Mapping of Three Genetic Determinants of Susceptibility to Estrogen-Induced Mammary Cancer within the Emca8 Locus on Rat Chromosome 5

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Abstract

The ACI rat model of 17β-estradiol (E2)-induced mammary cancer has gained wide use in the study of breast cancer etiology, prevention, and genetics. Emca8, a QTL that determines susceptibility to E2-induced mammary cancer, was previously mapped to rat chromosome 5 (RNO5) in an intercross between resistant Brown Norway (BN) and susceptible ACI rats. In this study, a panel of congenic rat strains, each of which carries BN alleles across a defined segment of RNO5 on the ACI genetic background, was generated and used to map more precisely the Emca8 determinants of mammary cancer susceptibility. Three distinct genetic determinants were localized within Emca8, and two of these were mapped to intervals of less than 15 megabases. Emca8.1 harbors Cdkn2a, Cdkn2b, and other genes and is orthologous to the 9p21 breast cancer locus identified in genome-wide and candidate gene association studies. Emca8.2 harbors Cdkn2c and other genes and is orthologous to the 1p32 locus in humans that is frequently deleted in breast cancers. Both Emca8.1 and Emca8.2 harbor copy number variants that are orthologous to copy number variant regions in humans. Gene expression profiles were defined for mammary tissues from E2-treated ACI and ACI.BN-Emca8 rats to define the impact of Emca8 on gene expression and identify differentially expressed genes residing within Emca8.1 and Emca8.2. This study further illustrates the relevance of the ACI rat model of E2-induced mammary cancer for identifying novel genetic determinants of breast cancer susceptibility and defining the mechanisms through which estrogens contribute to breast cancer development. Cancer Prev Res; 6(1); 59–69. ©2012 AACR.

Introduction

Breast cancer remains the second leading cause of cancer-related mortality among women in the United States in spite of numerous advances in diagnosis and treatment of this disease over the past 3 decades. Multiple factors contribute to, or otherwise influence, breast cancer development, including the female sex steroid hormones. The evidence implicating estrogens in breast cancer etiology is particularly convincing. Several population-based studies associate lifelong exposure to endogenous or exogenous estrogens with development of breast cancer (1–4). Moreover, data from the Women’s Health Initiative prospective study indicate that use by postmenopausal women of hormone replacement regimens that contain estrogens and a progestin significantly increases the risk of developing breast cancer (5, 6). Multiple studies indicate that inhibition of estrogen action through the use of selective estrogen receptor modulators (SERM) reduces breast cancer risk by 30% to 50% in study populations composed of either pre- or postmenopausal women (7–13). Data now emerging indicate that aromatase inhibitors, which block metabolism of androgen precursors to estrogens, are highly effective in preventing development of breast cancer in postmenopausal women (14). Although the association between estrogens and breast cancer is clear, the mechanisms through which estrogens contribute to development of breast cancer remain poorly defined, but may include estrogen receptor-α (ERα)-mediated events and oxidative stress/damage resulting from estrogen metabolism (3).

A family history of breast cancer is strongly associated with increased risk of this disease, and the extent to which familial risk is elevated increases as a function of the number of affected first-degree relatives and is inversely related to the age at which breast cancer is diagnosed in those relatives (15). Monozygotic twins are more concordant with respect to a diagnosis of breast cancer when compared with
dizygotic twins or non-twin siblings (16, 17). Together, these data indicate that shared genetic variants contribute to breast cancer risk independently of shared environment. Several genetic determinants of breast cancer risk have been identified, including mutant alleles of well-studied tumor suppressor genes such as BRCA1, BRCA2, TP53, and PTEN, which act as highly or moderately penetrant determinants of breast cancer risk in individuals inheriting those alleles (18, 19). However, because the frequency of mutant alleles of these genes in the general population is very low, these genes account for only approximately 25% of familial relative risk and less than 10% of all breast cancer cases. More recently, multiple loci have been identified in genome-wide association studies (GWAS) that harbor as yet unidentified genetic determinants of breast cancer risk (20–26). The main effects of the individual GWAS loci on breast cancer risk are small, and together they are estimated to explain approximately 8% of familial relative risk (19). Therefore, it is probable that many genetic determinants of breast cancer risk remain to be identified.

We are using the ACI rat model of 17β-estradiol (E2)-induced mammary cancer to define the mechanisms through which estrogens contribute to breast cancer development; identify and functionally characterize the genetic variants that determine susceptibility; and define the hormone—gene—environment interactions that influence development of mammary cancer in this physiologically relevant rat model. Female ACI rats are uniquely susceptible to mammary cancer when treated continuously with physiologic levels of E2 (27, 28). Induction of mammary cancer in female ACI rats occurs through a mechanism that is largely dependent on ERα (29, 30). Interestingly, progesterone is also required for development of mammary cancer in E2-treated ACI rats (27, 31). The mammary cancers that develop in E2-treated ACI rats are estrogen dependent and share multiple features in common with luminal-type breast cancers in humans, including chromosome copy number aberrations, expression of ERα, and expression of the progesterone receptor (Pgr; refs. 32–34). Interval mapping analyses of progeny generated in intercrosses between susceptible ACI rats and resistant Copenhagen (COP) or Brown Norway (BN) rats revealed 9 quantitative trait loci (QTL), designated Emca1 (Estrogen-induced mammary cancer) through Emca9, each of which harbors 1 or more genetic determinants of mammary cancer susceptibility (35–38). Interestingly, a subset of the loci identified in GWAS as determinants of breast cancer risk in humans appears to be orthologous to the previously mapped Emca loci, suggesting that these genetic determinants of breast cancer risk may be shared across species. The purpose of this study was to develop and employ congenic rat strains in a substitution-mapping approach to confirm the existence of, and to localize more precisely, the genetic determinants of mammary cancer susceptibility that reside within Emca8, which was mapped to rat chromosome 5 (RNO5) in intercrosses between the ACI and BN rat strains (37). Multiple congenic strains, each of which carries a distinct segment of RNO5 from the resistant BN strain on the genetic background of the susceptible ACI strain, were developed and characterized to further map Emca8 and define its effects on mammary cancer phenotypes. Regions of RNO5 within the Emca8 locus that differ in copy number between the ACI and BN genomes were identified using array comparative genomic hybridization (aCGH). Genes that reside within Emca8 and were differentially expressed between E2 treated ACI and ACI.BN-Emca8 congenic rats were identified as Emca8 candidates. Data presented herein indicate that at least 3 distinct genetic determinants of mammary cancer susceptibility reside within Emca8.

Materials and Methods

Care, treatment, and phenotypic characterization of animals

The Institutional Animal Care and Use Committee of the University of Nebraska Medical Center approved all procedures involving live animals. ACI and BN rats were obtained from Harlan Sprague Dawley, Inc. (Indianapolis, IN). The congenic rat strains discussed herein were generated as described below. The animals were housed in a barrier facility under controlled temperature, humidity, and 12-hour light/dark conditions. This facility was accredited by the American Association for Accreditation of Laboratory Animal Care and operated in accordance with the standards outlined in the Guide for the Care and Use of Laboratory Animals (DHHS Pub. 85–23). All procedures relating to care, propagation, and treatment of the experimental animals have been described previously (27, 28, 32, 36, 37). Beginning 7 weeks after initiation of E2 treatment, each rat was examined once or twice weekly for the presence of palpable mammary tumors. The location and size of each palpable tumor were noted at each examination. The rats were killed by decapitation when the largest palpable mammary tumor reached approximately 2.0 centimeters in its largest dimension, if necessitated by treatment-related moribundity, or following 196 ± 4 days of E2 treatment. Mammary tumor number, size, and location were recorded at necropsy. A portion of each tumor was subjected to histologic examination to confirm the presence of mammary carcinoma. To evaluate the impact of Emca8 on gene expression profiles, another set of animals was euthanized following 12 weeks of E2 treatment and the mammary glands were harvested, frozen in liquid nitrogen, and stored at −80°C.

Genotyping

Genomic DNA was isolated from tail clips or ear punches using DNasey columns according to the manufacturer’s protocol (Qiagen). Genetic markers that are polymorphic between ACI and BN were selected from the SSLP database in the Rat Genome Database. Oligonucleotide primers for genotyping were obtained from Invitrogen. When necessary, additional SSLP markers for genotyping specific genome regions were developed in our laboratory using the published rat genome sequence databases.
ACI rats were evaluated contemporaneously. Genotyping was carried out by PCR amplification and agarose gel electrophoresis as previously described (36, 37, 39).

**Generation and characterization of congenic rat strains**

The ACI.BN-D5Mgh17:D5Mgh15 congenic line (abbreviated ACI.BN-Emca8 or Emca8 line) was generated using a marker-assisted selection protocol as described previously (40). Briefly, BN female rats were crossed to ACI male rats to generate F1 progeny. The F1 males were then backcrossed to ACI females to produce the N2 generation. Males from the N2 generation were genotyped at a panel of markers distributed across the Emca8 locus on RNO5 (Supplementary Table S1, Tier 1). Animals heterozygous across Emca8 were genotyped at a panel of 42 markers distributed across the other autosomes to identify the rat that carried the fewest BN alleles at these background markers (Supplementary Table S1, Tier 2). This male was mated to ACI females to generate N3 progeny, and the marker-assisted selection protocol was repeated to generate N4 and subsequent generations of backcross progeny. A male was obtained at the N4 generation that was heterozygous for BN alleles across Emca8 but homozygous for ACI alleles at all 42 Tier 2 background markers used for the negative selection. Genotyping at 16 additional background markers was initiated at the N5 generation (Supplementary Table S1, Tier 3). At this generation, a male was identified that remained heterozygous across Emca8, but was homozygous for ACI alleles at all 58 background markers. Heterozygous N5 progeny of this male were intercrossed to produce congenic rats that were homozygous for BN alleles from D5Mgh17 through D5Mgh15. Additionally, male rats that were heterozygous across this interval were backcrossed to ACI females to generate rats harboring recombinations within the region of interest on RNO5. Animals harboring recombinant chromosomes were again backcrossed to ACI to generate male and female siblings carrying the same recombinant chromosome, and these siblings were intercrossed to generate 8 additional congenic lines for fine mapping (Table 1). Ultimately, the genetic background of each of these congenic lines was confirmed to be that of the recipient ACI strain by genotyping at a panel of 121 markers, 80 of which were unique from those used for negative selection, distributed across all autosomes other than RNO5 (Supplementary Table S1, Tier 4). Nomenclature of the resultant congenic strains is in accordance with the guidelines of the International Rat Genome Nomenclature Committee; the recipient strain is indicated first followed by the donor strain and the markers that flank the region known to be homozygous for the donor strain, followed lastly by the Institute for Laboratory Animal Research (ILAR) laboratory code designation (Table 1). Female rats from each of the congenic lines were treated with E2 as described earlier to evaluate their susceptibility to mammary cancer. Groups of ACI rats were evaluated contemporaneously.

**Identification of copy number variation between the ACI and BN genomes**

NimbleGen high-density oligonucleotide arrays were used in aCGH experiments to catalog copy number variants (CNV) between the susceptible ACI rat strain and the resistant BN rat strain. These arrays cover the nonrepetitive portion of the rat genome at an average density of 1 probe per 5 kb. DNAs were isolated from ACI and BN rats using DNeasy columns (Qiagen). Two independent experiments were conducted; DNA from the spleen was used in the first experiment and DNA from the liver of different individual rats was used in the second. Sample labeling, hybridization, and data collection were carried out by NimbleGen using conditions optimized to their platform. Duplicate labeling reactions and hybridizations were conducted in each experiment, and the Cy3 and Cy5 dye labels were reversed in the technical duplicates to eliminate potential bias relating to dye labeling. The resulting data were analyzed using SignalMap software (NimbleGen). Select CNVs were confirmed using PCR. The aCGH data generated in these analyses comprised part of a larger study in which multiple approaches were used to catalog CNVs in the rat genome (41). These data have been deposited in the EMBL ArrayExpress repository under accession number E-MEXP-1517.

**Evaluation of gene expression in the mammary gland**

Absolutely RNA Miniprep Kits (Stratagene) were used to isolate RNA from mammary tissues that were dissected from individual ACI and Emca8 rats (n = 5 each strain) that had been treated with E2 for 12 weeks, a time point that precedes development of palpable mammary cancer. The RNAs were labeled using One-cycle Target Labeling Kits (Affymetrix) according to the manufacturer’s specifications. Briefly, 2.5 μg of total RNA was used to generate labeled cRNA that was then fragmented and hybridized to Affymetrix Rat Genome 230 version 2.0 GeneChips. All RNA labeling and microarray hybridizations were carried out by the Microarray Core Facility at the University of Nebraska Medical Center. Assessment of data-quality parameters was carried out using the Gene Chip Operating System (GCGS; Affymetrix) according to the manufacturer’s recommendations. The primary microarray data have been deposited in the Gene Expression Omnibus under accession numbers GSE39788. The data from the 10 microarrays described in this article were normalized as part of a larger set of arrays using the Robust Multiarray Average (RMA) algorithm with quantile normalization (gcma function in Bioconductor gcma library). The 5 arrays for each strain were treated as a set to make pairwise comparisons between the 2 rat strains. P values for each gene in each comparison were calculated using an empirical Bayes moderated t-statistic method (eBayes function in the Bioconductor gcma library). The 5 arrays for each strain were treated as a set to make pairwise comparisons between the 2 rat strains. P values for each gene in each comparison were calculated using an empirical Bayes moderated t-statistic method (eBayes function in the Bioconductor gcma library).
Table 1. Genetic characteristics of congenic strains.

<table>
<thead>
<tr>
<th>Strain designation</th>
<th>Strain abbreviations</th>
<th>RGD IDa</th>
<th>ACI (Mb)b</th>
<th>BN (Mb)b</th>
<th>BN (Mb) ACI (Mb)</th>
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<tbody>
<tr>
<td>ACI.BN-Emca8</td>
<td>ACI.BN-Emca8a or Emca8</td>
<td>5135475</td>
<td>127.53</td>
<td>127.53</td>
<td>127.53</td>
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<td></td>
<td>5135476</td>
<td>129.75</td>
<td>129.75</td>
<td>129.75</td>
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<tr>
<td></td>
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<td>5135477</td>
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<tr>
<td></td>
<td></td>
<td>5135478</td>
<td>135.75</td>
<td>135.75</td>
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</tr>
</tbody>
</table>

aRat Genome Database.

bMicrosatellite marker and coordinate (Mb) on RNO5 (rat genome assembly version 3.4).

differential expression of 3 genes residing within Emca8 was confirmed by quantitative reverse transcription-PCR. Total RNA was isolated from mammary glands of 5 ACI and 5 Emca8 rats. Reverse transcription was carried out using the SuperScript III First-Strand Synthesis System (Invitrogen) and 900 ng total mammary RNA. Real-time quantitative PCR (qPCR) was carried out and the results were analyzed using the ABI 7500 PCR System (Applied Biosystems). Primer and probe sets for Tspan1 (Rn01416777_m1), Cd52 (Rn02132983_s1), and Wnt4 (Rn00584577_m1) were obtained from ABI Assays on Demand service. Standard curves were generated using cDNA reverse-transcribed from lung RNA (\( r^2 > 0.95 \)) and were used to calculate relative gene expression levels. Expression of Gapdh (4352338E, ABI) in each sample was analyzed simultaneously. Expression of each of the 3 genes was normalized to that of Gapdh.

Statistical analysis

Differences in latency to appearance of first palpable mammary tumor between strains were evaluated using the Logrank test (Mstat, v.5.4; University of Wisconsin, Madison, Wisconsin). The Wilcoxon rank-sum test was used to evaluate differences in the mean tumor number per rat (Mstat, v.5.4). Differences in gene expression were assessed using the Kruskal–Wallis ANOVA with Dunn post hoc tests (GraphPad Prism; San Diego California, California). \( P \) values equal to 0.05 or less were considered to be indicative of statistical significance.

Results

ACI.BN-Emca8 congenic rats exhibit reduced susceptibility to E2-induced mammary cancer relative to ACI rats

Emca8, a QTL on RNO5 for which the 95% confidence interval (95% CI) extends from D5Rat134 (52.43 Mb) to D5Rat37 (148.46 Mb), was identified by interval mapping analyses of progeny generated in a BN × ACI intercross (37). To confirm the existence of Emca8, we generated the ACI. BN-Emca8 congenic rat strain, which harbors BN alleles from D5Mgh17 (14.73 Mb) to D5Mgh15 (167.85 Mb) on the ACI genetic background, and characterized the susceptibility of this congenic rat strain to E2-induced mammary cancer. A group of 41 female ACI.BN-Emca8 rats was treated with E2 beginning at 9 weeks of age. The median latency to appearance of the first palpable mammary tumor in these animals was 188 days, and the incidence of mammary cancer at the completion of the 28-week course of treatment was 63% (Fig. 1). The mean latency for those animals that developed grossly apparent mammary cancer was 172 ± 21
A group of 16 E2-treated female ACI rats was evaluated contemporaneously with the ACI.BN-Emca8 congenic rats. The median latency in this group of ACI rats was 149 days, 100% of the animals at risk developed mammary cancer by 196 days of treatment, and the average number of mammary tumors observed at necropsy was 3.7 ± 3.2. The mammary cancer phenotypes exhibited by this group of ACI rats did not differ significantly from other groups of ACI rats evaluated during characterization of additional congenic rat strains described in the following sections. Therefore, the individual groups of E2-treated ACI rats were merged into a single population (n = 128) for further statistical analyses. Median latency to appearance of the first palpable mammary tumor in the merged population of E2-treated ACI rats was 147 days, incidence in the animals at risk was 94%, and the average number of tumors observed at necropsy was 5.3 ± 4.5 (Table 2). Relative to both the smaller and merged groups of ACI rats, the ACI.BN-Emca8 congenic rats exhibited significantly reduced susceptibility to E2-induced mammary cancer. Latency to appearance of the first palpable mammary cancer was prolonged, mammary cancer incidence was reduced, and tumor number per rat was lower in the E2-treated ACI.BN-Emca8 congenic rats, relative to the treated ACI rats (Fig. 1 and Table 2). These data confirm the existence of Emca8 as a QTL on RNO5 that harbors at least 1 genetic determinant of susceptibility to E2-induced mammary cancer.

**Emca8 harbors multiple genetic determinants of mammary cancer susceptibility**

Published interval mapping data revealed multiple local LOD peaks within the Emca8 95% CI, suggesting that multiple determinants of mammary cancer susceptibility

![Fraction tumor free](image)

**Figure 1.** The ACI.BN-Emca8 congenic rat strain exhibits reduced susceptibility to mammary cancer relative to the parental ACI rat strain. Ovary-intact female ACI and ACI.BN-Emca8 rats were treated with E2 beginning at 9 weeks of age. Each animal was thereafter examined at least once per week for the presence of palpable mammary cancer. Latency to appearance of mammary cancer was prolonged in treated ACI.BN-Emca8 rats (n = 41) relative to contemporaneously treated ACI rats (n = 16) or a population of ACI rats (n = 112) merged from other experiments described herein. Vertical ticks on each line represent censored animals.

![Table 2. Mammary cancer phenotypes](table)

**Table 2. Mammary cancer phenotypes**

<table>
<thead>
<tr>
<th>Strain</th>
<th>Median latency (days)a</th>
<th>P vs. ACIb</th>
<th>Hazard ratioa</th>
<th>Mean latency (days)b</th>
<th>Incidence at 196 daysc</th>
<th>Tumor number per rated</th>
<th>P vs. ACI</th>
<th>N²</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACI</td>
<td>147</td>
<td>—</td>
<td>1.00</td>
<td>140 ± 27</td>
<td>94%</td>
<td>5.3 ± 4.5</td>
<td>—</td>
<td>128</td>
</tr>
<tr>
<td>ACI.BN-Emca8</td>
<td>188</td>
<td>1.8 × 10⁻⁸</td>
<td>0.358</td>
<td>172 ± 21</td>
<td>63%</td>
<td>1.4 ± 1.2</td>
<td>4.1 × 10⁻⁹</td>
<td>41</td>
</tr>
<tr>
<td>ACI.BN-Emca8a</td>
<td>191</td>
<td>3.1 × 10⁻⁵</td>
<td>0.411</td>
<td>162 ± 29</td>
<td>68%</td>
<td>2.1 ± 1.9</td>
<td>5.4 × 10⁻⁵</td>
<td>30</td>
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<tr>
<td>ACI.BN-Emca8b</td>
<td>174</td>
<td>1.8 × 10⁻⁴</td>
<td>0.463</td>
<td>155 ± 26</td>
<td>76%</td>
<td>1.7 ± 2.0</td>
<td>2.2 × 10⁻⁷</td>
<td>35</td>
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<tr>
<td>ACI.BN-Emca8c</td>
<td>196</td>
<td>1.5 × 10⁻⁸</td>
<td>0.291</td>
<td>170 ± 25</td>
<td>56%</td>
<td>0.8 ± 0.9</td>
<td>2.8 × 10⁻¹⁰</td>
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<td>ACI.BN-Emca8b1</td>
<td>157</td>
<td>1.5 × 10⁻²</td>
<td>0.541</td>
<td>143 ± 20</td>
<td>63%</td>
<td>2.1 ± 2.6</td>
<td>2.1 × 10⁻³</td>
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<tr>
<td>ACI.BN-Emca8b3</td>
<td>170</td>
<td>4.4 × 10⁻³</td>
<td>0.411</td>
<td>154 ± 29</td>
<td>66%</td>
<td>1.2 ± 1.2</td>
<td>6.2 × 10⁻⁵</td>
<td>13</td>
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<tr>
<td>ACI.BN-Emca8d</td>
<td>155</td>
<td>0.0827</td>
<td>0.730</td>
<td>145 ± 18</td>
<td>100%</td>
<td>3.0 ± 2.9</td>
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<tr>
<td>ACI.BN-Emca8c1</td>
<td>153</td>
<td>0.1196</td>
<td>0.781</td>
<td>143 ± 25</td>
<td>86%</td>
<td>4.4 ± 3.8</td>
<td>0.3098</td>
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<td>ACI.BN-Emca8c2</td>
<td>8.6 × 10⁻⁷</td>
<td>0.240</td>
<td>161 ± 31</td>
<td>42%</td>
<td>0.5 ± 0.7</td>
<td>6.9 × 10⁻⁹</td>
<td>20</td>
<td>18</td>
</tr>
</tbody>
</table>

aCalculated using log rank test.

bCalculated for tumor positive rats.

cCalculated for population at risk.

dCalculated for all rats that were treated with E2 for at least 160 days and less than 200 days.

²Median number of rats treated with E2 (number treated with E2 for at least 160 days and less than 200 days).
Fine Mapping of Emca8.1 and Emca8.2

Additional congenic strains were generated and characterized to fine map the genetic determinants of mammary cancer susceptibility residing within the Emca8b and Emca8c intervals. The ACI.BN-Emca8b1 and ACI.BN-Emca8b3 rat strains harbor BN alleles across the proximal and distal portions of the Emca8b interval, respectively. Both of these congenic rat strains exhibited significantly reduced susceptibility to E2-induced mammary cancer when compared with E2-treated ACI rats, revealed by prolonged latency to appearance of palpable mammary cancer and reduced tumor number (Fig. 3 and Table 2). The ACI.BN-Emca8d congenic strain was generated specifically to evaluate the impact of genetic variants within or near several candidate genes known to function in cell-cycle regulation or mammary gland development, including Cdkn2a, Cdkn2b, Nfia, and Jun. Although latency to appearance of palpable mammary cancer in E2-treated ACI.BN-Emca8d congenic rats did not differ from that observed in ACI rats, the number of mammary cancers observed at necropsy was significantly lower in ACI.BN-Emca8d congenic rats relative to ACI rats (Fig. 3 and Table 2). Age-matched, sham-treated, ACI.BN-Emca8b1, ACI.BN-Emca8b3, and ACI.BN-Emca8d congenic rats did not develop mammary cancer. Together, these data localize a genetic determinant of mammary cancer susceptibility to a 14.6-Mb interval defined by D5Rat151 (104.23 Mb) and D5Rat25 (118.81 Mb) and designated Emca8.1.

The ACI.BN-Emca8c1 and ACI.BN-Emca8c2 congenic strains were generated to further evaluate the proximal portion of the Emca8c interval, the region of RNO5 that generated the peak LOD score during interval mapping of Emca8 (37). When treated with E2, ACI.BN-Emca8c1 rats developed mammary cancer in a manner that was indistinguishable from that of E2-treated ACI rats (Fig. 4 and Table 2). By contrast, the ACI.BN-Emca8c2 congenic strain exhibited dramatically reduced susceptibility to E2-induced mammary cancer. Latency to appearance of palpable mammary cancer was significantly prolonged and both the incidence of mammary cancer and tumor number per rat
were significantly reduced in E2-treated ACI.BN-Emca8c2 rats, relative to treated ACI rats. Age-matched, sham-treated, ACI.BN-Emca8c1 and ACI.BN-Emca8c2 congenic rats did not develop mammary cancer. These data localize a second genetic determinant of mammary cancer susceptibility to a 10-Mb interval on RNO5 defined by markers D5Got42 (130.75 Mb) and D5Rat86 (140.74 Mb), designated Emca8.2.

Histopathology of mammary tumors induced by 17β-estradiol

The histologic phenotypes of the mammary tumors that developed in each of the congenic rat strains in response to E2 treatment were similar to those that developed in ACI rats. All of the E2-induced tumors exhibited features of mammary carcinoma, including enlarged and pleomorphic nuclei with prominent nucleoli. Comedo features were frequently apparent. Although most of the tumors remained in situ, some were locally invasive and associated with a desmoplastic response. Overall, the tumors observed in this study did not differ discernibly from those described in previous studies (27, 32).

Emca8.1 and Emca8.2 harbor CNV regions

The genomes of ACI and BN rats were compared by aCGH using NimbleGen tiling path arrays to identify regions that vary in copy number between these inbred rat strains. These analyses revealed a total of 53 CNVs (data not shown), 2 of which reside within Emca8 on RNO5 (Fig. 5). The first of these CNVs extends over an approximately 100-kb region located within the Emca8.1 interval and harbors 4 genes that encode members of the interferon-α family of cytokines, including Ifna2. The second CNV extends over approximately 500-kb within the Emca8.2 interval. This CNV harbors 2 genes that encode members of the butyrophilin gene family and 4 pseudogenes. PCR analyses confirmed the existence of both of these CNVs and suggested the ACI genome lacks both of these gene segments when compared with the reference BN genome (data not shown). Interestingly, a search of the Database of Genomic Variants indicated the human genome similarly varies in copy number in the regions that are orthologous to these rat CNVs. Because the NimbleGen oligonucleotide array was constructed using the BN rat genome reference sequence (version 3.4) as the template, DNA segments that are present in the ACI genome but absent in the BN genome were not detectable using this platform.

Impact of Emca8 on gene expression in the mammary gland

To define the impact of genetic variants residing within Emca8 on gene expression in the mammary gland, microarray analyses were conducted on RNA isolated from grossly normal mammary glands of ACI and ACI.BN-Emca8 rats that were treated with E2 for 12 weeks, a time point that generally precedes appearance of palpable mammary cancer. Transcripts corresponding to 40 probe sets were differentially expressed between mammary glands of the E2 treated ACI and ACI.BN-Emca8 rats (Supplementary Table S2). The differentially expressed genes include Pgr (progesterone receptor) and Wnt4 (wingless-type MMTV integration site family, member 4), both of which are required for mammary gland development and were expressed at a higher level in ACI rats relative to ACI.BN-Emca8 congenic rats; and Spp1 (secreted phosphoprotein 1, also known as osteopontin), which is secreted by the mammary gland as a...
component of milk and extracellular matrix and was expressed at a lower level in the mammary gland of E2-treated ACI rats compared with glands of ACI.BN-Emca8 rats. Gene ontology enrichment analyses of the differentially expressed transcripts revealed a statistically significant association with the biological process tertiary branching involved in mammary gland duct morphogenesis. As expected, a disproportionately high fraction, 16 of 40 (40%), of the differentially expressed transcripts arise from genes that reside within the Emca8 congenic interval, including Tspan1, a putative mammary tumor suppressor gene that resides within Emca8.2 (45); Cd52, a protein expressed on the surface of lymphocytes and some epithelial cell types; Scl30a2, which encodes a zinc transporter and is regulated by prolactin–prolactin receptor signaling (46); and Wnt4, which functions downstream of a progesterone–progesterone receptor in the regulation of ductal branching (47). Quantitative real-time PCR (qRT-PCR) was carried out to confirm differential expression of a subset of the Emca8 candidate genes, Wnt4, Cd52, and Tspan1 (Supplementary Fig. S1). The data from these analyses confirm the microarray data and indicate that each of these genes was expressed at a significantly lower level in the mammary glands of E2-treated ACI.BN-Emca8 congenic rats relative to glands of E2-treated ACI rats.

Discussion

Data presented in this article confirm and extend a published interval mapping study of phenotypically defined (BNxACI)F2 rats that localized to RNO5 1 or more genetic determinants of susceptibility to E2-induced mammary cancer (37). By generating and characterizing a panel of novel congenic rat strains, we have now shown that at least 3 physically distinct genetic determinants of mammary cancer susceptibility reside on this chromosome. The first of these genetic determinants resides within the approximately 95-Mb segment of proximal RNO5 defined by markers D5Rat121 and D5Rat151; the second, designated Emca8.1, resides within the 14.6-Mb segment defined by markers D5Rat151 and D5Rat25; and the third, designated Emca8.2, resides within the 10-Mb segment of RNO5 defined by markers D5Got42 and D5Rat86 (Supplementary Fig. S2).

Other studies have also genetically associated RNO5 with susceptibility to E2-induced mammary cancer. Interval mapping analyses of F2 progeny from reciprocal intercrosses between susceptible ACI and resistant COP rats localized Emca1 to distal RNO5 (36). Moreover, loss of RNO5 was the most frequently observed somatic genetic abnormality when a panel of mammary cancers induced by E2 in ACI rats was evaluated by comparative genomic hybridization (33). Together, these data suggest that loss of function of 1 or more tumor suppressor genes residing on RNO5 may contribute to mammary cancer development in this rat model. Loci on RNO5 have also been mapped as driver events in breast cancer development (63). We are further exploring this apparent conservation of a breast cancer risk locus between humans and rats in comparative genetics and genomics-based studies to identify the causal genetic variants and define the organ site and mechanism through which they impact breast cancer development.

Emca8.2 harbors nearly 150 annotated genes, including 124 protein coding genes, and is orthologous to the 1p32 region of the human genome. To our knowledge, no evidence exists to associate germ-line variants at 1p32 with breast cancer risk. However, deletions at 1p32 have been reported to occur relatively frequently in breast cancers (64–66). In parallel studies, we have employed a congenic
substitution approach to localize \textit{Emca}1, a genetic determinant of susceptibility to E2-induced mammary cancer mapped to distal RNO5 in crosses between susceptible ACI rats and resistant COP rats (36), to the same region of RNO5 as \textit{Emca}8.2, suggesting the BN and COP strains may share resistance conferring alleles at this locus (unpublished data). Among the candidate genes residing with \textit{Emca}8.2 is \textit{Cldn}2c, which encodes the p18\textsuperscript{Ink4c} tumor suppressor protein. Mice that are homozygous for mutant alleles of \textit{Cldn}2c spontaneously develop tumors in the intermediate lobe of the pituitary gland (67). Moreover, \textit{Cldn}2c\textsuperscript{+/−} homozygotes and \textit{Cldn}2c\textsuperscript{−/−} heterozygotes exhibit increased susceptibility, relative to \textit{Cldn}2c\textsuperscript{+/+} littermates, to carcinogen-induced pituitary tumors and several other tumor types, indicating that haploinsufficiency of \textit{Cldn}2c predisposes to tumor development (68). Interestingly, \textit{Cldn}2c mutations, when harbored on the Balb/c genetic background, predispose to development of luminal-type mammary cancers and dysregulation of homeostasis within specific mammary epithelial cell populations (69), a phenotype that was not observed when the mutant \textit{Cldn}2c allele was harbored on the C57Bl/6 background.

An intriguing observation from this study is that \textit{Emca}8.1 and \textit{Emca}8.2 each contain a cluster of syntenic genes that appears to have arisen via duplication of an ancestral genome segment: \textit{Cldn}2b, \textit{Dmrt}a1, and \textit{Elavl}2 within \textit{Emca}8.1 and \textit{Cldn}2c, \textit{Dmrt}a2, and \textit{Elavl}4 within \textit{Emca}8.2. The \textit{Cldn}2 proteins regulate cell-cycle progression via inhibition of the cyclin D-dependent kinases \textit{Cdk}4 and \textit{Cdk}6. Because aberrant cyclin D signaling has been implicated in breast cancer etiology, we sequenced the ACI alleles of \textit{Cldn}2a, \textit{Cldn}2b, and \textit{Cldn}2c over their respective protein coding regions. The \textit{Cldn}2a coding regions for both p16\textsuperscript{Ink4a} and p19\textsuperscript{Arf} were identical between the ACI and BN rat strains. A coding region SNP was identified in the ACI alleles of both \textit{Cldn}2b and \textit{Cldn}2c, relative to their respective reference BN alleles (Supplementary Table S3). However, neither SNP resulted in a change in amino acid sequence, strongly suggesting that these SNPs are not functionally significant with respect to mammary cancer susceptibility.

Both \textit{Emca}8.1 and \textit{Emca}8.2 were shown to harbor CNVs. It is estimated that 5% to 20% of the genome is variant with respect to copy number within the human population (70). The distribution and functional significance of CNVs in rat appear similar to the human (41). Although it is clear that CNVs dramatically impact gene expression and influence risk of specific complex diseases, the impact of CNVs on cancer risk, in particular breast cancer risk, is not well defined. One recent study of 68 cases of familial or early-onset breast cancer revealed a total of 26 CNVs that occurred at least once in cases but not in 2 different control populations (71). A second recent study showed that the percentage of the germline genome that varies in copy number is not associated with the extent to which the somatic genome is aberrant in copy number in a panel of 28 breast cancers (72). The CNVs residing within \textit{Emca}8.1 and \textit{Emca}8.2 harbor genes that encode modulators of the immune system, and the human orthologs to both of these genome segments also exhibit variation in copy number, suggesting that these CNVs may determine breast cancer risk via regulation of immune surveillance. The impact of the CNVs residing within \textit{Emca}8.1 and \textit{Emca}8.2 on susceptibility to E2-induced mammary cancer is currently under investigation.

The mechanisms and sites of action of the \textit{Emca}8 genetic determinants of mammary cancer susceptibility are not known. Two observations suggest 1 or more of these determinants may function within the mammary epithelium. The first is that mammary cancers induced in ACI rats by E2 frequently exhibit loss of RNO5, suggesting that loss of function of 1 or more tumor suppressor genes on RNO5 contributes to mammary cancer development (33). The second is that the pattern of chromosome copy number changes exhibited by tumors induced in \textit{Emca}8 congenic rats differs from that exhibited by tumors in ACI rats, suggesting that introgression of BN alleles across the \textit{Emca}8 interval alters the pattern of somatic genetic events that occur during mammary cancer development (33). If the actions of the \textit{Emca}8 determinants of susceptibility are mammary autonomous, then identification of those genes that are differentially expressed between the mammary glands of E2-treated ACI and \textit{Emca}8 rats and reside within the \textit{Emca}8 congenic interval would reveal \textit{Emca}8 candidate genes whose expression is affected by genetic variants that reside within cis-acting regulatory elements. The genes that encode 40% of the differentially expressed transcripts identified in this experiment reside within the \textit{Emca}8 congenic interval, including \textit{Cyp}2\textit{j}10, which resides in \textit{Emca}8.1, and \textit{Tspan}1, which resides in \textit{Emca}8.2, and warrant further study to evaluate their potential role in mammary cancer development.

The ACI rat model of E2-induced mammary cancer exhibits many features in common with luminal-type breast cancers in humans and is gaining wide use in the breast cancer research community. The current study reveals the presence of at least 3 distinct genetic determinants of susceptibility to E2-induced mammary cancer on RNO5 (Supplementary Fig. S2) and further illustrates the relevance of this model to human breast cancer by identifying \textit{Emca}8.1 as a susceptibility locus that may be the functional ortholog to a genetic determinant of breast cancer risk in humans. Experiments are underway to further localize \textit{Emca}8.1 and \textit{Emca}8.2 to identify the causal genetic variants responsible for these 2 QTL and to define their sites and mechanisms of action.

### Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

### Authors’ Contributions

- **Conception and design:** J.D. Shull
- **Development of methodology:** J.D. Shull
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- **Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis):** B.S. Schaffer, S.G. Kurz, J.A. Colletti, C.L. Warren, J.D. Shull

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