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Genetic Mechanisms in Apc-Mediated Mammary Tumorigenesis

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Abstract

Many components of Wnt/β-catenin signaling pathway also play critical roles in mammary tumor development, yet the role of the tumor suppressor gene Apc (adenomatous polyposis coli) in breast oncongenesis is unclear. To better understand the role of Apc in mammary tumorigenesis, we introduced conditional Apc mutations specifically into two different mammary epithelial populations using K14-cre and WAP-cre transgenic mice that express Cre-recombinase in mammary progenitor cells and lactating luminal cells, respectively. Only the K14-cre-mediated Apc heterozygosity developed mammary adenocarcinomas demonstrating histological heterogeneity, suggesting the multilineage progenitor cell origin of these tumors. These tumors harbored truncation mutation in a defined region in the remaining wild-type allele of Apc that would retain some down-regulating activity of β-catenin signaling. Activating mutations at codons 12 and 61 of either H-Ras or K-Ras were also found in a subset of these tumors. Expression profiles of acinar-type mammary tumors from K14-cre; ApcCKO/+ mice showed luminal epithelial gene expression pattern, and clustering analysis demonstrated more correlation to MMTV-neu model than to MMTV-Wnt1. In contrast, neither WAP-cre–induced Apc heterozygous nor homozygous mutations resulted in predisposition to mammary tumorigenesis, although WAP-cre–mediated Apc deficiency resulted in severe squamous metaplasia of mammary glands. Collectively, our results suggest that not only the epithelial origin but also a certain Apc mutations are selected to achieve a specific level of β-catenin signaling optimal for mammary tumor development and explain partially the colon- but not mammary-specific tumor development in patients that carry germline mutations in Apc.

Introduction

Breast cancer is one of the most common malignancies in women in Western countries and it is the cause of death in approximately 20% of all females who die from cancer. Breast epithelium is a dynamic organ capable of rapid proliferation and functional differentiation upon pregnancy and lactation, followed by involution and remodeling at the end of each lactation period. The adult mammary gland consists of secretory alveoli organized into lobules and interconnected by a system of branching ducts. The entire mammary epithelium is enveloped by a basement membrane and embedded in a fatty connective tissue called the mammary fat pad. In the ducts and alveoli, the mammary epithelium is organized into two layers, a basal layer of myoepithelial cells and a luminal epithelial layer. The myoepithelial cells, like other basal epithelial cells, express basal keratins (in particular, K5 and K14), P-cadherin, and the transcription factor p63 [1]. They also contain smooth muscle-specific proteins, including the α-smooth muscle actin (α-SMA), which confer contractility. By contrast, luminal cells express K8 and K18, which are characteristics of simple epithelia and when fully differentiated, secrete milk proteins [1].

The molecular mechanisms of the initiation of breast cancer are well studied. Mutations in BRCA1 and BRCA2 result in increased susceptibility to breast cancer [2] and mutations in TP53 are found to be common in late stages of this cancer [3]. It has been shown that dysregulation of the Wnt signaling pathway is an important contributor to the initiation of breast cancer [4]. Adenomatous Polyposis Coli (APC) is a member of the Wnt/β-catenin signaling pathway that is involved in the maintenance of the progenitor cell population in the skin, intestine and other tissues. Mutations and/or altered expression of APC or altered expression in the tumor suppressor gene BRCA1 are found frequently in sporadic breast cancers [5–7] which implicates its role as a tumor suppressor in mammary epithelium. In mouse, activation of Wnt/β-catenin signaling in the mammary epithelium either by mutation in Apc (GenBank NM_007462) or by stabilization of β-catenin (NM_007614), contributes to tumorigenesis. For example, mice heterozygous for germline mutation in Apc (Apc1/2) spontaneously develop mammary tumors, although at a significantly lower incidence than intestinal tumors [8]. Transient expression of an activated form of β-catenin in secretory luminal epithelium driven by the MMTV promoter leads to both mammary gland hyperplasia and mammary adenocarcinoma [9]. Similarly, expression of a transcriptionally active form of β-catenin lacking the N-terminal 89 amino acids (ΔN89 β-catenin) results in precocious development, differentiation, and neoplasia in both male and female mouse mammary glands [10]. The K5 promoter-
Author Summary

Breast cancer is one of the most common malignancies in women in Western countries. Many components of Wnt/β-catenin signaling pathway are known to play critical roles in mammary tumor development, yet the role of the tumor suppressor gene Apc (adenomatous polyposis coli) in breast oncopogenesis is unclear. To study the role of Apc in mammary tumorigenesis, we introduced conditional Apc mutations specifically into two different mammary epithelial populations using K14 (Keratin 14)-cre and WAP (Whey Acidic Protein)-cre transgenic mice that express Cre recombinase in mammary progenitor cells and lactating luminal cells, respectively. In this study, we show that a specific type of Apc somatic mutations in mammary progenitor/stem cell population in mice induces mammary carcinomas with histological and molecular heterogeneity, but a complete deletion leads to squamous metaplasia. Our data show that mutations in a multilineage progenitor cell are important in certain mammary tumors. We also show that certain Apc mutations are selected to achieve a specific level of β-catenin signaling optimal for mammary tumor development and explain partially the reason why breast cancers do not develop as frequently as colorectal tumors in patients that carry germline mutations in Apc.

Results

Mammary Tumor Susceptibility in K14-cre; Apc<sup>CKO/+</sup> Mice but Not in WAP-cre–Induced Apc Mutant Mice

Apc<sup>CKO/+</sup> mice, a germline knockout strain derived from the Apc conditional mice die primarily due to development of multiple intestinal tumors [14]. We have found that these mice can occasionally develop mammary tumors, as in Apc<sup>Min/+</sup> mice [8] although at a low incidence (14.3%, 3 of 21). To further study the role of Apc in mammary tumor development without being hindered by the intestinal tumorigenesis, we induced Apc mutations specifically in mammary epithelium using either K14 or WAP promoters. We have previously shown that homozygous loss of Apc in K14-expressing embryonic cells results in abnormal skin phenotype associated with aberrant development and squamous metaplasia in many epithelial-derived tissues including teeth and thymus, and die prior to weaning [14]. In contrast to K14-cre; Apc<sup>CKO/CKO</sup> mice, the K14-cre; Apc<sup>CKO/+</sup> mice were phenotypically normal at birth, but upon aging showed decreased survival primarily due to mammary tumor susceptibility in female mice (Table 1, Figure 1A–G). The K14-cre; Apc<sup>CKO/+</sup> female mice (n = 19) had a median survival of 15 months. We were able to carefully analyze 17 of these mice for pathology. The differences in survival are statistically significant between the K14-cre; Apc<sup>CKO/+</sup> female mice and the cre-negative Apc<sup>CKO/+</sup> and Apc<sup>Min/+</sup> female mice (p = 0.02, log rank test). A large proportion of K14-cre; Apc<sup>CKO/+</sup> females invariably developed mammary tumors with focal squamous metaplasia (13 of 17, 76.5%, Figure 1B–G) and the mice were sacrificed when their tumors were over 2 cm in diameter. Of the four mammary tumor-free female mice, three died of hepatoma, histiocytic sarcoma and myososarcoma, respectively and one succumbed to severe dermatitis. We extensively performed a full histological autopsy on seven mammary tumor-bearing mice, of which two had lung metastasis. The mammary tumor susceptibility was also observed in K14-cre; Apc<sup>CKO/+</sup> female mice backcrossed to C57BL/6 (K14-cre; Apc<sup>CKO/+</sup>i-B6, n = 8). At the time of analysis, half of them (4 of 8, 50%) developed mammary tumors before reaching 12-months of age while the other half remained tumor-free for over 12-months.

Both WAP-cre positive heterozygous and homozygous Apc<sup>CKO</sup> mice were born in the expected Mendelian ratio with no bias towards either sex. All mice were phenotypically normal at birth, developed normally and were fertile. However, litters from WAP-cre; Apc<sup>CKO/CKO</sup> mothers could not thrive. When litters were transferred to foster mothers, these litters survived and developed normally, suggesting that it was due to lack of appropriate milk production by WAP-cre; Apc<sup>CKO/CKO</sup> mothers and consequent inability to nurse their litters properly. This observation is in agreement with the BLG-cre mediated inactivation of Apc [13].

Both WAP-cre positive heterozygous and homozygous Apc<sup>CKO</sup> female mice have been allowed to pass through four complete lactation cycles with the exception of the two mice that underwent three and were monitored up until they were 18-months of age. Nulliparous females of the same genotypes were also monitored as their controls. Unlike in the K14-cre; Apc<sup>CKO/+</sup> nulliparous female mice that developed mammary tumors spontaneously, neither mated WAP-cre positive Apc<sup>CKO/CKO</sup> nor Apc<sup>CKO/+</sup> mice showed mammary tumor susceptibility (Table 1). There were hardly any differences in either the survival or tumorigenicity between multiparous and nulliparous WAP-cre positive females of either Apc<sup>CKO</sup> genotypes and all of them lived as long as Cre negative controls (Table 1). Mammary tumors were occasionally observed in all four groups of WAP-cre positive females (Table 1). Mammary tumors developed in two out of 14 (21.4%) WAP-
Figure 1. Mammary tumorigenesis in K14-cre Apc\(^{-}\)\(^{CKO/+}\) female mice. (A) Survival Curve of K14-cre Apc\(^{-}\)\(^{CKO/+}\) mice. Kaplan-Meier survival plot of K14-cre, Apc\(^{-}\)\(^{CKO/+}\) (red solid line, n = 19), Apc\(^{-}\)\(^{D580/+}\) (blue solid line, n = 21), Apc\(^{-}\)\(^{CKO/CKO}\) (broken line, n = 37) and Apc\(^{-}\)\(^{CKO/+}\) mice (solid line, n = 33). Germline Apc heterozygous (Apc\(^{-}\)\(^{D580/+}\)) mice are predisposed to multiple intestinal tumorigenesis, but K14-cre driven Apc heterozygosity have decreased survival compared to the controls primarily due to predisposition to mammary tumors. (B, C) A mammary tumor (C) from a K14-cre; Apc\(^{-}\)\(^{CKO/+}\) female mouse (B) with grossly biphasic growth. Scale bar 1 cm. (D–G) K14-cre; Apc\(^{-}\)\(^{CKO/+}\) tumors show a spectrum of histological patterns from differentiated pilar (D), acinar (E), basosquamous (BS, F) to undifferentiated (UD, G), usually in combinations of these. Squamous metaplasia (arrows) is frequent in these tumors, showing transdifferentiation to epidermal and pilar structures. Insets are the area within respective red boxes at higher magnification. Scale bars 100 \(\mu\)m.

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Table 1. Incidence of tumorigenesis in Apc mutant female mice.

| Genotype       | Parity | Age | Median Survival Age/mo | N  | Mammary tumors % (n) | Intestinal tumors % (n) | Other % (n) | Malignancy % (n) |
|----------------|--------|-----|------------------------|----|----------------------|-------------------------|------------|-----------------|
| K14-cre        | CKO/+  | null| 15.2±4.8               | 17 | 76.5 (13)            | 0 (0)                   | 23.5 (4)   | 94.1 (16)       |
| WAP-cre        | CKO/+  | multi| 18.3±2.5               | 6  | 16.7 (1)             | 0 (0)                   | 0 (0)      | 16.7 (1)        |
| WAP-cre        | CKO/CKO| multi| 18.0±2.7               | 14 | 14.3 (2)             | 0 (0)                   | 21.4 (3)   | 35.7 (5)        |
| WAP-cre        | CKO/CKO| null | 17.9±4.3               | 8  | 12.5 (1)             | 0 (0)                   | 25.0 (2)   | 37.5 (3)        |
| + D580/+       | null   | 5.4±1.0                     | 21 | 14.3 (3)             | 100 (21)                | 0 (0)      | 100 (21)        |
| + CKO/+        | -      | 18.7±3.7                     | 33 | 3.0 (1)              | 0 (0)                   | 6.0 (2)    | 9.1 (3)         |
| + CKO/CKO      | -      | 18.9±4.5                     | 37 | 5.4 (2)              | 0 (0)                   | 8.1 (3)    | 13.5 (5)        |

N = total number of mice in the study.
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mous and pilar histological types with extensive keratinization, tumors (n = 4) developed were primarily composed of basosqua-

Histological Heterogeneity and the Expression of both Luminal and Myoepithelial Markers in K14-cre; Apc<sup>CKO/+</sup> Mammary Tumors but Not in WAP-Cre–Induced Apc Mammary Tumors

Tumors arising from stem or progenitor cells may show mixed lineage differentiation [15]. K14-expression starts embryonically, and some of those cells give rise to both basal and luminal cells of mammary gland [16], while WAP expression starts in adult luminal mammary epithelium following pregnancy and lactation [17]. To investigate whether Apc mutation-induced tumors arising from K14-cre positive cells and WAP-cre positive cells have similar histology and lineage differentiation, these tumors were histologically examined and stained for both K8, a marker for luminal epithelial cells, and α-SMA, K14 and p63, markers for basal myoepithelial cells.

The histology of mammary tumors that developed in the germline knockout strain, Apc<sup>Fl580/+</sup> mice were similar to those described for Apc<sup>Min/+</sup> mammary tumors [18]. All three of them were pilar tumors with extensive keratinization, and were adjacent to basosquamous components. The mammary tumors developed in K14-cre, Apc<sup>CKO/+</sup> mice, either in mixed or C57BL/6 background, exhibited a variety of histological patterns within a tumor similar to those found in other Wnt Pathway tumors [18]. Most of the tumors were adenocarcinomas with focal squamous metaplasia (Figure 1B–G, 2). Squamous metaplasia may be extensive as in pilar tumors or scattered as multiple foci. The most common histological pattern observed in 16 K14-cre, Apc<sup>CKO/+</sup> mammary tumors from mice in the mixed background were acinar (Figure 1E, 2A–E), often associated with basosquamous (Figure 1F, 2F–J) and pilar (Figure 1D, 2K–O) components but only occasionally with undifferentiated component (Figure 1G, 2P–T). Upon backcrossing to C57BL/6, the K14-cre, Apc<sup>CKO/+</sup> mammary tumors (n = 4) developed were primarily composed of basosqua-

Nature and Location of Second Hit Apc Mutations in K14 cre; Apc<sup>CKO/+</sup> Tumors

It is known that in Apc-mediated tumorigenesis, an important initial event is the loss or mutation of the second copy of the Apc locus. We examined the status of Apc in 20 K14-cre, Apc<sup>CKO/+</sup> (16 mixed, 4 C57BL/6 backgrounds) and five WAP-cre,Apc<sup>CKO</sup> (both WAP-cre,Apc<sup>CKO</sup> and WAP-cre;Apc<sup>CKO/CKO</sup>) mammary tumors. We performed 3 separate PCRs to respectively screen for the (i) wild-type (320 bp) and Apc<sup>CKO/+</sup> (430 bp) alleles, (ii) wild-type, Apc<sup>CKO/+</sup> and Apc<sup>Fl580</sup> (500 bp) alleles, and (iii) Apc<sup>Fl580</sup> allele alone to genotype tumor DNA as shown in Figure 3A, i–iii. Skin and mammary glands are the tissues known to have transgene expression in K14-cre mice [16] and the presence of the deleted allele of Apc can be detected in small quantities in normal mammary glands of K14-cre, Apc<sup>CKO/+</sup> mice only by the Apc<sup>Fl580</sup> allele-specific PCR (Figure 3A iii; G1–G3). In contrast, most K14-cre, Apc<sup>CKO/+</sup> tumors had Apc<sup>Fl580</sup> genotype, with no or reduced presence of Apc<sup>CKO</sup> allele (Figure 3A i and ii; T1–T3), showing that these tumors were derived from the clonal expansion of Apc<sup>Fl580</sup> cells. It is important to note that all K14-cre, Apc<sup>CKO/+</sup> derived mammary tumors (20 of 20) were heterozygous for Apc<sup>Fl580</sup> mutation but still retained the wild-type allele and did not show allelic loss. In WAP-cre positive Apc<sup>CKO</sup> mice, the presence of the Apc<sup>Fl580</sup> allele was only detected in multiparous WAP-cre,Apc<sup>CKO</sup> mammary glands (Figure S1E iii; G1–G3, G6, G7) but none in mammary glands of nulliparous WAP-cre,Apc<sup>CKO</sup> females (Figure S1E iii; G4, G5, G8, G9), confirming the specificity of the WAP promoter. A single prominent Apc<sup>Fl580</sup> band was detected by 3-
allele screening PCR in four out of five WAP-cre-induced Apc^CKO tumors irrespective of parity (Figure S1E ii; T5, T6, T7, T9), demonstrating the complete conversion of the conditional allele to the deleted allele. One WAP-cre;Apc^CKO/+ tumor from a multiparous female was heterozygous for Apc^D580 mutation with retention of the wild-type allele (Figure S1E ii; T3) while the other from a nulliparous female showed a reduced presence of the wild-type allele, suggesting an allelic loss (Figure S1E ii; T5). Those tumors that sporadically developed in cre-negative control mice were negative for the Apc^D580 allele (Figure S1E iii; T), implicating that their development was independent from Cre-induced Apc mutation. These genotyping results were further supported by RT-PCR of corresponding tumor RNA (data not shown).

To determine whether the inactivation of the remaining functional Apc allele was achieved by intragenic truncation mutations, we analyzed the tumor DNA by in vitro transcription and translation (IVTT) assay. In view of prior mutational analyses in humans and mice, the region of Apc considered most likely to contain mutations is the first 3 kb of exon 15 [19,20]. All mammary tumors that showed retention of the wild-type Apc allele were analyzed by IVTT, and truncated Apc products were detected in 19 of 20 (95%) K14-Cre; Apc^CKO/+ and all 3 (100%) Apc^D580/+ mammary tumors, as well as in a single WAP-Cre; Apc^CKO/+ mammary tumor that did not show loss of the wild-type allele (Table 2). One sporadic Apc^CKO/+ mammary tumor contained two distinct Apc mutations. The relevant PCR products

Figure 2. Histological heterogeneity in mammary tumors from K14-cre Apc^CKO/+ female mice. (A–E) Acinar tumor. (F–J) Basosquamous tumor with squamous metaplasia and ghost cells indicated by arrowheads. (K–O) Pilar tumor with extensive keratinization. (P–T) Undifferentiated tumor. (U–Y) Mammary tumor from a multiparous WAP-cre; Apc^CKO/+ female mouse. Stained with H&E for histology (A, F, K, P, U), K14 (B, G, L, Q, Y), α-SMA (C, H, M, R, W), K8 (D, I, N, S, X) and Ki67 (E, J, O, T, Y) antibodies as indicated at the top. Note the different patterns of cell lineage markers associated with different tumor descriptors. Scale bars are 100 μm for K–O, the rest are 50 μm.
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were subsequently cloned and sequenced. All 25 mutant sequences identified are shown in Table 2.

When histologically distinct portions of a tumor were grossly identifiable as in the tumor in Figure 1C, they were collected separately and were analyzed by IVTT. It was found that they shared the same somatic truncation mutation, further supporting that these histologically distinct tumors derived from a clonal expansion of the same progenitor cell that have acquired an Apc truncation mutation (Figure 3B, T4&T5). Most notably, despite the variety of mutant sequences, most of the mutations found were clustered further downstream, beyond codon 1500, than the mutation cluster region of Apc gene. One sporadic Apc\(^{1638\text{N}}\) mammary tumor contained two distinct Apc\(^{1638\text{N}}\) alleles, (i) Apc\(^{1638\text{N}}\) allele alone. The faint presence of the Apc\(^{1638\text{N}}\) allele (500 bp band) in K14-cre; Apc\(^{CKO/+}\) mammary glands is only detectable by allele specific PCR (iii), whereas the corresponding mammary tumors shows the prominent presence of the deleted allele over the Apc\(^{CKO/+}\) allele (430 bp band) in 3-allele PCR (ii). Note that the wild-type allele (320 bp band) is still intact in all the mammary tumor samples. Deleted Apc products are not detected in either liver or mammary tumors from K14-cre negative mice. L = Liver, G = Mammary Gland, MT or T = Mammary Tumor. (B) Wild-type allele-specific in vitro transcription and translation assay of Apc for detection of truncation mutations. The majority of tumors (19 of 20) showed truncated products (red arrows) within the analyzed region (codons 677–1674) of the remaining wild-type allele of Apc. Note that two histologically distinct regions, acinar (T4) and pilar (T5) analyzed individually share the same mutations. (C) Distribution of Apc mutations in K14-cre; Apc\(^{CKO/+}\) mammary tumors. Diagram of Apc between codons 677 and 1674 showing positions and characteristics of truncation mutations detected in K14-cre; Apc\(^{CKO/+}\) (red) and Apc\(^{1638\text{N}}\) (blue) mammary tumors (above). The mutation distribution of Apc\(^{1638\text{N}}\) intestinal tumors (50) is also shown for comparison (below). Each symbol, deletion (Empty triangle), insertion (filled triangle), substitution (pinhead), represents an independent mutation. Note the mutation cluster region (MCR) of mammary tumors is located further downstream than the region frequently observed in intestinal tumors. The three 15-aa (A,B,C) and four 20-aa (1, 2, 3, 4) \(\beta\)-catenin binding repeats and one SAMP repeat (S1) in this segment of Apc are indicated. (D) Mutations in the K-ras and H-ras gene. Representative examples of somatic mutations in the K-Ras and H-Ras cDNA from mammary tumors of the K14-cre; Apc\(^{CKO/+}\) mice. Sequence chromatograms of codons 12, 13 and 61 are shown. Mutant peaks are indicated by arrows. Mutations found in either K-Ras or H-Ras were mutually exclusive.

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Table 2. Sequence of Apc mutations in various Apc heterozygous tumors.

| Codon | Mutation | Consequence | Wild-type Sequence * | K14-Cre; ApcC/KO/+ | WAP-Cre; ApcC/KO/+ | ApcC/KO/+ | ApcC/KO/+ |
|-------|----------|-------------|----------------------|---------------------|---------------------|-----------|-----------|
| 924–928 | 14 bpΔ frameshift | AGA AGC - - - - - A CAC TCA | - | - | 1b | - |
| 1466 | +C frameshift | GAG AGT GGG CGT AAG CAG | 1 | - | - | - |
| 1521 | ΔAT frameshift | GAT GTA GAA TTA AGA ATC | - | - | 1 | |
| 1528 | C→T Gln→Stop | CCT CCA GTT CAG GAA AAC | 1 | - | 1b | - |
| 1529 | G→T Glu→Stop | GTT CAG GAA AAC GAC AAT | 1 | - | - | - |
| 1530 | +A frameshift | GTT CAG GAA AAC GAC AAT | 2 | - | - | - |
| 1530 | ΔAC frameshift | GTT CAG GAA AAC GAC AAT | 1 | - | - | - |
| 1534-1610 | 230 bpΔ frameshift | AAT GGG A - - - - - CCT GTG | 1 | - | - | - |
| 1542 | G→T Glu→Stop | CAG CCT GAG GAA TCA AAT | 1 | - | - | - |
| 1546 | G→T Glu→Stop | TCA AAT GAA AAC CAG GAT | - | - | 1 | - |
| 1547 | AC→T frameshift | TCA AAT GAA AAC CAG GAT | 1 | - | - | - |
| 1547 | +A frameshift | TCA AAT GAA AAC CAG GAT | 1 | - | - | - |
| 1551 | ΔA frameshift | CAG GAT AAA GAG GTA GAA | 1 | - | - | - |
| 1553 | G→T Glu→Stop | AAA GAG GTA GAA CCT GCT | 1 | - | - | - |
| 1554 | +A frameshift | GAG GTA GAA AAC CCT GAC | 1 | - | - | - |
| 1560-1565 | 14 bpΔ frameshift | GAA AAA GA - - - - - CCT GAT | 1 | - | - | - |
| 1561 | A→T Leu→Stop | TCT GAA AAA GAC TTA TTA | - | 1 | - | - |
| 1567 | ΔC frameshift | TCT GAT GAC GAT GAT ATT | 1 | - | - | - |
| 1567 | ΔAC frameshift | TCT GAT GAC GAT GAT ATT | 1 | - | - | - |
| 1568 | ΔT frameshift | TCT GAT GAC GAT GAT ATT | 1 | - | - | - |
| 1568 | ΔG frameshift | TCT GAT GAC GAT GAT ATT | 2 | - | - | - |
| 1570 | ΔT frameshift | GAT GAT ATT GAA ATA TTA | - | - | 1 | - |

*The wildtype sequence surrounding each mutation is shown and the site of mutation is shown in bold.

Activating Ras Mutations in K14-crc; ApcC/KO/+ Mammary Tumors

Wnt1-induced mammary tumors frequently contain activating H-Ras mutations [21] and mutations in K-Ras or N-Ras are frequently found in c-Myc-induced tumors [22]. To determine whether secondary somatic mutations in Ras are involved in Apc mutation-induced mammary tumorigenesis, cDNA copies of tumor Ras mRNAs were analyzed by direct sequencing. In our sequence-based analysis of exons 5 to 8 of the Tp53 gene was also carried out but Tp53 missense mutations were not detected.

Comparative Analysis of Expression Profiles of K14-crc; ApcC/KO/+ Mammary Tumors to Other Models

There are many mouse models of breast cancer that are different in histopathology and possibly in cell of origin [23,24].

Table 3. Histology and Kas mutations in mammary tumors.

| Genotype | Mammary Tumors | N | H-Ras | K-Ras |
|----------|----------------|---|-------|-------|
| K14-crc; ApcC/KO/+ | Acinar/Glandular | 6 | 2 (Q61L) | 0 |
| | Basosquamous/Pilar | 3 | 0 | 0 |
| | Undifferentiated | 2 | 0 | 1 (Q61R) |
| | Mixed | 6 | 0 | 3 (G12D, G12V) |
| Total | 17 | 2 | 4 |
| ApcC/KO/+ | Basosquamous/Pilar | 3 | 0 | 0 |
| WAP-crc; ApcC/KO/+ | Acinar/Glandular | 4 | 0 | 0 |
| | Mixed | 1 | 0 | 0 |
| Total | 5 | 0 | 0 |

*The wildtype sequence surrounding each mutation is shown and the site of mutation is shown in bold.

*Mutations found in the same mammary tumor.

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and these models also have distinct gene expression profiles [25,26]. To determine what types of mammary tumor models K14-cre, Apc(+/+), mice represent, gene expression profiles of three acinar-type mammary tumors, the most frequently found histological pattern in K14-cre, Apc(+/+) in the mixed background, and three cre-negative normal mammary gland samples were determined using Affymetrix GeneChip M430 2.0 arrays. All 3 tumors were heterozygous for Apc(+/+) mutation and the remaining allele contained a truncation mutation in Apc. Both Gene Set Enrichment analysis (GSEA) and Ingenuity Pathway analysis (IPA) results indicated that mouse tumor profiles have gene sets characteristics of cell cycle, cellular movement and cancer related genes (Dataset S3, S4, S5, and S6). To get additional insights into K14-cre, Apc(+/+) tumors, gene expression data from our model was compared to data set of multiple mouse mammary carcinoma models previously published [25]. Based on mouse model intrinsic gene set cluster analysis [25], a dendrogram and a heatmap were generated using dChip (http://biooul.harvard.edu/complab/dchip/) (Figure 4A-H). The gene expression pattern in dendrogram showed more correlations with luminal-type mammary tumors, which include MMTV-Neu, MMTV-PyMT and WAP-Myc [25]. K14-cre, Apc(+/+) tumors also expressed genes that are strongly expressed in human luminal tumors, such as ZBP1 and luminal cell marker K8 and K18, but were low in basal tumor-defining genes. These tumors also showed high expression of Folate receptor 1 (Folr1), which is commonly up-regulated in luminal tumor mouse models [25]. As with most mouse mammary tumors, our model was also negative for ER and many estrogen-regulated genes. In agreement with these data, K14-cre, Apc(+/+) acinar-type mammary tumors expressed K8 while K14 or α-SMA staining was restricted to a myoepithelial pattern (Figure 2B-D).

To confirm the initial comparative results, we further compared the gene expression of our K14-cre, Apc(+/+) model to those previously published for MMTV-Neu, MMTV-Wnt1 and MMTV-Wnt1/Neu bitransgenic mice [26]. A clustering diagram was obtained that clustered tumors from MMTV-Neu, MMTV-Wnt1 and MMTV-Wnt1/Neu bitransgenic samples the same way as indicated previously [26], with K14-cre, Apc(+/+) tumors clustering in a separate cluster when hierarchical clustering analysis was done by samples using rank correlation as distance measure for 19,581 probes. However if differentially expressed probes from K14-cre, Apc(+/+) tumors versus controls were used for clustering, K14-cre, Apc(+/+) tumors clustered next to MMTV-Neu with no effect on clustering between MMTV-Neu, MMTV-Wnt1 and MMTV-Wnt1/Neu samples. The same overall clustering was obtained using mouse model intrinsic gene set [25] (Figure 4A-H). These results support the view that acinar-type mammary tumors from K14-cre, Apc(+/+) model are luminal type that correlate more with MMTV-Neu than MMTV-Wnt1 model.

The elevated expression of Folr1 in mammary tumors detected by microarray analysis was confirmed by quantitative real-time RT-PCR. Since both the IPA and clustering analyses suggested a potential involvement of Neu/ErbB2 (NM_01003817) in K14-cre, Apc(+/+) mammary tumorigenesis (Figure S3A), we also included ErbB2 in our analysis. Over 30-fold increase in Folr1 (NM_008034) expression compared to the control was detected in acinar-type mammary tumors (108.7±23.3 vs 3.1±1.1, p = 0.0051) confirming the microarray results, but non-acinar type, including those tumors composed primarily of basosquamous, pilar, and undifferentiated structures, and Apc(+/+) mammary tumors showed no such differences (Figure 4I). There were no significant differences between tumors and the control for Ebb2 expression.

### Discussion

To delineate the role of Apc mutations in mammary gland, we used Cre-loxP technology to target inactivation of Apc gene in two different mammary epithelial cells, using K14-cre and WAP-cre transgenic mice. The Cre expression in our K14-cre transgenic mice is driven by the basal K14 promoter, which is active in progenitor cells that can give rise to both mammary luminal and myoepithelial lineages [27,28], whereas that of WAP-cre transgenic mice is specific to lactating luminal epithelial cells [17]. The availability of Apc mutant mice under two different promoters and their mammary tumors allowed us to study how Apc loss contributes to mammary tumorigenesis. In this study, we present several lines of evidence that target cells for Apc mutation-induced mammary tumorigenesis are progenitor/stem cells and that they require specific truncation mutations that partially retain β-catenin down-regulating function. First, K14-cre induced Apc(+/+) heterozygosity, but not WAP-cre induced Apc(+/+) heterozygosity or homozygosity, predisposes to mammary tumorigenesis. Second, K14-cre mediated mammary adenocarcinoma showed mixed lineage differentiation, in line with stem or progenitor cell origin, in contrast to WAP-cre mediated tumors that comprised essentially of luminal and abnormal α-SMA positive cells, lacking other basal markers. This is further supported by the fact that two grossly and histologically distinct regions of a tumor share the same somatic Apc truncation mutation, suggesting their origin from a common progenitor. Finally, the remaining wild-type allele of Apc is inactivated not by allelic loss, which is the common mechanism in intestinal tumorigenesis in Apc heterozygous mice, but preferentially by somatic truncation mutations specifically in a well defined region of the gene. This mutation cluster region was different to the one reported for intestinal tumors, implicating that the dosage-specific activation of downstream Wnt/β-catenin signaling pathway is necessary for mammary tumorigenesis.

We have previously shown that K14-creApc(+/+) mice have aberrant development and squamous metaplasia in many epithelial-derived tissues and die perinatally [14], not allowing the analysis of Apc loss in postnatal mammary gland. Analogous to K14-driven Apc(+/+) homozygosity, a complete inactivation of the Apc gene in WAP-expressing mammary luminal epithelial cells primarily led to the development of severe squamous metaplasia but rarely neoplasia. These observations suggest that constitutive activation of Wnt/β-catenin signaling pathway by Cre-mediated Apc deficiency, resulting in homozygous Apc (Apc(+/+)/ Apc(−/−)) mutations, invariably induce terminal squamous transdifferentiation of the mammary epithelium irrespective of cell origin of mutated cell, but do not develop tumors. This is in agreement with other Cre-mediated Wnt/β-catenin activation models in which induction of squamous metaplasia but not neoplasia was primarily observed [12,13,29].

Although homozygous Apc (Apc(+/+)/ Apc(−/−)) mutations induced either by K14 or WAP-promoters invariably results in squamous metaplasia, Cre-mediated Apc heterozygosity (Apc(+/−)) in K14-cre, Apc(+/+) mice developed mammary tumors with high penetrance. A similar tendency was also observed in K14-cre, Apc(+/+) mice backcrossed to C57BL/6, suggesting that the initiation of Apc-mediated mammary tumorigenesis is not affected by the genetic background. The majority of mammary tumors developed in K14-cre, Apc(+/+) mice had Apc(+/−) genotype and have somatically acquired truncation mutation in the remaining wild-type allele, unlike intestinal tumors in Apc(+/−) mice and other germline Apc heterozygotes in which the preferential mechanism of the wild-type Apc is allelic loss [14,30–32]. Most intriguingly, these truncation mutations were clustered around codon 1530 of Apc.
Figure 4. Comparison of expression profiles of K14-cre; Apc\(^{CKO/+}\) mammary tumors to MMTV-Wnt1 and MMTV-Neu tumors. (A) Dendrogram of K14-cre; Apc\(^{CKO/+}\), MMTV-Wnt1, MMTV-Neu and MMTV-Wnt1/Neu tumors [26], based on hierarchical clustering analysis of Affymetrix microarray data. K14-cre; Apc\(^{CKO/+}\) acinar mammary tumors (tumor 1, 2, 3) showing more correlation to MMTV-Neu. (B–G) Mouse models intrinsic gene set cluster analysis, as depicted in Herzchkowitz et al [25]. Red and blue indicate expression levels respectively above and below the median. The magnitude of deviation from the median is represented by the color saturation. (B) Luminal epithelial gene expression pattern. (C) Genes encoding components of basal lamina. (D) A second basal epithelial cluster genes. (E) Genes implicated in epithelial to mesenchymal transition. (F) A second mesenchymal cluster that is expressed in normal. (G) Estrogen-regulated genes. (H) Potentially estrogen-regulated genes. (I) Real-time RT-PCR analysis of Follr1 and Erbb2 transcript levels in mammary tumors of the K14-cre; Apc\(^{CKO/+}\) and Apc\(^{D580/+}\) mice. Bars represent the mean values ± S.E.M. for 7 control mammary glands (MG), 12 acinar and 6 non-acinar (undifferentiated or basosquamous) K14-cre; Apc\(^{CKO/+}\) and 4 Apc\(^{D580/+}\) (d580) mammary tumors normalized to the Hprt1 transcript levels. The difference in the Follr1 transcript levels was statistically significant between the control only in the acinar-type K14-cre; Apc\(^{CKO/+}\) mammary tumors (p<0.006), whereas no difference was detected for the Erbb2 transcript levels between the tumors and the control.

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(Figure 3C, Table 2), which is further downstream than the mutation cluster region typically observed in both human and mouse intestinal tumors [19,20,33]. Regulation of intracellular β-catenin levels is thought to represent one of the most important functions of the Apc tumor suppressor protein. Three different motifs in the central region of Apc are responsible for this activity. The three 15-amino acid (aa) repeats that bind β-catenin, the seven 20-aa repeats that both bind and down-regulate β-catenin [34,35], and the three SAMP motifs that bind conductin/axin [36,37]. The mutations found in mammary tumors would result in truncated Apc polypeptides retaining up to three of the seven 20-aa repeats but lack all SAMP motifs. It has been shown that loss of these functional motifs, especially those that lead to the elimination of at least five of the seven 20-aa repeats greatly reduced the β-catenin down-regulation activity of Apc [38]. However, Smits et al [39] showed that haploinsufficiency for the truncated Apc polypeptide that retains up to the third 20-aa repeat (Apk1638N/1638N) still retained some β-catenin down-regulation activity, resulting in a 5-fold increase in the transcriptional activity compared to a 30-fold increase in Apc mutation homozygosity (Apk1638N/1638N).

Since dosage of β-catenin is critical in determining epithelial cell fate in many organs and varying the level of β-catenin signaling during a cell fate program have been shown to switch the epithelial cell fate [40], it is possible that the homozygosity of Apc mutation (Apk1638N/1638N) results in too much β-catenin transcriptional activity, that may push cells into the signaling events that leads to squamous transdifferentiation rather than to hyperplasia of mammary epithelial cells and eventually to neoplasia. The Apk1638N homozygosity with somatic mutation of the remaining wild-type Apc allele that retains some β-catenin down-regulating domains may lead to the optimal dosage of β-catenin necessary for mammary tumorigenesis. Indeed, Apk1638N homozygosity induced by K14 promoter resulted in severe squamous metaplasia and ectopic hair follicle morphogenesis in many organs including skin and thymus [14] and the current data using WAP-cre also resulted in squamous metaplasia in mammary glands rather than tumor development. Since mutations found in mouse intestinal tumors result in either allelic loss or a somatic truncation mutation upstream of the third 20-aa repeats [14,19,20,30–32], deletion of the β-catenin binding domains seems to confer the main selective advantage in mouse intestinal tumorigenesis. Thus, our results and those of others indicate that there is an Apc-regulated level of β-catenin signaling optimal for tumor formation that differs tissue-specifically. The selection for an optimal β-catenin signaling level for tumor formation is also supported by the spectrum of somatic mutations observed in colorectal adenomas from Familial Adenomatous Polyposis (FAP) patients with different germline mutations in APC [41]. Our data also partly explain why breast cancers do not develop as frequently as colorectal tumors in FAP patients. It is likely that unless somatic truncation mutation optimal for breast oncogenesis is acquired in the APC gene, mammary epithelial cells are not initiated towards tumorigenesis but instead become metastatic. Such selection would reduce the incidence of tumorigenesis and require much longer latency, as demonstrated by Apk1638N and K14-cre, Apc1638N mouse models.

Our histopathological and molecular analyses showed that the majority of K14-cre,Apc1638N mammary tumors are adenocarcinomas with multiple foci of squamous metaplasia. These tumors are highly proliferative, ER-negative carcinomas, showing strong positivity for Tcry/β-catenin target genes, Myc and cyclin D1, with expression of both luminal and basal epithelial markers. They have many histological features common to Wnt pathway tumors previously described [18], but at the same time have expression profiles that correlate more to luminal tumor models. The latter observation could be explained partly by the predominance of acinar-type histology, which is a luminal type histology, found in the majority of K14-cre,Apc1638N tumors from the mixed background and was the histological type selected for the expression analysis in the current study. The selection of this particular histological type may have biased the expression profiles towards luminal expression pattern. Interestingly, the frequency of the acinar-type histology diminished and basosquamous/pilar structures predominated in the K14-cre,Apc1638N background tumors. Since either histological type of mammary tumors had the same mechanism of Apc inactivation irrespective of the genetic backgrounds, it suggests that the mode of initiation is the same but the progression to certain histological types is greatly influenced by modifier genes associated with the genetic backgrounds.

Comparison of our gene expression profiling data to published mouse and human breast cancers suggests that acinar-type tumors from K14-cre,Apc1638N mice are more similar to luminal type mouse models [25]. The similarities between mouse and human luminal tumors are limited by the fact that most human luminal epithelial cluster contains the ER and many estrogen-regulated genes, but many mouse mammary tumors, including K14-cre,Apc1638N+ tumors, are ER-negative. However, the expression profiles of K14-cre,Apc1638N+ acinar tumors also included a human luminal tumor-defining gene, XBP1 [42,43] and stained positive for Ki6. Our tumor set also showed elevated expression of Folr1, which is a gene included in luminal epithelial gene expression cluster that is highly expressed in MMTV-PyMT, MMTV-Neu, and WAP-cre tumors [25]. It was of interest that Folr1 expression level varied within K14-cre,Apc1638N+ mammary tumors depending on histology, and the ones that had elevated expression were those predominantly composed of acinar histology. The tumors from Apc1638N+ mice, which were of pilar and basosquamous histology, had very low Folr1 expression level. Although Folr1 is not associated with human luminal tumors, its overexpression and poor prognosis have been implicated in human breast cancers [44,45].

To determine whether other oncogenic pathways are involved in Apc mutation-induced mammary tumorigenesis, we examined the status of Ras oncogenes and Tp53 in these tumors. It has been previously shown that c-Myc induced mammary tumors in mice frequently harbor spontaneous activating mutations in K-Ras [22] while over 50% of MMTV-Neu tumors contain oncogenic mutations in H-Ras [21]. Jang et al also suggested that K-Ras activation strongly synergizes with both c-Myc and Wnt in mammary tumorigenesis and promotes the progression of tumors to oncogene independence, while H-Ras mutant Wnt-induced tumors remain oncogene dependent [46]. It is of interest that although their presence was mutually exclusive to each other, both H-Ras and K-Ras oncogenic mutations were found in a subset K14-cre,Apc1638N+ tumors. We could not find a strong association between histology, incidence of lung metastasis and Ras mutations, but those tumors that contained K-Ras mutations frequently had heterogeneous histology containing aggressive looking undifferentiated regions that have lost both lineage markers while those with H-Ras mutations were predominantly of acinar-type.

In conclusion, our study demonstrates that activation of Wnt/β-catenin signaling via inactivation of Apc leads to mammary tumorigenesis when the inactivation takes place in mammary epithelial progenitor cells rather than more differentiated secretory luminal cells; and when somatic truncation mutation is acquired in a particular region of the Apc gene, which may be necessary to achieve a certain level of β-catenin signaling activation required for mammary tumorigenesis. These initiated tumor cells develop
into heterogeneous tumor containing different histological types, each with different expression pattern of lineage markers, some acquiring more oncogenic mutations, such as in either H-Ras or K-ras genes. Our data indicate that only a specific subset of somatic mutations at the Apc gene will successfully lead to tumor formation in the mammary epithelium and there is a selection for Apc mutations that retain some down-regulating activity of β-catenin signaling. We propose that this selection is aimed at a specific level of β-catenin signaling optimal for mammary tumorigenesis, rather than at its constitutive activation achieved by deletion of all the β-catenin down-regulating domains in Apc, which invariably results in squamous metaplasia.

Materials and Methods

Mammary-Specific Inactivation of Apc

The Apc conditional (Apc<sup>CKO</sup>) and germline (Apc<sup>A580</sup>) knockout mice, WAP-cre and K14-cre transgenic mice have previously been described [14,16,17]. Apc<sup>A580/+</sup> mice have already been backcrossed to C57BL/6J background. The rest of the mice analyzed in this study were generated as follows: Apc<sup>CKO</sup> heterozygote mice of the F1 generation (C57BL/6J x 129/SvJ) were first crossed with either WAP-cre mice (C57BL/6J background) or K14-cre transgenic mice (FVB background). Cre-positive Apc<sup>CKO/+</sup> male mice thus generated were then crossed with Apc<sup>CKO/CKO</sup> females to generate homozygous and heterozygous Apc<sup>CKO</sup> offspring either with or without respective cre transgene. The mice were intercrossed thereafter for maintenance. Subsequently, K14-cre, Apc<sup>CKO/+</sup> female mice backcrossed for 4 generations to achieve >95% C57BL/6J background were also included in the analysis so that the results between two different promoters will be comparable. Females with genotypes WAP-cre, Apc<sup>CKO/+</sup> and WAP-cre, Apc<sup>CKO/CKO</sup> were mated and undergone pregnancies 4 times to facilitate WAP-cre-mediated deletion of exon 14 of Apc gene. Mice with genotype K14-cre; Apc<sup>CKO/CKO</sup> are perinatally lethal [14] and phenotypically normal K14-cre, Apc<sup>CKO/CKO</sup> littersmates were used for analysis. The mice were sacrificed when either they were moribund or their tumors reached at least 2 cm in diameter, following Institutional Animal Care and Use Committee guidelines.

Genotyping of Mice

Mouse tails tips obtained at ~10 days of age were lysed overnight in DirectPCR Lysis Reagent (Viagen Biotech) containing 0.1 mg/ml Proteinase K (Qiagen). The crude lysates were incubated at 85°C for 45 minutes and 0.5 μl of lysate was directly used per 25 μl PCR reaction. Detection of various Apc alleles and cre transgene was carried out as previously described [14].

Histological Analysis

Mice were sacrificed by CO₂ inhalation when they developed gross tumors or were moribund. The location and size of tumors were routinely recorded and pictures were taken from each mouse. Tumors were cut in portions and a portion was either fixed in 10% NBF or were moribund. The location and size of tumors were then compared. Females with genotype were analyzed for mutations at the Apc gene were analyzed for

DNA and RNA Extraction from Tumors

Both genomic DNA and RNA from tumors and various tissue samples collected at the time of autopsy were extracted as described previously [14]. Briefer, genomic DNA was extracted using DNeasy mini kit (QIAGEN). RNA was extracted by homogenizing tumors and tissues in 3 ml Trizol reagent (Invitrogen). After phase separation, an equal volume of 70% ethanol was added to the aqueous phase and purified through PureLink Microto-Midi Total RNA Purification System (Invitrogen), following manufacturer’s instruction. Concentrations of nucleic acids were determined by Nanodrop (Ribogreen, Molecular Probes, Eugene, Oregon, United States).

Analysis of Apc Status in Tumors

Tissue-specific recombination of the conditional alleles in tumors and various tissue samples was examined by analyzing both their extracted DNA and RNA as described previously [14]. Briefer, genomic DNA samples were examined by a semi-quantitative 3-primer genotyping PCR that will give 3 distinct sized products from the wild-type (320 bp), conditional (430 bp) and deleted (500 bp) alleles of Apc. In addition, two separate 2-primer PCRs were performed; one to check for the wild-type and Apc<sup>CKO</sup> alleles and the other to detect the presence of the Apc<sup>A580</sup> allele alone. The expression of full-length and truncated Apc alleles were examined by performing RT-PCR on RNA using SuperScript One-Step RT-PCR with Platinum Taq (Invitrogen), following manufacturer’s protocol.

Upon confirmation of the retention of the wild-type Apc allele, cDNA clones 677-1674 of the mouse Apc gene were analyzed for truncation mutations by PCR and in vitro transcription and translation (IVTT) assay as described previously [20,47] but with some modifications. All DNA amplifications were performed using Phi Ultra II fusion HS DNA polymerase (Stratagene) according to manufacturer’s instruction. The wild-type allele-specific amplifi-
cation of Apc was performed by nested-PCR to eliminate co-amplification of deleted Apc<sup>ADX20</sup> allele using the forward primer 5'-CATTCTCCCTACTTGAAGG and a reverse primer 5'-GGTGTCACTGAGGGTGGTG in the first PCR reaction. Two overlapping segments of the Apc gene covering codons 677–1234 and 1100–1674 were subsequently amplified from aliquots of the first reactions using two pairs of PCR primers specific for IVTT. Cycling conditions for the first stage PCR were one cycle of 94°C for 2 min, followed by 20 cycles of 94°C for 20 s, 50°C for 20 s and 72°C for 90 s, with one final extension cycle at 72°C for 3 min. Cycling conditions for the second stage PCR were as above except the cycle number was increased to 25. The PCR products were directly used for IVTT assay as described previously [20,47]. In order to facilitate the detection of Apc truncation mutations from tumor samples that are frequently co-harvested with adjacent normal tissues, we developed a method based on expression of Apc-GFP fusion polypeptides in bacteria, in which colonies derived from PCR products with mutation appear GFP-negative. The pTRcHis B Prokaryotic Expression Vector (Invitrogen) was modified to contain GFP coding sequence (Acc# U87625) between NheI and SacI sites. The sequence between NcoI and NheI sites, coding poly-histidine region was replaced with a BamHI site, such that insertion of amplified Apc fragments between BamHI and NheI sites restores the reading frame of GFP. For characterization of tumor-specific mutations, the PCR products were digested with BamHI and NheI, gel purified, and cloned into modified pTrc vector and transformed into bacterial cells using standard cloning procedures. Transformed bacterial cells were spread on LB plates containing final concentrations of 50 μg/ml ampicillin and 50 μM IPTG and incubated overnight at 37°C. The numbers of non-fluorescent and fluorescent colonies were counted under long-wave length UV light. When the percentage of non-fluorescent colonies over total was above the detection calls were used to remove 12,844 probes which had ‘Absent’ call across all samples. Data set with 32,322 probes was used as starting point for any subsequent analysis. To identify genes differentially expressed between tumor and control samples two-sample t-test was used (Dataset S1). T-test was performed using ComparativeMarkerSelection module of Gene Pattern (http://www.broad.mit.edu/cancer/software/genepattern/) [49]. Based on two-sample t-test results, any probes with fold differences below 2, t-test values below 4.5 were removed and only the probes that have either consistent absent or present calls were used as input for Ingenuity Pathway Analysis (IPA) Software (http://www.ingenuity.com/, Dataset S2). Ingenuity core analysis generated over 60 networks with nearly 600 network nodes in total, many of them involved in cell cycle, cell, growth, cell death, DNA replication, and cancer (Dataset S3, S4, S5, and S6).

Gene Set Enrichment Analysis (GSEA) was performed using java GSEA http://www.broad.mit.edu/gsea/ as previously described [49].

Comparison of Gene Expression Profiles with Other Mouse Models

To get additional insights in K14-cre, Apc<sup>CKO/+</sup> tumors, gene expression from our mouse model was compared to data set of multiple mouse mammary carcinoma models and human breast tumors previously published [25]. In particular, based on genes mainly in intrinsic gene set cluster analysis of mouse models a dendrogram was generated using dChip (http://biosun1.harvard.edu/complab/dchip/) (Figure 4A).

To further compare gene expression of K14-cre, Apc<sup>CKO/+</sup> model, gene expression probe level data (CEL files 430A 2.0) from Shixia Huang et al. for tumors from MMTV-Wnt1, MMTV-Neu and MMTV-Wnt1/MMTV-Neu bitransgenic mice were obtained [26]. MASS5.0 algorithm was used to estimate probe expression. Since 430 2.0 chips have additional probe sets compared to 430A 2.0 the subset corresponding to 430A 2.0 was used for MASS5.0 global method of scaling/normalization. Target Intensity value of 500 was used for all arrays. Prior to performing any other analysis, Affymetrix detection calls were used to remove 3,045 probes which had ‘Absent’ call across all samples. Data set with 19,581 probes was used as starting point for any subsequent analysis. Hierarchical clustering by samples was performed using data for all 19,581 probes as input and rank correlation as (Figure S3B). Subsequent-ly, 1,355 differentially expressed probes (fold differences above 2, t-test values above 4.5) from K14-cre, Apc<sup>CKO/+</sup> tumors versus controls were used for clustering analysis (Figure S3C).

Real-Time RT-PCR

The expression levels of Fohl1 and Ehhb2 in 17 K14-cre, Apc<sup>CKO/+</sup>, 5 WAP-cre, Apc<sup>CKO</sup> (Apc<sup>CKO/CKO</sup> and Apc<sup>CKO/+</sup> combined), 4 Apc<sup>ESM</sup>/+ mammary tumors were compared to those of 7 normal mammary glands by quantitative RT-PCR with HPRT1 as an internal control. Most of K14-cre, Apc<sup>CKO/+</sup> mammary tumors in the mixed background consisted of acinar-type, but there were a few which had distinct histology. Therefore, tumors were roughly divided into 2 groups; acinar and non-acinar. The latter group of mammary tumors primarily composed of undifferentiated, basosquamous and pilar-type histology. We analyzed 14 acinar-type, and 8 non-acinar type. The mammary tumors developed in Apc<sup>ESM</sup>/+ mice were mostly of basosquamous-type. TaqMan Gene Expression Assays for respective genes were used on 7500 Fast Real-Time PCR System (Applied Biosystem) according to the manufacturer’s protocol. Relative quantity was calculated using Sequence Detection Software version 1.4 (Applied Biosystem).
Supporting Information

**Figure S1** WAP-cre induced inactivation of Apc. (A) Whole-mount of a mammary gland showing development of severe squamous metaplasia in multiparous WAP-cre, Apc<sup>KD0/CKO</sup> female mouse. (B) H&E staining of another gland from the same mouse showing multiple metaplastic lesions throughout the gland. (C) H&E staining of a mammary tumor from a multiparous WAP-cre, Apc<sup>KD0/CKO</sup> female mouse with squamous metaplasia (arrows) which have less defined structures than those in K14-cre, Apc<sup>KO/+</sup> tumors. (D) K14 expression was only observed in these metaplastic lesions in WAP-cre induced tumors. Scale bars: 50 μm. (E) Genotyping for Apc in WAP-cre positive mammary glands and tumors, showing WAP-cre and parity-specific recombination of conditional alleles. Genotyping PCR for the (i) wild-type and Apc<sup>KD0/CKO</sup> alleles, (ii) wild-type, Apc<sup>KO/+</sup> and Apc<sup>AS/AS</sup> alleles, (iii) Apc<sup>AS/AS</sup> allele alone. The presence of the Apc<sup>AS/AS</sup> allele detected in mammary tumors from nulliparous WAP-cre positive females demonstrates that these tumors have derived from a clone of cells that have undergone Cre-mediated recombination. Found at: doi:10.1371/journal.pgen.1000367.s001 (3.0 MB PPT)

**Figure S2** Expression of Tcf/β-catenin-target genes in mammary tumors from K14-cre, Apc<sup>KD0/CKO</sup> female mice. A representative acinar-type mammary tumor stained with H&E for histology (A), Apc<sup>CKO/CKO</sup> H&E staining of a mammary tumor from a multiparous WAP-cre mouse. (B) H&E staining of another gland from the same mouse K14-cre analyses of expression profiles of which have less defined structures than those in K14-cre, Apc<sup>KO/+</sup> tumors. (C) Hierarchical clustering by samples for 1,335 differentially expressed probes (fold differences between tumors and control samples for 32,322 probes. Information on differential gene expression versus controls were used. Found at: doi:10.1371/journal.pgen.1000367.s003 (0.5 MB PPT)

**Figure S3** Ingenuity Pathway and Hierarchical Clustering analyses of expression profiles of K14-cre, Apc<sup>KD0/CKO</sup> mammary tumors. (A) A representative IPA network. Ingenuity core analysis generated over 60 networks, many of them involved in cell cycle, cell growth, cell death, DNA replication and cancer (see Dataset S3 for information for all networks). A representative network is shown, showing elevated expression of Fohl1. Green for elevated expression in tumor and red for elevation in control. (B) Hierarchical clustering by samples for 19,581 probes. A clustering diagram of K14-cre, Apc<sup>KD0/CKO</sup> tumors (1107 E,F,H), controls (1107 A,C,D), tumors from MMTV-Wnt1, MMTV-Neu and MMTV-Wnt1/MMTV-Neu bitransgenic mice. Rank correlation was used as distance measure. (C) Hierarchical clustering by samples for 1,335 probes. 1,335 differentially expressed probes (fold differences above 2, t-test values above 4.5) from K14-cre, Apc<sup>KD0/CKO</sup> tumors versus controls were used. Found at: doi:10.1371/journal.pgen.1000367.s002 (7.8 MB PPT)

**Table S1** Primer Sequences for Tp53 and Ras Mutational analysis. Found at: doi:10.1371/journal.pgen.1000367.s004 (0.05 MB DOC)

**Dataset S1** Differential gene expression between tumors and control samples. Information on differential gene expression between tumors and control samples for 32,322 probes. Found at: doi:10.1371/journal.pgen.1000367.s005 (21 MB XLS)

**Dataset S2** Input list of probes for Ingenuity Pathway Analysis. Information for 2,800 probes which were used as input for IPA. Out of data set with 32,322 probes that have been analyzed for differential expression by Gene Pattern, probes with fold differences below 2, t-test values below 4.5 were removed and only the probes that have either consistent absent (a) or present (p) calls, but not absent across all samples, i.e., ppp-ppp, aaa-ppp or ppp-aaa were used as input for Ingenuity Pathway Analysis Software. Overall 2,800 probes were used as input for IPA. Found at: doi:10.1371/journal.pgen.1000367.s006 (2.7 MB XLS)

**Dataset S3** Networks generated by Ingenuity Pathway Analysis. Information for all networks generated by Ingenuity Pathway Analysis. Found at: doi:10.1371/journal.pgen.1000367.s007 (0.04 MB XLS)

**Dataset S4** Molecules used in networks generated by Ingenuity Pathway Analysis. Information for all molecules used in networks generated by Ingenuity Pathway Analysis. Found at: doi:10.1371/journal.pgen.1000367.s008 (0.7 MB XLS)

**Dataset S5** Canonical Pathways. Information for Canonical Pathways identified by Ingenuity Pathway Analysis. Found at: doi:10.1371/journal.pgen.1000367.s009 (0.05 MB XLS)

**Dataset S6** Functions. Information on processes identified by Ingenuity Pathway Analysis. Found at: doi:10.1371/journal.pgen.1000367.s010 (0.2 MB XLS)

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**Author Contributions**

Conceived and designed the experiments: MK RK. Performed the experiments: MK NYOB. Analyzed the data: MK DS RTB. Contributed reagents/materials/analysis tools: MK RK. Wrote the paper: MK.
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