Clinical Studies

N-Myc Regulates Expression of the Detoxifying Enzyme Glutathione Transferase GSTP1, a Marker of Poor Outcome in Neuroblastoma

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Abstract

Amplification of the transcription factor MYCN is associated with poor outcome and a multidrug-resistant phenotype in neuroblastoma. N-Myc regulates the expression of several ATP-binding cassette (ABC) transporter genes, thus affecting global drug efflux. Because these transporters do not confer resistance to several important cytotoxic agents used to treat neuroblastoma, we explored the prognostic significance and transcriptional regulation of the phase II detoxifying enzyme, glutathione S-transferase P1 (GSTP1). Using quantitative real-time PCR, GSTP1 gene expression was assessed in a retrospective cohort of 51 patients and subsequently in a cohort of 207 prospectively accrued primary neuroblastomas. These data along with GSTP1 expression data from an independent microarray study of 251 neuroblastoma samples were correlated with established prognostic indicators and disease outcome. High levels of GSTP1 were associated with decreased event-free and overall survival in all three cohorts. Multivariable analyses, including age at diagnosis, tumor stage, and MYCN amplification status, were conducted on the two larger cohorts, independently showing the prognostic significance of GSTP1 expression levels in this setting. Mechanistic investigations revealed that GSTP1 is a direct transcriptional target of N-Myc in neuroblastoma cells. Together, our findings reveal that N-Myc regulates GSTP1 along with ABC transporters that act to control drug metabolism and efflux. Furthermore, they imply that strategies to jointly alter these key multidrug resistance mechanisms may have therapeutic implications to manage neuroblastomas and other malignancies driven by amplified Myc family genes. Cancer Res; 72(4); 1–9. ©2011 AACR.

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Introduction

Neuroblastoma is a solid tumor of embryonal neural crest origin and is the most common extracranial solid tumor of early childhood, accounting for 15% of all cancer related deaths in children (1). Patients diagnosed over one year of age often have disseminated, metastatic disease, often with MYCN amplification. While neuroblastomas typically respond to initial therapy regardless of risk group (2), the majority of patients with high-risk disease relapse with tumors that are refractory to treatment. There are no salvage regimens known to be curative for these patients (3). We have previously shown that the ATP-binding cassette transporter C1 (ABC1), a key component of phase III detoxification, is a powerful independent prognostic marker in neuroblastoma (4, 5). Consistent with this observation, ABC1 is able to efflux a wide range of chemotherapeutics (6), including many agents of importance in neuroblastoma therapy. However, several important chemotherapeutic agents to which resistance is observed, including cisplatin and cyclophosphamide, are not substrates of ABC1. Amongst the well-characterized contributors to multidrug resistance in other types of tumors are cellular
detoxification pathways. In particular, the phase II conjugating enzyme glutathione S-transferase P1 (GSTP1) is upregulated in a wide range of tumors and high GSTP1 expression is often associated with multidrug resistance (7–9). GSTP1 catalyses the conjugation of reduced glutathione to otherwise harmful electrophilic compounds, including cytotoxic drugs, and can sequester a range of nonsubstrate ligands (10). In addition to these roles, GSTP1 has been proposed to inhibit the mitogen-activated protein kinase (MAPK) pathway through direct interaction with c-Jun-NH2-kinase 1 (JNK1), decreasing sensitivity to drug-induced apoptosis (11). We have, therefore, extended our studies to investigate the prognostic value of this gene in neuroblastoma.

Here, we show that GSTP1 expression is an independent prognostic indicator of clinical outcome in primary neuroblastoma and, like ABCC1, is a direct transcriptional target of the N-Myc oncogene. The regulation of multiple components of drug metabolism pathways has implications for understanding drug insensitivity in patients with neuroblastoma with MYCN amplification and potentially in other malignancies with increased expression of Myc family proteins.

Materials and Methods

Patient tumor samples

All patient material used for gene expression analyses has been previously described (5, 12). In brief, a small discovery cohort of 51 primary tumors from previously untreated patients was obtained from either the Sydney Children’s Hospital, Sydney, Australia or the Neuroblastoma Tumor Bank of the Pediatric Oncology Group, USA (“SCH/POG” cohort; ref. 12) and a large validation cohort of 207 patients enrolled onto COG Neuroblastoma Biology Study 9047 was obtained from the Tumor Bank of the Children's Oncology Group, USA (“COG” cohort; ref. 5). The study was approved by the individual Institutional Review Boards, and informed consent was obtained for patients registered on the study. Publicly available data for GSTP1 expression from a customized oligonucleotide microarray data set of primary tumors from 251 patients with neuroblastoma from the German Neuroblastoma Trials NB90-NB2004 were also analyzed as a second independent validation cohort (“Oberthuer cohort”; GSTP1 probe = A_23_P202658). The patient cohort and microarray study are previously published (13). A summary of patient data for each cohort is provided as Supplementary Tables S1–S3.

Treatment

Treatments subsequently administered to patients were specific to their disease stage, age, and tumor biology and have been previously described for each of the SCH/POG (4), COG (5), and Oberthuer cohorts (14).

TH-MYCN mouse tumor samples

The TH-MYCN transgenic mouse model of neuroblastoma, which has the expression of the human MYCN oncogene targeted to mouse neuroectodermal cells via the rat tyrosine hydroxylase promoter, has been previously described (15–17). When medium palpable tumors (∼1 cm²) were detected, they were resected, measured, and snap frozen in liquid nitrogen for subsequent analysis. All experimental procedures were approved by the University of New South Wales Animal Care and Ethics Committee and were conducted under the Animal Research Act, 1985 (NSW, Australia) and the Australian Code of Practice for the Care and Use of Animals for Scientific Purposes (1997).

Real-time PCR methods

For tumor samples, total cytoplasmic RNA was isolated from human and mouse tumor material using a guanidinium thiocyanate-phenol-chloroform extraction method (4) and cDNAs were synthesized from 1 μg of RNA using random hexanucleotide primers and Moloney murine leukemia virus (MMLV) reverse transcriptase. Gene expression was determined by real-time PCR (RT-PCR) using either a Prism 7700 or 7900 Sequence Detection System (Applied Biosystems) with the following oligonucleotide primers and probes: human GSTP1, β-2 microglobulin (B2M) and MYCN and mouse Gstp1, Gsp2 (the 2 mouse genes corresponding to human GSTP1) and B2m. All sequences are shown in Supplementary Table S4.

For cell lines, RNA samples were prepared with Tri-Reagent (Sigma-Aldrich) and treated with DNase (DNAfree; Ambion). Reverse transcription and PCR were conducted by a SuperScript reverse transcription-PCR kit (Invitrogen). RT-PCR was carried out with iQ SYBR Green Supermix and the iQCycler thermocycler (BioRad) with primers and probes for human MYCN, GSTP1, NUC, and GUSB. All sequences are shown in Supplementary Table S4.

Gene expression levels were determined using the ΔΔCt method, normalized to the B2M control, and expressed relative to a calibrator (18).

Western blot analysis

Frozen tissue (∼50 mg) was pulverized on dry ice with a mortar and pestle in 500 μL lysis buffer (2× PBS, 1% NP-40, 0.5% sodium deoxycholate, and 0.1% SDS) containing a protease inhibitor cocktail (Sigma-Aldrich). Samples were centrifuged at 13,000 rpm in a benchtop centrifuge and the supernatants retained and quantitated by BCA assay (Pierce). Samples (20 μg) were electrophoresed on a 4% to 20% SDS-PAGE gel and transferred to nitrocellulose membrane (GE Healthcare). The membrane was blocked with 5% skim milk powder in Tris-buffered saline with 0.05% Tween 20, then incubated with an anti-GSTP1 antibody (mouse monoclonal 3F2C2, Abcam) followed by a horseradish peroxidase–conjugated secondary antibody. Membranes were developed with Supersignal reagent (Pierce), visualized on film and quantitated relative to α-tubulin by densitometry with QuantityOne software (BioRad).

Human neuroblastoma cell lines and culture

SH-EP Tet-21N cells (19) were cultured in Dulbecco's Modified Eagle's medium containing 10% heat-inactivated tetracycline-free FBS, whereas BE(2)-C and LA-N-5 cells were cultured in RPMI-1640 medium containing 20% FBS and
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Figure 1. GSTP1 is marker of poor prognosis in neuroblastoma. Kaplan–Meier curves for EFS (A) and overall survival (OS; B) in 51 patients with neuroblastoma from the SCH/COG cohort according to the expression of GSTP1. The level of GSTP1 expression was determined by RT-PCR and tumors dichotomized around the median value. Survival curves were analyzed by log-rank test. C, GSTP1 is expressed at a higher level in MYCN-amplified tumors in comparison with those without MYCN amplification. Graph shows relative expression as determined by ΔΔCt method ± SD (see Materials and Methods) with P value determined by the Student t test. D, GSTP1 protein levels in 6 representative neuroblastoma tumors. Relative expression at mRNA level is shown above the blots, while protein expression relative to α-tubulin, as determined using densitometry, is shown below. The drug-resistant neuroblastoma cell line BE(2)-C is used as a positive control. E, GSTP1 mRNA levels are closely correlated with GSTP1 protein levels in primary neuroblastoma tumors (r = 0.96, P = 0.002). The relationship was analyzed using linear regression.

Chromatin immunoprecipitation assays

The promoter region of GSTP1 was analyzed using bioinformatics techniques to identify putative N-Myc–binding sites, including the canonical E-box sequence CACGTG and other noncanonical sequences such as CATGTT and CACCGG. Promoter regions from −2,000 to −1,000 base pairs with respect to the transcription start site were considered for analysis. To test binding of N-Myc, quantitative chromatin immunoprecipitation (ChIP) was carried out as previously described (20, 21) using either SH-EP Tet-21N cells cultured in the absence of tetracycline (presence of N-Myc), BE(2)-C, or LA-N-5 cells. Antibodies used in this study were: IgG (Santa Cruz Biotechnology; sc-2027); N-Myc monoclonal antibody LA-N-5; and Max C-17 (Santa Cruz Biotechnology; sc-197). Specific pairs of primers used for quantitative ChIP are listed in Supplementary Table S5.

Statistical analysis

The relationship between levels of target gene expression and patient survival was analyzed using the Kaplan–Meier method with curves analyzed by log-rank test. Standard errors were calculated according to the method of Peto and Peto (23). Comparisons of outcome between subgroups in multivariable analyses were conducted using the Cox proportional hazards regression model. The relationship between levels of target gene expression was analyzed using the Spearman rank correlation. Differences in target gene expression between samples were assessed using a 2-sided Student t test. Statistical analyses were conducted using either Stata (StataCorp) or SPSS (IBM). Event-free survival (EFS) time was calculated from the time of enrolment onto the relevant study, or from diagnosis (SCH samples), to the time of the first occurrence of an event (relapse, progressive disease, secondary malignancy, or death) or to the date of last contact if no event occurred. Death was the only event considered for the calculation of overall survival time. All samples were deidentified, and researchers who conducted the gene expression analysis were blinded to all clinical characteristics and outcome of the subjects.

Tumors were categorized as having high expression of GSTP1 based on a range of cutoff points, including the median, upper quartile, and upper decile PCR values. The statistical methodology used to identify the optimal cutoff...
point to maximize the difference in outcome between groups with low versus high expression has previously been described in detail (24).

Results

Prognostic significance of GSTP1 in primary human neuroblastoma

To assess the prognostic significance of GSTP1 expression in neuroblastoma, we initially used RT-PCR to analyze its expression in a small cohort of 51 primary untreated tumors. When patients were dichotomized around the median RT-PCR value, high expression of GSTP1 was significantly associated with poorer EFS (P = 0.002, Fig. 1A) with 5-year survival rates of 92% ± 5.4% and 51% ± 11% for tumors with low and high GSTP1 expression, respectively, and also significantly associated with poorer overall survival (P = 0.006, Fig. 1B), with 5-year survival rates of 96% ± 3.9% and 63% ± 10% for tumors with low and high GSTP1 expression, respectively. Furthermore, GSTP1 expression was significantly higher in tumors with MYCN amplification than in nonamplified tumors (Fig. 1C, P = 0.024). To verify that GSTP1 gene expression accurately reflected expression at the protein level, we conducted Western blotting on 6 representative tumor samples, 3 with high GSTP1 gene expression and 3 with low gene expression (Fig. 1D). Protein levels were found to correlate strongly with gene expression in these samples (Fig. 1E; r = 0.96, P = 0.002). Full-length Western blots are presented in Supplementary Fig. S1.

Next, we extended these observations to 2 large patient cohorts. In the first, we analyzed GSTP1 expression by RT-PCR in 207 primary tumors (COG cohort). In the second, we analyzed publicly available microarray data (13) for GSTP1 expression in 251 primary tumors (Oberthuer cohort).

In the COG cohort, high GSTP1 expression was associated with worse outcome when patients were dichotomized around either the median or upper quartile RT-PCR values, although this failed to reach statistical significance at these cutoff points (not shown). However, at the upper decile, high GSTP1 expression was significantly associated with reduced EFS (P = 0.002; Fig. 2A). The 5-year EFS rate for patients with high GSTP1 expression was 52% ± 11% compared with 75% ± 3.3% for low GSTP1 expression. The prognostic significance of GSTP1 was also examined for patients with tumors lacking
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### Table 1. Multivariable Cox regression analysis of prognostic factors for neuroblastoma outcome

<table>
<thead>
<tr>
<th>Factor</th>
<th>EFS</th>
<th>Overall survival</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>COG-209</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tumor stage</td>
<td>HR (95% CI)</td>
<td>P</td>
</tr>
<tr>
<td>Age</td>
<td>4.6 (2.1–10.0)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>MYCN status</td>
<td>2.4 (1.1–5.1)</td>
<td>0.025</td>
</tr>
<tr>
<td>GSTP1 expression</td>
<td>1.8 (0.9–3.6)</td>
<td>0.086</td>
</tr>
<tr>
<td><strong>Oberthuer</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tumor stage</td>
<td>HR (95% CI)</td>
<td>P</td>
</tr>
<tr>
<td>Age</td>
<td>2.6 (1.2–5.5)</td>
<td>0.011</td>
</tr>
</tbody>
</table>

**NOTE:** Variables adjusted for in the multivariable analysis included tumor stage (1, 2, and 4S vs. 3, 4), age at diagnosis (<12 months vs. ≥12 months), MYCN status (amplified vs. nonamplified), and GSTP1 expression (dichotomized at the upper decile, low vs. high).

MYCN amplification. While these patients would be expected to have a relatively favorable outcome compared with patients with MYCN amplification, high levels of GSTP1 expression remained predictive of poorer outcome with a 5-year EFS rate of 60% ± 13% compared with 80% ± 3% for patients with low GSTP1 expression in their tumors (P = 0.025; Fig. 2B). Similarly, within poor prognosis patients (INSS stage 3 and 4), high levels of GSTP1 expression identified a subset with particularly poor outcome and a 5-year EFS rate of only 31% ± 14% compared with 52% ± 6% for patients with low GSTP1 expression (P = 0.022; Fig. 2C). In each case, similar effects were observed for overall survival (not shown).

Within the Oberthuer cohort, GSTP1 was strongly associated with EFS at the upper decile (P < 0.001; Fig. 2D) and also at the upper quartile and median (not shown). At the upper decile, the 5-year EFS rates for patients with high GSTP1 expression were 24% ± 13% compared with 74% ± 3% for low GSTP1 expression. In patients with tumors lacking MYCN amplification, 5-year EFS rates were 26% ± 20% and 78% ± 3% for those with high and low GSTP1 expression, respectively (P < 0.001; Fig. 2E). For those with poor prognosis (stage 3 and 4), high GSTP1 expression was associated with significantly worse outcome with 5-year EFS rates of 15% ± 12% and 55% ± 6% for high and low GSTP1 expression, respectively (P = 0.007; Fig. 2F). Within the stage 4 patients only, EFS was not significantly different for those with low and high GSTP1 expression in their tumors (P = 0.227), however, overall survival rates retained significance (P = 0.049) with 5-year survival rates of 51% ± 8.5% and 37% ± 14% for high and low GSTP1 expression, respectively (Supplementary Fig. S2).

Multivariable analysis was conducted to determine whether GSTP1 expression had prognostic significance independent of established prognostic indicators for neuroblastoma. Tumor stage (1, 2, or 4S vs. 3 or 4), age at diagnosis (<12 months vs. ≥12 months), MYCN status (amplified vs. single copy), and dichotomized GSTP1 expression were tested in a Cox proportional hazards model (Table 1). In the COG cohort, GSTP1 expression retained independent prognostic significance for EFS [HR = 2.6; 95% confidence interval (CI) 1.2–5.5; P = 0.011] and overall survival (HR = 2.21; 95% CI 1.0–4.8; P = 0.047). Likewise in the Oberthuer cohort, GSTP1 expression retained prognostic significance for both EFS (relative risk = 2.0; 95% CI 1.1–3.8; P = 0.029) and overall survival (relative risk = 2.3; 95% CI 1.1–4.9; P = 0.024). Finally, in a multivariable analysis for stage 4 patients only, including GSTP1 expression and age, GSTP1 expression approached significance for overall survival (relative risk = 2.1; 95% CI 0.99–4.6; P = 0.054), but was not significant for EFS (Supplementary Table S6).

Expression of GSTP1 correlates with MYCN in neuroblastoma tumors

As amplification of the transcription factor MYCN is a common feature of poor outcome in neuroblastoma, and GSTP1 expression was higher in MYCN-amplified tumors than in those without MYCN amplification (Fig. 1C), we sought to determine whether GSTP1 expression was regulated by MYCN. First, we assessed the correlation between GSTP1 expression and MYCN expression in the COG cohort after conducting RT-PCR analysis to determine relative MYCN expression levels. Using the Spearman rank correlation, GSTP1 levels were found to correlate with MYCN expression in both tumors with MYCN amplification (r = 0.61, P = 0.003; Fig. 3A) and those without (r = 0.73, P < 0.001; Fig. 3B). We also extended this analysis to the TH-MYCN transgenic mouse model of neuroblastoma (15), where the human MYCN transgene is expressed in cells of neuroectodermal origin by use of a tyrosine hydroxylase promoter. Using RT-PCR analysis, MYCN levels were found to correlate particularly closely with the expression of mouse Gstp1 (r = 0.91, P < 0.001; Fig. 3C). Similar results were observed for Gstp2 (not shown). Finally, we assessed the expression of GSTP1 using RT-PCR at various time points after tetracycline-induced suppression of exogenous MYCN expression in the neuroblastoma cell line SH-EP Tet-21N (19). GSTP1 expression was decreased after tetracycline exposure, along with MYCN (not shown).
Expression of \( \text{GSTP1} \) directly regulates \( \text{N-Myc} \) directly regulates \( \text{N-Myc} \) in cultured neuroblastoma cell lines, human neuroblastoma tumors, and tumors from a biologically relevant mouse model of neuroblastoma.

**N-Myc directly regulates \( \text{GSTP1} \) expression**

In light of these results, we assessed whether N-Myc directly regulates \( \text{GSTP1} \) expression. The promoter region of \( \text{GSTP1} \) was examined bioinformatically for putative N-Myc–binding sites within 2,000 bp on either side of the transcriptional start site. Two canonical (CACGTG) and 4 noncanonical (CAGCGG, CATGTG) E-box sites were identified over 5 distinct regions of the promoter (Fig. 4A). Next, we used ChIP assays to examine the physical association of N-Myc with each of the identified regions using the 3 independent human neuroblastoma cell lines SH-EP Tet-21N, LA-N-5, and BE(2)-C. In each cell line, the \( \text{GSTP1} \) promoter was directly bound by N-Myc, as well as its dimerization partner Max, at a noncanonical E-box proximal to the putative transcriptional start site (Fig. 4A). The fold enrichment for \( \text{GSTP1} \) was comparable with that of \( \text{APEX1} \), a well-known N-Myc target gene (25) indicating that the N-Myc/Max complex is strongly bound to the promoter.

Finally, to determine whether N-Myc directly activates \( \text{GSTP1} \) transcription, we cloned the \( \text{GSTP1} \) promoter upstream of a luciferase reporter gene and tested activity in SH-EP Tet-21N cells as a function of N-Myc expression. Luciferase activity was found to be dependent on N-Myc expression for the \( \text{GSTP1} \) reporter construct, as for \( \text{ABCC1} \), a positive control (26; Fig. 4B). Together, these data show that \( \text{GSTP1} \) is a direct transcriptional target of N-Myc in neuroblastoma cells.

**Discussion**

Using 3 independent patient cohorts, we have shown that high expression of \( \text{GSTP1} \) is a marker of poor prognosis in primary neuroblastoma. Furthermore, when included in multivariable analyses with the established prognostic indicators of age at diagnosis, \( \text{MYCN} \) amplification status and tumor stage as variables, \( \text{GSTP1} \) expression retained independent prognostic significance. This result raises the possibility that \( \text{GSTP1} \) contributes to the clinical behavior of neuroblastoma, consistent with its known roles in drug resistance and tumor biology. Whereas neuroblastomas typically respond to initial therapy regardless of risk group (2), the majority of patients with high-risk disease relapse with tumors that are refractory to treatment. It is as yet unclear whether this reflects the acquisition of multidrug resistance following exposure to chemotherapy, as a result of induction of one or more of the mechanisms which have previously been implicated as mediating multidrug resistance in neuroblastoma, such as \( \text{MRP1} \) overexpression (5) or \( \text{p53} \) mutation (27), or the selection and expansion of preexistent multidrug resistant tumor clones, as we have previously described for acute lymphoblastic leukemia (28). Future studies involving matched pairs of pre- and posttreatment tumor samples would be valuable to determine whether levels of \( \text{GSTP1} \) or other drug resistance–associated genes are elevated at relapse compared with levels at the time of diagnosis.

We also provide evidence that \( \text{GSTP1} \) is a direct transcriptional target of N-Myc. First, expression of \( \text{GSTP1} \) correlates with that of \( \text{MYCN} \) in both human tumors and the tumors derived from the TH-MYCN mouse neuroblastoma model. Second, the N-Myc protein, in complex with its dimerization partner Max, directly interacts with a noncanonical E-box proximal to the putative transcriptional start site of \( \text{GSTP1} \).
Finally, repression of MYCN expression reduces activity in a luminescent reporter assay using the GSTP1 promoter. Notably, both the multidrug transporter ABCC1, a phase III detoxification component that can efflux a number of glutathione-conjugated chemotherapeutic agents (29) and ABCC4, which can efflux both irinotecan and topotecan (12), are also independently prognostic of neuroblastoma outcome (4, 5, 12, 30) as well as directly regulated by N-Myc (26).

Figure 4. GSTP1 is a direct transcriptional target of N-Myc. A, N-Myc associates with the GSTP1 promoter. Quantitative ChIP was applied to the neuroblastoma cell lines BE(2)-C, LA-N-5, and SH-EP Tet21N cells expressing MYCN. Relative enrichment is compared with the preimmune serum. The results represent the mean ± SE of 5 independent ChIP experiments in which each region was amplified by RT-PCR in triplicate. Bent arrow, transcription start site; gray arrow, canonical E-box; black arrow, noncanonical E-box; and black boxes, amplicons. The chromosome and coordinates (bp) are also given. Quantitative ChIP for APEX1 in BE(2)-C cells is also shown. B, N-Myc regulates GSTP1 in a luciferase reporter assay. Firefly luciferase activity was determined following transient transfection of either a GSTP1 or ABCC1 reporter construct into SH-EP Tet21N cells. Cells were either not treated (NT; MYCN ON) or treated with tetracycline for 24 or 48 hours (TET 24 h or TET 48 h; MYCN OFF). Cloned regions are shown at left, with bent arrows denoting the transcription start site, the cloned DNA region (bp) indicated below the promoter map and fragment coordinates expressed relative to the transcription start point. The results are the means of the relative fluorescence units (RFU) ± SE of 3 independent transfections.
can, therefore, contribute to multidrug resistance in neuroblastoma through the upregulation of a suite of drug resistance genes covering a range of chemotherapeutic drugs. While previous in vitro studies suggest cooperativity between ABCB1 and GSTs (31, 32), GSTP1 has a relatively weak affinity for many anticancer drugs (7), implying that these proteins do not necessarily form sequential steps for the detoxification of a particular drug.

It is notable that of the 2 cohorts analyzed by RT-PCR, GSTP1 expression was significantly associated with poor outcome when dichotomized around the median RT-PCR value in the initial SCH/POG 51 sample cohort, whereas in the larger COG cohort, the association between high GSTP1 expression and poor outcome was evident but not significant at this cutoff point and in fact did not achieve prognostic significance until the data were dichotomized around the upper decile RT-PCR value. One contributing factor for this difference is most likely due to the differences between the patient characteristics of the 2 cohorts. Specifically, in the retrospectively accrued SCH/POG cohort of 51 tumors, 23.5% tumors were MYCN amplified and 55% were INSS stage 3 or 4 (12), whilst in the prospectively accrued COG cohort (5), only 10.1% of tumors were MYCN amplified and 42% were INSS stage 3 or 4. The underrepresentation of MYCN amplified, advanced stage tumors in the COG cohort can be related to the frequent diagnosis of stage 4 disease based on bone marrow sampling rather than tumor biopsy in that cohort, as we have previously described (5). As GSTP1 is transcriptionally regulated by N-Myc, and given the strong correlation between MYCN amplification and GSTP1 overexpression, it is, therefore, not surprising that GSTP1 expression is more predictive of outcome in a cohort with a higher proportion of MYCN-amplified tumors and less predictive in a cohort where MYCN-amplified tumors are underrepresented. Indeed, those MYCN amplified patients lost to the COG cohort would most likely only further strengthen the association between high GSTP1 expression and poor patient outcome evident in that cohort. The distributions of RT-PCR values for each cohort are shown in Supplementary Fig. S3.

The identification of GSTP1 as an N-Myc target gene also has importance for malignancies with high expression or amplification of c-Myc. N-Myc and c-Myc share a common set of target genes and are functionally interchangeable in the mouse (33). Furthermore, GSTP1 was one of a large number of genes identified as potential c-Myc transcriptional targets in a high-throughput ChIP study (25) and GSTP1 is transcriptionally regulated by c-Myc in osteosarcoma cell lines (G. Perini, manuscript in preparation). Finally, as Gstp1 is tightly coupled to MYCN expression in neuroblastomas arising in TH-MYC mice, this is likely to be a suitable preclinical model in which to assess the efficacy of GSTP1 inhibitors.

While the most familiar role for GSTP1 is the conjugation of reduced glutathione to cytotoxic drugs, GSTP1 may possess other functions that contribute to chemoresistance, including inhibition of JNK1 (34) and activation of extracellular signal–regulated kinase (ERK; ref. 35). In addition to potential roles in mediating drug resistance in neuroblastoma, GSTP1 could potentially impact other tumor properties through its ability to conjugate the cyclopentenone prostaglandins 15d-Δ12,14-PGJ2 and PGA2 (36), leading to their export through ABC1C and ABC3C (37) and its ability to sequester 15d-Δ12,14-PGJ2 in the cytosol independently of conjugation (38). Both mechanisms may prevent cyclopentenone prostaglandins from binding to the nuclear localized gamma isoform of the peroxisome proliferator-activated receptor (PPAR-γ), activation of which is antiproliferative, prodifferentiation, and proapoptotic (39) in cancer cells. In neuroblastoma, activation of PPAR-γ by 15d-Δ12,14-PGJ2 has been shown to induce apoptosis (40) and differentiation (41). While we cannot exclude these additional functions in our experiments, analysis of microarray data available for the Oberthuer cohort did not reveal any evidence of an association between GSTP1 expression and that of JNK1 (MAPK8), ERK1 (MAPK1) or PPARγ (PPARG; Supplementary Fig. S4), or with pathways associated with these genes (data not shown).

GSTP1 is upregulated in numerous human tumors and high GSTP1 expression is associated with chemoresistance (7–9). To our knowledge, this is the first study to reveal the prognostic significance of GSTP1 expression in neuroblastoma and the first to show that GSTP1 is a direct transcriptional target of the MYCN oncogene, which is frequently amplified in poor outcome neuroblastoma. These observations have significance both for MYCN-amplified neuroblastoma and for other diseases with amplification of Myc family oncogenes.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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References

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