3 pathway protein levels by Western blot (Supplementary Fig. S5E). Although total STAT3 remained relatively constant up to 500 μmol/L of S3I-201, phosphorylation was completely inhibited above 125 μmol/L. STAT3 transcriptional targets SOCS3 and MCL-1 were similarly reduced in a dose-dependent manner. STAT3 inhibition did not, however, reduce secretion of IL6, suggesting that IL6 regulation is upstream of STAT3 in the signaling pathway (Fig. 3F; Supplementary Fig. S5F).

EPP-secreted IL6 induces CD14+ monocytes to secrete key proinflammatory cytokine IL8

Transcriptomic analyses of Group A EPN identified that tumor-infiltrating myeloid cells contributed strongly to the inflammatory phenotype, and specifically IL8 expression, a hallmark of the IL6/STAT3 inflammation signature geneset, was highly enriched in Group A EPN patients (Fig. 1; Supplementary Fig. S1).

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targets, including IL8. To evaluate this, CD14+ myeloid cell STAT3 and upregulation of transcriptional inflammatory phenotype in a paracrine fashion, resulting in activation of STAT3 knockdown.

CD14+ monocytes were cultured in media harvested from CD14+ monocyte/CM culture cytokine levels to identify changes in monocyte-derived cytokines. There was a 9.2-fold increase (P = 0.043) in IL8 secretion from CD14+ cells treated with 811CM compared with that with media control alone (Fig. 4A). The remaining 12 cytokines tested did not show any significant differences (data not shown).

To determine whether IL8 production in CD14+ monocytes was induced by EPN-derived IL6, the experiment was repeated with the addition of IL6-neutralizing antibody (IL6NA) or IL6 receptor-neutralizing antibody tocilizumab. In both cases, production of IL8 by monocytes was significantly lowered by greater than 75% (Fig. 4B). Furthermore, flow cytometric measurement of pSTAT3 demonstrated significant induction of STAT3 phosphorylation (Tyr-705) in CD14+ monocytes, and this was reversed with addition of IL6NA (Fig. 4C and D). EGF, a potential alternative activator of STAT3, was shown not to drive STAT3 phosphorylation or IL8 release, as EGFR-blocking antibody cetuximab did not reverse this phenotype in 811 CM–treated myeloid cells (Supplementary Fig. S6B and S6C). Together, these data support our hypothesis that Group A EPN secretes IL6, which stimulates production of proinflammatory IL8 by myeloid cells via activation of STAT3 in the TME in a paracrine fashion.

IL8-mediated signaling between monocytes perpetuates inflammatory signaling in the TME

IL8 is a potent chemokine that has a variety of roles in inflammation. Although its most common function is to induce neutrophil infiltration, IL8 can also promote tumor-associated macrophages to secrete more cytokines and growth factors that further induce proliferation and tumor invasion (23). IL8 was the only cytokine we found to be significantly upregulated by monocytes in response to tumor cell paracrine signaling (Fig. 4A). We hypothesized that IL8 production by tumor-polarized monocyte could further polarize monocytes in a paracrine fashion. To test this hypothesis, freshly sorted CD14+ monocytes were cultured in media harvested from CD14+ monocytes that had been primed in either tumor-conditioned media (MonoCM) or control media (MonoO15) for 96 hours. Strikingly, a significant upregulation of CD163 was observed in cells cultured in MonoCM compared with those cultured in control media (Fig. 5A). In addition, MonoCM induced secretion of a number of common proinflammatory cytokines IL10, IL13, IL1β, IL6, IL7, and IL8 (Fig. 5B). Addition of IL8-neutralizing antibody to MonoCM prevented CD163 upregulation and was accompanied with upregulation of both HLA-DR and Fc-receptor CD64 expression (Fig. 5A). All proinflammatory cytokine production was reduced with the addition of IL8-neutralizing antibody to MonoCM (Fig. 5B).

Collectively, these studies provide evidence that EPN tumor cells induce paracrine polarization of monocytes through secretion of IL6. This inflammatory phenotype is then amplified between monocytes through upregulated IL8 production.
Discussion

Inflammatory response has been identified as a predominant transcriptomic phenotype in Group A EPN (1–3). The present study identifies tumor IL6/STAT3 pathway activation and cross-talk with myeloid cells as a potential mechanism underlying this phenotype. IL6/STAT3-mediated cross-talk between tumor and immune cells, resulting in inflammation, has been well documented in a number of tumors (20). Persistent IL6/STAT3 pathway activation is involved in various inflammation-associated cancers, most notably colorectal (14), gastric (15), and liver (16) cancers. It is known that oncogenic activation of STAT3, driven by IL6, increases cell proliferation, survival, and invasion as well as suppressing antitumor immunity (13). Tumor-derived IL6 affects the differentiation of myeloid lineages, including macrophages and dendritic cells, through STAT3 activation in these immune cell types (24). STAT3 activation in tumor-associated myeloid cells results in expression of procarcinogenic inflammatory mediators and upregulation of angiogenic factors and growth factors, leading to increased tumor growth in a paracrine fashion (20). In this study, EPN tumor cells were shown to release IL6, which activated myeloid cell STAT3 in a paracrine fashion. STAT3 activation resulted in increased IL8 production, which further polarizes myeloid cells to an inflammatory phenotype. In the central nervous system, oncogenic IL6/STAT3 signaling has been documented predominantly in GBM, the most common malignant brain tumor in adults, as important in proliferation, survival, and invasiveness of tumor cells and as a key regulator of the immunosuppressive microenvironment (25–29). GBM have been demonstrated to harbor protumor microglia/macrophages that are polarized by glioma stem cell–secreted factors (30). This cross-talk has been attributed to STAT3 activation (31). Therapeutic targeting of STAT3 has also shown promise in the most common malignant pediatric brain tumor, MED (17, 32). To our knowledge, the present study represents the only demonstration of such cross-talk in EPN. Given that IL6 and IL8 gene expression is elevated in Group A EPN when compared with other brain tumors, including GBM and MED, it emphasizes the particular importance of IL6/STAT3 signaling and immune cross-talk in the biology of this tumor.

The EPN Group A IL6/STAT3 activation gene set includes critical effectors of the key phenotypic characteristics of Group A EPN (1–3), namely inflammation [IL6, CCL2, PTGS2 (COX2)], mesenchymal transition (CHI3L1), invasiveness (TIMP1, MMP2, MMP9), angiogenesis (VEGFA), and antiapoptosis (MCL1, BIRC3). Thus, constitutive IL6/STAT3 signaling may underlie a number of the characteristic oncogenic phenotypes of Group A EPN, representing a "molecular hub" as has previously been ascribed to STAT3 in gliomas (33). A recent epigenomic study of EPN revealed that Group A, unlike Group B, exhibits a CpG island methylator phenotype (CIMP), suggesting epigenetic modifiers as rational therapeutic candidates in this molecular subgroup (34). Both IL6 and STAT3 have been shown to drive hypermethylation, potentially linking the IL6/STAT3 pathway with CIMP in this subgroup (35–37). Given these potentially pivotal roles of IL6/STAT3 in Group A EPN tumor biology, therapeutic exploration of STAT3 and/or IL6 inhibition is warranted.

We have previously shown that immunity affects outcome in pediatric EPN (19). Subsequently, we characterized immunologic differences in posterior fossa EPN, identifying an immunosuppressed phenotype in Group A when compared with Group B (3). Specifically, T cells derived from Group A tumors did not respond to stimulation with appropriate cytokine release and appeared to
have an exhausted phenotype compared with those derived from Group B tumors, a finding also seen in GBM (38). Thus, in Group A EPN, there is an association of IL6/STAT3-mediated inflammation with an immunosuppressed phenotype. Numerous mechanisms have been demonstrated to link inflammation to immunosuppression, such as generation of myeloid-derived suppressive cells (39) and immunosuppressive T-cell subsets (40). STAT3 has been shown to inhibit expression of antitumor T helper type immune-stimulating molecules, and promote expression of immunosuppressive factors, and is therefore likely drives immunosuppression in Group A EPN (41). With the recent success of cancer therapies that inhibit immunosuppressive factors, most notably CTLA-4 and PD-1 (42, 43), identification of a tumor-associated myeloid cell–mediated immunosuppressive mechanism in Group A EPN has particular clinical relevance. Reversal of myeloid cell–mediated immunosuppressive phenotypes for therapeutic gain has been achieved by T-cell activation strategies, such as IL12 treatment that results in reprogramming of tumor-associated myeloid cells (44). Alternatively, directly targeting tumor-associated myeloid cells has shown promise, as achieved by CSF-1R inhibition in GBM (45). The ability of IL6 receptor antagonist tocilizumab, which is FDA approved for treatment of rheumatoid arthritis (46), to abrogate IL6/STAT3-mediated tumor/myeloid cell cross-talk in the present study provides yet another therapeutic approach. Group A EPN has a poor outcome and little evidence that it is responsive to standard chemotherapy. Our work is highly suggestive that in the realm of pediatric brain tumors, this specific subgroup of EPN would be a strong candidate for the development of immunotherapy.

Disclosure of Potential Conflicts of Interest

R. Vibhakar reports receiving commercial research support from Epizyme. No potential conflicts of interest were disclosed by the other authors.

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Inflammatory IL6/STAT3 Signaling in Ependymoma

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Several studies have shown that the interleukin-6 (IL-6) pathway is involved in the spread of gastric cancer, and that the expression of interleukin-6 (IL-6) is associated with circulating carcinoembryonic antigen (CEA) in patients with hepatocellular carcinoma (HCC) [1, 2].

It has been observed that the expression of IL-6 is associated with poor prognosis in patients with colorectal cancer [3]. A recent study has shown that IL-6 expression is associated with a higher risk of recurrence and metastasis in patients with colorectal cancer [4].

Moreover, a study has shown that the expression of IL-6 is associated with a higher risk of recurrence and metastasis in patients with colorectal cancer [5].

In conclusion, the expression of IL-6 is associated with a higher risk of recurrence and metastasis in patients with colorectal cancer. Further studies are needed to elucidate the role of IL-6 in the progression of colorectal cancer.
Interleukin-6/STAT3 Pathway Signaling Drives an Inflammatory Phenotype in Group A Ependymoma

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