Human Breast Cancer: Correlation of Relapse and Survival with Amplification of the HER-2/*neu* Oncogene

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The HER-2/*neu* oncogene is a member of the *erbB*–like oncogene family, and is related to, but distinct from, the epidermal growth factor receptor. This gene has been shown to be amplified in human breast cancer cell lines. In the current study, alterations of the gene in 189 primary human b east cancers were investigated. HER-2/*neu* was found to be amplified from 2- to greater than 20-fold in 30% of the tumors. Correlation of gene amplification with several disease parameters was evaluated. Amplification of the HER-2/*neu* gene was a significant p e-dictor of both overall survival and time to relapse in patients with b east cancer. It retained its significance even when adjustments were made for other known prognostic factors. Moreover, HER-2/*neu* amplification had greater p ognostic value than most currently used prognostic factors, including hormonal-receptor status, in lymph node–positive disease. These data indicate that this gene may play a role in the biologic behavior and/or pathogenesis of human b east cancer.

THE EVIDENCE LINKING PROTO-ONCOGENES TO THE INDUCtion or maintenance of human malignancies is largely circumstantial, but has become increasingly compelling. This circumstantial evidence is derived from studies of animal models, tumor cell lines, and actual human tumors. Data from animal models and cell lines include: (i) sequence homology between human proto-oncogenes and the viral oncogenes of transforming retroviruses that are known to be tumorigenic in some species (*1, 2*); (ii) transfection studies showing the transforming potential of proto-oncogenes in NIH 3T3 cells and primary embryo fibroblasts (*3–5*); and (iii) the central role of certain proto-oncogenes in tumorigenesis by chronic transforming retroviruses such as avian leukosis virus (*6*). Data from human tumors include: (i) increased expression of specific proto-oncogenes in some human malignancies (*7, 8*); (ii) localization of proto-oncogenes at or near the site of specific, tumor-associated chromosomal translocations (*9*); and (iii) amplification of proto-oncogenes in some human tumors (*10, 11*).

Additional data linking proto-oncogenes to cell growth is their expression in response to certain proliferation signals (*12, 13*) and their expression during embryonic development (*14, 15*). More direct evidence comes from the fact that, of the 20 known proto-oncogenes, three are related to a growth factor or a growth factor receptor. These genes include c-*sis*, which is homologous to the transforming gene of the simian sarcoma virus and is the β chain of platelet-derived growth factor (PDGF) (*16, 17*); c-*fms*, which is homologous to the transforming gene of the feline sarcoma virus and is closely related to the macrophage colony-stimulating factor receptor (CSF-1R) (*18*); and c-*erbB*, which encodes the EGF receptor (EGFR) and is highly homologous to the transforming gene of the avian erythroblastosis virus (*19*). The two receptor-related proto-oncogenes, c-*fms* and c-*erbB*, are members of the tyrosine-specific protein kinase family to which many proto-oncogenes belong.

Recently, a novel transforming gene was identified as a result of transfection studies with DNA from chemically induced rat neuroglioblastomas (*20*). This gene, called *neu*, was shown to be related to, but distinct from, the c-*erbB* proto-oncogene (*21*). By means of v-*erbB* and human EGFR as probes to screen human genomic and complementary DNA (cDNA) libraries, two other groups independently isolated human *erbB*–related genes that they called HER-2 (*22*) and c-*erbB*-2 (*23*). Subsequent sequence analysis and chromosomal mapping studies revealed all three genes (*neu*, c-*erbB*-2, and HER-2) to be the same (*22, 24, 25*). A fourth group, also using v-*erbB* as a probe, identified the same gene in a mammary carcinoma cell line, MAC 117, where it was found to be amplified five- to ten-fold (*26*).

This gene, which we will call HER-2/*neu*, encodes a new member of the tyrosine kinase family; and is closely related to, but distinct from, the EGFR gene (*22*). HER-2/*neu* differs from EGFR in that it is found on band q21 of chromosome 17 (*22, 24, 25*), as compared to band p11–p13 of chromosome 7, where the EGFR gene is located (*27*). Also, the HER-2/*neu* gene generates a messenger RNA (mRNA) of 4.8 kb (*22*), which differs from the 5.8- and 10-kb transcripts for the EGFR gene (*28*). Finally, the protein encoded by the HER-2/*neu* gene is 185,000 daltons (*21*), as compared to the 170,000-dalton protein encoded by the EGFR gene. Conversely, on the basis of sequence data, HER-2/*neu* is more closely related to the EGFR gene than to other members of the tyrosine kinase family (*22*). Like the EGFR protein, HER-2/*neu* has an extracellular domain, a transmembrane domain that includes two cysteine-rich repeat clusters, and an intracellular kinase domain (*21*), indicating

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that it too is likely to be a cellular receptor for an as yet unidentified ligand.

As a result of the published data showing amplification of HER-2/*neu* in a human mammary carcinoma cell line, and as part of an ongoing survey in our laboratory of proto-oncogene abnormalities in human tumors, we evaluated alterations of the HER-2/*neu* gene in a large series of human primary breast cancers. Our results show that amplification of this gene occurs relatively frequently in breast cancer, and that it is associated with disease relapse and overall patient survival.

Factors that are known to be important in the prognosis of breast malignancies in individual patients include: size of the primary tumor, stage of disease at diagnosis, hormonal receptor status, and number of axillary lymph nodes involved with disease (positive nodes) (*29*). The current study, which was conducted in two parts, involved the evaluation of tissue from 189 separate breast malignancies that were part of a breast cancer study ongoing at the University of Texas, San Antonio. This cohort of tumors was of interest because considerable information was available on the majority of the specimens including size of the primary tumor, estrogen receptor status, progesterone receptor status, age of patient, disease stage, and status of the axillary lymph nodes.

In the initial survey, tissue from 103 primary breast cancers was evaluated for alterations in the HER-2/*neu* gene. DNA from individual tumors was prepared as described (*30*), digested with Eco RI, and subjected to Southern blot analysis with a ^{32}P-labeled HER-2/*neu*-1 probe, which is known to detect a 13-kb hybridizing band in human DNA (22). Examples of tumors from the initial survey are shown in Fig. 1. Of the 103 samples examined, 19 (18%) showed evidence of HER-2/*neu* gene amplification. The degree of amplification in individual cases was determined by dilution analysis (Fig. 2A), as well as soft laser densitometry scanning. To determine that the amount of DNA loaded in each lane was equivalent, all filters were washed and rehybridized with a ^{32}P-labeled arginase gene probe (*31*). This probe identifies a 15-kb hybridizing band on Eco RI–digested human DNA, and was selected as a control because it more appropriately assesses the relative amount and transfer of high molecular weight species than a probe hybridizing with low molecular weight species, which transfer more readily on Southern blotting. All lanes were shown to contain equivalent amounts of high molecular weight DNA (Fig. 2B). Individual tumors were assigned to groups containing a single copy, 2 to 5 copies, 5 to 20 copies, and greater than 20 copies of the HER-2/*neu* gene (Fig. 1). Assignment of tumors to the various groups was done

Table 1. Association between HER-2/*neu* amplification and disease parameters in 103 breast tumors.

Factor*	Number of tumors					P†
	Single copy	2 to 5 copies	5 to 20 copies	>20 copies	Total	
Hormonal receptor status						
ER+	53	2	9	1	65	0.99
ER−	31	1	2	4	38	
PgR+	42	2	6	2	52	0.85
PgR−	42	1	5	3	51	
Tumor size (centimeters)						
≤2	13	1	1	0	15	0.82
2–5	34	1	5	1	41	
>5	17	1	2	2	22	
Unknown	20	0	3	2	25	
Age at diagnosis (years)						
≤50	21	1	2	1	25	0.83
>50	52	2	7	4	65	
Unknown	11	0	2	0	13	
Number of positive lymph nodes						
0	30	0	3	1	34	0.11
1–3	20	0	1	1	22	
>3	17	2	4	2	25	
Unknown	17	1	3	1	22	

*Receptor status was analyzed as described (*39*). ER, estrogen receptor: + and − refer to the presence or absence of ≥3 fmol of receptor per milligram of protein. PgR, progesterone receptor: + and − refers to the presence or absence of ≥5 fmol of receptor per milligram of protein. †Statistical analyses for correlation of HER-2/*neu* amplification with disease parameters were performed by the χ^2 test. *P* values were computed after combining the cases with 5 to 20 and >20 copies.

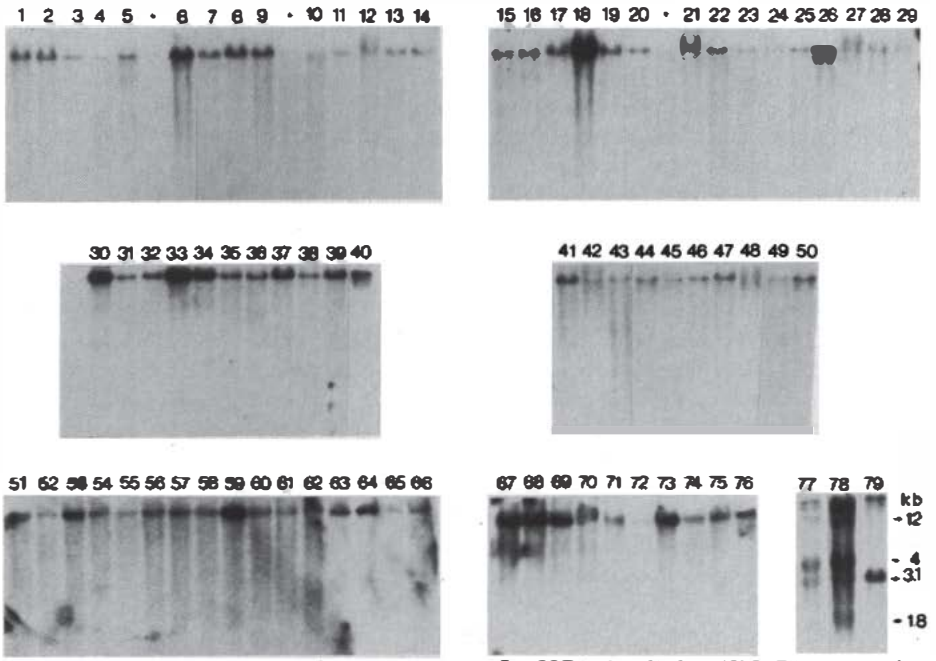

Fig. 1. Analysis of alterations of the HER-2/*neu* gene in human breast cancer. Shown are 79 of the 189 breast tumors used in this analysis. Tumors with a single cop of ER-2/*neu*: 3, 4, 10 to 15, 20, 23 to 25, 27 to 29, 31, 38, 42 to 46, 48, 49, 52, 55, 61, 65, 66, 71, 72, and 74. Tumors with two to five copies of ER-2/*neu*: 1, 2, 5, 7, 9, 16, 17, 19, 21, 22, 32, 35, 36, 47, 50, 54, 56 to 58, 60, 62, 70, and 75 to 77. Tumors with 5 to 20 copies of HER-2/*neu*: 6, 8, 26, 34, 37, 39 to 41, 51, 53, 63, 64, 67, 69, 73, and 79. Tumors with more than 20 copies of ER-2/*neu*: 18, 30, 33, 59, 68, and 78. Examples of tumors 77 to 79 have rearrangements in the HER-2/*neu* gene. DNA was extracted from tissues and digested with Eco RI as described (*30*). A total of 12 μg of Eco RI–digested DNA was loaded onto 0.8% agarose gels, separated by electrophoresis, and transferred onto nylon filter papers (Biodyne) (*30*). All filters were baked in a vacuum oven for 3 hours at 80°C, prehybridized in 5× SSC (standard saline citrate) containing 50% formamide, 10% dextran sulfate, 0.1% SDS, denatured salmon sperm DNA (1 mg/ml), and 4× Denhardts solution for 12 hours, then hybridized in the same solution containing ^{32}P-labeled nick-translated HER-2 probe (*21*) specific activity of 1×10^8 cpm per microgram of DNA; 2×10^6 cpm/ml. Hybridization occurred at 42°C for 48 hours, followed washing of filters under the following conditions in succession: 2× SSC for 20 minutes at room temperature; two washes of 30 minutes each in 2× SSC, 0.1% SDS at 65°C; one wash of 30 minutes in 0.5× SSC, 0.1% SDS at 65°C. Filters were then exposed to XAR-5 x-ray film (Kodak) for autoradiography.

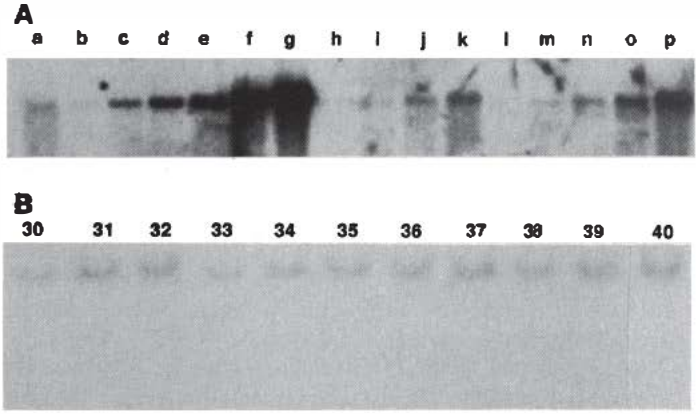

Fig. 2. (**A**) Example of dilutional analysis to assess degree of HER-2/*neu* gene amplification. Lanes a, g, k, and p were loaded with 12 μg of Eco RI–digested breast tumor DNA. Lane a is DNA from tumor 31 (Fig. 1), which represents a tumor with a single copy of the HER/2-*neu* gene. Lane g is DNA from tumor 33, which represents a tumor with >20 copies of the HER-2/*neu* gene. Lanes b to f are serial dilutions (1:100, 1:20, 1:10, 1:5, and 1:2, respectively) of the DNA sample in lane g. Lane k is DNA from tumor 35 (Fig. 1), which represents a tumor containing two to five copies of the HER-2/*neu* gene. Lanes h to j are serial dilutions (1:10, 1:5, and 1:2, respectively) of the DNA sample in lane k. Lane p is DNA from tumor 34 (Fig. 1), which represents a tumor with 5 to 20 copies of the HER-2/*neu* gene. Lanes l to o are serial dilutions (1:20, 1:10, 1:5, and 1:2, respectively) of the DNA sample in lane p. The filter was prepared and hybridized with a ^{32}P-labeled HER-2 probe as in Fig. 1. (**B**) Example of arginase probe hybridization to demonstrate that equivalent amounts of tumor DNA were loaded into each lane. Rehybridization of filter containing lanes 30 to 40 (Fig. 1). The filter was first stripped of label by washing in a buffer made up of 50% formamide, 3× SSC, and 0.1% SDS at 65°C for 20 minutes, following by three successive washes of 5 minutes each in 0.1× SSC at room temperature. Filters were exposed overnight on XAR-5 film (Kodak) to ensure removal of all radioactive probe, then rehybridized as in Fig. 1 with a ^{32}P-labeled human arginase gene probe (*31*).

in a blinded fashion, in that they were made without knowledge of disease parameters. Analysis of the data for association between gene amplification and a number of disease parameters was then performed.

Of 103 tumors evaluated in the initial survey, there was essentially no correlation between gene amplification and estrogen receptor status, progesterone receptor status, size of tumors, or age at diagnosis (Table 1). However, when analysis was performed for association between HER-2/*neu* amplification and number of positive lymph nodes, a trend was noted. This analysis showed that 4/34 (11%) of patients with no involved nodes, 2/20 (10%) with 1 to 3 involved nodes, and 8/25 (32%) with >3 involved nodes had gene amplification ($P = 0.11$). If these data were examined by comparing 0 to 3 positive nodes versus >3 positive nodes, the correlation with gene amplification became more significant ($P < 0.05$). Thus, there was a significant increase in incidence of HER-2/*neu* gene amplification in patients with >3 axillary lymph nodes involved with disease. A multivariate regression analysis to correlate HER-2/*neu* amplification with various disease parameters identified the number of positive nodes as the only significant factor, either alone or in combination, to correlate with amplification.

This initial study indicated that it might be possible to discriminate among node-positive patients on the basis of HER-2/*neu* gene amplification. It is well known that the number of positive nodes is the best prognostic factor for disease recurrence and survival in patients with breast cancer (*29*). Given the correlation between number of nodes positive and HER-2/*neu* amplification, one might predict that amplification of this gene might also have some prognostic value. No long-term follow-up data, however, were available on the 103 patients analyzed in the initial study. For this reason, a second study was conducted on 100 breast cancer samples from patients with positive axillary lymph nodes. All of the information available for the first group of 103 patients was available for these patients. In addition, relapse and survival information was available, since these cases had a median follow-up of 46 months (range 24 to 86 months). Of these 100 samples, 86 yielded sufficient DNA for study. Amplification of the HER-2/*neu* gene was measured as in the initial survey, and examples of tumors from this study are shown (Fig. 1). Amplification was found in 34/86 (40%) of these patients. For this larger sample of node-positive patients, several statistically significant or nearly significant relationships were observed. In agreement with the preliminary survey, there was an association between number of involved lymph nodes and HER-2/*neu* amplification (Table 2). In addition, the presence of gene amplification was correlated with estrogen receptor status and size of primary tumor (Table 2). Together, these two surveys yielded data on 189 patients and the association of HER-2/*neu* amplification with various disease parameters in the combined group is shown in Table 3.

While these correlations were of interest, the strong relationship

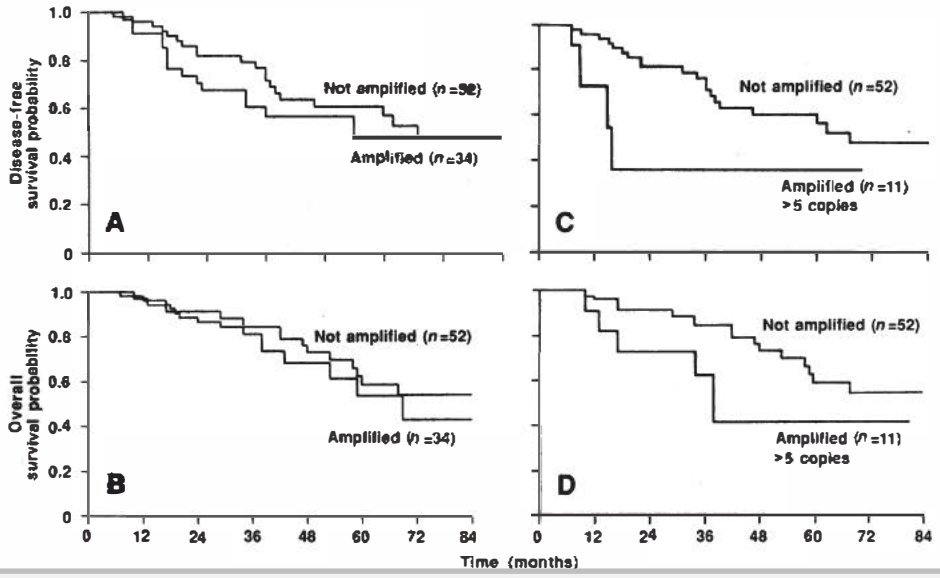

Fig. 3. Actuarial curve for relapse in (**A**) node-negative patients with no amplification versus node-positive patients with any amplification (>2 copies) of HER-2/*neu* and (**C**) node-positive patients with no amplification versus node-positive patients with greater than 5 copies of HER-2/*neu*. Actuarial curve for overall survival in (**B**) node-positive patients with no amplification versus node-positive patients with any amplification (>2 copies) of HER-2/*neu* and (**D**) node-positive patients with no amplification versus node-positive patients with greater than 5 copies of HER-2/*neu*. Actuarial curves for both relapse and overall survival were computed by the method of Kaplan and Meier (*44*) and compared by the log rank test (*42–44*).

between HER-2/*neu* amplification and nodal status ($P = 0.002$) indicated that information on amplification of this gene may correlate with disease behavior; that is, recurrences and survival. To test this, univariate survival analyses were performed in which amplification was compared to relapse and survival in this patient group. A total of 35 patients had a recurrence of the disease, and 29 had died at the time of the analyses. Median times to relapse and death were 62 months and 69 months, respectively. The median follow-up time for patients still alive was 47 months, ranging from 24 to 86 months. A total of 71 of the 86 patients (83%) received some form of therapy after mastectomy: adjuvant systemic therapy alone, 47%; adjuvant systemic therapy plus local radiation, 19%; and local radiation alone, 17%. A strong and highly statistically significant correlation was found between the degree of gene amplification and both time to disease relapse ($P = <0.0001$) and survival ($P = 0.0011$) (Table 4). Moreover, when compared in univariate analyses to other parameters, amplification of HER-2/*neu* was found to be superior to all other prognostic factors, with the exception of the number of positive nodes (which it equaled) in predicting time to relapse and overall survival in human breast cancer (Table 4). The association between HER-2/*neu* amplification and relapse and survival can be illustrated graphically in actuarial survival curves (Fig. 3, A to D). While there was a somewhat shortened time to relapse and shorter overall survival in patients having any amplification of the HER-2/*neu* gene in their tumors (Fig. 3, A and B), the greatest differences were found when comparing patients with >5 copies of the gene to those without amplification (single copy) (Fig. 3, C and D). Patients with greater than five copies of HER-2/*neu* had even shorter disease-free survival times ($P = 0.015$) and overal survival times ($P = 0.06$) when compared to patients with no amplification. The phenomenon of greater gene copy number correlating with a worse prognosis has also been seen in evaluations of N-*myc* gene amplification in human neuroblastomas (*32*).

To determine if amplification of HER-2/*neu* was independent of other known prognostic factors in predicting disease behavior, multivariate survival analyses were performed on the 86 node-positive cases. Amplification of the gene continued to be a strong prognostic factor, providing additional and independent predictive information on both time to relapse and overall survival in these patients, even when other prognostic factors were taken into account (Table 4).

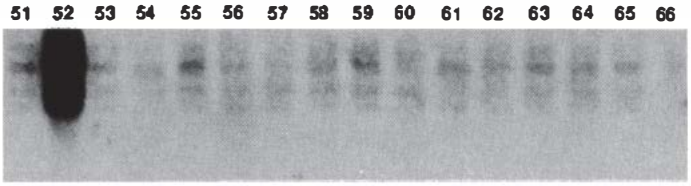

Fig. 4. Example of rehybridization of filter with human EGFR probe. Filters were stripped as in Fig. 2B, and hybridized with ^{32}P-labeled human EGFR probe (*28*), as in Fig. 1. Shown are the lower molecular weight bands hybridized with ^{32}P- abeled EGFR probe in filter-containing lanes 51 to 66 (Fig. 1). The bands from top to bottom are 2.8 2.2, and 1.8 kb, respectively. Lane 52 is an example of a tumor showing marked amplification (>50 copies) of the EGFR gene.

Rearrangement of the HER-2/*neu* gene was rare. Of the total 189 tumors evaluated, three showed evidence of rearrangement, and in two of the three cases, the rearrangement was identical (Fig. 1, cases 77 to 79). Also, two of the rearranged HER-2/*neu* loci were amplified (Fig. 1, cases 78 and 79). The incidence of HER-2/*neu* rearrangement as determined by Eco RI digestion was too small to attempt statistical correlations.

To determine whether the phenomenon of amplification of HER-2/*neu* in breast cancer extended to related growth factor receptors, all filters were analyzed with the EGFR probe (Fig. 4). Amplification of the EGFR gene was found in 4/189 (2%) of the cases, and rearrangement of the EGFR gene was found in one of those four cases. The incidence of EGFR amplification and rearrangement was too smal to attempt statistical correlation. Comparison of HER-2/*neu* amplification (53/189 or 28%) with that of the EGFR gene reveals the incidence of the former to be 14 times greater than that of the latter, indicating that the phenomenon of gene amplification is not a general one for a related tyrosine kinase–specific receptor in human breast cancer. Moreover, studies examining alterations of two other tyrosine kinase–specific proto-oncogenes, *abl* and *fes*, in breast cancer did not show amplification of these genes (*33*). Alterations of non–tyrosine kinase–related proto-oncogenes in these

Table 2. Association between HER-2/*neu* amplification and disease parameters in 86 breast tumors from node-positive patients.

Factor*	Single copy	2 to 5 copies	5 to 20 copies	>20 copies	Total	P†
Hormonal receptor status						
ER+	38	21	5	1	65	0.05
ER−	14	2	4	1	21	
PgR+	31	18	4	1	54	0.14
PgR−	21	5	5	1	32	
Tumor size (centimeters)						
≤2	18	8	3	0	29	0.09
2–5	28	12	2	1	43	
>5	6	3	4	1	14	
Age at diagnosis (years)						
≤50	16	12	6	1	35	0.06
>50	36	11	3	1	51	
Number of positive lymph nodes						
1–3	31	7	5	0	43	0.06
>3	21	16	4	2	43	

*ER and PgR are as described in Table 1. †Statistical analyses for correlation of HER-2/*neu* amplification with various disease parameters were performed by the χ^2 test. *P* values were computed after combining the 5 to 20 and >20 cases, since there were so few samples in the >20 group.

Table 3. Association between HER-2/*neu* amplification and disease parameters in combined surveys (189 patients).

Factor*	Single copy	2 to 5 copies	5 to 20 copies	>20 copies	Total	P†
Hormonal receptor status						
ER+	91	23	14	2	130	0.05
ER−	45	3	6	5	59	
PgR+	73	20	10	3	106	0.06
PgR−	63	6	10	4	83	
Tumor size (centimeters)						
≤2	31	9	4	0	44	0.19
2–5	62	13	7	2	84	
>5	23	4	6	3	36	
Unknown	20	0	3	2	25	
Age at diagnosis (years)						
≤50	37	13	8	2	60	0.11
>50	88	13	10	5	116	
Unknown	11	0	2	0	13	
Number of positive lymph nodes						
0	30	0	3	1	34	0.002
1–3	51	7	6	1	65	
>3	38	18	8	4	68	
Unknown	17	1	3	1	22	

*ER and PgR are as described in Table 1. †Statistical analyses for correlation of HER-2/*neu* amplification with various disease parameters were performed by the χ^2 test. *P* values were computed after combining the cases with 5 to 20 and >20 copies.

Table 4. Univariate and multivariate analyses comparing disease-free survival (relapse) and overall survival to prognostic factors in node-positive patients.

Factor	Univariate (*P*)		Multivariate*			
	Survival	Relapse	Survival		Relapse	
Number of positive nodes	0.0001	0.0002	0.0003	(0.0938 ± 0.0256)	0.001	(0.0849 ± 0.0266)
HER-2/*neu*	0.0011	<0.0001	0.02	(0.0872 ± 0.0388)	0.001	(0.1378 ± 0.0425)
Log (PgR)	0.05	0.05				
Tumor size	0.06	0.06				
Log (ER)	0.15	0.10	0.03	(−0.5158 ± 0.2414)		
Age	0.22	0.61				

*Cox's partially nonparametric regression model was used to evaluate the predictive power of various combinations and interactions of prognostic factors in a multivariate manner (*42–44*). Results are shown as *P* (regression coefficient ± SE).

tumors have been examined. In a survey of 121 primary breast malignancies, amplification of the c-*myc* gene was found in 38 (32%) (*34*). Attempts to correlate c-*myc* gene amplification with stage of disease, hormonal receptor status, histopathologic grade, or axillary node metastases showed no association. There was a statistically significant association between c-*myc* amplification and age at diagnosis >50 years in a group of 95 of these patients (*34*). Data on relapse and survival were not presented in this study; however, there was no correlation between c-*myc* amplification and nodal status to indicate an association with disease behavior.

The exact role of various proto-oncogenes in the pathogenesis of human malignancies remains unclear. One line of evidence implicating abnormalities of these genes in human disease is association of their amplification with tumor progression in specific cancers. The N-*myc* gene is frequently amplified in human neuroblastomas and neuroblastoma cell lines (*35, 36*). Studies on the N-*myc* proto-oncogene were the first to show a direct association between abnormalities in a proto-oncogene and clinical behavior of a human tumor. N-*myc* amplification and expression correlate both with stage of disease and overall survival in patients with neuroblastoma (*10, 32, 37*). Moreover the greater the N-*myc* gene copy number, the worse the patient prognosis for all stages of the disease (*32*). Taken together, these data indicate a role for the N-*myc* gene in the pathogenesis of neuroblastoma (*32*).

Neuroblastoma is a relatively rare disease with an incidence of one per 125,000 children. Carcinoma of the breast, however, is a common malignancy affecting one of every 13 women in the United States. There are 119,000 new cases per year, and approximately 40,000 women will die of the disease in 1986 (*38*). Current treatment decisions for individual patients are frequently based on specific prognostic parameters. The major prognostic factors for breast cancer include presence or absence of tumor in the axillary nodes, size of the primary tumor, and presence or absence of hormonal receptors (*29*). The current study indicates that amplification of the HER-2/*neu* gene is a significant predictor of both overall survival and time to relapse in node-positive patients with breast cancer. Amplification of the gene retains its prognostic significance in multivariate analysis, even when adjustments are made for other known prognostic factors. Moreover, amplification of HER-2/*neu* has greater prognostic value than most currently used prognostic factors, including progesterone and estrogen receptors, and is equivalent to and independent of the best known prognosticator—number of positive lymph nodes. Finally, the degree of HER-2/*neu* amplification appears to have an effect on survival, with greater copy number being associated with a worse prognosis (Fig. 3, C and D). A similar phenomenon has been observed for N-*myc* gene amplification in human neuroblastoma (*32*).

The potential role of HER-2/*neu* in the pathogenesis of breast cancer is unknown. Like N-*myc*, the correlation of HER-2/*neu* amplification with disease progression indicates it may be an important gene in the disease process. The role of other cell receptors in the biology of breast cancer is well established (*29, 39, 40*). It is easy to speculate that a gene encoding a putative growth factor receptor, when expressed in inappropriate amounts, may give a growth advantage to the cells expressing it. Alternatively, alteration in the gene product itself may lead to a critical change in the receptor protein. A single point mutation in the transmembrane domain of the protein encoded by the rat *neu* oncogene appears to be all that is necessary for the gene to gain transforming ability (*41*). Whether this or a similar alteration is found in the amplified HER-2/*neu* gene in human breast cancer will require sequence analysis of the homologous region in the amplified human gene. In addition, studies evaluating the expression of this gene at the RNA and/or protein level will prove important in determining if HER-2/*neu* amplification results in an expected increased gene expression. The question of amplification of HER-2/*neu* in metastatic as compared to primary lesions in a given patient is important. The current study utilized only primary breast tumors for analyses. It would be of interest to determine if HER-2/*neu* copy number is altered as the tumor metastasizes. A recent study evaluating N-*myc* copy number in human small cell carcinoma of the lung showed no difference between primary and metastatic lesions (*11*).

The initial survey from the current study showed that 15% of breast cancer patients with stage I disease (node-negative) have HER-2/*neu* amplification. Unfortunately, no long-term follow-up data were available for these patients. This stage I setting may be an additional group in which HER-2/*neu* measurements will have an impact in predicting biologic behavior of the tumor, and as a result, in design of treatment strategy. Finally, if the HER-2/*neu* gene product functions as a growth factor receptor that plays a role in the pathogenesis of breast cancer, identification of its ligand and development of specific antagonists could have important therapeutic implications.

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