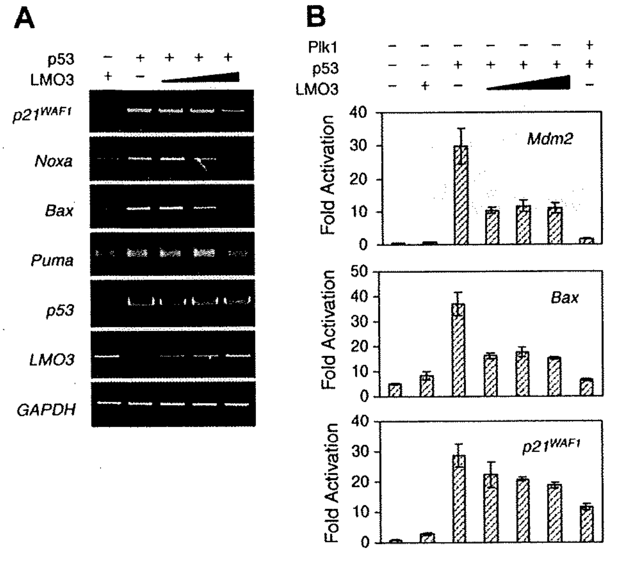

Fig. 2. LMO3 inhibits the transcriptional ability of p53. (A) mRNA levels of p53 target genes following p53 overexpression in p53-deficient H1299 cells, with co-expression of an increasing amount of LMO3 plasmid. Total RNA was extracted and subjected to RT-PCR analysis of *Noxa*, *Bax*, *p21*^{WAF1} and *Puma*; detection of *GAPDH* was used as a loading control. (B) Luciferase gene reporter assay of *p21*^{WAF1}, *Bax* and *Mdm2* promoter regions. H1299 cells were transiently transfected with the indicated combination of p53 and increasing LMO3 plasmid. Results are the mean of three independent experiments ± standard deviation.

p53-mediated activation of *p21*^{WAF1}, *Bax*, and *Mdm2* promoter regions was reduced by co-expression of FLAG-LMO3 when compared to transfection of p53 alone. Therefore, both endogenous mRNA transcription and activation of p53-responsive promoter elements were reduced upon co-expression with LMO3. These findings signify that LMO3 acts as a co-repressor of p53, suppressing p53-mediated transcriptional regulation.

Promoter recruitment of p53 is affected by LMO3

We attempted to clarify the mechanism by which LMO3 represses p53-mediated gene activation. For this, we employed ChIP assays to characterize the recruitment of p53 onto p53-response elements in the *p21*, *Bax* and *Puma* promoters. Both p53 and LMO3 proteins could be expressed in H1299 cells, detected by western blot (Fig. 3A). This experimental system revealed that specific recruitment of exogenously expressed p53 onto the promoters of *p21*, *Bax*, and *Puma* genes in the presence or absence of HA-LMO3 (Fig. 3B). The specificity of the anti-p53 antibody to precipitate p53 bound chromatin is shown by the lack of PCR product in the absence of p53, LMO3 only transfection, and ChIP with normal mouse IgG. The effect of LMO3 on p53 recruitment to these regions appears to be promoter specific, as a clear increase in recruitment of p53 to the *p21* promoter was observed when LMO3 was present in cells. A similar tendency at *Bax* and *Puma* promoters was observed to a lesser extent.

Discussion

LMO3 can act as an oncogene by promoting cell survival when highly and abnormally expressed in neuroblastoma [14]. Furthermore, we report here that LMO3 inhibits p53, one of the key molecules in protection against cancer. This oncogenic action of LMO3 is comparable to the activity of other LIM-only protein family members against tumor suppressor proteins [19]. Additionally, the compensatory roles of LMO1 and LMO3 in development [6] suggest common mechanisms of activity between LIM-only proteins. Yet the timing of expression levels and topography result in subtly distinct outcomes. Taken together with our previous studies, recent results are consistent with the notion that LIM-only proteins are regulatory proteins which have essential functions in transcriptional regulation, while they can be potent oncogenes under conditions of abnormal expression.

We demonstrated that LMO3 represses p53-mediated activation and transcription of apoptosis-related genes. The loss of p53 activation provides tumor cells with several selective advantages, such as an increased tolerance to growth arrest and apoptosis-inducing protective mechanisms, in addition to genetic instability [3,5]. This indicates that p53 is either inactivated or repressed by LMO3, even though p53 still retains nuclear localization and DNA-binding capability. Additionally, activation of the DNA-damage response by CDDP treatment demonstrated a functioning p53 pathway in SH-SY5Y cells including the transcriptional activation of *p21* (Supplementary Fig. 1). Interestingly, p53 recruitment to the *p21*^{WAF1} promoter was increased by LMO3 expression. However, in all p53-activated genes studied, LMO3 could repress their transcription by p53. Thus, LMO3 expression can influence p53 recruitment in a promoter selective manner but this may not be the main mechanism of repression.

As no enzymatic activity has been reported for LMO3, we propose that de-regulation of LMO3 expression leads to abnormal complex formation because of inappropriate LMO3 interactions. Our ChIP assay suggests that LMO3 does not suppress p53-mediated gene activation by interfering with DNA-binding. Therefore, another repression mechanism must exist. Accumulating evidence has demonstrated that post-translational modification of histones correlate with gene transcriptional regulation. Generally, Histone acetylation is associated with gene activation [20]. Physical and functional interactions of histone-acetyltransferases with p53, such as CBP and p300, demonstrate targeted acetylation of histones at promoter regions [21–23]. ChIP assays may indicate mod-

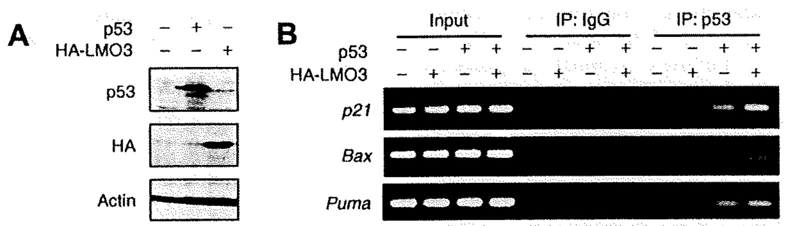

Fig. 3. Recruitment of p53 to promoters of apoptosis-related genes. (A) Immunoblotting showing expression of p53 and HA-LMO3 in p53-deficient H1299 cell line. (B) Chromatin immunoprecipitation with anti-p53 antibody or control mouse IgG in H1299 cells transfected with the indicated combinations of p53 and HA-LMO3 expression plasmids.

ification of histone acetylation by overexpression of LMO3 in the chromatin of p53-target genes. Future studies should examine the potential protein–protein interactions and the nature of LIM-only protein complexes involved in epigenetic modifications of chromatin.

The discrepancy between increased p53 recruitment and repression of gene activation could be explained by the following mechanisms. p53 receives a complex assortment of post-translational modifications including phosphorylation, ubiquitination, sumoylation, methylation and acetylation. These modifications affect many aspects of p53 status and activity, such as protein stability, DNA-binding activity, promoter selection and target-gene activation and/or repression. Regarding the repression of p53-mediated transcription by LMO3, we could not find any reduction in protein stability (data not shown) and DNA-binding activity of p53 to the *p21*, *bax*, and *puma* promoters. This suggests that LMO3 regulation of p53 may affect the association with its co-activators and repressors. It has been proposed that LIM-only proteins exert their effect by mediating protein–protein interactions and competing for interacting domains in the assembly of protein complexes [24,25]. Thus, LMO3 may directly compete for recruitment of negative transcriptional regulators to the p53 DNA-binding complex and promoter regions. Alternatively, LMO3 could recruit post-translational modifiers of p53 affecting transcriptional activation via an indirect mechanism. One other possibility, although not yet established for LIM-only proteins, is that binding by LMO3 affects the protein folding of p53, allowing recruitment to its response element yet interferes with assembly of the transcription machinery.

We expected that alterations in LMO3 transcriptional complexes have an inappropriate regulatory effect on downstream targets. Indeed, this is supported by our findings that the interaction of LMO3 with p53 represses p53-mediated transcription. This seems to be a common theme among LIM-only proteins. For example, LMO4 inhibits the transcriptional activity of BRCA1, a major tumor suppressor in breast cancers [10,19]. Intriguingly, Simonis et al. [26] found that *LMO3* is activated by chromosomal translocations of the T-cell receptor beta locus associated with T-cell lymphomas. In view of this study, the activities and molecular pathways of LMO3 activity identified here and in our previous report may be applicable to T-ALL. For future studies of LMO3, the regulation of gene expression itself needs to be clearly defined.

Long term survival, especially for those over 18 months of age for children with advanced neuroblastoma is currently unsatisfactory. Regardless of a myriad of treatments, recovery rates are poor. Present treatment regimes include surgery, radiation therapy, chemotherapy, retinoic acid and immunotherapy with anti-GD2 monoclonal antibody. Currently, in high risk groups (around half of all patients) overall survival is less than 40% [2]. There is an urgent necessity for specific therapies that can selectively eliminate cancer cells while limiting damage to normal cells and tissues. In particular, identification of novel targets and pathways through studies of abnormal gene expression, mutations, and genetic abnormalities in the various stages of neuroblastoma is crucial. Inhibition of LMO3 may be useful in treatment of presently difficult to treat neuroblastomas. The potential for interference of LIM-only protein multi-complexes and subsequent inhibition of normal and tumorigenic roles has been demonstrated using vector mediated expression of an anti-LMO2 single chain Fv antibody fragment [27,28]. Recent advances which will allow for individual gene profiling of tumors and the ability to design specific inhibitors may lead to a personalized treatment regime based on expression of individual oncogenes. Therefore, specific targeting of LMO3 in highly expressing tumors may simultaneously permit activation of the p53 pathway and inhibit LMO3-mediated pro-survival mechanisms.

Acknowledgments

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.bbrc.2009.12.010.

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Imaging, Diagnosis, Prognosis

Clinical Cancer Research

Accurate Outcome Prediction in Neuroblastoma across Independent Data Sets Using a Multigene Signature

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Abstract

Purpose: Reliable prognostic stratification remains a challenge for cancer patients, especially for diseases with variable clinical course such as neuroblastoma. Although numerous studies have shown that outcome might be predicted using gene expression signatures, independent cross-platform validation is often lacking.

Experimental Design: Using eight independent studies comprising 933 neuroblastoma patients, a prognostic gene expression classifier was developed, trained, tested, and validated. The classifier was established based on reanalysis of four published studies with updated clinical information, reannotation of the probe sequences, common risk definition for training cases, and a single method for gene selection (prediction analysis of microarray) and classification (correlation analysis).

Results: Based on 250 training samples from four published microarray data sets, a correlation signature was built using 42 robust prognostic genes. The resulting classifier was validated on 351 patients from four independent and unpublished data sets and on 129 remaining test samples from the published studies. Patients with divergent outcome in the total cohort, as well as in the different risk groups, were accurately classified (log-rank $P < 0.001$ for overall and progression-free survival in the four independent data sets). Moreover, the 42-gene classifier was shown to be an independent predictor for survival (odds ratio, >5).

Conclusion: The strength of this 42-gene classifier is its small number of genes and its cross-platform validity in which it outperforms other published prognostic signatures. The robustness and accuracy of the classifier enables prospective assessment of neuroblastoma patient outcome. Most importantly, this gene selection procedure might be an example for development and validation of robust gene expression signatures in other cancer entities. *Clin Cancer Res; 16(5); 1532–41. ©2010 AACR.*

One of the main challenges in clinical cancer research remains accurate prediction of outcome, enabling better choice of risk-related therapy. This is particularly true for neuroblastoma, a pediatric tumor of the sympathetic nervous system, which is characterized by a remarkably heterogeneous clinical course. Tumors that are found in infants frequently regress spontaneously or show differentiation features on treatment, whereas tumors diagnosed in children >1 year of age often metastasize, causing accelerated cancer-related death despite intensive therapies. Accordingly, different therapeutic schemes exist ranging from watch-and-see approaches to multimodal therapies. Four major risk stratification systems are currently being used in various parts of the world (Europe, United States, Japan, and Germany) based on a combination of clinicopathologic and genetic parameters, such as age at diagnosis, tumor stage, *MYCN* gene status, histopathologic classification, ploidy, and chromosome 1p and 11q status (1–8). Clinical experience within these systems indicates that the stratification is useful, but misclassifications occur, resulting in overtreatment or undertreatment. Identification of more specific and sensitive markers for response to therapy and outcome prediction is clearly required and is expected to result in better choice of risk-related therapy.

As differences in outcome are considered to reflect underlying genetic and biological characteristics that have

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Translational Relevance

Prognostic classification of heterogeneous diseases such as neuroblastoma remains challenging. In this study, a unique data-mining approach was applied for establishment of an accurate and robust gene expression classifier to predict clinical outcome of neuroblastoma patients. Using both published and unpublished microarray expression data of 933 primary neuroblastomas, a 42-gene classifier was developed and successfully validated. The powerful and independent prognostic value of the 42-gene classifier is shown using several lines of evidence. First, patients with divergent outcome were accurately classified. Second, multivariate analysis showed that the classifier is an independent prognostic factor, contributing to more accurate assessment of prognosis when considering the conventional risk factors alone. This was further confirmed within a subgroup of high-risk patients. Moreover, the excellent performance of the classifier across different expression platforms clearly shows its robustness. The presented gene selection procedure is suitable for the development of gene expression signatures in other cancer entities.

their effect on mRNA gene expression profiles, several microarray expression profiling studies have been undertaken to predict patient outcome in different cancer entities.

An important limitation of many published gene expression profiling studies is the lack of statistical power to identify markers and lack of independent validation. Typically, around 30,000 to 40,000 transcripts are tested, generating hundreds of thousands of data points for a relatively small subset of tumors (between 20 and 100). When such a high number of genes are evaluated as prognostic markers, there is a substantial chance that a random association between a gene and the prognostic classes is observed (9, 10). Consequently, many published studies do not classify patients better than chance due to lack of internal validation by repeated random sampling of training sets or external validation on independent samples. As such, there are a few inherent but often overlooked statistical issues, such as data overfitting, unstable gene lists, and lack of study power (11).

In this study, we established a prognostic 42-gene classifier for children with neuroblastoma by reanalysis of four published gene expression studies from four different microarray platforms comprising 582 patients in total (12–15). To facilitate data comparison across different platforms, probe annotations were updated with respect to the original publications. When available, clinical follow-up information was updated. All these aspects critically contribute to the success of our multigene signature. Successful validation of the multigene signature in four independent unpublished data sets shows its robust performance and platform independence.

Materials and Methods

Gene expression data sets. Four published studies were used for selecting the genes and building the prognostic classifier (phase 1 data sets), and four unpublished data sets were used as independent validation sets (phase 2 data sets).

The phase 1 data sets were downloaded either from the National Center for Biotechnology Information Gene Expression Omnibus (GSE2283 and GSE3960; refs. 14, 15) or from the European Bioinformatics Institute ArrayExpress database (E-TABM-38; ref. 13), or from the authors' Web site[10] (12).

A trained multigene correlation signature was validated on the four independent phase 2 data sets from which the 42 genes (when present) were extracted and standardized (per gene, the median value across the samples was subtracted followed by division by the SD of the gene): (*a*) hgu95av2 Affymetrix gene expression data from 106 neuroblastoma patients (validation set 1; 40 genes present), (*b*) hgu133plus2 Affymetrix gene expression data from 53 neuroblastoma patients (validation set 2; 40 genes present), (*c*) data set for 91 neuroblastoma patients obtained using an 11K custom Agilent oligonucleotide microarray (validation set 3; 41 genes present), and (*d*) Human Exon 1.0 ST Affymetrix expression data from 101 neuroblastoma patients (validation set 4; 42 genes present; standardized data of the 42-gene selection as well as clinical data are available in Supplementary Tables S1 and S2; Fig. 1).

For the remainder of the article, we will label the data sets according to the first author for the published phase 1 studies [Oberthuer (13), Wang (15), Berwanger (12), and Ohira (14)] and as validation sets 1, 2, 3, and 4 for the unpublished phase 2 studies.

Data preprocessing. To make the data from the different microarray platforms maximally comparable, annotation information of the probes was updated using the MatchMiner tool (16) for the custom-made cDNA or oligonucleotide arrays (12–14) and using the latest version of the R packages hgu95av2 and hgu133plus2 for the Affymetrix array data (15). Probe identification numbers were converted into gene symbols to enable straightforward comparison of the gene lists between the different studies. Throughout the text, the number of unique gene symbols (represented by one or more array probes) in each study is indicated.

Updated clinical information with regard to progression-free survival (PFS) and overall survival (OS) times was obtained from the authors (14, 15) or was publicly available (13). For the Berwanger and Ohira studies and validation set 1, only OS data were available.

[10] http://www.imt.uni-marburg.de/microarray/download.html

Patients were divided in two clearly defined risk groups. The low-risk subgroup was defined by stage I, II, or IVS without *MYCN* amplification, and the high-risk subgroup comprised patients with age of diagnosis >1 y with stage IV tumors (irrespective of *MYCN* status) or with stage II and III tumors with *MYCN* amplification. To develop our classifier, as many patients as possible from the four phase 1 data sets were divided in the two risk groups with maximally divergent clinical course (Table 1), that is, low-risk patients with PFS time (or OS time for Berwanger and Ohira data sets) of at least 1,000 d and high-risk patients that died from the disease. The patients that did not belong to the above-mentioned low- or high-risk subgroups were used as independent test set.

Statistical analysis. Identification and validation of prognostic classifiers (for each single phase 1 data set) were done by prediction analysis of microarray (PAM) classification with 10-times repeated 10-fold cross-validation in

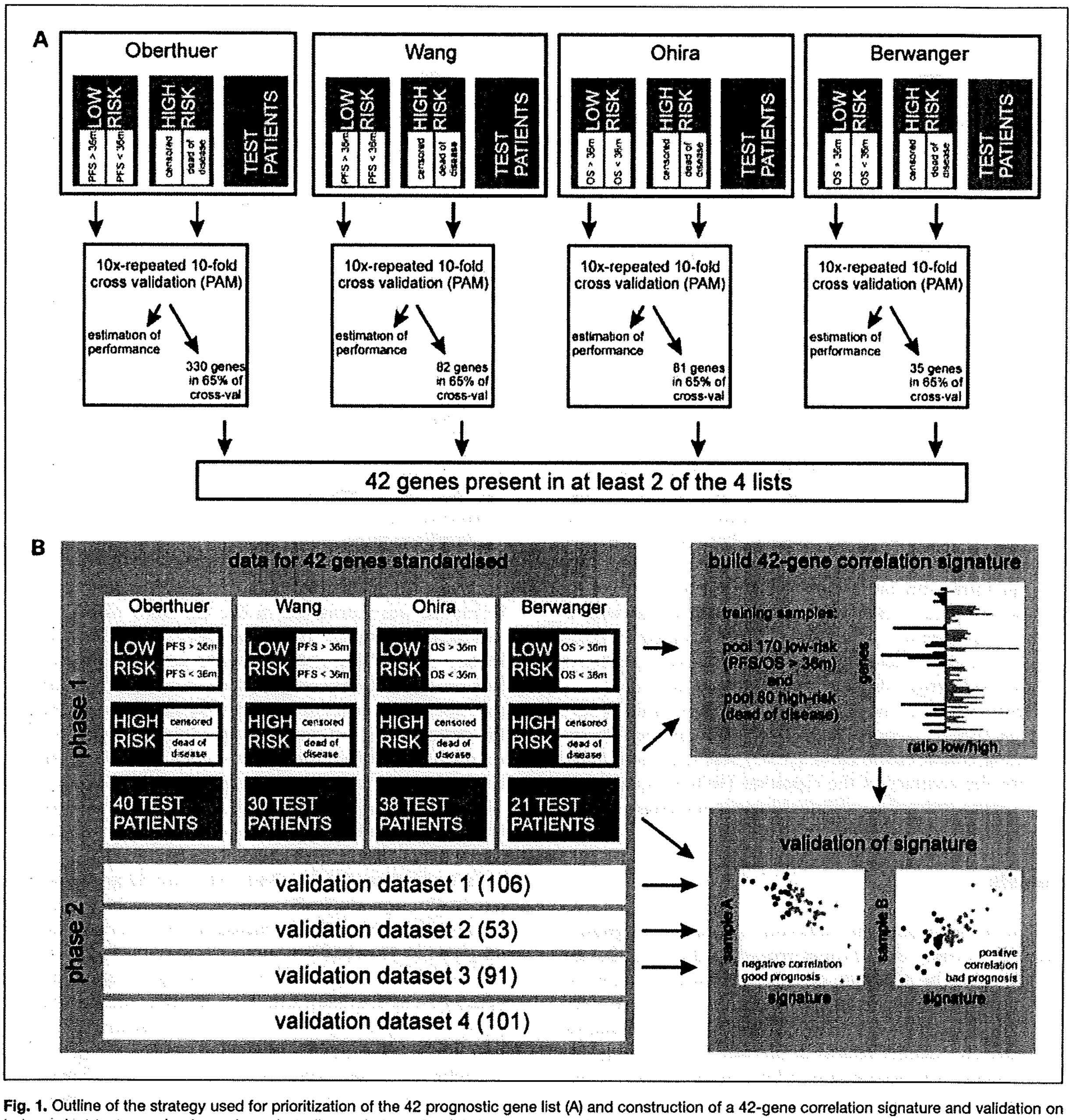

Fig. 1. Outline of the strategy used for prioritization of the 42 prognostic gene list (A) and construction of a 42-gene correlation signature and validation on independent test samples from phase 1 studies and phase 2 validation data sets (B). m, months.

Table 1. Published phase 1 studies used for training the classifier, with indication of the number of (training) samples, median OS or PFS (in months), and estimation of the performance of the study-specific PAM classifier for prediction of unfavorable outcome (OS)

	Berwanger	Oberthuer	Ohira	Wang
No. patients	94	251	136	101
No. low-risk training samples	22	87	43	18
No. high-risk training samples	13	25	20	22
Median OS/PFS (mo)	OS = 43	PFS = 55	OS = 46	PFS = 48
Specificity	0.955	0.977	0.814	1.000
Sensitivity	1.000	0.960	0.950	0.773
Negative predictive value	0.929	0.923	0.704	1.000
Positive predictive value	1.000	0.988	0.972	0.783
Accuracy	0.971	0.973	0.857	0.875
Performance (AUC)	0.977	0.969	0.882	0.886

the R statistical language using the Bioconductor package MCRestimate (Fig. 1A; refs. 13, 17). Forty-two genes were present in at least two of the four resulting gene lists.

A cross-platform gene signature was built using standardized expression data of the 42 genes (if present on the respective arrays, see Supplementary Data 2) from four published phase 1 studies. The correlation method was used to build and test a cross-platform prognostic signature (Fig. 1B). Log-transformed data were merged in one file (if more than one probe was present for a certain gene, the probe with the highest expression value was selected), and for each of the 42 genes, the mean expression value in low-risk neuroblastoma patients with PFS of at least 1,000 d was subtracted from the mean expression value in high-risk neuroblastoma patients that died of disease. For classification, the Pearson's correlation coefficient of the signature with the standardized expression values of independent test patients was calculated. Patients with a correlation coefficient below 0 were predicted to have good prognosis, whereas the other patients were predicted to have bad prognosis [according to Liu et al. (18)].

Kaplan-Meier survival analysis was done with the R survival package (R version 2.6.1). The area under the receiver operating characteristic curve (AUC) was used as a measure for the accuracy of the classifiers (ROCR R-package). Multivariate forward conditional logistic regression analysis was done using SPSS version 16.

Results

Gene prioritization for inclusion in a robust prognostic classifier. A complete 10-times repeated 10-fold cross-validation using the PAM algorithm (13, 19) was done on the training patients belonging to one of the two clearly defined risk groups from the four published phase 1 studies separately to identify robust prognostic markers (Fig. 1). This process was accompanied by determination of the classification accuracy, providing a first estimation of the utility of the expression data to predict outcome (Table 1).

For each data set, we selected the probes that were included in at least 65 of the 100 cross-validation gene lists, as these genes are likely to be the ones with the highest prognostic value as determined by Oberthuer et al. (13). The resulting prognostic gene lists from the four studies showed significant overlap (Table 2; Supplementary Data 1). Two genes were in common between three lists (i.e., *MYCN* and *NTRK1*), whereas 40 genes were in common between two lists. Thirty-two were previously reported in at least 1 of 10 published prognostic gene lists, of which only 10 were found in 2 or more published prognostic lists (12–14, 20–26). The occurrence of the 42 genes in at least two of the four lists makes them robust, platform-independent, prognostic markers.

Classification performance of the 42-gene list. Next, we investigated whether the 42-gene list is able to predict prognosis across different data sets. The classification performance was estimated in the different phase 1 data sets using a complete 10-times repeated 10-fold cross-validation method using all patients from the two clearly defined risk groups. For this analysis, it is important to note that not all 42 genes are present on all platforms; hence, the performance test was inherently done with a different number of genes for the different data sets (Supplementary Data 2). As already indicated, the 10-times repeated 10-fold cross-validation provides a good estimate for the classification performance using the expression data of the selected gene list.

As a reference, the 35-, 330-, 81-, and 82-gene lists obtained through single PAM analysis of each of the four phase 1 data sets were evaluated in the same way as the 42-gene list. The classification performance was also tested for a subset of 11 genes (from the 42-gene list) that were present on all four platforms. This analysis showed that all performance parameters for the 42-gene list are best or second best for all studies compared with the other gene lists, whereby the overall accuracy is highest for the 42-gene list subset (AUC = 0.935; Supplementary Data 2). This analysis also shows that the performance of a classifier built for a given data set is not always best, which indicates the power and utility of our meta-analysis for the identification of a prognostic gene list by using expression data of 250 training samples (170 low risk and 80 high risk). When only 11 genes of the 42-gene list were selected that are present on all four platforms, the overall accuracy was lower due to loss in sensitivity and positive predictive value. The 42-gene classifier was also compared with two published classifiers (13, 27) and showed that the 42-gene classifier performs best.

Table 2. Genes that are in common between the 42-gene list and the different individual classifier gene lists (number of common genes in list/total number of genes in list)

	Berwanger (10/35)	Oberthuer (38/330)	Ohira (12/81)	Wang (26/82)	published lists
AHCY		–	–		2
AKR1C1		+		+	1
ARHGEF7		+	+		2
BIRC5	–		–		1
CADM1		+		+	0
CAMTA2		+		+	0
CDCA5	–	–			2
CDKN3		–		–	2
CLSTN1		+		+	1
DDC		+	+		1
DPYSL3		+	+		1
ECEL1		+	+		0
EPB41L3		+		+	0
EPHA5	+	+			1
EPN2		+		+	0
FYN			+	+	1
GNB1		+	+		1
HIVEP2		+		+	1
INPP1	+			+	1
MAP7	+	+			1
MAPT		+	+		1
MCM2		–		–	0
MRPL3		–		–	1
MYCN	–	–	–		4
NCAN		–		–	0
NME1	–	–			2
NRCAM		+		+	2
NTRK1		+	+	+	4
ODC1	–			–	1
PAICS		–		–	1
PLAGL1	+	+			1
PMP22		+		+	1
PRKACB		+		+	2
PRKCZ		+		+	1
PTN		+		+	1
PTPRN2		+	+		0
SCG2		+		+	1
SLC25A5		–		–	1
SNAPC1		–		–	0
TYMS		–		–	1
ULK2		+		+	0
WSB1	+	+			4

NOTE: The number of published prognostic gene lists (other than the four reanalyzed studies) in which these genes are found is indicated in the last column. –, associated with poor outcome; +, associated with favorable outcome.

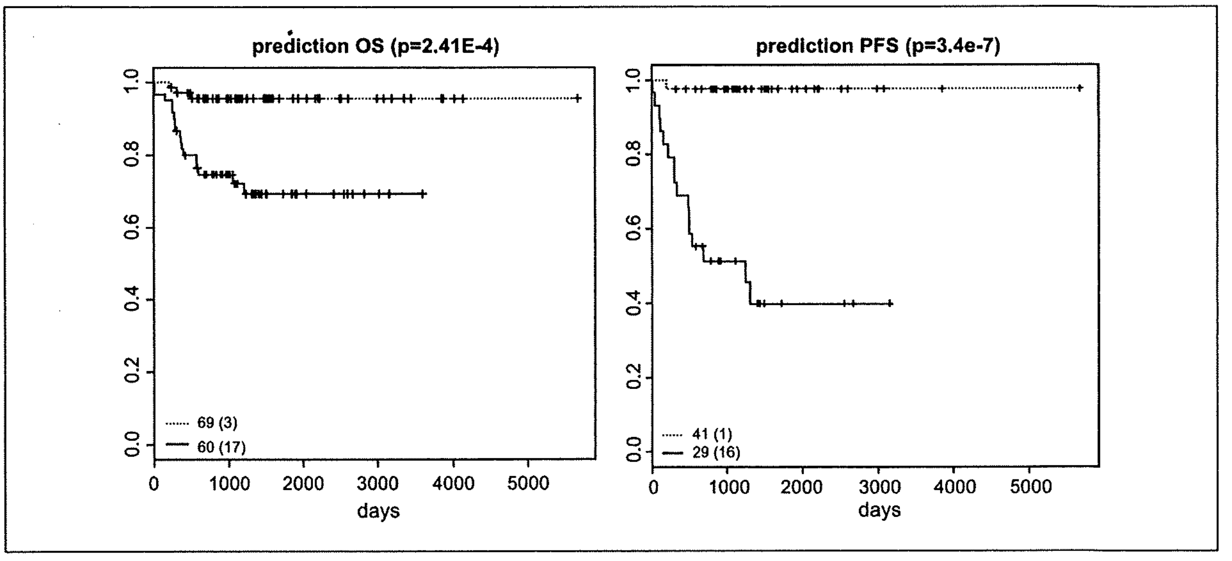

Fig. 2. Kaplan-Meier and log-rank analysis of 129 test patients (OS) and 70 test patients (PFS) from the four published phase 1 studies classified using the prognostic correlation signature. Legend, number of patients in predicted subgroups; between brackets, number of patients with event (relapse, progression, or death).

Validation of a cross-platform prognostic 42-gene correlation signature for neuroblastoma. A major disadvantage of the PAM classification method is the need for a training set of samples that are analyzed on the same gene expression measurement platform as the one used to evaluate the test samples. We therefore applied an alternative method to build a classifier based on the 42-gene list that can be used for completely independent data sets even on other platforms.

The prognostic signature is determined using 250 training samples from the four phase 1 studies. A 42-gene classification vector was created and tested using the correlation method (see Materials and Methods; Fig. 1).

First, the correlation signature was tested on the 129 test samples (patients not belonging to the low- and high-risk subgroup) from the four phase 1 studies and revealed a very high predictive power for OS (log-rank P = 2.41E−4) and PFS (log-rank P = 3.40E−7; Fig. 2).

Next, this correlation signature was evaluated on the four independent phase 2 data sets (351 patients), whereby the patients could be clearly separated into groups with significant differences in OS (log-rank P = 2.17E−23) and PFS (log-rank P = 2.03E−21; Fig. 3A). Kaplan-Meier analysis of patients stratified using known risk factors (i.e., age, stage, and *MYCN* gene status) showed that the correlation signature outperforms these risk factors (P < 0.001, except for *MYCN*-amplified samples; Supplementary Fig. S2). This was confirmed using multivariate logistic regression analysis evaluating age, stage, *MYCN* status, and the gene classifier, indicating that the 42-gene signature is an independent predictor for PFS and OS in the four phase 2 data sets as well as in the test samples of the phase 1 data sets (Table 3). Of note, whereas phase 2 data sets are representative of the general neuroblastoma population, test samples from the phase 1 data sets only represent intermediate risk patients.

As the different validation data sets include patients stratified using different risk stratification systems (Europe, United States, and Germany), we defined a common low- and high-risk group (Supplementary Data 3). As there was only 1 patient of 50 that died of disease within the common low-risk group of patients, we did not do Kaplan-Meier analysis. However, we could show that this single patient was classified in the high-molecular risk group using our classifier. Most interestingly, the correlation signature could partition patients within the common high-risk subgroup into groups with significant differences in OS and PFS (Fig. 3B) and was an independent prognostic marker (odds ratios, >4; Supplementary Table S4). To exclude that the significant survival differences in high-risk tumors is solely due to the effect of the *MYCN* amplification and related downstream *MYCN* signaling, we also tested the survival in high-risk tumors without *MYCN* amplification and could show that the classifier also significantly discriminates these patients with respect to outcome (Fig. 3C; Supplementary Table S4). In line with this, inspection of the 42-gene list indicated that not all 42-genes are related to *MYCN* amplification (Supplementary Data 4).

Discussion

In this study, we developed and validated a 42-gene prognostic classifier for children with neuroblastoma through a reanalysis strategy of published data complemented with gene expression data from 351 patients from

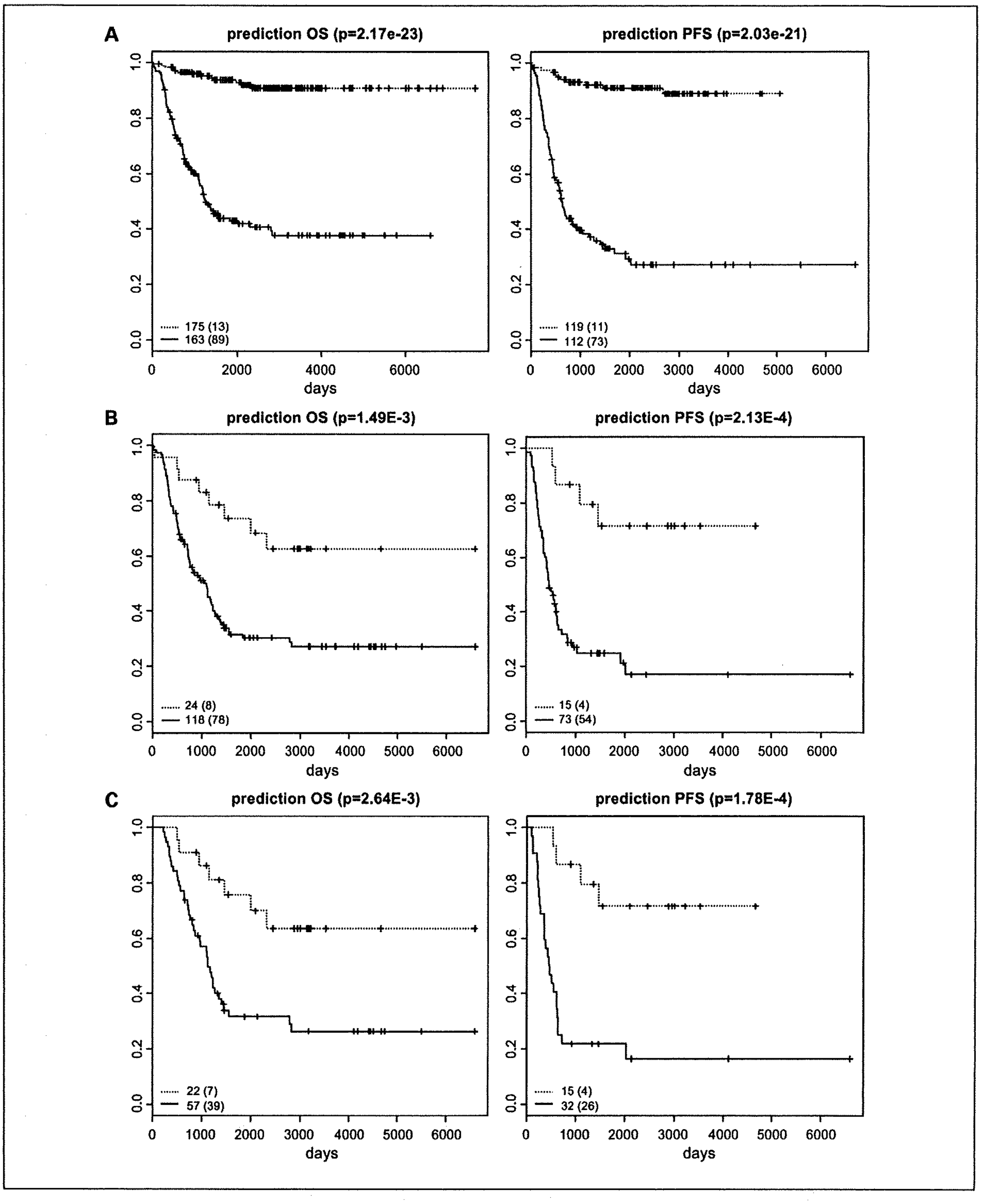

Fig. 3. Kaplan-Meier and log-rank analysis of the patients from four independent unpublished phase 2 validation data sets classified using the prognostic correlation signature for all patients together {5-y OS of 93.9% [95% confidence interval (95% CI), 90.2-97.6] for low molecular risk versus 43.1% (95% CI, 35.6-52.2) for high molecular risk and 5-y PFS of 91.1% (95% CI, 86.0-96.6) for low molecular risk versus 30.4% (95% CI, 22.1-41.8) for high molecular risk; A}, for the common high-risk subgroup (B), and for the common high-risk subgroup without MYCN amplification (C). Legend, number of patients in predicted subgroups; between brackets, number of patients with event (relapse, progression, or death).

Table 3. Multivariate logistic regression analysis (with correlation signature classification, MYCN status, International Neuroblastoma Staging System stage, and age at diagnosis; A) and sensitivity, specificity, and accuracy (AUC with 95% CI) results (follow-up time of at least 36 mo; B) for correlation signature prediction in the independent test samples from the phase 1 data sets and in the phase 2 validation data sets

A

		OS		PFS	
		P	OR (95% CI)	*P*	OR (95% CI)
Test samples from phase 1 data sets	Correlation signature	3.16E−2	5.11 (1.16-22.58)	3.12E−4	54.00 (6.17-472.41)
	MYCN amplification	7.80E−5	21.50 (4.69-98.54)	1.26E−1	—
	Stage (IV versus other)	1.80E−1	—	2.65E−1	—
	age (<1 or >1 y)	1.52E−1	—	8.65E−1	—
Phase 2 validation data sets	Correlation signature	9.07E−7	7.02 (3.23-15.28)	1.1E−14	16.45 (8.09-33.48)
	MYCN amplification	4.19E−2	2.23 (1.03-4.84)	3.13E−1	—
	Stage (IV versus other)	1.35E−2	2.50 (1.21-5.16)	2.16E−1	—
	age (<1 or >1 y)	1.45E−4	4.14 (1.99-3.66)	1.1E−4	4.18 (2.03-8.64)

B

	Test samples from phase 1 data sets	Phase 2 validation data sets
Sensitivity OS	17/20 = 0.85	89/102 = 0.87
Specificity OS	41/67 = 0.61	140/195 = 0.72
Performance, AUC (95% CI), OS	0.731 (0.612-0.850)	0.795 (0.742-0.849)
Sensitivity PFS	16/17 = 0.94	93/110 = 0.85
Specificity PFS	27/35 = 0.77	95/119 = 0.80
Performance, AUC (95% CI), PFS	0.856 (0.748-0.964)	0.822 (0.764-0.879)

NOTE: —, not analyzed.
Abbreviation: OR, odds ratio.

four unpublished data sets (Fig. 1). To accomplish this, four published microarray studies comprising >500 neuroblastoma patients were reanalyzed generating four new prognostic gene lists with a high overlap of genes between them. Comparison of the genes in the classifiers showed that 42 unique genes were present in at least two of the four lists. Not surprisingly, this set of 42 predictor genes contains numerous genes that have been reported in the context of neuroblastoma (e.g., *MYCN, NTRK1, NME1, CADM1, FYN, ODC1*, and *WSB1*). The finding of these genes in at least two independent studies indicates their robustness as prognostic markers. Comparison of the performance of the 42-gene list with the lists that were generated on the individual phase 1 studies and with two published prognostic gene lists (13, 27) showed that the classifier based on the 42-gene list has the highest overall accuracy while using the lowest number of genes. However, we have to keep in mind that this observed superiority of the 42-gene set might in part be due to the fact that, for some of the other gene lists, a large proportion of genes were not present on the platform (Supplementary Table S3).

The high prognostic classification performance of the 42-gene list is undoubtedly due to our unique reanalysis approach. First, annotations of the probes on the different platforms were updated according to the latest genome build. Second, a uniform risk definition was applied to select training patients across the different studies. Only patients with maximally divergent courses were used for training. Third, the same powerful algorithm with built-in cross-validation was used for identification of prognostic genes in four major published data sets, enabling the generation of relatively stable prognostic gene lists with high overlap.

This list of 42 prognostic genes was used to build a cross-platform classification signature. As the PAM algorithm is not suitable for cross-platform classification, we used a more intuitive, alternative method for building a 42-gene classifier. In this study, we generated a prognostic correlation signature based on expression data of the 42 genes in 250 training samples of the four phase 1 data sets. The signature was subsequently applied on independent test samples from the phase 1 data sets and on four independent and unpublished phase 2 data sets, generated on different expression profiling platforms, totaling 480 patients. The excellent prognostic performance of the 42-gene list (Table 3) further shows the validity of our meta-analysis approach and the utility of the recognized prognostic markers for neuroblastoma. The classifier predicts overall (OS) and PFS for the patients from the four phase 2 studies as well as for the test patients from the phase 1 studies (which could not be unequivocally classified in the low- or high-risk subgroups using known risk factors) with high sensitivity and specificity (Table 3). Importantly, the classifier was shown to be an independent predictor for both PFS and OS when stratifying for known risk factors such as age, stage, and *MYCN* status. Indeed, the 42-gene list does not only contain *MYCN*-regulated genes and, thus, not only reflects the *MYCN* copy number status of the samples. This is further substantiated by the excellent performance of the classifier in the high-risk neuroblastoma patients without *MYCN* amplification.

Thus far, this is the largest prognostic meta-analysis study in neuroblastoma, totaling >900 patients, including 351 patients from four independent and unpublished validation data sets. In contrast to other studies on neuroblastoma gene expression classifiers (13, 14, 21, 25, 27, 28), we could show an excellent performance of our classifier on these four independent data sets involving patients from different risk protocols from Germany, Europe, and United States by using a smaller gene set and a more intuitive classification method.

This survival classifier will definitely help to identify patients with increased risk in the current risk groups and to make a better choice of risk-related therapy. For example, low-risk patients with high molecular risk might benefit from more aggressive treatment protocols, whereas more intensive follow-up and new experimental therapies might be considered for high-risk patients with high molecular risk.

In conclusion, we applied a unique meta-analysis strategy for the identification of a robust set of 42 prognostic genes for outcome prediction in neuroblastoma. Furthermore, we propose a prognostic gene signature that is significantly associated with outcome prediction in neuroblastoma samples from independent studies using different technological platforms, making it a useful and practical classifier for risk stratification in neuroblastoma patients. The signature remains to be tested in a prospective clinical validation. The low number of genes makes this signature very well suited for cost-effective and fast PCR-based analysis, requiring only minimal amounts of tumor material, as exemplified by a recently published quantitative PCR study in which a 59-gene classifier containing the 42 genes from this study was trained, tested, and independently validated on a large cohort of patients (29). The outlined strategy for robust selection of prognostic markers and the use of a cross-platform correlation signature have wide application potential in other cancer entities.

In the search of an optimal prognostic classifier, it could prove useful to do an integrated analysis to determine the combined prognostic power of a mRNA gene expression signature along with gene copy number levels, microRNA gene expression patterns, and epigenetic modifications.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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