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Exquisite Sensitivity of TP53 Mutant and Basal Breast Cancers to a Dose-Dense Epirubicin–Cyclophosphamide Regimen

Philippe Bertheau, Elisabeth Turpin, David S. Rickman, Marc Espie, Aurélien de Reyniès, Jean-Paul Feugeas, Louis-François Plassa, Hany Soliman, Mariana Varna, Anne de Roquancourt, Jacqueline Lehmann-Che, Yves Beuzard, Michel Marty, Jean-Louis Misset, Anne Janin, Hugues de Thé

ABSTRACT

Background

In breast cancers, only a minority of patients fully benefit from the different chemotherapy regimens currently in use. Identification of markers that could predict the response to a particular regimen would thus be critically important for patient care. In cell lines or animal models, tumor protein p53 (TP53) plays a critical role in modulating the response to genotoxic drugs. TP53 is activated in response to DNA damage and triggers either apoptosis or cell-cycle arrest, which have opposite effects on cell fate. Yet, studies linking TP53 status and chemotherapy response have so far failed to unambiguously establish this paradigm in patients. Breast cancers with a TP53 mutation were repeatedly shown to have a poor outcome, but whether this reflects poor response to treatment or greater intrinsic aggressiveness of the tumor is unknown.

Methods and Findings

In this study we analyzed 80 noninflammatory breast cancers treated by frontline (neoadjuvant) chemotherapy. Tumor diagnoses were performed on pretreatment biopsies, and the patients then received six cycles of a dose-dense regimen of 75 mg/m² epirubicin and 1,200 mg/m² cyclophosphamide, given every 14 days. After completion of chemotherapy, all patients underwent mastectomies, thus allowing for a reliable assessment of chemotherapy response. The pretreatment biopsy samples were used to determine the TP53 status through a highly efficient yeast functional assay and to perform RNA profiling. All 15 complete responses occurred among the 28 TP53-mutant tumors. Furthermore, among the TP53-mutant tumors, nine out of ten of the highly aggressive basal subtypes (defined by basal cytokeratin [KRT] immunohistochemical staining) experienced complete pathological responses, and only TP53 status and basal subtype were independent predictors of a complete response. Expression analysis identified many mutant TP53-associated genes, including CDC20, TTK, CDKN2A, and the stem cell gene PROM1, but failed to identify a transcriptional profile associated with complete responses among TP53 mutant tumors. In patients with unresponsive tumors, mutant TP53 status predicted significantly shorter overall survival. The 15 patients with responsive TP53-mutant tumors, however, had a favorable outcome, suggesting that this chemotherapy regimen can overcome the poor prognosis generally associated with mutant TP53 status.

Conclusions

This study demonstrates that, in noninflammatory breast cancers, TP53 status is a key predictive factor for response to this dose-dense epirubicin–cyclophosphamide regimen and further suggests that the basal subtype is exquisitely sensitive to this association. Given the well-established predictive value of complete responses for long-term survival and the poor prognosis of basal and TP53-mutant tumors treated with other regimens, this chemotherapy could be particularly suited for breast cancer patients with a mutant TP53, particularly those with basal features.
mutations, but also explores other dysfunctions, such as which not only determines the functional impact of TP53 survival than those with normal tumors often have poor responses to therapy and/or shorter that mutant treatments, but also the intrinsic aggressiveness of the disease. which incorporates not only the efficiencies of the different chemotherapy efficiency, survival is a composite endpoint, tumors disappearance is a direct and unambiguous measure of part because of technical difficulties in establishing given cytotoxic treatment in patients is largely unsettled, in given molecular determinants for conventionally dosed chemotherapy responses are only emerging [6–8], and very little is known regarding prediction of response to dose-dense treatments.

**Introduction**

Breast cancers are a heterogeneous group of tumors. While most breast cancer patients receive chemotherapy, less than 20% of those receiving neoadjuvant treatment will reach complete pathological response (disappearance of invasive tumor cells in pathological tissue samples), which strongly predicts long-term survival [1–5]. Predictive molecular determinants for conventionally dosed chemotherapy responses are only emerging [6–8], and very little is known regarding prediction of response to dose-dense treatments.

**Tumor protein p53 (TP53),** the prototypic tumor suppressor gene, is a master gene of stress response that plays a key role in cancer development. TP53 is a transcription factor that controls the expression of many genes implicated in apoptosis (PUMA and BAX) or cell-cycle regulation (SFN and CDKN1A). In animal or cell-line models, TP53 was shown to play a critical role in the response to DNA damage induced by a number of anti cancer therapies [9]. In fact, TP53 inactivation may promote an exquisite sensitivity to some agents, but resistance to others [10].

The role of TP53 status in determining the response to a given cytotoxic treatment in patients is largely unsettled, in part because of technical difficulties in establishing TP53 status in the clinical setting, and because most studies analyzed survival rather than initial tumor response. While tumor disappearance is a direct and unambiguous measure of chemotherapy efficiency, survival is a composite endpoint, which incorporates not only the efficiencies of the different treatments, but also the intrinsic aggressiveness of the disease. In hematological malignancies, several studies have found that mutant TP53 status is associated with treatment failure [11,12]. Similarly, in breast cancer, patients with TP53-mutant tumors often have poor responses to therapy and/or shorter survival than those with normal TP53 [13–17].

Here, we have used a highly sensitive functional TP53 assay, which not only determines the functional impact of TP53 mutations, but also explores other dysfunctions, such as splicing defects [18], to analyze a group of breast cancer patients treated with a neoadjuvant dose-intense chemotherapy regimen.

**Methods**

**Patients**

Two hundred and six patients with inflammatory and noninflammatory breast cancers treated at a single institution from 1997 to 2003 underwent open incisional biopsy (0.5–3 cm in size) followed by first-line chemotherapy and consented to the study (Tables 1 and S1). One hundred and twenty-six patients were not included for the following reasons: inflammatory breast cancer (78 tumors), frozen tumor tissue absent or unsuitable for RNA analysis (29 tumors), absence of further mastectomy (16 cases) or undefined response (three cases: patients P80, P81, P83; see below). The 80 remaining patients were treated with exactly the same regimen (75 mg/m^2_ eriurubicin and 1,200 mg/m^2_ cyclophosphamide, delivered every 14 d [19] with granulocyte-colony stimulating factor support in case of febrile neutropenia) and had unambiguous pathological response data. Of the 80 patients, 35 were included in the microarray profiling analysis, as these two additional TP53-mutant tumor samples previously excluded from the treatment response analysis as the patients had received another treatment (patient P81) (see Table S1) or had an initial biopsy that may have removed most of the tumor (patient P80). A third additional patient with TP53 mutant tumor (patient P83) (Table S1) was included for validation studies. Patients were staged IIB, IIIa, IIIb, or IV [20], except four patients (Tables 1 and S1) with a T2N0M0 (stage Ila) disease who had documented tumor doubling time of less than 6 mo (two cases) or who had tumors over 3 cm in size (two cases). The group of 80 patients included in the study was not different from the 48 excluded patients with noninflammatory breast cancer patients in terms of age and TNM Classification of Malignant Tumors stage [20] with, respectively, median age 48 y (24–76 y) and 52 y (29–74 y) and TNM: T1, 0% and 5%; T2, 14% and 19%; T3, 45% and 43%; T4, 41% and 33%; N+, 75% and 71%; and M+, 19% and 13%. Tumors were graded according to the modified Scarff, Bloom, and Richardson system [21]. All patients were screened for metastasis at diagnosis with at least chest x-ray, liver ultrasound, or thoraco-abdomino-pelvic CT scan and bone scintigram. At the time of diagnosis 11 patients had metastases (Table S1). After completion of the planned six cycles of primary chemotherapy—thus approximately 3 mo after diagnosis—the patients underwent mastectomy and axillary lymph node dissection. Pathologically assessed complete response was defined by the complete disappearance of invasive tumor cells in the mastectomy specimen and in the lymph nodes or a single microscopic invasive focus (P4) or residual breast in situ carcinoma (P42, P46, and P69), as previously described [22].

**TP53 Typing**

TP53 status was determined by the yeast functional assay, in which mutant TP53 transcripts yield red yeast colonies and wild-type transcripts yield white ones [23]. Tumors were considered TP53 mutant when: (i) more than 15% of the yeast colonies were red, (ii) analysis using the split versions of the test could identify the defect in the 5’ or 3’ part of the gene, confirming the initial determination [24], and (iii) sequence

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<tr>
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Table 1. Description of the 80 Patients Analyzed for Chemotherapy Response

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analysis from mutant yeast colonies could identify an unambiguous genetic defect (mutation, deletion, or splicing defects) (Table S2). All tumors with more than 15% red colonies fulfilled these three criteria. Note that the four tumors with low percentage of mutant colonies (15%-25%) all exhibited stop or frame-shift mutations, defects known to be associated with nonsense mediated RNA decay, resulting in low mRNA abundance (Table S2). Prediction of dominant negative activity was performed using IARC software (http://www-p53.iarc.fr/index.html).

RNA Analysis
RNA was prepared as previously [22], yielding 2–83 μg (mean 17 μg) of RNA. Its quality was verified by Agilent bioanalyzer (http://www.home.agilent.com), and Affymetrix arrays (http://www.affymetrix.com) were performed after a single or a double round of amplification (Table S1). RT-PCR was performed using Gene Expression Assays (Applied Biosystems, http://www.appliedbiosystems.com), except for the CDKN2A locus for which we designed specific primers (available upon request).

Immunohistochemistry
Immunohistochemical analyses were carried out on paraffin sections using antibodies directed against estrogen receptor 1 (ESR1) (clone 6F11) (Novoceastra, http://www.vision-bio.com), keratin 5/6 (KRT5/6) (clone D5/16 B4) (Dako-Cytomation, http://www.dako.com), keratin 17 (KRT17) (clone E3) (DakoCytomation), cyclin-dependent kinase inhibitor 2A (CDKN2A [p16] (clone E6H4) (DakoCytomation), and on frozen sections using antibodies directed against prominin 1 (PROM1 [CD133]) (clone AC133) (Miltenyi Biotec, http://www.miltenyibiotec.com). Basal KRT (5/6 or 17) or PROM1 were scored positive if strong cytoplasmic staining was observed in any invasive carcinoma cells [25,26]. For all other antibodies, there was either no staining (negative cases) or a positive staining in more than 10% of tumor cells (positive cases) either in nucleus (ESR1, CDKN2A) and/or in cytoplasm (CDKN2A).

Statistics and Bioinformatics
Microarray data analysis was based on 37 tumor samples (Table S1): 29 (set S1) processed using the one-cycle target labeling protocol (Affymetrix), and eight (set S2) processed using the two-cycle target-labeling protocol. RT-PCR data analysis was based on 82 tumor samples: 37 from the microarray series (S1 + S2) and 45 new samples (set S3). Except as indicated, all transcriptome analysis was carried out using either an assortment of R-system software (version 1.9.0) packages including those of Bioconductor (version 1.1.1) (http://www.bioconductor.org) or original R code. Raw feature data from Affymetrix HG-U133A GeneChip microarrays were normalized using RMA method (R package affy version 1.4.32), which yielded log 2 intensity expression summary values for each of the 22,283 probe sets. Each set (S1 and S2) was normalized independently. Individual feature data from set S1 and S2 were normalized in batches along with an additional 17 (one-cycle) and 19 (two-cycle) samples unrelated to this study, respectively. Probe sets corresponding to control genes or having an “x” annotation were masked, leaving 19,987 probe sets for further analyses. Clustering analysis of the samples was performed using DNA-Chip Analyzer software (dChip version 1.3, http://www.dchip.org) with (1 – Pearson correlation coefficient) as distance metric and Centroid linkage. The RNA normalized data of 37 samples (S1 + S2) were used in this analysis, based on a subset of 990 probe sets. These 990 probe sets were selected using only set S1 based on the following criteria: (i) a robust coefficient of variation (rCV) superior to the 95th rCV percentile and below 10, and (ii) a p-value of a variance test (see below) less than 0.01. For each probe set, rCV was calculated by first eliminating the highest and lowest expression values for that probe set out of all of the samples. From the remaining samples we divided the standard deviation of the expression values by the mean expression values. This yielded an rCV value for each probe set. The variance calculated for each probe set P (variance across all samples) was compared to the median variance from all 19,987 probe sets. The statistic used was \[(n – 1) \times \text{Var}(P)/\text{Var}_{\text{med}}\] where n refers to the number of samples. This statistic was compared to a percentile of the Chi² distribution with (n – 1) degrees of freedom (this criterion is used in the BRB Array Tools filtering tool, described in the user's manual [http://limus.nci.nih.gov/BRB-ArrayTools.html]) and yielded a p-value for each probe set.

We performed all univariate t- and F-tests using BRB Array Tools (version 3.0 b2) on the RNA normalized data for the 19,787 probe sets. We designated a significance level of each univariate test of \(p < 0.001\) (except when otherwise indicated). To evaluate the number of false positives (due to multiple testing), we used a Monte Carlo approach (implemented in BRB comparison tool) based on 1,000 random sample label permutations. This method calculates the false discovery rate (with a probability of 90%), on the basis of the number (n) of probe sets (n first probe sets ordered by their p-value from the univariate test) identified where the false discovery is relative to the chosen level of significance for the univariate test (e.g., \(p = 0.001\)). This method also evaluates the number n’ of probe sets (n’ first probe sets ordered by their p-value from the univariate test) for which the number of false discoveries is less than 10 (with a probability of 90%). See Dataset S1 for the statistics related to the definitions of the genes associated with the C1, C2, and C3 groups.

Based on the t-tests of TP53 status described above, we sorted the 1,599 obtained probe sets by fold change (ratio of the geometric mean intensity in the 17 TP53 mutant samples versus the geometric mean intensity in the 12 TP53 wild-type samples). We then selected the ten well-characterized probe sets having the highest fold change: 204304_s_at (TP53) [PRKACG], 205347_s_at (TMSNB), 209016_s_at (KRT7), 213338_at (RIS1), 209805_s_at (PHLD2A), 36711_at (MAFF), 202912_at (ADM), 204822_at (TTK), 209870_s_at (CD20), and 207039_at (CDKN2A) (219010_at [FLJ10901] which was filtered, as it is not well characterized). We also selected ESR1 (second highest inverse fold change). This yielded 12 gene transcripts for further study with RT-PCR (for CDKN2A we used two targets: p14 and p16). Due to a lack of sample RNA, only 948 data points (Ct [gene, sample]) from a total of 984 possible data points (12 genes × 82 samples) were available. These Ct values were normalized to yield ddCt values, based on the following calculation: for a given sample S, ddCt_{gene}\(s\) = dCt_{gene}\(s\) – (Median of dCt_{gene} across all samples), with dCt_{gene}\(s\) = Ct_{gene}\(s\) – Ct_{calibrator}\(s\), using the gene TBP (TATA-binding protein) as the reference gene. See
Page 2

**A**

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| STRATIFICATION            |     |       |                  |              |            |          |    |      |     |
|----------------------------|-----|-------|------------------|--------------|------------|----------|---|------|
| Event Free Survival        |     |       |                  |              |            |          |    |      |     |
| Overall Survival           |     |       |                  |              |            |          |    |      |     |

**Figure 1.** Response to Chemotherapy

(A) Top: distribution of the pathological response to chemotherapy of the 80 patients according to TP53 status as well as other clinical or biological annotations. T, T stage from the TNM classification. *p*-Values are below each contingency table. Bottom: results from adjusted Chi² tests. The variables tested for the prediction of complete response are shown in the columns; the stratification variable is listed in the first column. The *p*-values are color coded (dark yellow and bold type, *p* < 0.0001; light yellow, 0.0001 < *p* < 0.01).

(B) Left graph: Kaplan-Meier analysis of the event-free survival of the patients without metastatic extension at diagnosis, all treated with the same regimen (including patient P80, see Table S1). Note that all five relapses in the TP53 mutant group occurred in the first 18 months, while in the TP53 wild-type group, relapses were still observed when survival of many patients was censored. Right graph: overall survival stratified by TP53 status and complete response.

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Dataset S1 for the statistics associated with the RT-PCR data of these 12 genes.

**Statistical Methods for the Analysis of the Clinical Data**

The association between treatment response and potential prognostic variables (age, tumor grade, cytoplasmic staining of CDKN2A, presence of KRT5/6 or 17, ERBB2 mRNA expression, ESR1 protein expression, T stage from TNM classification, and TP53 mutation status) was tested using Fisher’s exact test. Because the age of the patients represents a continuous variable, patients were divided into two classes using a cutoff at age 50. Stratified association analyses were performed using the Mantel-Haenszel test. Kaplan-Meier survival curves and log-rank *p*-values were calculated on the basis of either event-free survival (considering local relapse or distant metastasis as an event) in the population of patients that were free of metastasis at diagnosis or overall survival on the complete population.

**Results**

All Complete Responses to a Dose-Dense Chemotherapy Harbor TP53 Mutations

We had previously observed, in 49 of our 206 patients, that complete responses were preferentially achieved when tumors bore TP53 mutations [22]. Analysis of the consecutive cohort of 31 patients independently validated this association (*p* = 0.0003), which became compelling (*p* = 10⁻⁸) when the initial subset and the consecutive cohort were pooled (Figure 1A). Indeed, not a single tumor with a normal TP53 genotype (52 cases) had a complete response, while 15 out of 28 TP53-mutant tumors exhibited complete pathological responses. The predicted effects of the observed mutations and the distribution of R72P polymorphism were not significantly different in tumors with complete or incomplete responses (Table S2).

**TP53 Status and Basal Features Are Independent Predictors of Complete Response**

Many studies have demonstrated that mutant TP53 status is tightly associated with ESR1neg and grade 3 breast cancers. In addition, ESR1pos status was previously associated with chemotherapy resistance [7]. To elucidate the respective contribution of these factors in predicting chemotherapy response, we analyzed the distribution of age, T stage (from TNM classification), tumor grade, TP53 status, staining for ESR1, KRT5/6 or 17, and ERBB2 RNA expression among the 80 patients (Figure 1A; Tables 1 and S1). We also included staining for CDKN2A, a major tumor suppressor whose
expression is tightly associated with TP53 status (see below). High transcript and protein levels of CDKN2A are associated with cytoplasmic staining (Figure S1). Therefore we used the cytoplasmic staining pattern as the criteria for deeming a sample CDKN2A positive or negative, as in previous studies [27–29]. No or weakly significant differences in age, T stage, or ERBB2 status were found between complete and incomplete responses. In contrast, grade, TP53 status, ESR1, KRT5/6 or 17, and cytoplasmic CDKN2A (p16) staining were all strongly associated with response (Figure 1A). As there are no complete responses in the TP53 wt group, the estimation of a regression coefficient using the multivariate logistic regression model is impossible, this coefficient being theoretically infinite in such a situation, precluding a multivariate analysis. Yet, TP53 status remained significantly linked to a response in univariate analyses, irrespective of the stratification (age, T stage or tumor grade, KRT5/6 or 17 presence, CDKN2A cytoplasmic staining [p16], ERBB2 mRNA, or ESR1 protein expression) in Mantel-Haenszel tests (Figure 1A). In contrast, with the exception of basal features (KRT5/6 or 17 positivity), all the other individually significant variables significantly associated with complete response prior to stratification for TP53 (Figure 1A) no longer remained significant after stratification for TP53 status (Figure 1A). Moreover, among the patients with TP53 mutations, the 15 tumors with a complete response had sizes and grades (six T2s, five T3s, and four T4s, all grade 3) comparable to the 13 who did not reach a complete response (three T2s, five T3s, and five T4s, all but one grade 3). Altogether, despite the impossibility of a formal multivariate regression analysis, it appears that TP53 and, to a lesser extent, basal features are the only important predictors of complete pathological response.

TP53 Status and Survival

When patients with metastatic disease at diagnosis were excluded from the analysis, most patients with a TP53 mutant tumor had favorable event-free survival, although with the current median follow-up (46 mo, range 3–103 mo), it did not reach statistical significance (Figure 1B, left graph; Table S1). Patients with a basal phenotype or complete responses also had favorable outcomes (Table S1), in line with the well-known association between a complete response and prolonged survival [1–5]. This observation is particularly remarkable, because TP53 mutant tumors have been reported in several studies to have a shorter survival than TP53 wild-type ones [13,14,30,31]. Patients with wild-type TP53 tumors had a relatively favorable overall survival, despite the lack of complete response (Figure 1B, right graph, red curve). Interestingly, patients with TP53-mutant tumors who did not reach complete response had a significantly shorter overall survival than other tumors (p = 0.02) (Figure 1B, right graph, orange curve). Again, absence of complete responses in the wild-type TP53 group precluded a multivariate survival analysis.

Can Transcriptional Profiling Predict Complete Response?

In an attempt to better characterize the responsive tumors, we performed expression analyses using microarrays. Of the 83 (three additional TP53 mutant tumor samples were considered for the profiling study, see Methods) breast tumors considered for gene-profiling analysis, 37 had enough high-quality RNA extracted from biopsies before chemo-therapy to be analyzed with the arrays, leaving the remaining 46 samples for validation studies. Consistent with previous reports [32], hierarchical cluster analyses of these 37 cancers identified three robust clusters of patients (C1, C2, and C3), as well as the genes defining these patients’ clusters (Figure 2A; Tables S3–S5).

To define genes specifically associated with complete responses, we then performed t-tests based on the Affymetrix data on the 28 tumors (nine complete responses and 19 incomplete responses) processed using a single amplification step (see Methods). We identified 77 probe sets using a p-value threshold of 0.001, with a high false discovery rate of 26% (Table S6). Using the same sample population, we identified 1,599 TP53 mutant–associated genes, with a false discovery rate less than 0.1%. As expected, the great majority (54 of 77) of genes associated with complete response were also TP53-associated genes, the others most likely being false positive (Table S7). Importantly, within the subgroup of TP53 mutant tumors, t-tests failed to identify more genes associated with complete responses than would be expected by chance.

Examining the genes associated with TP53 status, we found that, as expected, wild-type TP53 tumors overexpressed many ESR1-associated genes [30,32,33], as well as ribosomal protein genes (Figure 2B). In contrast, TP53 mutant tumors overexpressed, among others, a number of master genes (such as PROM1, cell division cycle 20 homolog [CDC20], CDKN2A, TTK protein kinase [TTK], and adrenomedulin [ADM]) (Figure 2B; Table S7). Most of these mutant TP53 associated genes did not overlap with the ones described in a recent study that used direct TP53 sequencing and a different chip [14]. To exclude the possibility that the genes associated with TP53 mutant status might merely reflect ESR1wt status, we repeated this analysis within the subgroup of ESR1pos tumors. We again found six out of the top ten genes previously identified among 15 top genes differentiating TP53-mutant versus wild-type tumors (Table S8) within the ESR1pos subgroup, demonstrating that the TP53-mutant genes that we have identified do not simply reflect ESR1wt status. In order to validate these mutant TP53-associated genes, we then assessed by quantitative RT-PCR the levels of expression of the first ten genes with the largest fold difference (Figure 2B; Table S7), as well as ESR1. Most of the 12 gene transcripts tested showed significant differences between TP53-mutant or wild-type tumors, not only in the tumor set used to select those genes, but also in the rest of the samples, the ESR1pos subgroup, and the complete population (Dataset S1; Figure 3).

To characterize the highly chemosensitive tumors that express the KRT5/6 or KRT17 proteins by immunohistochemistry, we performed t-tests based on the Affymetrix data of TP53 mutant tumors and found overexpression of basal cytokeratins and many genes previously identified in myoepithelial cells, consistent with the proposed origin of these tumors (Table S9) [26].

Lastly, we compared transcript levels to the immunohistochemical detection of ESR1, CDKN2A (p16), PROM1, KRT5, and KRT17 in all samples, which demonstrated very significant differences in mRNA levels between immunohistochemistry (IHC)+ and IHC− tumors (p < 0.001) (Figure S1). In particular, in most of the TP53-mutant and nine out of ten of the basal tumors (defined as KRT5− or KRT17-staining), PROM1 staining was strongly positive in a few cancer cells that could be breast cancer stem cells.
Discussion

We show that in noninflammatory breast cancers, TP53 mutations are highly predictive of complete responses to a dose-intense neoadjuvant epirubicin–cyclophosphamide chemotherapy regimen. Why did previous studies fail to identify this relationship? We believe that the results reported here reflect the use of a very aggressive DNA-damaging regimen and of a highly efficient technique to determine TP53 status, which detects not only mutations and deletions, but also abnormal splicing events [18]. It is also possible that some previous studies were biased by the presence of inflammatory breast cancers in the study population.

As TP53 is a master gene controlling acute DNA-damage response, its functional integrity was expected to control cell survival, particularly after a dose-dense regimen triggering both double-strand breaks and DNA cross-links. TP53 activation induces a plethora of biological responses (transient cell cycle arrest, senescence, and/or apoptosis) that may have opposing effects on cancer therapy responses [34]. TP53 or CDKN1A deficiencies, which impede chemotherapy-induced cell-cycle arrest, dramatically increase anthracyclinduced cell death ex vivo [10]. TP53-induced cell-cycle arrest should also protect cells from cyclophosphamide, which, in vivo, only kills rapidly cycling cells [35]. Note that one of the few genes induced by chemotherapy in breast cancers is p21, CDKN1A [36]. In contrast, TP53-mutant cells that cannot arrest in the cell cycle would subsequently progress towards mitotic catastrophe [10,37]. Topoisomerase II A (TOP2A) expression is an important determinant of epirubicin response [38]. When we investigated the expression of TOP2A by RT-PCR in all the samples, no significant differences in transcript levels were observed between responsive and unresponsive tumors, independently of their TP53 status (unpublished data). We suggest that the very high dose of cyclophosphamide used here bypasses the influence of TOP2A in controlling response to epirubicin. Whatever the exact mechanism(s) involved, the exquisite chemosensitivity of
TP53 mutant breast cancers strongly favors the hypothesis that here, TP53 activation principally blocks cell cycle progression, rather than triggering a cell death program [34]. In line with our observations, transient pharmacological inhibition of TP53 was recently proposed to boost chemotherapy efficacy [39].

The expression studies performed here have identified and validated a transcriptional profile associated with mutant TP53 status (and hence indirectly to response), but failed to identify, within the TP53 mutant group, a specific profile associated with complete response. Yet, many of these TP53 mutant–associated genes would be helpful tools in characterizing the pathophysiology of these tumors. PROM1, a marker of normal or cancer stem cells [40], is the gene with the highest fold-difference in TP53-mutant breast tumors (Figure 2B) or several other tumor types (unpublished data). Basal cancers, which were proposed to have a stem cell origin, are virtually all TP53 mutant and express high levels of PROM1 transcript and protein (Figures 3 and S1). Very high expression of CDKN2A transcript was associated with cytoplasmic p16 staining (Figure S1) and was almost exclusively observed in TP53 mutant tumors, consistent with the absence of selection pressure for silencing of the CDKN2A locus when TP53 is mutated. Note that several studies have shown that cytoplasmic p16 was associated with poor survival [27–29], while here it predicts responsiveness (Figure 1A).

Finally, a large number of cell-cycle checkpoint genes (CDKN2A, CKS2, TTK, CDC20, CENPA, CCNB1, CCNB2, and BUB1) were overexpressed in TP53-mutant tumors, which may facilitate the execution of mitotic catastrophe upon chemotherapy exposure [41].

Several studies have repeatedly demonstrated worse outcomes for patients with TP53-mutant breast tumors when treated with a standard regimen, implying that mutant TP53 is a poor prognostic factor [13,14,16,30]. In our study, mutant TP53 was the major independent predictive factor of complete pathological responses, which itself is the major predictor of long-term survival in patients previously treated with the same protocol [3]. Accordingly, TP53-mutant patients from this study appeared to have a more favorable event-free survival than those with a wild-type TP53 (Figure 1B). However, if patients with TP53-mutant tumors failed to reach a complete response, their survival was significantly worse than those with TP53 wild-type, unresponsive tumors (p = 0.02, Figure 1B), consistent with previous studies. The coexistence, among TP53-mutant tumors, of two very different types of tumors (i.e., the responsive ones with good prognosis and the unresponsive ones with very poor prognosis) may account for the conflicting results of the literature regarding the prognostic value of TP53 status in breast cancer. The apparent paradox between the results of this study and previous ones is likely treatment-related, as the
regimen used here had a dose intensity two to four times higher than most others, with only two-week intervals between courses. However, some recent studies are in line with our data; ESR1** breast cancers (which are mostly TP53 mutant) were found to be more sensitive to neoadjuvant chemotherapy [7] and, in a pilot study, TP53 staining was associated with favorable responses to preoperative anthracyclines [42]. Despite the small number of cases analyzed, our data also suggest that basal cancers, described as having a dismal prognosis in all other studies [25,26,33,43], are exquisitely sensitive to this association, possibly because of cyclins [42]. Despite the small number of cases analyzed, our associated with favorable responses to preoperative anthra-

Table S2. Summary of the Data on the 28 TP53 Mutations in Patients Studied for Pathological Response to Chemotherapy

Table S3. Genes Specific for Patient Cluster 1

Table S4. Genes Specific for Patient Cluster 2

Table S5. Genes Specific for Patient Cluster 3

Table S6. List of the 77 Probe Sets That Are Differentially Expressed between Tumors That Exhibited a Complete Response to Chemotherapy and Those That Did Not

Table S7. List of the Probe Sets with the Highest Differential Expression in TP53-Mutant Versus TP53 Wild-Type Tumors

Table S8. List of Probe Sets Associated with TP53 Mutant Status in the Subgroup of ESR1** Tumors

Table S9. Genes Identified by t-Tests of TP53-Mutant KRT5/6** or KRT17** Tumors Versus KRT5/6 ** and KRT17** Tumors

Accession Numbers

The primary data for the microarrays were deposited at the European Bioinformatics Institute (EBI) Web site (http://www.ebi.ac.uk) (ArrayExpress number E-TABM-43). Accession numbers for the genes and corresponding proteins cited in the main text are given below in PubMed format (gene, NM_; protein, NP_;):
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This work is dedicated to the memory of Claude Savelli who was lost to breast cancer at a young age.


References

9. delattre, M. H. Stern, E. Cvitkovic, and J. Zucman. Microarrays were performed at the Institut de Génétique et de Biologie Moléculaire et Cellulaire (http://www-igbmc.u-strasbg.fr) by C. Thibault.
The normal human breast contains several types of cell, any of which can become malignant. In addition, there is more than one route to malignancy—different sets of genes can be mutated. As a result, breast cancer is a heterogeneous disease that cannot be cured with a single type of treatment. Ideally, oncologists would like to know before they start treating a patient which therapeutic approach is going to be successful for that individual. Recently, researchers have begun to identify molecular changes that might eventually allow oncologists to make such rational treatment decisions. For example, laboratory studies in cell lines or animals indicate that the status of a gene called TP53 determines the chemotherapy agents (drugs that preferentially kill rapidly dividing cancer cells) to which cells respond. p53, the protein encoded by TP53, is a tumor suppressor. That is, in normal cells it prevents unregulated growth by controlling the expression of proteins involved in cell division and cell death. Consequently, p53 is often inactivated during cancer development.

Why Was This Study Done? Although laboratory studies have linked TP53 status to chemotherapy responses, little is known about this relationship in human breast cancers. The clinical studies that have investigated whether TP53 status affects chemotherapy responses have generally found that patients whose tumors contain mutant TP53 have a poorer response to therapy and/or a shorter survival time than those whose tumors contain normal TP53. In this study, the researchers have asked whether TP53 status affects tumor responses to a dose-intense chemotherapy regimen (frequent, high doses of drugs) given to women with advanced noninflammatory breast cancer before surgery. This type of treatment is called neoadjuvant chemotherapy and is used to shrink tumors before surgery.

What Did the Researchers Do and Find? The researchers collected breast tumor samples from 80 women before starting six fortnightly cycles of chemotherapy with epirubicin and cyclophosphamide. After this, each woman had her affected breast removed and examined to see whether the chemotherapy had killed the tumor cells. The researchers determined which original tumor samples contained mutated TP53 and used a technique called microarray expression profiling to document gene expression patterns in them. Overall, 28 tumors contained mutated TP53. Strikingly, all 15 tumors that responded completely to neoadjuvant chemotherapy (no tumor cells detectable in the breast tissue after chemotherapy) contained mutated TP53. Nine of these responsive tumors were basal-cell–like breast tumors, a particularly aggressive type of breast cancer; only one basal-cell–like, TP53-mutated tumor did not respond to chemotherapy. Patients whose tumors were unresponsive to the neoadjuvant chemotherapy but contained mutated TP53 tended to die sooner than those whose tumors contained normal TP53 or those with chemotherapy-responsive TP53-mutated tumors. Finally, expression profiling identified changes in the expression of many p53-regulated genes, but did not identify an expression profile in the TP53-mutated tumors unique to those that responded to chemotherapy.

What Do These Findings Mean? These findings indicate that noninflammatory breast tumors containing mutant TP53—in particular, basal-cell–like tumors—are very sensitive to dose-dense epirubicin and cyclophosphamide chemotherapy. Intensive regimens of this type have rarely been used in previous studies, which might explain the apparent contradiction between these results and the generally poor response to chemotherapy of TP53-mutated breast tumors. More tumors now need to be examined to confirm the association between complete response, TP53 status and basal-cell–like tumors. In addition, although complete tumor responses generally predict good overall survival, longer survival studies than those reported here are needed to show that the tumor response to this particular neoadjuvant chemotherapy regimen translates into improved overall survival. If the present results can be confirmed and extended, dose-dense neoadjuvant chemotherapy with epirubicin and cyclophosphamide could considerably improve the outlook for patients with aggressive TP53-mutant, basal-cell–like breast tumors.

Additional Information. Please access these Web sites via the online version of this summary at http://dx.doi.org/10.1371/journal.pmed.0040090.

- The US National Cancer Institute provides patient and physician information on breast cancer and general information on understanding cancer
- Cancer Research UK offers patient information on cancer and breast cancer
- The MedlinePlus encyclopedia has pages on breast cancer
- Emory University’s CancerQuest discusses the biology of cancer, including the role of tumor suppressor proteins
- Wikipedia has pages on p53 (note that Wikipedia is a free online encyclopedia that anyone can edit)