Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures


Abstract

Mammographic density measures adjusted for age and body mass index (BMI) are heritable predictors of breast cancer risk, but few mammographic density-associated genetic variants have been identified. Using data for 10,727 women from two international consortia, we estimated associations between 77 common breast cancer susceptibility variants and absolute dense area, percent dense area and absolute nondense area adjusted for study, age, and BMI using mixed linear modeling. We found strong support for established associations between LSP1 and rs3817198 (\(P < 10^{-5}\)) and adjusted absolute and percent dense areas, respectively. Of 41 recently discovered breast cancer susceptibility variants, associations were found between rs1432679 (EBF1), rs17817449 (ESR1), and rs12710696 (2p24.1), and rs3757318 (ESR1) and adjusted absolute and percent dense areas, respectively. There were associations between rs6001930 (MKL1) and both adjusted absolute dense and nondense areas, and between rs17356907 (NTN4) and adjusted absolute nondense area. Trends in all but two associations were consistent with those for breast cancer risk. Results suggested that 18% of breast cancer susceptibility variants were associated with at least one mammographic density measure. Genetic variants at multiple loci were associated with both breast cancer risk and the mammographic density measures. Further understanding of the underlying mechanisms at these loci could help identify etiologic pathways implicated in how mammographic density predicts breast cancer risk. Cancer Res; 75(12); 2457-67. ©2015 AACR.
Introduction

Mammographic density refers to the white or light areas on a mammogram, which are thought to reflect differing amounts of epithelial and stromal tissue within the breast, as distinct from radiographically lucent fatty tissue. For women of the same age and body mass index (BMI), those with more extensive amounts of either absolute or percent dense area are more likely to develop breast cancer (1). The underlying biologic processes are not clear.

Twin and family studies have shown that a substantial variation in the mammographic density measures could be due to genetic factors (2–4). Moreover, these heritable mammographic density measures are thought to explain about 10% to 20% of the association of family history with breast cancer risk (5, 6).

Finding genetic variants that are associated with both breast cancer risk and the mammographic density measures that predict breast cancer has the potential to reveal underlying biologic pathways that explain the associations between those mammographic measures and cancer, resulting in a better understanding of the etiology of breast cancer. The use of large-scale genotyping projects to discover common genetic variants (single-nucleotide polymorphisms, or SNPs) associated with breast cancer risk has opened up the possibility of achieving this. The international DENSNP consortium previously studied the associations of 15 independent breast cancer susceptibility variants with age- and BMI-adjusted mammographic density measures for 17,000 women. This confirmed prior associations found between the variant rs381798 (in the region of LSP1; refs. 7, 8) and adjusted absolute and percent dense area and provided evidence for an association between rs10483813 (in the region of RAD51L1) and adjusted percent dense area (9). Two genome-wide association studies (GWAS) conducted by the Markers of Density (MODE) consortium found that there was an association between rs10995190 (in the ZNF365 locus), independently shown to be associated with breast cancer risk (10), and adjusted percent dense area, and weaker evidence for associations with the variants rs2046210 (in the region of ESR1) and rs3817198 (see above; ref. 11). More recently, MODE identified novel loci associated with dense area (rs10034692 from AREG, rs703556 from IGF1, rs7289126 from TMEM184B, rs17001868 from SGSME/MKL1), nondense area (rs7816345 from PTRN6, rs7816345 from PTRN6, and rs7289126 from TMEM184B; ref. 11). Furthermore, using a GWAS of both breast cancer and mammographic density, MODE investigators found that adjusted percent dense area and breast cancer risk have a shared genetic basis that is mediated by, at least in theory, a large number of common variants (12).

A further 41 independent breast cancer susceptibility common variants have been discovered by a study of 45,290 cases and 41,880 controls using a custom genotyping array designed, in part, by the Breast Cancer Association Consortium (BCAC; ref. 13). Of these new variants, a recent report from several coauthors found novel associations between breast cancer SNPs in 8q25: rs9485372 (TAB2) and rs9383938 (ESR1) with a volumetric measure of mammographic density (14). They also found novel associations between breast cancer SNPs rs6001930 (MKLI) and rs17356907 (NTN4) with absolute nondense volume. Here, we provide the largest and most comprehensive report to date of the associations between the current total of 77 known breast cancer susceptibility SNPs and three area-based mammographic density measures using data from over 10,000 women participating in the DENSNPs and MODE consortia.

Materials and Methods

Subjects

Genotypes, mammographic density measures, and information on conventional breast cancer risk factors were available for 10,727 self-reported women of European Ancestry from 13 studies described previously (4, 9, 11, 15). A summary of study design, sample sizes, mammographic, and genotyping characteristics is given in Supplementary Table S1. Each study obtained informed consent and had relevant ethics and institutional approvals. Only anonymized data were used for analyses.

Mammographic density measures

All mammographic density measurements were performed on digitized analogue films using either the Cumulus (16), Madena (17), or MDEST (18) programs. All approaches apply a thresholding
technique to measure total area of the breast and absolute dense area, from which percent dense area and absolute nondense area are derived. Absolute dense and nondense area values were converted to cm² according to the pixel size used in the digitization. All measurements were conducted by observers blind to genotype, case status (if applicable), and breast cancer risk factor data. For cases, mammograms prior to diagnosis were used or, when this was not possible, those from the contralateral breast taken at the time of diagnosis (Table 1).

The mammographic density readings were performed on both craniocaudal (CC) and mediolateral oblique (MLO) views but these have been consistently shown to have high correlation (range, 0.87–0.90; ref. 19).

Genotyping
The 77 currently known breast cancer susceptibility SNPs were genotyped for the 13 studies either as part of a GWAS (11, 15) or by genotyping of a custom Illumina iSelect genotyping array comprising 211,155 SNPs [described in Michailidou and colleagues (Table 1; ref. 13)]. Quality control was conducted at the study level; for all SNPs in these analyses their call rates were >95%. Five SNPs (from three studies) with Hardy–Weinberg equilibrium $P < 0.001$ were excluded.

Statistical methods
Distributions of covariates summarized by frequency and percentages are summarized by breast cancer status (affected/unaffected). Primary analyses used individual level data and included a fixed study effect to adjust for potential differences due to study. Analyses were conducted using the square root of the density measures as the outcome variables, and examination of the distributions of the residuals after adjustment for age and BMI showed an approximately normal distribution.

Primary analyses were conducted using fixed effects ordinary linear regression adjusting for age (continuous), 1/BMI, and study. Analyses considered SNP associations as additive by defining an ordinal covariate as the number of copies of the minor allele (0, 1, or 2) producing per-allele estimates that are reported as $\beta$ and standard error $(SE)$. (For imputed genotypes from the two GWAS studies, the imputed allelic dosage values were used.) Secondary analyses were performed to evaluate potential confounding with other covariates such as case–control status, menopausal status (pre- and perimenopausal combined vs. postmenopausal), and postmenopausal hormone use (ever vs. never use). To measure the extent to which the mammographic measures mediated the SNP associations with breast cancer risk, we estimated the proportion of change in the regression coefficient for each SNP after adjustment for breast cancer status and calculated 95% confidence intervals based on methods described by Lin and colleagues (20).

We performed a series of analyses to test the robustness of the association between mammographic density measures and the 77 SNPs. First, we performed an overall test of whether there was no association between any of the variants and a given mammographic measure by testing whether the distribution of the 77 $P$ values deviated from the uniform distribution on the interval 0, 1. The Fisher exact test of uniformity tests the sum of the $-2 \ln P_i$ across all loci where $P_i$ is the $P$ value for the $i^{th}$ variant, against $\chi^2$ distribution with $2n$ degrees of freedom, where $n$ is the number of independent variants (21). Second, to try to determine the “best” model fit (i.e., the set of independent SNPs that give the
Results

Table 2 shows summary characteristics for each study. The majority of women were older than 60 years, more than 80% were postmenopausal, 55% had BMI ≥ 25 kg/m², and 35% were breast cancer cases.

Percent and absolute dense area were negatively associated with age, BMI, parity, and postmenopausal status and positively associated with postmenopausal hormone therapy use (Supplementary Table S1). Conversely, absolute nondense area was positively associated with age, BMI, and parity and negatively associated with hormone therapy use. All of the above associations were similar in direction and magnitude for cases and controls (data not shown). None of the density measures were statistically significantly different by mammogram view (Supplementary Table S1).

Of the 77 variants, nine were associated with at least one adjusted mammographic density measure, using the threshold of 0.00065 (Table 3, results for all SNPs in Supplementary Table S1). Figure 1 is a forest plot of all 77 breast cancer susceptibility variants sorted by magnitude of association with breast cancer risk in these studies; the nine variants are highlighted in bold. The findings confirm previously identified associations with both adjusted percent and absolute dense areas for rs10995190 in the ZNF365 gene (β = 0.16, SE = 0.028, P = 8.5 × 10^-9 and β = 0.25, SE = 0.038, P = 4.7 × 10^-11, respectively), rs2046210 in the region of ESR1 (β = 0.098, SE = 0.021, P = 2.4 × 10^-6 and β = 0.14, SE = 0.029, P = 1.7 × 10^-6, respectively) and rs3817198 in the region of LSP1 (β = 0.087, SE = 0.021, P = 4.4 × 10^-6 and β = 0.16, SE = 0.029, P = 1.3 × 10^-7, respectively). None of these three variants showed evidence of association with adjusted nondense area (Table 3). There were marginal associations between two independent variants (r² = 0.003) in the region of RAD51L1; rs999737 (P = 0.003 and P = 0.01) with both adjusted percent and absolute dense area [reported in our previous DENSNP study (9)] and rs2588809 (P = 0.002, P = 0.04, and
Figure 1.
Associations between the 77 common breast cancer susceptibility SNPs and breast cancer (BC), adjusted percent dense area (PD), adjusted dense area (DA), and adjusted nondense area (NDA), ordered by the magnitude of the association with breast cancer.
P = 0.02) with adjusted percent dense area, dense area, and nondense area respectively (Supplementary Table S2).

For the 41 recently identified breast cancer loci, we found evidence of novel associations between at least one of the adjusted density measures and six variants (Table 3). The minor G allele of rs1432679 (EBF1) was positively associated with adjusted dense area and negatively associated with adjusted nondense area, and hence was positively associated with adjusted percent density (b = 0.087, SE = 0.020, P = 1.1 \times 10^{-5}). The minor G allele of rs6001930 in the region of MKL1 was negatively associated with both adjusted absolute dense and nondense areas (b = −0.18, SE = 0.044, P = 3.2 \times 10^{-5} and b = −0.23, SE = 0.048, P = 1.7 \times 10^{-5}, respectively), but was not associated with adjusted percent density (P = 0.04). The A allele of rs17356907 in the region of NTN4 was negatively associated with adjusted dense area (b = −0.12, SE = 0.033, P = 2.4 \times 10^{-4}), but not with adjusted dense area or percent density. The A allele of rs3757318 (close to ESR1) was positively associated with adjusted dense area (b = 0.19, SE = 0.054, P = 4.6 \times 10^{-4}), but not with either of the other density phenotypes.

Further adjustment for case-control status showed evidence that of rs1432679 and dense area included the bolded variants in Table 3 plus three others, including rs12710696 (2p24.1), rs4808801 (SSBP4:ISYNA1:ELL), and rs12422552 (12p13.1), which, when combined, explained 1.2% of the variation in the adjusted percent dense area trait. Similarly, the best fitting model from Lasso regression of adjusted dense area included the six boulded variants in Table 3 and rs1432679 (EBF1), rs17817449 (MIR1972-2:FTO), and rs4808801 (SSBP4:ISYNA1:ELL). When combined, they explained 1.4% of the variation in adjusted dense area. Finally, the best fitting model for adjusted nondense area included only the three boulded variants in Table 3, which, when combined, explained 0.4% of the variation.

When we removed the variants resulting from the best fitting Lasso models for each phenotype noted above, the distribution of the remaining P-values still deviated from the null hypothesis of no association between the genetic variants for both percent and absolute dense area (P = 0.00005 for percent density, P = 0.00006 for dense area) but not nondense area (P = 0.01). Sequentially removing the variants most strongly associated with the mammographic density measure until the test no longer found deviation from the null using a P value threshold of 0.00065, we found evidence of one more SNP associated with each percent dense and absolute dense area (rs999737 and rs6678914, respectively).

We also compared the quantile-quantile plots before and after exclusion of the top 14 breast cancer variants (nine identified via ordinary linear regression and five others identified via LASSO regression) most strongly associated with the mammographic density measures (see Fig. 2). On the basis of the analysis described above and the lack of departure from the 45° line once the top 14 variants have been removed (indicative of a probable threshold of commonly shared variants), we estimate that there is an approximate 18% overlap between breast cancer- and mammographic density-associated variants.

Discussion

This is the largest and most comprehensive study to date of the associations between breast cancer risk-predicting mammographic density measures and the 77 independent established breast cancer susceptibility common variants, 41 of which were recently identified by large-scale genotyping (13). In addition to previously reported associations between common breast cancer susceptibility SNPs in the regions of ZNF365, ESR1, and LSP1 and age- and BMI-adjusted absolute and percent dense area, we found strong evidence of novel associations between SNPs with all three adjusted mammographic density measures (in the region of EBF1); with adjusted dense area or percent dense area (MIR1972-2:FTO, 2p24.1, and another in the region of ESR1 independent of the initially reported SNP, rs2046210); adjusted dense and nondense area (MKL1) and nondense area only (NTN4). The directions of these associations were consistent with that of their associations with breast cancer risk, with the exception of MKL1 and 2p24.1 that were both negatively associated with dense area (and percent dense area) but are reportedly positively associated with breast cancer risk. Furthermore, these mammographic measures show evidence for mediating the association of several of these SNPs and breast cancer risk.

These findings are consistent with those recently reported by our coauthors’ Swedish study (14). Despite differences in phenotypes (area vs. volume), both studies independently showed novel associations between absolute measures of dense tissue with rs2046210 (ESR1) and between absolute measures of...
Figure 2.
Quantile-quantile plots before and after exclusion of the top 14 breast cancer susceptibility SNPs most strongly associated with the mammographic density measures. A, percent dense area; B, dense area; C, nondense area.
nondense tissue with rs17356907 (NTN4). Both studies also reported strong negative associations between and absolute measures of dense and nondense tissue with rs6001930 (MKL1). The other novel association reported in Brand and colleagues (14) between percent dense volume and rs9485372 (TAB2), a variant associated with breast cancer risk in Asian women, was not investigated in this study. The Swedish study did not replicate the previously reported association with rs3817198 (LSP1) nor our novel associations with rs12710696 (2p24.1) and rs17817449 (MIR19722-2:FTO), underscoring the differences in the volumetric and area phenotypes. Of note, both volumetric and area-based density measures have been shown associated with breast cancer risk, with similar magnitude of association (23).

Although the standard approach using linear regression identified nine variants associated with mammographic density, the nonuniform distributions of the remaining P values suggest that there are additional genetic variants associated with both breast cancer risk and the mammographic density measures that predict risk. In total, there is evidence of at least 14 breast cancer susceptibility variants (18%) associated with at least one mammographic density measure; approximately 10%, 12%, and 4% of the breast cancer susceptibility SNPs were associated with percent dense area, dense area and nondense area, respectively. Our estimate of 18% is consistent with empirical estimates that the percentage of overlap between genetic determinants of breast cancer and the risk-predicting mammographic density measures is 14% (95% CI, 4–39%; refs. 5, 12).

The nine density-associated variants identified here (using the standard approach) account for only a small proportion of the between-woman variation in the three risk-predicting mammographic density phenotypes (≤1.5% for each), but the contribution of the true causal variants could be larger. Also, it has been estimated that there are more than 1,000 loci involved with breast cancer susceptibility (13) and therefore it is possible that a considerable subset of these will also be associated with the mammographic density measures. Importantly, several of the SNP associations with breast cancer appear to be mediated by the mammographic density phenotypes. In fact, 15% to 20% of the associations reported in this study would be the same for bra cup size, although none of the variants overlap those examined in this study (33). The ESR1 variant reported by Eriksson and colleagues (34) is in moderate LD with both the ESR1 variants reported on here (r² = 0.23 with rs2046210 and with rs375318, although the mutual LD between these is just 0.07), and Eriksson’s MKL1 variant (rs73167017) is also in moderate LD with MKL1 rs6001930 reported here (r² = 0.33), but the ZNF365 variant, rs7089814, is independent of rs1095190 (r² = 0.04). Within MKL1, rs6001930 is correlated with rs995871 (r² = 0.75), which has been recently reported to be associated with mammographically measured female breast size, which correlates strongly with nondense area. Little is known about the functionality of any of the density-associated variants identified in this study.

Our study benefited from its large sample size and genotyping performed using the same custom Illumina iSelect genotyping array in 11 of the 13 studies. We also used the same stringent quality controls for all studies except the two GWAS, and exclusion of data from these two GWAS-based studies did not substantially affect the findings reported here (data not shown). Mammographic density measurements were performed using well-established methods shown to have high repeatability by trained observers, with all analyses being adjusted for study to reduce the impact of any between-study differences in the type of films available, digitizer used, quality of the density readings, and source of covariate data and other unmeasured confounders. We reproduced established associations between the three risk-predicting density phenotypes and measured breast cancer risk factors as well as prior genetic associations with breast cancer variants. Because over 80% of our sample population were postmenopausal, these results are generally applicable to postmenopausal women. However, based on previous work using longitudinal twin data, we have shown that the familial/genetic component of mammographic density is established before mid-life (35) and therefore, we believe that the direction of the associations reported in this study would be the same for premenopausal women.
More than 40 studies have found an association between mammographic density and breast cancer risk, many using different qualitative or quantitative methods of measuring mammographic density [19, 36]. This suggests that mammographic density, as currently measured, is a useful biomarker. Our previous collaborations [9, 37] have demonstrated that data from multiple mammographic density studies can be combined to produce internally consistent results. One reason for this is the very wide variation in mammographic density measures within populations, even for women of the same age and BMI.

In summary, our findings provide further support for shared genetic determinants of breast cancer risk and the mammographic density measures that predict risk, presumably representing shared etiologic pathways. Although the contributions of the genetic risk markers identified to date explain little of the phenotypic variance, uncovering the cause of familial aggregation (the so-called “missing heritability”) of the mammographic density measures that predict breast cancer could substantially increase understanding of the biologic pathways involved in the development of the disease.

Disclosure of Potential Conflicts of Interest
P.A. Fasching has received speakers bureau honoraria from Novartis, Pfizer, Roche, Agen, and Genomic Health. No potential conflicts of interest were disclosed by the other authors.

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