Somatic Mutation of p53 Leads to Estrogen Receptor α-Positive and -Negative Mouse Mammary Tumors with High Frequency of Metastasis

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ABSTRACT

Approximately 70% of human breast cancers are estrogen receptor α (ERα)-positive, but the origins of ERα-positive and -negative tumors remain unclear. Hormonal regulation of mammary gland development in mice is similar to that in humans; however, most mouse models produce only ERα-negative tumors. In addition, these mouse tumors metastasize at a low rate relative to human breast tumors. We report here that somatic mutations of p53 in mouse mammary epithelial cells using the Cre/loxP system leads to ERα-positive and -negative tumors. p53 inactivation under a constitutive active WAPCre in prepubertal/pubertal mice, but not under MMTVCre in adult mice, leads to the development of ERα-positive tumors, suggesting that target cells or developmental stages can determine ERα status in mammary tumors. Importantly, these tumors have a high rate of metastasis. An inverse relationship between the number of targeted cells and median tumor latency was also observed. Median tumor latency reaches a plateau when targeted cell numbers exceed 20%, implying the existence of saturation kinetics for breast carcinogenesis. Genetic alterations commonly observed in human breast cancer including c-myc amplification and Her2/Neu/erbB2 activation were seen in these mouse tumors. Thus, this tumor system reproduces many important features of human breast cancer and provides tools for the study of the origins of ERα-positive and -negative breas tumors in mice.

INTRODUCTION

Breast carcinogenesis requires multiple genetic changes including inactivation of tumor suppressor genes and activation of oncogenes (1). Mutations in p53 are observed in close to half of human cancers including breast carcinomas (2). p53 is also mutated in families with Li-Fraumeni syndrome in which early-onset female breast cancer is the most prevalent type of tumor (3). p53 is a transcription factor that regulates genes critical for cell cycle arrest and for apoptosis after genotoxic stress, thus preventing genome instability (4–6). In addition, amplification and/or overexpression of c-myc, Her2/Neu/erbB2, and cyclin D1 are observed in 70% of ERα-positive breast tumors (12, 20) metastasize. Genetic alterations commonly observed in human breast cancer including c-myc amplification and Her2/Neu/erbB2 activation were seen in these mouse tumors. Thus, this tumor system reproduces many important features of human breast cancer and provides tools for the study of the origins of ERα-positive and -negative breast tumors in mice.

Targeting Vector Construction. A 10.75-kb clone covering exons 1–10 of p53 was isolated from a 129sv mouse genomic library. The 3.4-kb XhoI-HindIII fragment containing exons 2–9 was subcloned into pBR322. A replacement-type targeting vector was made by inserting the first loxP site into a BamHI site located in intron 6. A neo-cassette flanked by two loxP sites was inserted into the PvuII site in intron 4. The resulting construct was cleaved with XhoI and HindIII, blunt-ended and subcloned into p��2TK (27). The finished targeting construct is designated p53neo/loxP2TK.

MMTVCre Transgenic Construction. The backbone of the MMTVCre transgene is pBSKCR3 (28) containing part of the rabbit β-globin gene (the end of exon 2, intron 2, and exon 3), and the polyadenylation site. A 1.6-kb BigII-HindIII fragment composed of the Cre transgene with a nuclear localization signal was inserted within exon 3 of the globin gene of pBSKCR3. A 1.5-kb HindIII-Nhel fragment containing the MMTV-LTR was cut from pMAM (Clontech, Palo Alto, California) and subcloned 5’ to exon 2 of the globin gene. The finished transgene construct is designated pMMTVCre.

MMTVCre-Transgenic Mice Production. The 4.3-kb XhoI fragment containing the MMTVCre transgene was excised and purified. The transgenic...
founders were generated by microinjecting the MMTVCre transgene fragment into the male pronucleus of fertilized eggs derived from CB6F1 × C57BL/6 intercrosses. Transgenic founders were confirmed by Southern analysis or PCR of tail DNA. The primers for the Cre transgene (363-bp amplified) were CreF (5'-GGGTGCTCAATTCTAAGTACG-3') and CreR (5'-CCGATTCGCCCGCATACCAAGT-3'). All mice were maintained in accordance with the guidelines of the Laboratory Animal Research Committee of The University of Texas Health Science Center at San Antonio and Institutional Animal Care and Use Committee of University of California, Irvine.

**Generation of Conditional p53 Mutant Mice.** J1 embryonic stem cells were electroporated with Sall-linearized p53neolox2TK and selected with G418 and 1-(2-deoxy-2-fluoro-β-D-arabinofuranosyl)-5-iodouracil. Embryonic stem cells harboring homologous recombination were identified by Southern blotting using a 3' probe external to the targeting region. The neo-cassette was removed from targeted embryonic stem cells by transient expression of p53Cre. Of 231 clones analyzed by Southern blotting, two contained a recombination that removed only neo. These two clones were expanded and injected into C57BL/6 blastocysts. Chimeric males were mated with C57BL/6 females, and germline transmission of the mutant allele was verified by Southern and PCR analyses. Subsequently, p53lox/p53MTTVCre mice were generated by crossing p53lox/mice with MMTVCre mice. For PCR analysis, the following primers were used: primer x (5'-TGGGAGCAGCAGAACGGATCTGTA-3'); y (5'-GGTCCGTCACCATCTCGAT-3'); z (5'-CATGCAGGAGCTATTACAC-3'); and p (5'-TACTCTTCCCCCTCTAATAAGCTAT-3'). Primers y and z flank the loxP site in intron 6 and amplify a 119-bp fragment from wild-type p53 and 158 bp from the FP allele. Primer pair x/z amplifies a 500-bp fragment from the deleted allele after Cre-mediated recombination. Primer pair p/q amplifies a 327-bp product in the wild-type allele as well as a 253-bp fragment for the pseudogene.

In vivo functional analysis of Cre recombinase in double-transgenic mice carrying Cre and R26R reporter transgenes. To evaluate Cre activity in vivo, Cre mice were crossed with the Rosa 26 reporter (R26R) strain (29). Mammary glands from double-transgenic Cre; R26R mice were collected at different developmental stages and stained with X-gal for lacZ expression (30).

**Histology and Immunohistochemistry.** Collected tissues were fixed in 4% paraformaldehyde and processed through paraffin embedding following standard procedures. Sections were stained with H&E for histopathological evaluation. Immunostaining was performed following the protocol described in the Vectastain Elite ABC kit (Vector Laboratories, Burlingame, CA). For antigen retrieval, slides were heated for 20 min in 10 mM citrate buffer (pH 6.0) in a microwave oven. The antibodies used were CK8 and CK14 (1:2,000 and 1:300; The Binding Site, Birmingham, United Kingdom), ERα (1:2,000, MC-20; Santa Cruz Biotechnology, Santa Cruz, CA), PR and Neu/erbB2 (1:200 and 1:2,000; Dianova, Hamburg, Germany), and β-catenin (1:500; C20, NovoCasta Laboratories, Newcastle, United Kingdom).

**Western Analysis and Fluorescence Microscopy.** Tumor cells were grown in DMEM/F12 medium containing 15% fetal bovine serum, 10 ng/ml epidermal growth factor, and 1 μg/ml insulin. Cell lysates were prepared using EBC (50mM Tris-HCl, 120 mM NaCl, 1 mM EDTA, pH 8.0, 50 mM NaF, 0.5% NP-40) buffer, and lysates (50 μg) were separated by 10% gel electrophoresis and electrophoretically transferred to nitrocellulose paper. The nitrocellulose paper was incubated with anti-ERα (1:1,000, MC-20; Santa Cruz Biotechnology), anti-ERβ (1:1,000, PAI-31; Affinity Bioreagents, Golden, CO) or anti-actin (1:20,000; Sigma, St. Louis, MO) antibodies, followed by incubation with horseradish peroxidase or alkaline phosphatase-conjugated secondary antibodies, and developed using an enhanced chemiluminescence (ECL) or 5-bromo-4-chloro-3-indolyl phosphate/nitroblue tetrazolium solution. Tumor cells were infected with Ad-25ERE-GFP adenoviruses at a multiplicity of infection of ~100. Cells were preincubated in serum-free DMEM/F12 for 1 day and treated with 10 μM 17-β estradiol. Green fluorescent protein fluorescence was detected 24 h after 17-β estradiol treatment.

**RESULTS**

**Generation of the Floxed p53 Allele.** We engineered the floxed p53 allele (designated p53fl) by inserting the loxP sites into introns 4 and 6 of p53 through a two-step process (Fig. 1, A and B). The phosphoglycerate kinase neomycin resistance cassette was subsequently removed by transient expression of Cre recombinase. Deletion of exons 5 and 6 led to an in-frame deletion of 99 codons (codons 123–221) that encode part of the DNA-binding domain. The presence of loxP sites in introns 4 and 6 did not interfere with the transcription of p53, and the full-length p53 protein was detected in p53fl mice embryonic fibroblasts in the absence of Cre recombinase (Fig. 1C). A smaller protein product of expected mass of 39 kDa, designated p53flΔ5-6, was detected in p53fl mouse embryonic fibroblasts infected with Cre adenoviruses (Fig. 1C). IR-induced responses demonstrate that p53flΔ5-6 is transcriptionally inactive and fails to increase p21 target gene transcription. In contrast to wild-type p53, mutant p53flΔ5-6 protein was not stabilized after IR (Fig. 1D). No p53 protein was detected from mouse embryonic fibroblasts derived from p53-null (p53−/−) mice (Fig. 1, C and D).

**Characterization of Cre-Transgenic Mice.** To introduce somatic p53 mutation in the mammary gland, different lines of mice expressing Cre under the control of MMTV-long terminal repeat, MMTVCreα, and MMTVCreβ (collectively termed MMTVCre) were generated. In addition, to express Cre specifically in mammary luminal epithelial cells, WAPrtTACre-transgenic mice in which Cre is regulated by the whey acidic protein (WAP) promoter were also used (31). In the MMTVCreα line, Cre activity was restricted to the mammary gland, whereas in MMTVCreβ and WAPrtTACre lines, Cre-mediated deletion was observed in many tissues (Fig. 2A). In contrast to the founder mice, when the WAPrtTACre transgene was bred to floxed p53 or reporter mice (see below), its activity became independent of doxycycline and pregnancy, likely attributable to modification of the transgene, and/or the unstable nature of the multicopy transgene. The altered transgene will be referred to as WAPCre hereafter.

Because transgene activity varies depending on promoter and insertion sites, Cre-transgenic mice were crossed with R26R mice expressing LacZ after the removal of the floxed stop sequence by Cre (29) to identify the cell types targeted by Cre-mediated recombination in the mammary gland (Fig. 2B; Table 1; data not shown). In nulliparous MMTVCreα; R26R mice, LacZ was detected in ~0.7% cells of mammary gland. The expression remained low during 1st pregnancy and reached ~2.9% at 2nd pregnancy in both luminal epithelial and myoepithelial cells but not in stromal fibroblasts and adipocytes. In MMTVCreβ; R26R mice, LacZ expression was also found in 5.6% of those cells in 2-week-old and ~20% in 7-week-old nulliparous mice. The expression increased to >60% in pregnant mice. The increased percentage of targeted cells in multiparous mice is expected, because MMTV promoter activity is up-regulated during pregnancy. In WAPCreα; R26R mice, LacZ activity was robust with 66% positive cells in 1-week-old and >90% in 17-day-old and 6-week-old nulliparous and pregnant mice. Thus, there are significantly higher numbers of targeted cells in WAPCre than in MMTVCre mice during prepubertal/subpubertal stages.

**Effects of p53 Inactivation on Spontaneous Mammary Carcinogenesis.** As expected, these mice develop tumors with different spectrums. The most common tumor type is mammary tumor, and the majority of mammary tumor-bearing mice (60–80%) had multiple primary mammary tumors (Fig. 3; Table 2). Mammary tumor latency varied depending partly on numbers of targeted cells and parity of mice. Nulliparous p53fl/MTTVCreα females developed mammary tumors between 14 and 24 months of age with a median tumor latency (MTL) of 17.5 months with almost complete penetrance (23 of 24 mice), whereas all multiparous p53fl/MTTVCreα mice developed mammary tumors with a significantly shortened latency, between 11.5 and 24 months of age with a MTL of 15.5 months (P = 0.004, generalized Wilcoxon statistic). Both larger numbers of targeted cells as well as pregnancy-mediated cell proliferation could contribute to the shortened MTL. Nulliparous p53fl/MTTVCreβ females developed mammary tumors between 6 and 14 months of age with an MTL of 10.5 months in nearly 50% of mice (9 of 19 mice), whereas
multiparous \( p53^{fp/fp} \)MMTV\(^{Cre}\) mice developed mammary tumors between 7 and 12 months of age with an MTL of 11 months in 60% of mice (12 of 20 mice). The MTL of \( p53^{fp/fp} \)MMTV\(^{Cre}\) mice is significantly shorter than that of \( p53^{fp/fp} \)MMTV\(^{Cre}\) mice (\( P / H11021 0.001 \)), indicating distinct mammary carcinogenesis kinetics in mice with 1 or 3% versus 20% of \( p53 \)-mutated cells. However, there is no statistical difference in the median MTL between 20% targeted cells in nulliparous and 60% in multiparous \( p53^{fp/fp} \)MMTV\(^{Cre}\) mice (\( P / H11005 0.29 \)). The lower penetrance of mammary tumors in \( p53^{fp/fp} \)MMTV\(^{Cre}\) was attributable to the presence of other tumor types leading to early death. In \( p53^{fp/fp} \)WAP\(^{Cre}\) mice, mammary tumors developed between 8 and 12.5 months of age with a MTL of 9.5 months with high penetrance (13 of 14 mice). Consistent with the findings in \( p53^{fp/fp} \)MMTV\(^{Cre}\), increasing targeted cells to >90% did not shorten the MTL further (\( P = 0.29 \)). Of note, only one 23.5-month-old multiparous heterozygous \( p53^{+/fp} \)MMTV\(^{Cre}\) mouse developed palpable mammary tumor in a cohort of mice between 20 and 26 months of age (\( n = 12 \); data not shown). The apparent long tumor
Fig. 2. Characterization of Cre activity. A. PCR analysis of Cre-mediated excision of floxed p53 alleles in p53<sup>fl/fl</sup> Cre mice. Primer pair x/z amplified a ~500-bp product in the deleted allele and a 377-bp fragment for the pseudogene, and primer pair p/q amplified a 327-bp product in the wild-type allele as well as a 253-bp fragment for the pseudogene. Tissue DNA samples were derived from p53<sup>fl/fl</sup>MMTVCre<sup>a</sup> (a), p53<sup>fl/fl</sup>MMTVCre<sup>b</sup> (b), and p53<sup>fl/fl</sup>WAPCre<sup>c</sup> (c) mice. Nontransgenic, non-Cre-transgenic mammary gland; Mg (1st), (3rd), (4th), and (parous), mammary gland of 1st, 3rd, 4th pregnancy and of a parous female. B. β-galactosidase staining of cells in the mammary gland of Cre: R26R mice. a-c, mammary gland from MMTVCre<sup>a</sup>; R26R mice, nulliparous (a), 1st pregnancy (b), 2nd pregnancy (c). Arrow in c indicates β-galactosidase detection in a myoepithelial cell. d-f, mammary gland from MMTVCre<sup>b</sup>; R26R mice, 2-week-old (d), nulliparous (e), 1st pregnancy (f). g-i, mammary gland from WAPrtTACre: R26R mice, 1-week-old (g), nulliparous (e), 1st pregnancy (f). Counterstained with nuclear fast red. Original magnifications, ×200.
latency suggests that the internally truncated mutant p53 protein expressed under the endogenous promoter might not work in a dominant-negative manner.

Mammary tumors in all groups of mice are heterogeneous including adenocarcinoma, myoepithelial adenocarcinoma, adenosquamous carcinoma, and spindle cell tumor (Fig. 4, A-D). The majority of tumors were poorly differentiated invasive adenocarcinomas that share the most histopathological similarity with human tumors. In addition to mammary tumors, a few p53<sup>fl/fl</sup>MMTV<sup>Cre</sup> mice also developed lymphoma caused by a very low level of Cre activity in the lymphocytes or a low spontaneous incidence in aged C57BL/6 × 129sv mice. On the other hand, other tumor types were found in p53<sup>fl/fl</sup>MMTV<sup>Cre</sup> and p53<sup>fl/fl</sup>WAP<sup>Cre</sup> mice caused by a broader Cre expression pattern (Table 2; Fig. 2A).

Importantly, up to half of p53<sup>fl/fl</sup>MMTV<sup>Cre</sup> mice had mammary tumor metastasis either in lung and/or liver after gross examination (Table 2; Fig. 4, E and F). Metastatic mammary tumor foci were also detected in p53<sup>fl/fl</sup>MMTV<sup>Cre</sup> and p53<sup>fl/fl</sup>WAP<sup>Cre</sup> mice (Table 2).

**Molecular Characterization of Mammary Tumors.** Estrogen is critical in the etiology of breast cancer and ERα mediates estrogen responsiveness in breast cancer. Significantly, 40% of the p53<sup>fl/fl</sup>WAP<sup>Cre</sup> mice (n = 15) had both ERα- and ERβ-positive tumors (Fig. 4H), compared with 42 tumors from p53<sup>fl/fl</sup>MMTV<sup>Cre</sup> mice that were all ERα- and PR-negative (Fig. 4G). The percentage of ERα-positive cells in ERα-positive tumors is over 90% whereas in ERα-negative tumors, no ERα-positive tumor cells were seen. The expression of ERα in tumors from p53<sup>fl/fl</sup>WAP<sup>Cre</sup> but not p53<sup>fl/fl</sup>MMTV<sup>Cre</sup> mice was further confirmed by Western blotting analysis (Fig. 4L). In contrast to ERα, ERβ was expressed in all tumors (Fig. 4L and data not shown). The closely correlated expression of ERα and PR, a downstream target of ER, suggests that ERα is functional in ERα-positive tumors. To further test this notion, adenoviruses carrying green fluorescent protein regulated by estrogen-response elements (EREs; 32) were used to infect tumor cells prepared from p53<sup>fl/fl</sup>MMTV<sup>Cre</sup> and p53<sup>fl/fl</sup>WAP<sup>Cre</sup> mice. After treatment with estradiol, green fluorescent protein-positive cells were detected in tumor cells from p53<sup>fl/fl</sup>WAP<sup>Cre</sup> but not p53<sup>fl/fl</sup>MMTV<sup>Cre</sup> mice (Fig. 4M). Thus, ERα in the ERα-positive p53<sup>fl/fl</sup>WAP<sup>Cre</sup> tumors is transcriptionally active.

Deregulation of ERα expression during the premalignant stages of human breast carcinogenesis has been reported (33). Correspondingly, an increase of ERα-positive cells as well as clusters of ERα-positive cells (Fig. 4, J–K), in contrast to singularly distributed ERα-positive cells in the normal gland, was observed in mammary intraepithelial neoplasia (34) but not in hyperplasia without atypia (Fig. 4I). Thus, similar to human breast cancer, there are multistep histopathological changes and alterations in the ERα expression pattern during the progression of mammary carcinogenesis in these models.

Frequent genetic changes and prognostic markers of human breast cancer have been identified. To test whether this mouse model parallels human breast cancer in these alterations, selected genes were

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**Table 1 Cre-mediated recombination in Cre; R26R mice**

| Cre transgene | Nulliparous pregnant | Site | X-gal positive cells (%) (mean ± SE) |
|---------------|----------------------|------|------------------------------------|
| MMTV<sup>Cre</sup> | Nulliparous (d42) | End bud/duct | 0.73 ± 0.37 (n = 12) |
| 1st pregnancy | Alveoli | 0.22 ± 0.12 (n = 12) |
| 2nd pregnancy | Alveoli | 2.85 ± 0.44 (n = 12) |
| MMTV<sup>Cre</sup> | Nulliparous (d50) | End bud/duct | 18.97 ± 3.19 (n = 12) |
| 1st pregnancy | Alveoli | 56.71 ± 0.06 (n = 12) |
| WAP<sup>Cre</sup> | Nulliparous (d44) | End bud/duct | 90.73 ± 0.02 (n = 12) |
| 1st pregnancy | Alveoli | 96.80 ± 0.02 (n = 24) |

*SE, standard error.

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**Table 2 Tumor formation in p53<sup>fl/fl</sup>; Cre mice**

| Cre transgene | MMTV<sup>Cre</sup> (Nulliparous) | MMTV<sup>Cre</sup> (Multiparous) | MMTV<sup>Cre</sup> (Nulliparous) | MMTV<sup>Cre</sup> (Multiparous) | WAP<sup>Cre</sup> (Parous) |
|---------------|-------------------------------|-------------------------------|-------------------------------|-------------------------------|--------------------------|
| Total number of mice | 14 | 37 | 19 | 20 | 12 |
| Mammary tumor | 14 (100%) | 37 (100%) | 9 (47%) | 12 (60%) | 11 (92%) |
| Lymphoma | 2 (14%) | 6 (16%) | 15 (79%) | 15 (75%) | 5 (42%) |
| Other tumor types<sup>a</sup> | - | - | - | - | 2 (17%) |
| Metastasis<sup>b</sup> | 7 (50%) | 13 (35%) | 1 of 3 (33%), IC<sup>c</sup> | 1 of 4 (25%), IC<sup>c</sup> | 4 (36%) |
| Multiple mammary tumors | 11 (79%) | 22 (59%) | 3 of 4 (75%), IC | 7 of 10 (70%), IC | 8 (67%) |
| Median tumor latency (months) | 17.5 | 15.5 | 10.5 | 11 | 9.5 |

<sup>a</sup> Other tumor types, such as soft tissue tumors.

<sup>b</sup> The number of mammary tumor bearing-mice had metastasis of mammary tumor origin.

<sup>c</sup> IC, incomplete.
examined (Fig. 5). Amplification or overexpression of c-myc proto-oncogene is frequently observed in human breast cancer (35). In this model, c-myc amplification is found in \( \text{H1101} \) 35% of mammary tumors from \( \text{p53fp/fpMMTVCre} \) mice (Fig. 5A). About two-thirds of tumors from \( \text{p53fp/fpMMTVCre} \) and \( \text{p53fp/fpWAPCre} \) mice showed Neu/erbB2 overexpression by immunostaining and Western blot analysis using anti-Neu/erbB2 and phosphotyrosine antibodies (Figs. 4H and 5B). Overexpressed Neu/erbB2 appears to be active because tyrosine residues of the receptors are phosphorylated (Fig. 5B). In addition, the activity of matrix metalloproteinase (MMP), matrix metalloproteinase

Fig. 4. Histological characterization of mammary tumors. Primary mammary tumors from \( \text{p53fp/fpMMTVCre} \) mice showed various histological features, including adenocarcinoma (A), myoepithelial adenocarcinoma (B), squamous cell carcinoma (C), and spindle cell tumor (D). Metastatic mammary tumors in the liver (E) and lung (F). Immunphenotypes of mammary tumors showing estrogen receptor \( \alpha \) (ER\( \alpha \)) and PR-negative staining (G), and ER\( \alpha \), PR-, Neu-, and p53-positive staining (H). I-K, premalignant lesions of mammary gland. I, hyperplasia without atypia with negligible ER\( \alpha \) expression (inset). J-K, mammary intraepithelial neoplasia (MIN) with increased ER\( \alpha \) expression (inset). L, Western analysis of ER\( \alpha \) and ER\( \beta \) expression in tumors from \( \text{p53fp/fpMMTVCre} \) (FM110) and \( \text{p53fp/fpWAPCre} \) (FW473) mice. M, estrogen and estrogen receptor responsiveness of tumor cells. Fluorescence microscopy analysis of ER\( \alpha \)-negative tumor cells (FM110) and of ER\( \alpha \)-positive tumor cells (FW473) infected with Ad-25ERE-GFP in the presence or absence of estradiol. Original magnifications, \( \times 200 \) (A-F) and \( \times 400 \) (G-K).
and myoepithelial cells were targeted by Cre recombinase, as indicated by the Rosa26 reporter strain (29). Heterogeneous tumor types (adenocarcinomas, myoepithelial adenocarcinomas, adenosquamous carcinomas, and spindle cell tumors) were seen in all mouse strains (Fig. 4). The majority of tumors were poorly differentiated invasive adenocarcinomas, which were also the most similar to human tumors histopathologically. Nonmammary tumors were also found, probably attributable to Cre expression in other tissues (Table 2; Fig. 2A). About 50% of mammary tumors metastasize to lung or liver (Table 2). Both histopathology and microarray analyses (data not shown) support that lung lesions are indeed tumor metastases. The metastasis frequency correlated with neither specific Cre-transgenic line nor tumor latency, consistent with previous observations (40). This tumor system recapitulates the high frequency of metastasis seen in advanced human breast cancer. By contrast, the experience of some investigators indicated that most mouse tumor models represent an early nonmetastatic stage of tumor development (41). Lung metastasis was also found in p53<sup>−/−</sup>-BALB/c mammary gland transplant models (42); however, the precise metastasis rate is not clear.

These mouse mammary tumors exhibit a pattern of mutation and gene dysregulation similar to human breast cancer. Amplification or overexpression of the c-myc and erbB2 proto-oncogenes is frequently observed in human breast cancer (7, 35). About 35% of these mammary tumors were found to have c-myc amplification and two-thirds showed erbB2 overexpression. Matrix metalloproteinase 9 and cell cycle regulators such as AYK1 (STK15), CDC25B, cyclin E2, and MCM6 were up-regulated in these tumor cells. This is consistent with the recent results showing that overexpression of these genes in human breast cancer reflects poor prognosis (36, 37). The high frequencies of c-myc amplification and overexpression of erbB2 and cell cycle regulators in p53-mutated tumors suggest that these genetic alterations have pivotal roles during tumor progression.

An inverse relationship between the number of targeted cells and MTL was observed. It is reasonable to assume that larger numbers of targeted cells are more likely to acquire critical genetic changes leading to tumor development with shorter latency. Indeed, similar genetic (e.g., c-myc) and gene expression changes (e.g., Neu/erbB2, AYK1, CDC25B, cyclin E2, and MCM6) were seen at high frequencies in tumors of both short and long latency. Intriguingly, when the number of targeted cells exceeded 20%, MTL did not shorten further. To explain this phenomena, we assume that cancer initiation depends in part on the accumulation of a certain number of key mutations (43). If the key rate-limiting process was simply the accumulation of one additional mutation, then after the average cell has gone through <i>T</i> rounds of cell division, the probability of obtaining the key mutation is <i>N</i><sup>u</sup><i>T</i><sup>−1</sup>. If we suppose <i>u</i> is approximately 10<sup>−6</sup>, and there are about <i>T</i> = 10 rounds of cell division, then saturation would happen when <i>N</i> is of the order 10<sup>10</sup>, which is probably much higher than the actual number of cells at saturation. Thus, to explain the saturation kinetics, there are two alternatives. First, the mutation rate per cell division may be higher than 10<sup>−6</sup>. This may occur because mutations of p53 increase the mutation rate per cell division. Second, some precancerous clonal expansion may be occurring, which would increase the number of rounds of cell division and therefore decrease the number <i>N</i> of initial predisposing target cells needed to achieve saturation. On the basis of results of the <i>MMTVCre<sup>b</sup></i> line, it can be concluded that a saturation kinetic is reached by targeting ~20% of mouse mammary epithelial cells. In the WAPCre<sup>e</sup> line, it is likely that a different population of mammary epithelial cells is targeted; however, the tumor kinetics is similar to that of <i>MMTVCre<sup>b</sup></i>. In addition to the number of targeted...
cells, it is plausible that the tumor latency might also be reflective of the type of cells targeted. Because multiple cell types are targeted in the models described here, the contribution of cell numbers and types of cells cannot be clearly determined.

On the basis of microarray profiling analysis, human breast cancers can be classified into five subtypes (44). It is not clear whether these heterogeneous tumor types are originated from different cells of the mammary gland or specific cancer-initiating cells are targeted and heterogeneity develops subsequently during tumor progression. Recent studies have revealed that a population of breast cancer cells possess stem cell-like properties (45). However, it remains to be studied whether cancer-initiating cells of ERα-positive and -negative tumors are different. In WAPCre mice both ERα-positive and -negative mammary tumors were found, although mutations of p53 in MMTVCre mice resulted in only ERα-negative tumors. Parity may not be relevant because ERα-positive tumors were found in both nulliparous and parous p53−/−WAPCre mice. It is plausible that ERα-positive stem cells, in addition to ERα-negative stem cells, are targeted in WAPCre mice. In contrast, in MMTVCre mice, only ERα-negative stem cells are targeted. Because nearly 90% of cells are LacZ-positive during second pregnancy in MMTVCre mice (data not shown), this might suggest that only a small population of cells give rise to ERα-positive tumors in these adult parous mice. The Cre transgenes are active at different developmental stages in WAPCre and MMTVCre mice. Whether developmental stages affect the abundance of ERα-positive progenitor cells is not clear. Because it is feasible to isolate ERα-positive epithelial cells from normal mammary glands and tumors (32), molecular mechanisms underlying ERα-positive and -negative mammary carcinogenesis can be systematically addressed using this model.

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