Poor Outcome in Estrogen Receptor–Positive Breast Cancers Predicted by Loss of *Plexin B1*

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Abstract

Purpose: A common characteristic of mammary carcinomas is an inverse relationship between the estrogen receptor (ER) status and the proliferative activity of the tumor. Yet, a subset of ER-positive breast cancers is characterized by a high proliferation, suggesting malfunctions in ER responsiveness that influence the biological and therapeutic behavior of tumor cells. The expression of several ER-dependent genes seems to be dysregulated among those "uncoupled" tumors. One of those genes is *plexin B1*, a cell-surface receptor for the semaphorin Sema4D (CD 100). However, the biological role of plexin B1 in breast cancer is largely unknown.

Experimental Design: Expression data of plexin B1 were obtained from Affymetrix microarray analysis of $n = 119$ breast cancer specimens. Validation was done by quantitative real-time PCR and protein expression was evaluated by immunohistochemistry. Expression data were compared with clinical characteristics as well as follow-up data of the disease.

Results: Low plexin B1 expression levels characterize a more aggressive tumor phenotype. The expression of plexin B1 is strongly correlated with the ER status. However, even among ER-positive tumors, loss of plexin B1 is associated with an impaired prognosis of breast cancer patients in both univariate (all patients, $P = 0.0062$; ER positive, $P = 0.0107$) and multivariate analyses (all patients, $P = 0.032$; ER positive, $P = 0.022$). Immunohistochemistry reveals that the tumor cells themselves and not the endothelial cells are the major source of plexin B1 expression in the tumor.

Conclusion: Plexin B1 acts not only as a new important prognostic but should also represent a predictive marker indicating an endocrine resistance. These data give a new insight in markers that could be involved in endocrine dysregulation of breast cancer.

Plexins are cell-surface receptors for semaphorin molecules. They have been shown to be widely expressed in various epithelial cells and their interaction governs cell adhesion and migration in a variety of tissues [for recent reviews, see Kruger et al. (1) and Bussolino et al. (2)]. Plexins belong to the c-Met family of scatter factor receptors but lack an intrinsic tyrosine kinase domain. Their ligands, the semaphorins, are cell-surface and secreted proteins and were first identified as repulsive axonal guidance molecules governing neuronal growth. Later on, it was recognized that these ligand receptor pairs regulate cell motility in many cell types. Giordano et al. (3) reported that plexin B1 triggers invasive growth, a complex program that includes cell-cell dissociation, anchorage-independent growth, and branching morphogenesis. Because plexins are broadly expressed, additional biological roles for semaphorin-plexin signaling in development and disease will probably be elucidated. Several groups presented evidence for essential roles for semaphorins in organizing several nonneural tissues like heart (4–6), lung (7), mammary gland (8), and bone homeostasis (9). In addition, autocrine loops of semaphorin-plexin signaling have been suggested to have tumor suppressor function in normal epithelial cells, and loss of heterozygosity of these genes might potentially foster deregulated tumor cell adhesion and migration (10–13). In contrast, because of the observation that plexin B1 couples with the receptor tyrosine kinases Met (3) and ErbB2 (14), it has been speculated that plexin B1 may trigger invasive growth of epithelial cells (3).

To date, there is only limited knowledge about the expression of plexins and semaphorins in breast cancer, their regulation, and their roles in disease prognosis and prediction. We identified *plexin B1* among dysregulated genes in breast cancers with disturbed ER signaling. Here, we show by a combination

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of Affymetrix microarray profiling, quantitative real-time PCR, and immunohistochemical analysis that loss of plexin B1 is a marker for poor prognosis in breast cancer, which was verified on independent published data sets.

Materials and Methods

Breast cancer samples. Tissue samples were obtained from consecutive patients undergoing surgical resection between December 1996 and July 2003 at the Department of Gynecology and Obstetrics at the Johann Wolfgang Goethe University in Frankfurt. Patients were selected for this study if they had received adjuvant chemotherapy (cyclophosphamide-methotrexate-5-fluorouracil or epirubicin-cyclophosphamide) and sufficient follow-up data of more than 2 years were available (n = 119). Patients with positive hormone receptor status received additional tamoxifen for 5 years. All tissue samples were stored in liquid nitrogen. Clinical characteristics of the patients are given in Table 1.

Microarray analysis. Isolation of RNA and expression profiling using Affymetrix Human Genome U133A microarrays was done as described elsewhere (15). Briefly, hybridization intensity data were automatically acquired and processed by Affymetrix Microarray Suite 5.0 software. The expression level of each gene was determined by calculating the average of differences in intensity (perfect match-mismatch) between its probe pairs. Scans were rejected if the scaling factor exceeded 2 or "chip surface scan" revealed scratches, specks, or gradients affecting overall data quality (Refiner, GeneData AG, Basel, Switzerland). The data were subsequently analyzed by using the Cluster and TreeView software package (16). Before cluster analysis, gene chip expression values were adjusted by log transformation and median centering of the gene chips. Hierarchical gene clustering was done by the similarity metric "absolute correlation (centered)."

Assessment of ER, ErbB2, proliferative status, and plexin B1 expression of the samples. Samples were characterized according to standard pathology including the estrogen receptor (ER) status by ligand binding assays or immunohistochemistry. In addition, immunohistochemistry data of the progesterone receptor and ErbB2 were available for most cases. Because differences existed between the two methods used for determining the ER status and data for some samples were missing, the "molecular" status for the receptors was additionally determined based on Affymetrix expression data resulting in concordance of >90%. The molecular ER status was determined using a cutoff value of 1,000 for the Affymetrix probe set 205225_at corresponding to the estrogen receptor gene (*ESR1*), as has been by others (17). Identical results were obtained for 113 of the 119 samples when genes dependent on the ER status described by Gruvberger et al. (18) were used to cluster the samples into two groups. For use as an ordinal variable, the ranking of all samples according to the *ESR1* probe set 205225_at was used. For Affymetrix data on ErbB2 mRNA expression, a cutoff of 4,500 was identified for probe set 216836_s_at by using samples with a 3+ staining in immunohistochemistry with HER2 antibody. This cutoff also correlated very well with the ErbB2-like subtype based on the "intrinsic gene set" of Sorlie et al. (19) as previously shown (20). To obtain a quantitative metric for the molecular proliferation state, we used a cluster of 136 highly correlated genes well known for their association with proliferation (see Supplementary Fig. S9; Supplementary Table S4) similar to the method proposed by Sotiriou et al. (21). For plexin B1 Affymetrix data (probe set 215807_s_at), a cutoff value of 500 was determined by comparison with the ER status (see Results).

Table 1. Correlation of plexin B1 expression with clinical characteristics of breast cancers

	Total, N = 119	Plexin B1 expression (Affymetrix value)		P
		High (>500), n = 54	Low (≤500), n = 65	
Age (y)				
<50	59	33	26	0.027
≥50	60	21	39	
Tumor stage				
1	60	30	30	n.s.
2	49	18	31	
3	4	3	1	
4	6	3	3	
Nodal status				
Negative	66	29	37	n.s.
Positive	51	25	26	
Unknown	2	0	2	
Histology				
Ductal	87	29	58	<0.001
Lobular	25	20	5	
Mixed	3	3	0	
Other	4	2	2	
Molecular grading				
High proliferation	60	15	45	<0.001
Low proliferation	59	39	20	
ER status				
Positive	79	52	27	<0.001
Negative	40	2	38	
HER2 status				
Positive	23	5	18	0.018
Negative	96	49	47	
Molecular subtype				
Basal-like	31	4	27	<0.001
Erbb2-like	20	3	17	
Luminal A	67	46	21	
Luminal B	1	1	0	

Analysis of mRNA expression by quantitative real-time PCR. Total RNA from human primary mammary carcinomas was isolated by the guanidinium isothiocyanate method as described (22) in combination with affinity purification (RNeasy, Qiagen, Hilden, Germany). Real-time PCR analyses were done using the ABI 7700 Sequence Detection System (PE-Applied Biosystems, Foster City, CA). cDNAs were generated by random primed reverse transcription (ProSTAR cDNA-synthesis kit, Stratagene, La Jolla, CA) as previously described (23, 24). PCR reactions were done according to the manufacturer's protocols (PE-Applied Biosystems). VIC-fluorophore–labeled glycerol-3-phosphate dehydrogenase (GPDH) TaqMan probes served as reference quantification markers. Each quantitation was reproduced thrice and normalized to GPDH using the ΔC_t method. Pearson correlation was used to compare the ΔC_t values to Affymetrix microarray data. Primer sequences used for plexin B1 detection were as follows: PlxnB1-U1, 5′-ACCACAAGCTGGGC-CGGGACTCCC-3′; PlxnB1-L1, 5′-GATGTCTGCATAGTACCTTTCCAC-3′.

Immunohistochemical detection of plexin B1 protein expression. Frozen breast cancer tissues were cut into 5-μm sections and placed on superfrost charged slides. Immunohistochemistry was done according to standard procedures. Briefly, the slides were fixed for 10 min in acetone (−20°C) and incubated at room temperature with a primary monoclonal anti–plexin B1 antibody (Santa Cruz Biotechnology, Santa Cruz, CA; 1:100 dilution) for 1 h. Cy3-labeled antimouse secondary antibody (Dianova, Hamburg, Germany) was used to detect plexin B1 by fluorescence. Sections were counterstained with 4′,6-diamidino-2-phenylindole and then mounted with a coverslip. Basic routine H&E staining (modified Schmidt's hematoxylin) was done for all specimens to ensure tissue quality. Staining of the tissues with the anti–plexin B1 antibody was only observed in breast cancers positive for plexin B1 mRNA expression. Furthermore, as a positive control, the anti–plexin B1 antibody was independently verified by staining human skin (Supplementary Fig. S10).

Analyses of published data sets. The ONCOMINE 2.0 database (25)[7] was used as an interface to access published breast cancer microarray data sets. These data sets were analyzed for differential expression of plexin B1 among the class distinctions stored in the ONCOMINE database. The SymAtlas web application[8] was applied to analyze Affymetrix microarray data of normal human tissues stored in the SymGene database (26). Genome-wide gene expression data for 295 samples from the study of van de Vijver et al. (27) were downloaded from the website of Rosetta Inpharmatics.[9]

Statistical analysis. Subjects with missing values were excluded from the analyses and all reported P values were two sided. $P < 0.05$ was considered to indicate a significant result. For use as a binary variable, Affymetrix mRNA expression data of plexin B1 were categorized using a cutoff value of 500. In addition, a conservative procedure of median splitting was used for each independently analyzed sample group. Although it is also possible to use plexin B1 expression as a continuous prognostic factor, it is more appropriate and practical to group the tumors into two risk categories by use of a cutoff point when it is biologically meaningful, allowing, for example, direct comparison of Kaplan-Meier curves between groups. We chose the cutoff based on the expression level of plexin B1 in ER-negative tumors (see Results). This cutoff decision makes immediate biological sense because the gene was originally identified as a marker for ER-positive tumors, which display a behavior similar to that of ER-negative tumors. However, the results of the analyses did not change substantially when nearby cutoff points were used or plexin B1 levels were used in a continuous fashion (see Results). χ^2 test was used to test for associations between plexin B1 expression of tumors and standard clinical and molecular parameters. Survival intervals were measured from the time of surgery to the time of death from disease or of the first clinical or radiographic evidence of disease recurrence. Data for women in whom the envisaged end point was not reached were censored as of the last follow-up. We constructed Kaplan-Meier curves and used the log-rank test to determine the univariate significance of the variables. A Cox proportional hazards regression model was used to examine simultaneously the effects of multiple covariates on survival. The effect of each variable was assessed with the use of the Wald test and described by the hazard ratio with a 95% confidence interval. The stepwise Cox proportional hazards models initially included age, tumor size, lymph node status, molecular grading, ER, ErbB2, as well as plexin B1 expression. The final model was developed by dropping each variable in turn from the model and conducting a likelihood ratio test to compare the full and the nested models. A significance level of 0.1 as the cutoff to exclude a variable from the model was used. All analyses were done using SPSS 11.0 (SPSS, Inc., Chicago, IL).

Results

Plexin B1 expression in different human tissues and breast cancers. To gain further insight into the function of the *plexin B1* gene, we started our analysis with a survey of plexin B1 mRNA expression in various normal human tissues by using public available resources including the SymGene database (26). Plexin B1 expression was detected in a variety of human tissues (see Supplementary Fig. S5). Highest levels were observed in several regions of the brain, placenta, prostate, heart, colorectal adenocarcinoma, liver, lung, kidney, and thyroid, pointing to a role of plexin B1 in cells of ectodermal origin, which also constitute the progenitors of mammary epithelial cells. Furthermore, in previous microarray analyses of breast cancer samples, we and others identified *plexin B1* among genes that are most dependent on the ER status of the tumor (24), indicating an ER-driven regulation of plexin B1 in mammary epithelial cells.

Dysregulation of plexin B1 in ER-positive tumors. We have recently identified a subtype of breast cancers with stem cell–like features ("SCL" type) by gene expression profiling (28). A characteristic feature of those tumors was the perfect inverse correlation of ER expression and proliferative activity seen in this subgroup. In contrast, tumors that did not show this stem cell–like expression signature ("non-SCL" type) seemed to be frequently uncoupled from this tight link and displayed alterations in several ER-dependent transcriptional units, suggesting malfunctions in distinct branches of the ER regulatory network. The unique characteristic of SCL tumors allowed us to screen for altered expression in "uncoupled" tumors among 157 genes known to be dependent on the ER status. One of the genes that resulted from this screen was plexin B1, detected as part of a coregulated gene cluster containing a number of known genes involved in cellular adhesion. As shown in Supplementary Fig. S6, plexin B1 expression is strictly dependent on ER positivity but significantly reduced among those ER-positive samples in whom the proliferative activity was uncoupled from the ER status. In fact, *plexin B1* gene expression represents a link between those two vectors with a positive correlation to ER (*ESR1*) gene expression and a negative correlation to proliferative activity (see Supplementary Fig. S8). The correlation of plexin B1 expression with the ER status provides a clue for defining a reasonable cutoff point for Affymetrix microarray expression values of plexin B1. As presented in Fig. 1, only 2 of 40 (5%) ER-negative samples displayed an Affymetrix expression value >500 for plexin B1.

[7] http://www.oncomine.org
[8] http://symatlas.gnf.org/SymAtlas/
[9] http://www.rii.com/publications/2002/nejm.html

However, 27 of 79 (34%) of the ER-positive samples did show a negative result for plexin B1 when using this threshold.

Clinical characteristics of patients with plexin B1 expression. The clinical characteristics of patients with plexin B1 expression are presented in Table 1. Whereas we detected no correlation of tumor size and lymph node status with plexin B1 expression, a negative association with the age of the patient was observed. As stated above, a strong negative correlation of plexin B1 expression with the proliferative activity of the tumor was seen. Furthermore, plexin B1–expressing breast cancers are highly correlated with a lobular histology and a positive ER status, whereas ErbB2 was associated with low plexin B1 expression. These results are in line with low plexin B1 expression in the basal-like and ErbB2-like molecular subtypes when tumors were classified according to Sorlie et al. (19).

Loss of plexin B1 predicts poor outcome in ER-positive breast cancers. As shown in Fig. 2, plexin B1 displayed a significant prognostic value for disease-free survival. This effect was seen both in all patients (Fig. 2A) and in the ER-positive subgroup (Fig. 2B). In addition, plexin B1 seems to be of prognostic value in patients with a negative as well as a positive lymph node status (Fig. 2C and D, respectively) and independent of the type of chemotherapy used (epirubicin-cyclophosphamide or cyclophosphamide-methotrexate-5-fluorouracil; data not shown). Moreover, when comparing plexin B1 in univariate analysis to standard parameters, as denoted in Table 2, plexin B1 mRNA expression (Affymetrix value >500) displayed the highest prognostic value. This result was obtained for the whole sample group ($P = 0.0062$) as well as the subset of ER-positive patients ($P = 0.0107$). Even a very conservative approach of median splitting of plexin B1 Affymetrix values among each individual sample group resulted in high prognostic values ($P = 0.0173$ and $P = 0.0526$). Finally, as stated in Table 2, in a stepwise multivariable Cox regression model starting with all standard parameters, only plexin B1 ($P = 0.032$ and 0.022), tumor size ($P = 0.017$ and 0.026), and ErbB2 ($P = 0.048$ and 0.004) remained significant among all patients as well as ER-positive patients only. Here, it should be noted that the high prognostic value of ErbB2 among ER-positive patients is based only on 9 (11.4%) ErbB2-expressing tumors in this subgroup (see Table 2). Similar results were obtained when using log plexin B1 expression as a continuous variable in the Cox regression model ($P = 0.020$; hazard ratio, 0.33, 95% confidence interval, 0.13-0.84; for log of plexin B1 among ER-positive patients).

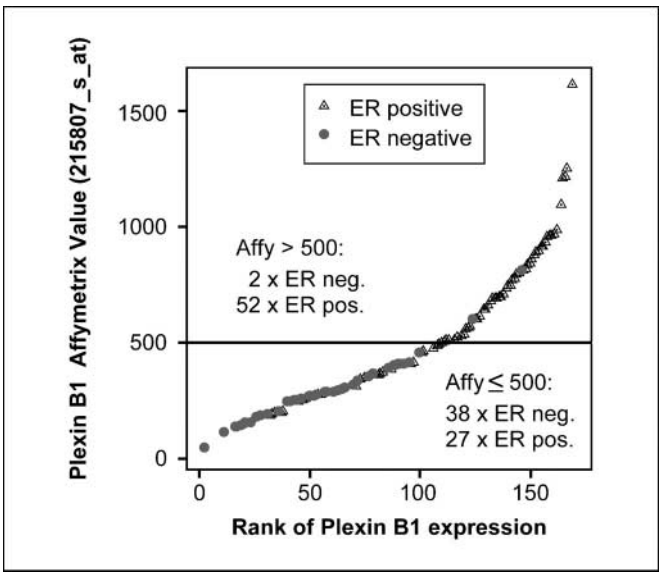

Fig. 1. Correlation of ER status and plexin B1 defines a threshold for plexin B1 Affymetrix expression values. Scatter plot of Affymetrix expression values of plexin B1 (probe set ID 215807_s_at) versus the rank of expression among 119 breast cancer samples. Triangles, ER-positive samples; gray dots, ER-negative samples. Horizontal line, Affymetrix expression value of 500, which was adopted as a biological threshold based on plexin B1 expression in ER-negative samples. The absolute numbers of ER-positive and ER-negative samples above and below this threshold are given.

Validation of plexin B1 mRNA expression by quantitative real-time PCR. Quantitative reverse transcription–based real-time PCR was used to validate the mRNA expression data obtained from the Affymetrix platform. Independent tissue samples were obtained from 29 of the tumors that were previously profiled on Affymetrix microarrays. Plexin B1 mRNA expression was measured using a SYBR green real-time PCR assay and the ΔC_t method was used to obtain relative expression values of plexin B1 as compared with GPDH. Both platforms display a highly significant correlation ($P = 0.001$). Supplementary Fig. S7 shows the box plot of ΔC_t values (plexin B1 versus GPDH) compared with qualitative data on plexin B1 expression as determined by microarray using >500 as cutoff value. From the plot, it can be deduced that this cutoff value roughly corresponds to a ΔC_t of ~ 5.

Prognostic value of plexin B1 expression can be verified on independent data sets. To verify our results on independent expression data, we analyzed published microarray data sets using the ONCOMINE database (25) as an interface. The data sets were investigated for differential expression of plexin B1 among the class distinctions stored in the ONCOMINE database. In line with our data, plexin B1 was dependent on the ER status in most studies (Supplementary Table S3). The highest significance ($P = 0.00005$) was obtained in the study of Wang et al. (29), which used the same Affymetrix microarray (HG-U133A) as in the work presented here. In addition, in three studies, a higher grading was correlated with reduced plexin B1 expression. Finally, reduced plexin B1 expression was correlated with early metastasis in the studies from the Netherlands Cancer Institute (27, 30). For a more detailed examination, we analyzed genome-wide gene expression data from van de Vijver et al. (27). The sample group was median split according to the expression value of the plexin B1 reporter (AB007867) on the microarray. As depicted in Fig. 3, plexin B1 expression showed a significant prognostic value both among all patients and in the ER-positive subgroup in this data set (Fig. 3A and B, respectively).

Plexin B1 protein is expressed by epithelial carcinoma cells. Recent observations (31, 32) suggested an additional function for plexin B1 in endothelial cells, and it was proposed that some carcinomas might exploit a proangiogenic effect of Sema4D as a chemoattractant on plexin B1–expressing endothelial cells (33). Accordingly, it could be speculated that expression of plexin B1 by the tumor cells themselves might sequester the secreted Sema4D and reduce its proangiogenic effect. In this case, the loss of plexin B1 would also be of

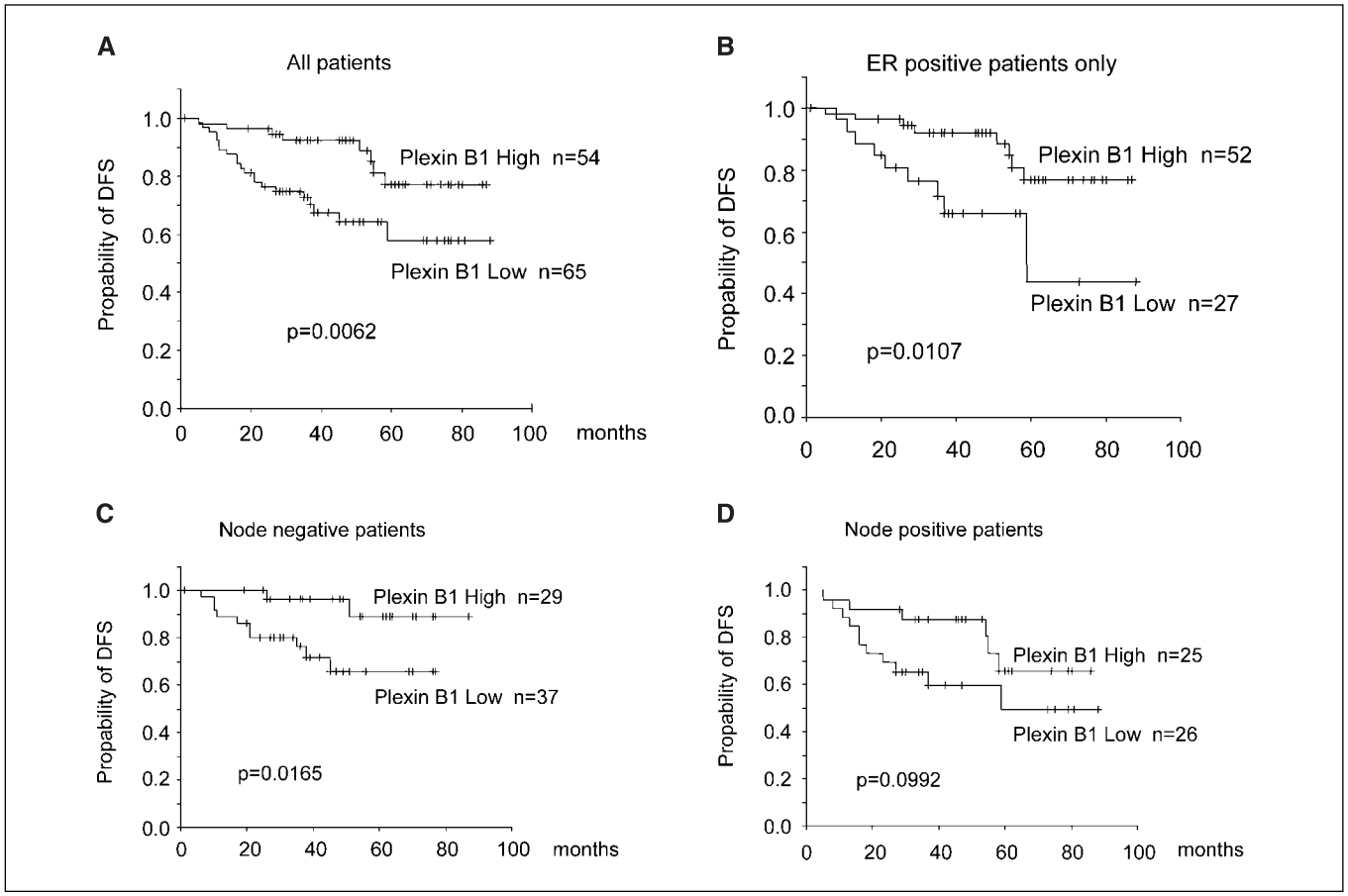

Fig. 2. Prognostic significance of loss of plexin B1 expression. Kaplan-Meier estimates of the disease-free survival of patients with tumors stratified by plexin B1 expression (Affymetrix threshold of 500) are given. Individual curves are presented for all patients (*A*), the ER-positive subgroup (*B*), all lymph node – negative patients (*C*), as well as lymph node – positive patients (*D*).

advantage for the tumor cells. In light of these different possibilities, a critical question is whether the tumor cells themselves or endothelial cells are the major source of plexin B1 expression in the tumor. Thus, we carried out immunohistochemistry to detect plexin B1 protein in those breast cancer samples with high *plexin B1* gene expression. As shown in Fig. 4 and Supplementary Fig. S4, expression of plexin B1 was detectable in ductal mammary epithelial cells.

Table 2. Univariate and multivariate analyses of standard parameters and plexin B1 in relation to disease-free survival

Parameter	All patients (*N* = 119)		ER-positive patients only (*n* = 79)	
Univariate analysis	*P*	*n*	*P*	*n*
Age (≤50 vs >50 y)	0.3129	59 vs 60	0.2731	44 vs 35
Tumor size (>2 vs ≤2 cm)	0.0232	59 vs 60	0.0747	39 vs 40
Lymph node (positive vs negative)	0.1308	51 vs 66	0.1139	39 vs 39
Molecular grading (above vs below median proliferation)	0.0395	60 vs 59	0.0872	39 vs 40
ER status (negative vs positive)	0.1653	40 vs 79	n.a.	n.a.
HER2 mRNA (Affymetrix value >4,500 vs ≤4,500)	0.0690	23 vs 96	0.0121	9 vs 70
Plexin B1 mRNA median (below vs above median Affymetrix-value in each individual sample group)	0.0173	60 vs 59	0.0526	40 vs 39
Plexin B1 mRNA (Affymetrix value ≤500 vs >500)	0.0062	65 vs 54	0.0107	27 vs 52
Multivariate Cox regression	*P*	Hazard ratio (95% CI)	*P*	Hazard ratio (95% CI)
Tumor size (≤2 vs >2 cm)	0.017	0.35 (0.15-0.83)	0.026	0.25 (0.08-0.85)
Plexin B1 mRNA (Affymetrix-value >500 vs ≤500)	0.032	0.40 (0.17-0.93)	0.022	0.31 (0.12-0.85)
HER2 mRNA (Affymetrix value >4,500 vs ≤4,500)	0.048	2.41 (1.01-5.76)	0.004*	6.12 (1.81-20.7)*

*High hazard ratio based on only 9 (11.4%) HER2-expressing patients in this ER-positive subgroup.

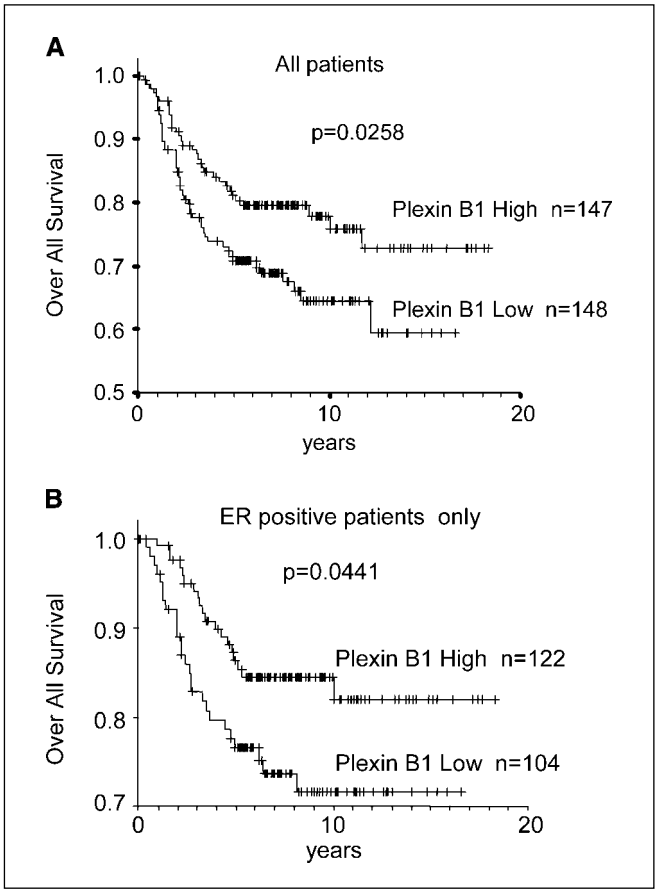

Fig. 3. Prognostic value of plexin B1 expression in published microarray data sets. The sample group of 295 breast tumors from the study of van de Vijver et al. (27) was median split according to the expression value of the plexin B1 reporter (AB007867) on their microarray. Kaplan-Meier estimates of survival of patients according to this stratification are given both for all patients (*A*) and the ER-positive subgroup (*B*).

Discussion

Using several complementing methods, we found that patients with breast cancers that are characterized by reduced plexin B1 expression display a poor prognosis. These results might suggest that plexin B1 suppress the invasive behavior of the tumor. However, the precise function of plexin B1 in tumors is not yet clear. On one hand, it was shown that plexin B1 couples with the receptor tyrosine kinases Met (3) and ErbB2 (14), and in both cases, Sema4D stimulates receptor kinase activity. This led researchers to speculate that the plexin B1-Met interaction may trigger invasive growth of epithelial cells by regulating MET signaling through its effectors like Grb2, Src, or phosphatidylinositol 3-kinase and the mitogen-activated protein kinase pathway (3). On the other hand, the semaphorins are well known as repellants defining areas of exclusion for plexin- and neuropilin-expressing neurons in the developing nervous system (34, 35). Both plexin A1 and plexin B1 signal repulsion when activated by their semaphorin ligands. Analogous to governing the repulsive growth of neurons, plexin D1 and Sema3E are required for the exclusion of vasculature from somites during development. Sema3E is expressed by the somites and functions as a stop sign for plexin D1–expressing endothelial cells, preventing vessels to colonize the somites (36). Consistently, Sema4D signaling through plexin B1 in the breast carcinoma cell line SKBR3 inhibits cell migration (37). The discovery that plexins have intrinsic GTPase-activating protein activity toward R-Ras (38) provided a link between the various aspects of semaphorin biology, suggesting that many of their effects relate to the plexin-mediated regulation of integrins by R-Ras. The repellent effect to turn away from the semaphorin source can thus be explained by R-Ras–mediated disruption of integrin binding to the extracellular matrix by semaphorin-plexin engagement on one side of the cell. An increased integrin binding to extracellular matrix on the opposing side where no semaphorin plexin interaction occurs leads to growth and migration. Thus, it has been suggested that any activation of plexin signaling might suppress metastasis by activating the GTPase-activating protein activity of plexins toward R-Ras, leading to decreased integrin binding. R-Ras is itself oncogenic (39–41). Constitutively active R-Ras has been found to increase cell migration of T47D breast epithelial cells (42) and cervical epithelial C33A cells (39) toward collagen. Consequently,

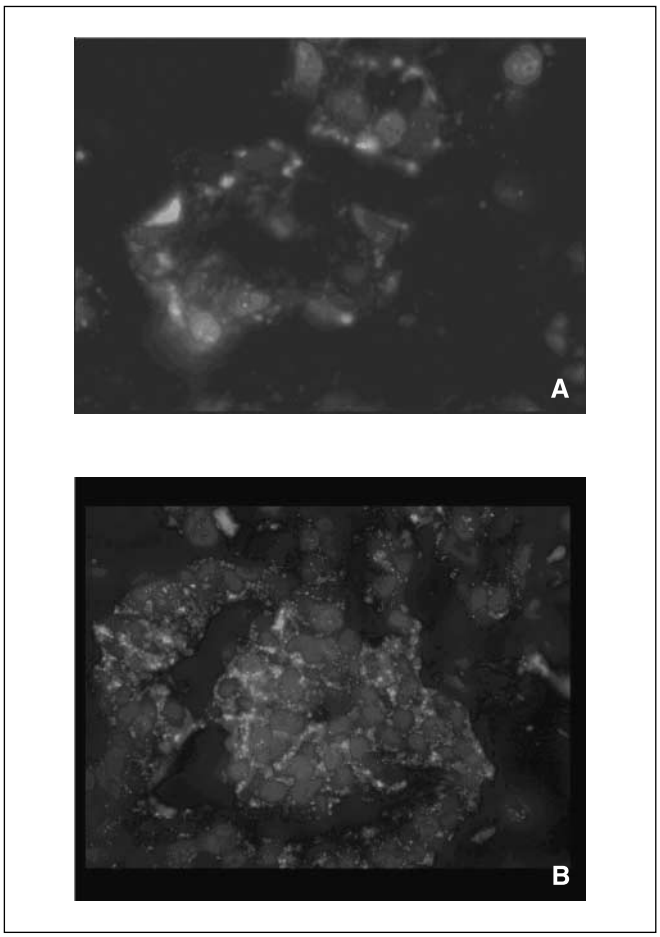

Fig. 4. Detection of plexin B1 protein on tumor cells. Plexin B1 protein was detected in 5-μm sections of tumor tissue from a breast cancer patient using a monoclonal antibody directed against plexin B1 and visualized with a Cy3-labeled secondary antibody. 4′,6-Diamidino-2-phenylindole was used to counterstain the nuclei of cells. *A,* normal mammary epithelial cells; *B,* tumor cells of an invasive ductal mammary carcinoma. No staining was seen when mammary carcinomas without plexin B1 mRNA expression were analyzed (data not shown). A color version of this figure is available online in Supplementary data (Suppl. Fig. S4).

semaphorin-stimulated plexin GTPase-activating protein activity might decrease cell migration in certain cancers. In conclusion, loss of plexin B1 expression could allow tumor cells to grow in opposite direction toward a repelling semaphorin gradient. This feature could promote an invasive behavior and enhance the distortion of normal tissue structure by the tumor cells. Our data emphasize that loss of plexin B1 characterizes a more aggressive tumor phenotype because low plexin B1 expression levels are associated with an impaired prognosis of breast cancer patients in both univariate (all patients, $P = 0.0062$; ER positive, $P = 0.0107$) and multivariate (all patients, $P = 0.032$; ER positive, $P = 0.022$) analyses, outperforming standard prognostic parameters such as tumor size, nodal status, ER status, etc. This observation is not only confined to our study cohort but can also be verified in microarray analyses of several authors, underlining the validity of our findings. Furthermore, differential expression of plexin B1 was validated by PCR analysis confirming the results of our microarray data.

Factors that are regulatorily involved in expression of plexin B1 are largely unknown. Here, we can show that plexin B1 expression is strongly correlated with expression of ER and low proliferative state of mammary carcinoma cells (see Supplementary Fig. S8). Yet loss of plexin B1 expression was observed in the subset of ER-positive tumors with high proliferation (uncoupled tumors), contrasting the normal inverse relationship between the ER status and the proliferative activity of the tumor (43, 44). When classifying tumors according to the intrinsic gene set described by Sorlie et al., the loss of plexin B1 is mainly confined to the basal-like and ErbB2-like tumors. However, roughly one third of all luminal A tumors show a low plexin B1 expression ≤500 (see Table 1).

Recent results (31, 32) also propose an additional function for plexin B1 in endothelial cells. Here, Sema4D promotes endothelial cell migration and tubulogenesis *in vitro* and the formation of blood vessels *in vivo*. A new study (33) even suggested that head and neck squamous cell carcinomas and other epithelial-derived tumors, including breast carcinomas, might indeed exploit the proangiogenic effect of Sema4D to promote tumor growth and survival and enhance their metastatic potential. In this scenario, Sema4D would be a chemoattractant rather than a repellent for plexin B1–expressing endothelial cells. Accordingly, it could be speculated that expression of plexin B1 by the tumor cells themselves might sequester the secreted Sema4D and reduce its proangiogenic effect. In this case, the loss of plexin B1 would also be of advantage for the tumor cells. Thus, an important aspect of our results is the immunohistochemical demonstration that the tumor cells themselves and not the endothelial cells are the major source of plexin B1 expression in the tumor.

In conclusion, plexin B1 represents an important new prognostic marker for breast cancer. Moreover, because of the normal inverse link between ER status and proliferation seen in plexin B1–expressing tumors, loss of plexin B1 might also act as a predictive marker indicating an endocrine resistance. The use of estrogen and progesterone receptor status to select for endocrine therapy is undeniably crucial. However, novel markers of a functional ER signaling like plexin B1 may also predict response to endocrine therapy as has been suggested for ErbB2 (45). To evaluate this potential role of plexin B1, further clinical investigations should be done.

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