A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11.

Genome-wide association studies (GWAS) of breast cancer defined by hormone receptor status have revealed loci contributing to susceptibility of estrogen receptor (ER)-negative subtypes. To identify additional genetic variants for ER-negative breast cancer, we conducted the largest meta-analysis of ER-negative disease to date, comprising 4754 ER-negative cases and 31 663 controls from three GWAS: NCI Breast and Prostate Cancer Cohort Consortium (BPC3) (2188 ER-negative cases; 25 519 controls of European ancestry), Triple Negative Breast Cancer Consortium (TNBCC) (1562 triple negative cases; 3399 controls of European ancestry) and African American Breast Cancer Consortium (AABC) (1004 ER-negative cases; 2745 controls). We performed in silico replication of 86 SNPs at P<= 1 × 10(-5) in an additional 11 209 breast cancer cases (946 with ER-negative disease) and 16 057 controls of Japanese, Latino and European ancestry. We identified two novel loci for breast cancer at 20q11 and 6q14. SNP rs2284378 at 20q11 was associated with ER-negative breast cancer (combined two-stage OR = 1.16; P = 1.1 × 10(-8)) but showed a weaker association with overall breast cancer (OR = 1.08, P = 1.3 × 10(-6)) based on 17 869 cases and 43 745 controls and no association with ER-positive disease (OR = 1.01, P = 0.67) based on 9965 cases and 22 902 controls. Similarly, rs17530068 at 6q14 was associated with breast cancer (OR = 1.12; P = 1.1 × 10(-9)), and with both ER-positive (OR = 1.09; P = 1.5 × 10(-5)) and ER-negative (OR = 1.16, P = 2.5 × 10(-7)) disease. We also confirmed three known loci associated with ER-negative (19p13) and both ER-negative and ER-positive breast cancer (6q25 and 12p11). Our results highlight the value of large-scale collaborative studies to identify novel breast cancer risk loci.