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## Genetic variation in sensitivity to estrogens and breast cancer risk

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#### **Abstract**

Breast cancer risk is intimately intertwined with exposure to estrogens. While more than 160 breast cancer risk loci have been identified in humans, genetic interactions with estrogen exposure remain to be established. Strains of rodents exhibit striking differences in their responses to endogenous ovarian estrogens (primarily 17β-estradiol). Similar genetic variation has been observed for synthetic estrogen agonists (ethinyl estradiol) and environmental chemicals that mimic the actions of estrogens (xenoestrogens). This review of literature highlights the extent of variation in responses to estrogens among strains of rodents and compiles the genetic loci underlying pathogenic effects of excessive estrogen signaling. Genetic linkage studies have identified a total of the 35 quantitative trait loci (QTL) affecting responses to 17β-estradiol or diethylstilbestrol in 5 different tissues. However, the QTL appear to act in a tissue-specific manner with 9 QTL affecting the incidence or latency of mammary tumors induced by 17β-estradiol or diethylstilbestrol. Mammary gland development during puberty is also exquisitely sensitive to the actions of endogenous estrogens. Analysis of mammary ductal growth and branching in 43 strains of inbred mice identified 20 QTL. Regions in the human genome orthologous to the mammary development QTL harbor loci associated with breast cancer risk or mammographic density. The data demonstrate extensive genetic variation in regulation of estrogen signaling in rodent mammary tissues that alters susceptibility to tumors. Genetic variants in these pathways may identify a subset of women who are especially sensitive to either endogenous estrogens or environmental xenoestrogens and render them at increased risk of breast cancer.

#### Keywords

Estrogen; Estrogen Receptors; Xenoestrogens; Quantitative Trait Loci; Breast Cancer

#### Estrogens and breast cancer risk

Estrogens have diverse actions in directing development and maintenance of tissues. However, prolonged exposure to estrogens has been implicated in initiation and progression of cancers primarily in breast, endometrium, and ovary (Burns and Korach 2012). Given the diverse roles, the health benefits and risks of estrogen supplementation was examined in postmenopausal women in the Women's Health Initiative (WHI). This study demonstrated an increased incidence of breast cancer among women receiving postmenopausal hormone therapy and a lack of clear beneficial effects in other tissues (Prentice and Anderson 2008; Prentice et al. 2008). The risk associated with postmenopausal hormone therapy was also observed in the Million Women Study (Beral 2003). Both studies reported a modest increase in risk of breast cancer associated with estrogen alone therapies but was significantly higher when progestins were included. Exposure to estrogens is also significant for women prior to menopause. Higher levels of circulating estradiol were associated with increased breast cancer risk among premenopausal women (Eliassen et al. 2006). Breast cancer risk was also increased by early menarche and late menopause (Bernstein 2002; Tamimi et al. 2016).

Together these associations suggest that lifetime exposure to estrogens play an important role in the pathogenesis of breast cancer (Pike 1987).

Although estrogens participate in the initiation and progression, the majority of women do not develop detectable breast cancers (American Cancer Society, 2017) despite exposures to both endogenous estrogens produced during each ovarian cycle. During pregnancy, estrogens reach concentrations that are approximately 10-fold higher than in postmenopausal women. Rather than increased risk, these levels of estrogen along with other hormones during pregnancy have an overall long-term protective effect reducing the risk of breast cancer by up to 50% (Albrektsen et al. 2005; Chie et al. 2000; MacMahon et al. 1970). The major estrogen produced by the ovaries is 17β-estradiol. Administration of 17βestradiol alone or in combination with progesterone was to sufficient to mimic the protective effects of pregnancy in rodents (Dunphy et al. 2008; Guzman et al. 1999; Rajkumar et al. 2001; Rajkumar et al. 2007; Sivaraman et al. 1998). Similarly, for the subset of women in WHI without benign breast disease or family history of breast cancer, estrogen-only postmenopausal hormone therapies were associated with measurable decreases in breast cancer and an overall decrease in mortality (Anderson et al. 2012). While these observations are not sufficient to warrant use of estrogen treatments for risk reduction, they do highlight the paradoxical roles of estrogens in preventing as well as promoting breast cancer and suggest a complex balance of responses within breast tissue.

Genetic variation in estrogen signaling has the potential to determine the balance of responses to estrogens within breast tissues and modify the risk of breast cancer associated with exposure to estrogens. As estrogen receptor alpha (ERa) is expressed in a majority of breast cancers and is a target of therapies to block signaling, genetic variants within the *ESR1* locus have been examined for associations with breast cancer risk in women (Dunning et al. 2016). While these genetic variants have a significant effect, the overall impact on breast cancer risk is modest with odds ratios of less than 1.2. In contrast, genetic differences rendering strains of rats sensitive or resistant to the tumorigenic effects of estrogens reveal the potency of the underlying regulatory pathways (Shull et al. 2001; Shull et al. 1997). Differences in sensitivity to estrogen signaling among strains of rodents have the potential to define critical pathways affecting breast cancer risk in humans as well as provide new therapeutic targets. In this review, we have summarized data examining differences in sensitivity to estrogens among strains of mice and rats and the genetic basis for the variation.

#### Variation in responses to estrogenic compounds among strains of rodents

PubMed was searched to identify publications where estrogenic compounds were evaluated in strains of rats or mice. The initial search retrieved 265 publications that included the terms "strain differences estrogen". This set was refined by selecting those using rat or mouse models. The set was manually curated to identify studies in which at least 2 strains of rats or mice were compared. Studies that included treatments with  $17\beta$ -estradiol are emphasized as this is the most active of the estrogens produced by ovaries and provides a reference for comparisons. Studies using well-characterized agonists of estrogen receptors (*e.g* ethinyl estradiol, diethylstilbestrol) were also included. Environmental chemicals were evaluated for estrogenic activity, referred to as xenoestrogens, were included when comparisons with

either  $17\beta$ -estradiol or estrogen agonists were available. While effects in mammary tissue were of primary interest, all tissues were included in the search to assess whether strain-effects were consistent across tissues. The data are also selected to emphasize inbred strains of mice (BALB/c, C3H, C57BL/6, DBA, 129) and rats (ACI, BN, COP, DA, F344, WKY). However, Sprague Dawley (SD) outbred rats are included because they were used across many studies. The Holzman strain (Holz) is outbred and was derived from SD. Long-Evans and SD outbred strains are related to the Wistar (Wis) strain from which they were derived. Similarly, outbred CD-1 mice were compared in some reports. Most studies examined only single doses of compounds. This limits the ability to detect non-monotonic differences in responses among strains and sensitivity would be overlooked if saturating doses were used. Therefore, the data may underestimate the extent of genetic variation. The selected studies are summarized in Table 1.

Given the prominent role in breast cancer, effects of estrogen exposures in the mammary gland were of primary interest. However, only 5 publications compared responses across strains of mice or rats and differed greatly in doses and duration of treatments. Acute exposure to 17β-estradiol for 4 days was evaluated in C57BL/6J and C3H/H3J mice that were ovariectomized prior to puberty (Wall et al. 2014a). Branching of mammary ducts was greatest in C57BL/6J females, whereas C3H/HeJ exhibited a greater ductal length. The proliferative response was greater in C57BL/6J, but was balanced by higher levels of apoptosis. Acute treatment of C57BL/6J mice with 17β-estradiol also increased the ductal area to a greater extent than in CD-1 mice. However, the difference appears related to the near complete arrest of ductal elongation upon ovariectomy in C57BL/6J females whereas modest ductal growth continued in CD-1 even in the absence of ovaries (Wadia et al. 2007). Long-term exposure to diethylstilbestrol (DES) increased ductal branching to a similar extent in wild type BALB/cJ and 129/SvEv female mice but no mammary tumors were observed in either strain (Bennett et al. 2000). Effects of chronic treatment with 17βestradiol were also compared in ACI and BN rats (Ding et al. 2013). ACI rats had dramatic proliferative responses after 1 week which were sustained throughout the 12-week treatment period. In contrast, BN rats exhibited a transient increase in proliferation during 1–3 weeks but returned to baseline levels by 12 weeks. Unlike C57BL/6J mice where increased proliferation was balanced by increased apoptosis, no difference in apoptosis was detected between ACI and BN rats using cleaved caspase as a marker. While 17β-estradiol stimulated proliferation and hyperplasia of the mammary epithelium in ACI rats, differentiation was the major effect in BN rats as indicated by the increased expression of milk proteins. ACI rats also developed mammary tumors with chronic exposure to 17β-estradiol or DES (Shull et al. 2001; Shull et al. 1997; Stone et al. 1979). While treatments and endpoints varied among these studies, they demonstrate clear differences in estrogen-induced proliferation, apoptosis and morphogenesis of the mammary ducts among the strains.

The uterus is also very sensitive to estrogens and responses have been compared in multiple strains of rats and mice. The outbred SD were used across 5 studies providing a common reference. To test acute responses, rats were ovariectomized then treated with 17β-estradiol, estrogen agonists or environmental compounds to test for xenoestrogen activity with uterine weight as a common endpoint. Increases in uterine weight in response to the estrogen agonist ethinyl estradiol (EE) were similar for the F344 and SD rats (McKim et al. 2001).

EE increased uterine weights to a greater extent in Wis and DA/Han strains compared to SD (Diel et al. 2004; Geis et al. 2005). The outbred LE rats also had a greater increase in uterine weight in response to the estrogen analog PEP compared to SD rats (Lawson et al. 1984). The Wis rats were more sensitive to 17β-estradiol when compared to the WKY (Mitsui et al. 2013). As the SD strain is outbred and derived from the Wis strain, it appears that genetic variants determining uterine responses may be segregating within the populations used in the experiments. In mice treated with the estrogen analog E2-DP, the increase in uterine weight in the 129 strain was 2-fold that in the C57BL/6 and C3H/He strains with intermediate responses in C3H/JFe and DBA/1 (Drasher 1955). However, in subsequent studies using 17β-estradiol (Roper et al. 1999), responses were greater in C57BL/6J compared C3H/HeJ strains (3.5-fold vs 2.1-fold, respectively). The C57BL/6J strain also exhibited a stronger recruitment of macrophages compared to C3H/HeJ mice (Griffith et al. 1997).

The strain-differences in the uterus are more complex when comparing responses to environmental xenoestrogens. Although SD and F344 rats responded similarly to the estrogen analog EE, responses to octametthylcylotetrasioxane (D4) were greater in SD compared to F344 rats (McKim et al. 2001). However, bisphenol A (BPA) stimulated a 3fold increase in proliferation of the vaginal epithelium in the F344 strain while responses in SD rats were negligible, yet responses to  $17\beta$ -estradiol were similar for the two strains (Long et al. 2000). The strains did not differ in clearance of BPA, indicating genetic variation in intracellular signaling. In mice, low doses of DES increased uterine weights to a greater extent in C57BL/6J mice indicating that this strain is more sensitive than the BALB/c (Greenman et al. 1977). Prolonged treatment with DES induced neoplastic lesions in the uterus of 129/SvEv mice, but not BALB/cJ. But this response was limited to the uterus as there were no lesions detected in the mammary glands (Bennett et al. 2000). It is not clear from these studies whether the estrogenic responses are mediated by estrogen receptors as drugs to block these receptors were not included. Nonetheless, genetic variants determining sensitivity to xenoestrogens appear to be distinct from variants determining sensitivity to 17β-estradiol. Therefore, the relative potency of xenoestrogens across strains cannot be inferred from responses to 17β-estradiol.

Estrogen-stimulated proliferation of lactotrophs within the pituitary and secretion of prolactin have also been compared in strains of rats. Both 17 $\beta$ -estradiol and DES have been used and elicited consistent responses. The ACI and F344 strains are generally more responsive (Moy and Lawson 1992; Spady et al. 1999b; Stone et al. 1979; Wiklund and Gorski 1982) compared to the related outbred strains (SD, Holz, Wis). In contrast, the BN, COP and WKY strains had modest responses detectable at early time points, but were transient (Spady et al. 1999a). Tissue differences were especially striking in comparisons of Wis and WKY strains (Mitsui et al. 2013). While pituitary responses to 17 $\beta$ -estradiol were negligible in WKY rats, uterine weights were increased ~5-fold. Strain differences were also prominent following chronic stimulation with 17 $\beta$ -estradiol resulting in 5-fold higher levels of plasma prolactin in SD and Wis rats compared to BN (Blankenstein et al. 1984). This is similar to the relative sensitivity for estrogen-induced pituitary growth reviewed previously (Spady et al. 1999a) where F344 are most sensitive, SD being intermediate and BN being the least sensitive.

While estrogen agonists induce proliferative responses in mammary, uterine and pituitary, they cause regression in other tissues. DES induced thymic regression in both C57BL/6 and BALB/c strains (Greenman et al. 1977). Although the strains differed in initial thymus weights, both exhibited similar ~1.5 g decreases following DES treatment (Greenman et al. 1977). In rats, the F433 strain was most responsive in pituitary and uterine tissues, but DES-induced thymic regression was greatest in the SD strain compared to F344 and BN (Gould et al. 2000). Treatment with 17 $\beta$ -estradiol elicited striking reductions in testicular weights in C57BL/6J males compared to outbred CD-1 mice (Spearow et al. 1999; Spearow et al. 2001). Similarly, hair regrowth is suppressed by 17 $\beta$ -estradiol in C57BL/6, C3H and CD-1 mice but did not differ among these strains (Smart et al. 1999). Therefore, it appears that genetic variants regulating estrogen-induced repression in these tissues differ from the variants mediating growth in other tissues.

The striking differences among strains in responses to estrogenic compounds demonstrates genetic diversity in the signaling pathways. It is especially notable that proliferation was transient in spite of continuous exposure in some strains. This was most notable in the pituitary and mammary tissues of BN and COP rats indicating an ability to attenuate signaling (Ding et al. 2013; Gould et al. 2000) but not in ACI and F344. In the case of mammary epithelium of C57BL/6J mice, proliferation in response to 17β-estradiol appeared to be balanced by an increase in apoptosis (Wall et al. 2014a). In contrast, ACI rats have a persistent proliferative response to DES in mammary epithelium without a compensatory increase in apoptosis and was associated with extensive hyperplasia (Ding et al. 2013). Thus, strains of rodents appear to have adopted different strategies to achieve tissue homeostasis. The ability to attenuate signaling also appears to differ among tissues. An example is the formation of neoplastic lesions in the uterus of 129/SvEv mice treated with DES, but no lesions developed in the mammary glands of these mice (Bennett et al. 2000). The diversity of responses among strains of rats and mice suggests that effects would be similarly variable among humans (Spearow and Barkley 2001). Thus, the genes and pathways regulating these responses can significantly affect whether exposure to endogenous levels of 17β-estradiol poses a significant risk. The genetic variation could also affect the risk associated with postmenopausal hormone therapies and exposures to environmental xenoestrogens.

#### Genetic variants determining responses to estrogen

Linkage mapping has been used to identify the genetic basis for the variation in responses to estrogens among strains of rodents. Searches of rat and mouse genome databases and PubMed were conducted to compile relevant loci. These are summarized in Figure 1 with details provided in Supplementary Table 1.

The pathogenic effects of prolonged estrogen stimulation on mammary tumorigenesis are best described in rats. ACI rats are highly susceptible to mammary tumors while COP are resistant and BN are highly resistant. In genetic crosses between these inbred rat strains, susceptibility to  $17\beta$ -estradiol-induced mammary tumors behaves as an incompletely dominant trait (Shull et al. 2001). A total of 9 QTL (designated *Emca*) influencing susceptibility to mammary tumors (latency and/or number of mammary tumors) were identified (Figure 1). QTL mapped to rat chromosomes 5 and 18 in  $17\beta$ -estradiol-treated F2

progeny generated in intercrosses between ACI and COP rats and chromosomes 2, 3, 4, 5, 6, 7, and 18 in progeny from intercrosses between ACI and BN rats (Gould et al. 2004; Schaffer et al. 2006; Shull 2007). The existence of each of these mammary tumor QTL has been confirmed through generation and characterization of congenic rat strains. The QTL exhibit orthology to a region of the human genome that has been linked to breast cancer risk and/or mammographic breast density in genome wide association studies, strongly suggesting these genetically defined rat models are relevant to understanding the genetic bases of breast cancer susceptibility in humans (Colletti et al. 2014; Schaffer et al. 2013).

Strain differences in the responsiveness of the anterior pituitary lactotroph to estrogens have also long been recognized (Spady et al. 1999a) allowing multiple QTL to be mapped (designated *Edpm* and *Ept*, Figure 1). F344 and ACI rats are highly sensitive to the stimulatory actions of estrogens on lactotroph proliferation, resulting in rapid development of lactotroph hyperplasia and adenoma. COP rats exhibit an intermediate sensitivity while BN rats are highly insensitive to estrogen-induced proliferation of lactotrophs. When pituitary weight was used as a phenotypic indicator of estrogen stimulated lactotroph proliferation, five QTL were identified upon characterization of DES treated female F2 progeny generated in an intercross between F344 and BN rats (Wendell and Gorski 1997). One additional QTL was mapped during characterization of backcross progeny generated using these same strains (Wendell et al. 2000). When ACI rats were utilized as the sensitive strain, six QTL were mapped upon characterization of DES treated male F2 progeny generated in reciprocal intercrosses between ACI and COP rats and two additional QTL were mapped upon characterization of 17β-estradiol-treated female F2 rats generated in a BNxACI intercross (Shull et al. 2007; Strecker et al. 2005). Each of the QTL mapped in these studies of estrogen action on the pituitary lactotroph resides in a distinct region of the rat genome, although the mapping resolution for Edpm3 and Ept2, both of which reside on rat chromosome 3, is insufficient to demonstrate conclusively that these two QTL are distinct entities. Several of these QTL that harbor genetic determinants of responsiveness of the rat pituitary gland to estrogens have been isolated as congenic rat strains, which will allow the genetic variants that impact responsiveness to estrogens to be mapped to higher resolution and their molecular actions to be further elucidated (Dennison et al. 2015; Kurz et al. 2014; Kurz et al. 2008; Pandey et al. 2004; Wendell et al. 2002). The presence of multiple loci regulating responses to estrogens and that these are distinct for mammary gland and uterus highlights the tissue-specific nature of estrogen signaling and its complexity.

In the rat uterus, estrogens exert strain specific actions on induction of pyometritis, which is thought to develop as a consequence of extensive over proliferation of the uterine epithelium. In this regard, BN rats are highly sensitive relative to ACI or F344 rats revealing 2 genetic loci (Figure 1). *Eutr1*, a QTL that influences pyometritis development, was mapped to the proximal region of rat chromosome 5 in a study in which F2 progeny generated in an intercross between BN and ACI rats were treated with 17β-estradiol (Gould et al. 2005). A second QTL, *Eutr2* was mapped to the same region of chromosome 5 through characterization of DES treated congenic rats in which BN alleles across proximal chromosome 5 were introgressed onto the F344 genetic background (Pandey et al. 2005).

In contrast to the mammary epithelium, pituitary and uterus, estrogens inhibit proliferation of thymocytes in mice and rats (Gould et al. 2000; Greenman et al. 1977). QTL that modify the extent of the repression have been identified in rats (Figure 1). Treatment with DES identified QTL influencing repression on chromosome 10 (Esta1) and chromosome 2 (Esta2) and Esta3) in a study using male F2 progeny from a BN x ACI intercross (Gould et al. 2006). QTL associated with regression of testes induced by DES were identified on chromosomes 1 and 7 (Figure 1) in recombinant inbred male rats (Tachibana et al. 2006). Although no linkage was detected for pituitary adenoma development in male rats in the recombinant inbred strains, the markers associated with regression of testes (D1Wox25, D7Mit4) are in close proximity to a locus affecting pituitary adenomas on chromosome 1 (Ept10) and the locus involved in mammary tumors and pituitary adenomas (Emca4, Ept7) on chromosome 7 (Figure 1). The mammary tumor and pituitary phenotypes were identified in different crosses (ACI x COP and BN x ACI respectively) while the testicular phenotype was mapped in panel of 30 recombinant inbred strains derived from crosses of LE/Stm x F344/DuCrj rats (LEXF/FXLE). Therefore, while the locus may be the same, it is likely that the polymorphisms responsible for the tissue-specific effects differ among the strains.

Comparisons of estrogen responses in uterus and mammary glands of C3H/HeJ and C57BL/6J female mice reveal a complex set of modifiers in each tissue as well. Treatment with 17β-estradiol increased uterine weights 3.3-fold in C57BL/6J compared to a 2.2-fold increase in C3H/HeJ (Roper et al. 1999; Wall et al. 2013). The greater sensitivity to estrogen in the C57BL/6J strain was dominant in F1 hybrids. Therefore, linkage analysis was performed using backcross of F1 progeny to C3H/HeJ which identified 5 QTL (designated Est, Supplementary Table 1). Differences in estrogen-stimulated uterine weight was linked to chromosomes 5 and 11. Infiltration of eosinophils in the uterus induced by 17β-estradiol administration was linked to loci on chromomosomes 4, 10 and 16 as well as interactions between D10Mit180 and the loci on chromosomes 4 and 5. The effects on uterine weight in C57BL/6J and C3H/HeJ were not due to proliferative responses, but rather a higher level of apoptosis in the C3H/HeJ mice (Wall et al. 2013). Treatment with 17β-estradiol also stimulates expansion of the of ductal branching in mammary glands. The extent of development was nearly 2-fold greater in C57BL/6J mice compared to C3H/HeJ (Wall et al. 2014a). Although estrogen stimulates increases in tissue mass in both the mammary epithelium and uterus, little overlap was observed in transcriptional profiles induced by 17βestradiol in these tissues (Wall et al. 2014b). Therefore, it appears that the OTL regulating responses to estrogenic stimulation are distinct among mammary epithelium and uterus in these strains of mice.

These studies indicate that the genetic variants controlling responsiveness to estrogens do so in a tissue and/or cell-type specific manner. For example, the QTL that influence development of pituitary lactotroph hyperplasia/adenoma are physically distinct from those that influence susceptibility to mammary cancer; the only exception being Ept7 and Emca4, which both map to the same region of rat chromosome 7 (Kurz et al. 2014; Schaffer et al. 2006; Shull et al. 2007). The tissue-specific actions of these loci allowed development of a novel rat model of  $17\beta$ -estradiol-induced mammary tumors that lacks the deleterious morbidities associated with pituitary lactotroph hyperplasia/adenoma (Dennison et al. 2015). As a result, studies of regulation of estrogen signaling must be studied in the appropriate

tissue. Despite the limited genetic diversity in ACI, COP and BN strains, a total of 9 QTL were identified that modify sensitivity to mammary tumors induced by chronic exposure to  $17\beta$ -estradiol. This suggests that a much larger number of loci and variants may participate in regulating the consequences of exposure to estrogenic compounds in the human population.

### Effects of estrogens on mammary gland development and breast cancer risk

Estrogen is a primary driver of mammary gland development during puberty. Estrogen receptor alpha (ERa) plays a principal role as deletion of the gene encoding ERa (Esr1) causes a profound failure of mammary gland development (Feng et al. 2007). Therefore, differences among strains in mammary development during puberty offers an additional approach to evaluate estrogen sensitivity and actions. A survey of mammary gland architecture was performed using 43 recombinant inbred strains of mice that comprise the Mouse Diversity Panel (Hadsell et al. 2015). Tissues were evaluated during puberty (42 day old) and at maturity (12 weeks) for 15 different measures of area, branching and density of the mammary ducts. The phenotypes were largely consistent at both ages within strains, and therefore, not simply a consequence of differences in the onset of puberty. Hierarchical clustering defined 4 patterns of development represented by C3H/HeJ, 129S1/SvlmJ, C57BL/6J and BALB/cByJ (Clusters 1–4, respectively). This is consistent with the differences in ductal growth between C57BL/6J and C3H/HeJ strains (Table 1) following acute treatment with 17β-estradiol (Wall et al. 2014a). The analysis of mammary gland development identified 20 mammary ductal quantitative trait loci (Mdq, Table 3). Of these, 9 were found to be within, or close to, orthologous regions associated with risk for breast cancer in humans.

Differences in mammary structure among the strains in the Mouse Diversity Panel also appear to provide insights into pathways underlying breast density. Most notably, the lead SNP for *Mdq15* maps to within 0.5 Mbp of a locus on 12q24 associated with mammographic density in women (Stevens et al. 2012). The most significant SNP (rs1265507) is in close proximity to the *Tbx3* gene, which is required for the ERa expressing lineage of mammary epithelial cells (Davenport et al. 2003; Kunasegaran et al. 2014) and breast cancer (Douglas and Papaioannou 2013; Krstic et al. 2016; Stephens et al. 2012). In addition, the lead SNP in Mdq8, which was associated with ductal branch density, maps to within 0.11 Mbp of an orthologous region in the human containing the breast cancer associated SNP, rs11814448 (Michailidou et al. 2015; Michailidou et al. 2013). This particular SNP is located between the genes *Dnajc1* and *Bmi1*. *Bmi1* is regulated by ERa and has been implicated in a number of behaviors in breast cancer cells including epithelialto-mesenchymal transition (Wang et al. 2014). Therefore, the genetic modifiers that regulate ductal development in mice appear to overlap with breast cancer risk loci in women. Although it is unclear whether the *Mdq* loci regulated by development or are dependent on estrogen exposure, A search of ChIP-seq databases for H3K4me2 binding was used to identify regulatory elements within the Mdq loci and colocalize binding of progesterone receptor within 15 (Mbp) of the loci suggesting hormonal regulation (Hadsell et al. 2015).

The role of the *Mdq* in mammary tumorigenesis has not been tested directly. As a means to address their relationship with susceptibility to mammary tumors, the authors combined previously published data on strain dependent variation in mammary tumorigenesis and the incidence of lung metastases in the polyoma middle T-antigen model with their own data on variation in normal mammary ductal development. Modifiers of mammary tumorigenesis and lung metastasis have been mapped using mice expressing the oncogenic polyoma middle T-antigen (MMTV-PyMT) in crosses with 28 strains (Le Voyer et al. 2000; Le Voyer et al. 2001; Lifsted et al. 1998). Of these previously studied 28 strains, measures of normal branch density were available for 21. By plotting strain means, mammary ductal branch density and incidence of lung metastasis were found to be highly correlated (R<sup>2</sup>>0.7) indicating that at least a portion of the loci involved in ductal structure were related to tumor development and/or metastasis (Hadsell et al. 2015).

#### Modifiers of estrogen signaling --- challenges and opportunities

The studies in rodents demonstrate the presence of genetic variants that can limit or amplify the pathogenic effects of estrogenic compounds in mammary glands. A total of 29 QTL have been identified that influence the effects of estrogens on development of the mammary ductal network and susceptibility to mammary tumors (Figure 1 and Table 2). These loci are orthologous to polymorphisms associated with breast cancer risk in humans suggesting that variation in estrogen signaling may be a common mechanism underlying breast cancer risk. Furthermore, the risk posed by chronic exposure to estrogens would be of greatest concern for a subset of individuals who are particularly sensitive. This highlights the potential impact of gene x environment interactions in determining risk associated with estrogen exposures.

Several hurdles hamper the ability to detect genetic variants that interact with levels of estrogen exposure to influence breast cancer risk in humans. The difficulty of accurately estimating levels of estrogen exposure in large populations of women is a major challenge. The magnitude of risk associated with genetic variants is often modest and, without very large studies, the statistical power to detect interactions can be limiting (Rudolph et al. 2016). However, relationships between mammographic breast density and estrogen exposure suggest that genetic interactions may be important. Mammographic density is among the strongest predictors of breast cancer risk and is determined, in part, by estrogen exposure. Estrogen plus progestin hormone therapies increase breast density and can explain the increased risk associated with the use of exogenous hormones (Byrne et al. 2017; Chlebowski et al. 2013). Conversely, inhibition of signaling through estrogen receptors by Tamoxifen reduced mammographic density and was associated with decreased risk of subsequent breast cancer (Cuzick et al. 2011). Identification of genes involved in estrogen signaling among the 11 loci associated with differences in mammographic density in GWAS (Lindstrom et al. 2014) reinforces the potential interactions between estrogen exposure and breast cancer risk. Candidate genes linked to polymorphisms include the gene encoding ERa (ESR1) and estrogen-responsive target genes (Amphiregulin, Insulin-like growth factor 1) as well as lymphocyte-specific factor 1 (LSPI). A targeted screen of genes linked to breast cancer risk (Odefrey et al. 2010) also found significant associations between mammographic breast density and polymorphisms in LSP1. Similar to the effects in ACI rats (Ding et al. 2013), genetic variants in humans that impair the ability to attenuate

estrogen signaling may render individuals susceptible to breast cancer associated with postmenopausal hormone therapies. The reduction in breast density in response to Tamoxifen has been shown to vary substantially among women (Cuzick et al. 2011) and genetic variants that are permissive to estrogen signaling may play a role in limiting the efficacy of Tamoxifen in these individuals. Thus, the challenge is to identify the rate-limiting steps in estrogen signaling and pathogenic responses in breast tissue.

Genetic variation in responses to estrogenic stimulation among strains of rodents provides an incisive approach to define critical pathways in mammary tissue. The dose, duration and types of estrogenic compounds can be controlled in experimental settings. Study designs allow effects of modest magnitude to be detected. The availability of genetically diverse strains of mice represented in the Collaborative Cross and Diversity Outbred panels (Harrill and McAllister 2017) offer new opportunities to expand the number of loci influencing sensitivity to elevated levels of endogenous estrogens or estrogen therapies. These studies would provide a foundation for selection of strains to evaluate the risks posed by environmental xenoestrogens. The loci in humans that are orthologous to the rodent loci regulating estrogen sensitivity can be used in targeted screens for interactions with estrogenic exposures (endogenous or environmental sources) providing greater statistical power to detect associations. The pathways identified in rodents would provide insights into risk alleles in humans rendering individuals sensitive to the pathogenic effects of estrogenic exposures as well as provide biomarkers for assessing risk in breast tissues.

#### **Supplementary Material**

Refer to Web version on PubMed Central for supplementary material.

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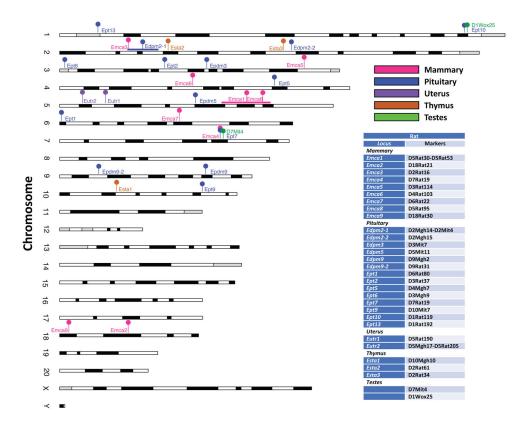
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**Figure 1. Positions of QTL regulated responses to estrogens in 5 tissues in rats**The phenotypes and strains used to define the quantitative trait loci (QTL) are indicated. The localization of QTL is based on the polymorphic markers used in mapping experiments. An interval is indicated using a horizontal line for *Emca1* and *Eutr2*.

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Table 1

Variation in responses to estrogens among strains of rodents.

Sp./Sex	Strains <sup>a,b</sup>	Compound	Doses	Trt Duration	Phenotypes	Reference
Mammary						
Mus, Female	C57BL/6J, C3H/HeJ	E2	40 μg/kg daily injections	Acute, 4 days	Proliferation: C57BL/6J > C3H/HeJ Apoptosis: C57BL/6J > C3H/HeJ	(Wall et al., 2014a)
Mus, Female	C57BL/6J, CD-1	E2 BPA	0.25–50 µg/kg/d 250 ng/kg/d	Acute, 10 days E2	Ductal area, E2: C57BL/6J > CD-1 TEB/Ductal area; E2: C57BL/6J > CD-1 TEB/Ductal area: BPA: C57BL/6J > CD-1	(Wadia et al., 2007)
Mus, Female	BALB/cJ, 129/SvEv	DES	15 ppb <i>po</i>	Chronic, 6 months	Ductal branching: 129/SvEv = BALB/cJ	(Bennett et al., 2000)
Ratus, Female	ACI, BN	E2	27 mg in silastic implant	Chronic, 1–12 weeks	Proliferation: ACI > BN Apoptosis: ACI = BN	(Ding et al., 2013)
Ratus, Female	ACI, SD	DES	5 mg implants	Chronic, 10–214 days	Mammary tumors: ACI > SD Chronic stimulation resulted in mammary tuors in ACI but not SD rats.	(Stone et al., 1979)
Uterus and vagina	jina					
Ratus, Female	SD, F344	EE DES-DP CE D4	1–30 µg/kg/d po 0.5–15 µg/kg/d po 10–150 mg/kg/d po	Acute, 18-21 days old	Uterine weight, EE: SD = F344 Uterine weight, DES-DP: SD = F344 Uterine weight, CE: SD = F344 Uterine weight, D4: SD > F344	(McKim et al., 2001)
Ratus, Female	DA/Han, SD, Wis	EE BPA OCT Gen	100 µg/kg/d <i>po</i> 5–200 mg/kg/d <i>po</i> 5–200 mg/kg/d <i>po</i> 25–100 mg/kg/d <i>po</i>	Acute, 3 days	Uterine weight, EE: Wis = DA/HAN > SD Potency rank was similar for BPA, OCT, Gen.	(Diel et al., 2004)
Ratus, Female	SD, Long-Evans	PEP	$25-100~\mu g~sc$	Acute, 1 day	Uterine weight: Long-Evans > SD	(Lawson et al., 1984)
Ratus, Female	SD, F344	E2 BPA	0.02–2.0 µg/kg <i>ip</i> 0.2–150 mg/kg <i>ip</i>	Acute, 1 day	Proliferation, E2: SD = F344 Proliferation, BPA: F344 > SD	(Long et al., 2000)
Ratus, Female	SD, Wis	EE Gen	100 µg/kg/d 50–200 mg/kg/d	Acute, 3 days	Uterine weight: EE: Wis $>$ SD Uterine weight, Gen: Wis $=$ SD	(Geis et al., 2005)
Ratus, Female	Wis, WKY	E2	2 mg, <i>ip</i>	Chronic, 3 weeks	Uterine weight: Wis > WKY BrdU labeling: Wis > WKY	(Mitsui et al., 2013)
Ratus, Female	F344, Holz	DES	2.5 mg implants	Chronic, up to 8 weeks	Uterine growth: F344 = Holz	(Wiklund et al., 1981)
Mus, Female	129, С57ВL/6, С3Н/Не, С3Н/ЈFе, DBA/1	E2-DP	1 μg/d <i>ip</i>	Acute, 3 days	Uterine weight: 129 > C3H/JFe = DBA/1 > C57BL/6 = C3H/He	(Drasher, 1955)

Sp./Sex	$Strains^{a,b}$	Compound	Doses	Trt Duration	Phenotypes	Reference
Mus, Female	C57BL/6J, C3H/HeJ, B6C3	E2	40 μg/kg/d <i>sc</i>	Acute, 2 days	BM8+ macrophages: C57BL/6J > C3H/HeJ	(Griffith et al., 1997)
Mus, Female	C57BL/6J, C3H/HeJ, B6C3-F1	E2	$40~\mu \mathrm{g/kg/d}~sc$	Acute, 2 days	Uterine weight: C57BL/61>C3H/HeJ=B6C3-F1	(Roper et al., 1999)
Mus, Female	C57BL/6J, CD-1	E2 BPA	0.25–50 µg/kg/d 250 ng/kg/d	Acute, 10 days E2	Uterine weight, E2: CD-1 > CS7BL/6J Uterine weight: BPA: CD-1 = CS7BL/6J	(Wadia et al., 2007)
Mus, Female	BALB/c* C57BL/6J, C57BL6.BALB/c-F1	DES	2.5–1000 ppb <i>po</i>	Acute, 6 days	Uterine weight: $C57BL/6J = F1 > BALB/c$	(Greenman et al., 1977)
Mus, Female	BALB/cJ, 129/SvEv	DES	15 ppb	Chronic, 6 months	Neoplasia: 129/SvEv > BALB/cJ	(Bennett et al., 2000)
Pituitary						
Ratus, Female	ACI, SD	DES	5 mg implants	Chronic, 10–214 days	Pituitary weights: ACI > SD	(Stone et al., 1979)
Ratus, Male	F344, Holz	DES	2.5 mg implants	Acute, 4–56 days	Proliferation: F344 > Holz	(Wiklund and Gorski, 1982)
Ratus, Female	SD, Long-Evans	PEP	$25$ – $100~\mu g~sc$	Acute, 1 day	Prolactin secretion: Long-Evans > SD Pituitary weight: Long-Evans = SD	(Lawson et al., 1984)
Ratus, Female	F344, Holz	DES	2.5 mg implants	Chronic, up to 8 weeks	Pituitary weight: F344 > Holz	(Wiklund et al., 1981)
Ratus, Female	F344, Holz	E2 DES	100 µg/kg/d 50–200 mg/kg/d	Chronic, up to 8 weeks	Plasma prolactin, E2: F344 = Holz Plasma prolactin, DES: F344 > Holz	(Moy and Lawson, 1992)
Ratus, Female	SD, Wis WAG/Rij, BN/BiRij	E2	20 mg implants	Chronic, 2–52 weeks	Plasma prolactin: SD > Wis WAG/Rij > BN/BiRij	(Blankenstein et al., 1984)
Ratus, Female	Wis, WKY	E2	2 mg, <i>ip</i>	Chronic, 3 weeks	Pituitary weight: Wis > WKY BrdU labeling: Wis > WKY	(Mitsui et al., 2013)
Ratus, Male	ACI, COP	DES	5 mg implants	Chronic, 12 weeks	Pituitary weights: ACI > COP	(Spady et al., 1999)
Thymus						
Mus	BALB/c* C57BL/61, C57BL6.BALB/c-F1	DES	2.5–1000 ppb <i>po</i>	Acute, 6 days	Decrease thymic weight: BALB/c* ~ C57BL/6J = F1 Initial thymic weights significantly greater in BALB/c*.	(Greenman et al., 1977)
Ratus, Female	BN, F344, SD	DES	5 mg implants	Chronic, 1–28 days	Decrease thymic weight: $SD > F344 = BN$	(Gould et al., 2000)
Testis						
Mus, Male	C17/Jls, C57BL/6J, CD1	E2	0-40 µg implants	Chronic, 20 days	Inhibition of testes: C17/JIs = C57BL/6J > CD-1	(Spearow et al., 2001)

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Sp./Sex	$Strains^{a,b}$	Compound <sup>c</sup> Doses	Doses	Trt Duration	Phenotypes	Reference
Skin/Hair follicle	cle					
Mus, Female	Mus, Female C57BL/6, C3H, CD-1	E2	10 nM topical treatment	Chronic, 20 weeks	Inhibition of hair growth: $C57BL/6 = C3H = CD-1$ (Smart et al., 1999)	(Smart et al., 1999)

# Abbreviations:

ats Strains: ACI=AxC-Irish; BN=Brown Norway; COP=Copenhagen; F344=Fischer 344; Holz=Holzman LE=Long-Evans; SD=Sprague-Dawley; Wis=Wistar; WKY=Wistar Kyoto

HMDS=Hexamethyldisiloxane; OCT=p-tert-octylphenol; PEP=Polyestradiol Phosphaste

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Compounds: BPA=Bisphenol A; CE=Coumestrol; D4=Octamethylcyclotetrasiloxane; DES=Diethylstilbestrol; E2=17β-estradiol; E2-DP=Estradiol Diproprionate; EE=Ethinyl Estradiol; Gen=Genestein; bouse Strains: BALB/c\*=BALB/c-StCrlfC3Hf/Nctr; B6C3-F1=C57BL/61xC3H/HeJ

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Table 2

Overlap between mouse Mdq loci and breast cancer risk loci in humans<sup>1</sup>

QTL	Lead SNP	а	Effect Size <sup>a</sup>	Human locus	Human Syntenic Location <sup>b</sup>	Breast Cancer Risk Loci	Nearest BrCa SNP	GWAS P	Distance to Mouse <sup>b</sup>	iCOGS P¢	Combined GWAS iCOG P <sup>C</sup>
Mdq1	rs29972830	9.E-12	0.26	7q32.3	132.73	$AES^d$	rs4593472	3.E-05	2.06	4.E-06	2.E-09
Mdq2	rs32398376	2.E-09	0.21	1q25.3	183.13	ON	rs11249433	7.E-10	61.85		
Mdq3	rs13483228	3.E-09	0.21	18q12.1	28.16	YES	rs1436904	1.E-03	3.59	5.E-06	3.E-08
Mdq4	rs33051600	3.E-08	0.2	2q24.3	169.07	YES	rs2016394	1.E-02	3.90	2.E-06	8.E-06
Mdq5	rs30095733	6.E-08	0.17	5q11.2	51.23	YES	rs889312	7.E-20	4.81	3.E-27	1.E-39
Mdq6	rs46013670	8.E-08	0.18	3q21.1	122.88	ON	rs1053338	2.E-02	58.91	2.E-07	9.E-09
Mdq7	rs50444438	1.E-07	0.17	7p15.3	21.90	ON	rs6977610	2.E-04	6.64		
Mdq8	rs27176282	1.E-07	0.17	10p12.3	22.21	YES	rs11814448	4.E-05	0.11	3.E-13	6.E-17
6bpW	rs36588132	1.E-07	0.16	3p22.3	33.06	YES	rs12493607	4.E-02	2.38	7.E-08	1.E-08
Mdq10	rs29830755	2.E-07	0.16	7p15.1	28.64	ON	rs6977610	2.E-04	13.38		
Mdq11	rs3696903	4.E-07	0.17	11p15.2	16.42	ON	rs909116	7.E-07	14.48		
Mdq12	rs33753649	5.E-07	0.17	22q12.1	25.95	YES	rs132390	1.E-03	3.67	4.E-07	3.E-09
Mdq13	rs30305626	7.E-07	0.15	7q31.2	117.30	ON	rs2048672	6.E-06	13.35		
Mdq14	rs27275156	8.E-07	0.15	20p13	4.75	ON	rs6109595	1.E-04	8.11		
Mdq15	rs29778211	8.E-07	0.14	12q24.21	114.97	YES	rs1265507	1.E-08	0.54		
Mdq16	rs31558147	8.E-07	0.15	4q12	56.08	YES	rs11732323	6.E-05	0.43		
Mdq17	rs46415121	1.E-06	0.15	12q13.13	52.83	ON	rs10506095	1.E-05	20.03		
Mdq18	rs27336088	1.E-06	0.16	20q12	40.01	ON	rs6109595	1.E-04	27.15		
Mdq19	rs29782631	2.E-06	0.14	11q22.1	100.83	ON	rs948725	2.E-04	23.58		
Mdq20	rs36274122	2.E-06	0.14	1q24.3	171.86	ON	rs1538472	5.E-05	73.77		

<sup>/</sup>Mouse loci from Hadsell et al 2015 (Hadsell et al. 2015); Human loci from Phengeni (http://www.ncbi.nlm.nih.gov/gap/phegeni), and

 $<sup>^{</sup>C}_{\rm Michailidou\ et\ al.\ (Michailidou\ et\ al.\ 2013;\ Michailidou\ et\ al.\ 2013)}$ 

 $d_{\rm Less}$  than 5Mbp apart; iCOGS data provide larger sample sizes