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Breast Cancer Research

RESEARCH

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Development and validation of a risk prediction model for premenopausal breast cancer in 19 cohorts

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Abstract

Background Incidence of premenopausal breast cancer (BC) has risen in recent years, though most existing BC prediction models are not generalizable to young women due to underrepresentation of this age group in model development.

Methods Using questionnaire-based data from 19 prospective studies harmonized within the Premenopausal Breast Cancer Collaborative Group (PBCCG), representing 783,830 women, we developed a premenopausal BC risk prediction model. The data were split into training (2/3) and validation (1/3) datasets with equal distribution of cohorts in each. In the training dataset variables were chosen from known and hypothesized risk factors: age, age at menarche, age at first birth, parity, breastfeeding, height, BMI, young adulthood BMI, recent weight change, alcohol consumption, first-degree family history of BC, and personal history of benign breast disease (BBD). Hazard ratios (HR) and 95% confidence intervals (CI) were estimated by Cox proportional hazards regression using age as time scale, stratified by cohort. Given that complete information on all risk factors was not available in all cohorts, coefficients were estimated separately in groups of cohorts with the same available covariate information, adjusted to account for the correlation between missing and non-missing variables and meta-analyzed. Absolute risk of BC (in situ or invasive) within 5 years, was determined using country-, age-, and birth cohort-specific incidence rates. Discrimination

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(area under the curve, AUC) and calibration (Expected/Observed, E/O) were evaluated in the validation dataset. We compared our model with a literature-based model for women < 50 years (iCARE-Lit).

Results Selected model risk factors were age at menarche, parity, height, current and young adulthood BMI, family history of BC, and personal BBD history. Predicted absolute 5-year risk ranged from 0% to 5.7%. The model overestimated risk on average [E/O risk = 1.18 (1.14–1.23)], with underestimation of risk in lower absolute risk deciles and overestimation in upper absolute risk deciles [E/O 1st decile = 0.59 (0.58–0.60); E/O 10th decile = 1.48 (1.48–1.49)]. The AUC was 59.1% (58.1–60.1%). Performance was similar to the iCARE-Lit model.

Conclusion In this prediction model for premenopausal BC, the relative contribution of risk factors to absolute risk was similar to existing models for overall BC. The discriminatory ability was nearly identical (< 1% difference in AUC) to the existing iCARE-Lit model developed in women under 50 years. The inability to improve discrimination highlights the need to investigate additional predictors to better understand premenopausal BC risk.

Keywords Risk prediction model, Premenopausal breast cancer, Young-onset breast cancer

Introduction

Breast cancer (BC) is the leading cancer diagnosis and the leading cause of cancer death among women worldwide [1–4]. While diagnosis prior to menopause is less common than postmenopausal diagnosis, younger age at diagnosis often involves a more aggressive form of disease and is associated with worse prognosis [2, 5–7]. Moreover, younger women are less likely to be diagnosed through screening, as the World Health Organization and most country-specific commissions recommend mammographic screening for average risk women beginning at 50 years of age [8–10], though the US has recently lowered the recommended starting age to 40–45 years [11, 12]. Rising incidence of premenopausal BC globally in recent decades [2, 13] highlights the need to understand risk of BC in young women better, to inform clinical surveillance among younger women.

While several risk prediction models for overall BC with similar sets of risk factors are widely used, including Gail [14], Tyrer-Cuzick [15], and BOADICEA [16, 17] models, most have been developed among primarily postmenopausal women [18]. This limits generalizability to premenopausal women, especially given that associations of some established risk factors, such as adiposity [19, 20], differ by menopausal status, and other risk factors, such as breastfeeding [21] and recent weight change [22], are hypothesized to be more strongly associated with BC risk in premenopausal women. Thus, performance of existing models is generally worse for premenopausal v. postmenopausal women, with lower discriminatory ability and overestimation of risk seen among the premenopausal group [23–25]. Only one model to date has been specifically developed for women < 50 years of age, though relative risk contributions were derived from existing literature and not modeled within cohort data (iCARE 'synthetic' model, hereafter: iCARE-Lit) [26–29].

Here, we leveraged a large international consortium, the Premenopausal Breast Cancer Collaborative Group (PBCCG), to select model risk factors from a set of previously established and hypothesized risk factors that are widely available from standard survey questionnaires and develop a 5-year absolute risk prediction model in premenopausal women. We considered reproductive and lifestyle factors, anthropometrics, and personal and family history.

Methods

Cohort

The PBCCG was created to study risk factors for premenopausal BC by combining data from prospective cohort studies across Europe, North America, Asia, and Australia. Details on cohort design and data harmonization have been described [30]. Briefly, cohorts were eligible to join PBCCG if they had more than 100 cases BC diagnosed before age 55. To date, 22 cohorts have provided baseline questionnaire data, follow-up questionnaire data (where available, N= 17 cohorts), and incident case information to one of two centralized data repositories. Cases (in situ and invasive BC) diagnosed before menopause were identified by self-report, medical record, and/or linkage to cancer registries. Menopausal status was defined using data from multiple questionnaire cycles by (a) self-reported age at menopause (31%), or, where missing, (b) age first known to be postmenopausal if under 50 (1%), or (c) age last known premenopausal if over age 50 (15%), or (d) age 50 if no information on menopausal status was provided (53%). At least one follow-up cycle after age 55 was requested from each cohort to enable retrospective classification of menopausal status if necessary [30, 31]. Variables for future analyses were harmonized using a common protocol at the data centers [30].

Nineteen cohorts were included in this analysis, representing Asia (N= 2), Europe (N= 6), the United States (N= 10), and Australia (N= 1).

Statistical analyses

Individuals were assigned to multiple 5-year risk intervals based on age throughout follow-up, with covariates updated over time based on the most recent questionnaire, with censoring at age of menopause. Within individual cohort studies, if missing for only some individuals, age at menarche, alcohol consumption, BMI at age 18–24 years, and breastfeeding duration were imputed with median values (Table S1). This method was used given low within-cohort missingness (< 10% for each variable within each cohort, details provided in: Supplemental Methods "Within-cohort imputation") and given that low correlations between BC risk factors inhibits usefulness of conditional imputation. Yearly BMI was imputed using linear interpolation to allow for the calculation of recent weight change.

To facilitate internal model validation, the sample was split randomly within cohorts (two-thirds allocated to training dataset and one-third to validation dataset). Model building steps were performed within the training dataset, using STATA version 16 [32]. Cox proportional hazards regression [33, 34], with age as the underlying time-scale and stratified by cohort, was used to estimate hazard ratios (HR) and 95% confidence intervals (CI) for premenopausal BC. Availability of model variables of interest varied by cohort due to either lack of initial cohort data collection or lack of integration into the version of the harmonized dataset used in this analysis. Variables were selected from the following set of established and hypothesized risk factors if $p < 0.05$ by groupwise forward selection: first-degree family history of BC, reproductive factors (age at menarche, parity, age at first birth, breastfeeding), anthropometrics (height, BMI, BMI at age 18–24, recent weight change), current alcohol intake, and personal history of BBD. This method was used to enable incorporation of data from all cohorts in variable selection, despite differences in availability of certain variables. Details on the selection of variables are provided in the Supplemental Methods. To ensure that variables identified as model predictors were not dependent on this selection method, we also performed backwards selection within the set of cohorts with information available on all variables of interest ($N = 8$ cohorts).

After selection, linearity was assessed using Martingale residuals and the assumption of proportional hazards was tested visually by checking plots of Schoenfeld residuals by age in the full model and -ln(-ln(Survival probability) vs. ln(age), and statistically, by interaction tests between each variable and age. No substantial deviations from linearity or proportional hazards were detected (see Supplemental Methods). Because some variables selected into the final model were not available in all cohorts, final risk model coefficients (HRs) were estimated using covariance adjustment and a generalized meta-analysis approach [35]. First, cohorts were grouped based on which of the required regression variables were available. Cox models were run for each group of cohorts. For groups missing the same set of covariates, coefficient estimates for the available covariates were adjusted using the covariance matrix from the studies with complete covariate data. Adjusted estimates were then meta-analyzed with weighting by the inverse variance (see Supplemental Methods). Model coefficients were compared to those derived directly from the subset of cohorts with complete covariate data.

Absolute risk estimates were calculated as:

$$5y\ absolute\ risk = years\ in\ age\ group_j \times \frac{IR_{ijk}}{RR_{ijk}} \times exp^{lp}$$

where $i =$ country, $j = 5\text{-}year$ age groups, $k =$ birth year, and $lp =$ linear predictor from the Cox model. Incidence rates (IR_{ijk})were obtained from the International Agency for Research on Cancer (IARC)'s Global Cancer Observatory (GCO) project (2020), available by region, country, 5-year age groups, and birth cohort from various cancer registries [36, 37]. To align with absolute risk assignment used in existing risk models and ensure incident rates represented average rates within our cohort [14], the obtained IR_{ijk} was divided by RR_{ijk}, the mean relative risk (exp^{lp}) in country i, age group j, and birth year k in our training data sets [14].

Model performance was evaluated in the validation dataset. Discrimination was measured by the area under the curve (AUC) based on (1) linear predictor deciles and (2) absolute risk deciles. Expected and observed relative and absolute risks were calculated and plotted by training data-determined relative or absolute risk deciles, respectively [38]. For calibration within individual studies, deciles were recalculated based on the training data for each study.

We compared performance of our model among the subset of women < 50 y of age with that of the iCARE-Lit model [26–29]. Five-year age group-specific SEER incidence rates were applied when calculating absolute risk for both prediction models. Details are provided in Supplemental Methods.

Invasive-only model

Given that knowledge of risk of in situ or invasive BC can inform screening in younger women, we focused on BC overall as our primary outcome. However, because etiologies of invasive and in situ BC may differ, it is important to separately consider invasive cases. We repeated all analyses using invasive BC as the outcome to account for potential biological differences, to ensure accurate

assignment of global incidence rates, and to facilitate comparison of this model with iCARE-Lit, which was developed among invasive cases [29, 38]. Individuals who developed in situ BC were censored at time of diagnosis.

Among invasive BC cases, we further included a sensitivity analysis testing model variable selection and model performance for ER + and ER- BC separately, censoring at time of BC diagnosis of opposite or unknown subtype.

Results

The analytic cohort included 783,830 premenopausal women, with 9,618 incident premenopausal BC cases followed for 8.1 years on average (max = 25.2 y). The majority of participants were from North America and Western Europe (Table 1) and were White (58%) and non-Hispanic (99%) (Table 2). The average age at baseline questionnaire was 39.9 years (standard deviation, SD = 6.9 y). Most (79%) were parous, with mean age at first birth of 25 years, and 2 births and 15 months of breastfeeding on average. Approximately 10% of the cohort reported a first-degree family history of BC and 17% reported a personal history of BBD. Average BMI at most current questionnaire cycle was 24.0 kg/m^2 (SD = 4.5 kg/m^2), with a lower BMI reported in young adulthood [mean (SD) = 21.2 (3.1) kg/m^2]. Mean four-year weight change prior to the most current questionnaire was + 0.5 kg (Table 2). Approximately 50% of the cohort were current alcohol drinkers. Aside from variables missing by design (Table S2), missingness was low within-cohorts (< 10%) (Supplemental Methods). Compared to the full cohort, in the subset of cohorts with no model variables missing by design (N = 426,128, cases = 5,704), BBD history was more common (31% vs. 17%), while means and proportions of other variables were similar (Table S3).

Relative risk model

Variables selected in the model were age at menarche, parity, height, BMI (current and young adulthood), personal history of BBD, and first-degree family history of BC (Table 3). Variables were consistent when selecting among studies with complete covariate data only and coefficients for the prediction model determined from generalized meta-analysis were similar to those calculated for this subset (N = 284,149, cases = 3,777) (Table 3, Table S4). Lower risk of premenopausal BC was observed with increasing age at menarche [adjusted

Table 1 Distribution of 19 cohorts in the PBCCG (N = 783,830, breast cancer cases = 9,618)

Cohort	Acronym	N (%)	Cases (%)
Europe			
BCN Generations Study	BGS	61,303 (7.8%)	458 (4.8%)
Etude Epidemiologique aupres de femmes de la Mutuelle Generale de L'Education Nationale	E3 N	58,360 (7.5%)	1081 (11.2%)
European Prospective Investigation into Cancer and Nutrition	EPIC	89,464 (11.4%)	921 (9.6%)
The HUNT2 Study	HUNT2	16,955 (2.2%)	44 (0.5%)
Norwegian Women and Cancer Study	NOWAC	76,001 (9.7%)	427 (4.4%)
Swedish Mammography Cohort	SMC	26,329 (3.4%)	157 (1.6%)
The Swedish Women's Lifestyle and Health Study	SWLHS	47,371 (6.0%)	243 (2.5%)
North America (United States)			
California Teachers Study	CTS	46,251 (5.9%)	628 (6.5%)
Campaign against Cancer and Heart Disease	CLUEII	4,099 (0.5%)	47 (0.5%)
Mayo Mammography Health Study	MMHS	5,017 (0.6%)	53 (0.6%)
Nurses'Health Study	NHS	95,012 (12.1%)	1937 (20.1%)
Nurses'Health Study II	NHSII	115,623 (14.8%)	2397 (24.9%)
NYU Women's Health Study	NYUWHS	6,688 (0.9%)	197 (2.0%)
The Sister Study	SIS	16,877 (2.2%)	374 (3.9%)
Southern Community Cohort Study	SCCS	14,126 (1.8%)	55 (0.6%)
US Radiologic Technologists Cohort	USRTC	52,559 (6.7%)	412 (4.3%)
Asia			
Shanghai Women's Health Study	SWHS	33,707 (4.3%)	85 (0.9%)
Singapore Chinese Health Study	SCHS	9,989 (1.3%)	38 (0.4%)
Australia			
Melbourne Collaborative Cohort Study	MCCS	8,099 (1.0%)	64 (0.7%)
Total		**783,830**	**9,618**

Table 2 Characteristics of participants from 19 cohort studies within the PBCCG ($N = 783,830$, breast cancer cases = 9,618)

Characteristic	Mean (SD) or N (%)[a]
Race/Ethnicity	
White	455,286 (58%)
Black	18,836 (2.4%)
Asian	49,200 (6.3%)
Hispanic	5,094 (< 1%)
Other/Unknown	251,791 (32%)
Age at baseline questionnaire (years)	39.9 (6.9)
Age at menarche (years)	12.8 (1.5)
Height (cm)	164.2 (6.5)
BMI (kg/m^2)	24.0 (4.5)
Missing	11,310 (1.4%)
BMI age 18–21 (kg/m^2)[b]	21.2 (3.1)
Missing	23,602 (3.0%)
4-y weight change (kg)[b]	0.5 (1.8)
Missing	35,403 (4.5%)
Current alcohol drinker (yes)	393,978 (50%)
Missing current alcohol use	241,439 (31%)
Alcohol (drinks/week, among current drinkers)[b]	4.2 (8.1)
Missing	40,716 (65%)
Family history of BC[b]	77,747 (9.9%)
Missing	55,482 (7%)
History of benign breast disease[b]	134,266 (17%)
Missing	348,889 (44%)
Parous	618,405 (79%)
Parity (among parous)	2.2 (1.1)
Missing	6 (<0.1%)
Age at first birth (among parous)	25.2 (4.5)
Missing	4,670 (0.8%)
Breastfeeding months (among parous)[b]	15 (11.8)
Missing	120,085 (19%)
Breast cancer cases	**9,618 (1.2%)**
Age at diagnosis (years)	46.4 (4.8)
In situ	1673 (17%)
Invasive	7,914 (82%)
Stage I	2393 (25%)
Stage II	1843 (19%)
Stage III	605 (6.3%)
Stage IV	123 (1.3%)
Unknown	3460 (32%)
In situ vs. invasive status missing	31 (0.3%)
ER Status	
Positive	4,735 (49%)
Negative	1,517 (16%)
Borderline/Unknown	3,366 (35%)
PR status	
Positive	4,097 (43%)
Negative	1,717 (18%)
Borderline/Unknown	3,799 (39%)
HER2 Status	
Positive	657 (6.8%)
Negative	2,877 (30%)
Borderline/Unknown	6,084 (63%)

ER Estrogen receptor, *PR* Progesterone receptor, *HER2* Human epidermal growth receptor 2

[a] Mean (SD) and N (%) after within-cohort imputation

[b] Among cohorts without variable missing by design

Table 3 Beta coefficients and hazard ratios (HR) and 95% confidence intervals (CI) for the PBCCG risk model for premenopausal breast cancer

	Full Dataset[a]		Subset with complete covariate data[b]
Variable	Beta	HR (95% CI)[c]	HR (95% CI)[d]
Age at menarche (per year)	−0.046	0.96 (0.94–0.97)	0.95 (0.93–0.98)
Parity (per child)	−0.131	0.88 (0.84–0.91)	0.89 (0.87–0.92)
Height (cm)[e]	0.110	1.12 (1.03–1.21)	1.17 (1.11–1.23)
BMI (kg/m^2)[f]	−0.124	0.88 (0.82–0.95)	0.92 (0.88–0.95)
BMI age 18–24 (kg/m2)[f]	−0.079	0.92 (0.85–1.01)	0.89 (0.83–0.96)
History of BBD	0.440	1.55 (1.45–1.66)	1.55 (1.45–1.67)
Family history of BC	0.541	1.72 (1.59–1.85)	1.72 (1.58–1.87)

BBD Benign breast disease, *BMI* Body mass index, *PBCCG* Premenopausal Breast Cancer Collaborative Group

[a] Estimates from training dataset, $N = 522,700$ Cases = 6,392

[b] Cohorts include those with no model variables missing by design: BCN Generations Study, E3 N, Nurses' Health Study, Nurses' Health Study II, The Sister Study, Women's Lifestyle and Health Study, Shanghai Women's Health Study. Estimates from training data, $N = 284,149$, Cases = 3,777

[c] Beta estimates calculated following generalized meta-analysis with random effects model, mutually adjusted for all listed variables

[d] Beta estimates calculated directly from Cox PH model results among complete case dataset, mutually adjusted for all listed variables

[e] Estimated per 10 cm

[f] Estimated per 5 kg/m2

HR (aHR) per year (95% CI) = 0.96 (0.94–0.97)], parity [aHR per child = 0.88 (0.84–0.91)], current BMI [aHR per 5 kg/m^2 = 0.88 (0.82–0.95)], and BMI in young adulthood (aHR per 5 kg/m^2 = 0.92 (0.85–1.01)], while higher risk was observed with height [aHR per 10 cm = 1.12 (1.03–1.21)], personal history of BBD [aHR = 1.55 (1.45–1.66)], and first-degree family history of BC [aHR = 1.72 (1.59–1.85)]. The magnitude of the linear predictor, which estimates the log relative risk for an individual based on their covariate distribution, varied substantially by cohort (Table S5).

Absolute risk & model calibration

Five-year absolute risk of BC ranged from 0.00017% to 5.65% for all individuals (Table S5). Overall, the model overestimated absolute risk of premenopausal BC [E/O (95% CI = 1.18 (1.14–1.23)] (Table S6), though calibration varied widely across cohorts. Overestimation was similar in the subset with complete covariate data [E/O = 1.19 (1.14–1.25)] (Table S7). The absolute risk of developing BC was underestimated in lower deciles of absolute risk and overestimated in higher deciles of risk, (Table 4, Fig. 1A). Calibration of relative risk based on covariate-determined risk score deciles showed less overestimation in the upper tails (Fig. 1B). In the subset with complete covariate data, absolute risk calibration was similar, and relative risk was well-calibrated (Figure S1 A, S1B).

Model discrimination was modest, with an AUC of 59.1% (58.1–60.1%) for the full model (Table S6) and similar discrimination in the complete case subset (AUC = 60.2%, 95% CI = 58.9–61.4%) (Table S7). Overestimation was particularly high for the Asian cohorts with limited case numbers.

Comparison with iCARE-Lit < 50 model

Most variables are the same between our model and the iCARE-Lit model, with the exception of alcohol consumption and oral contraceptive use (both used in iCARE-Lit). Given the lack of consistent information on current oral contraceptive use in PBCCG, we considered all participants to be missing this variable when calculating the iCARE-Lit risk. When restricting to women < 50 years of age and comparing our model to the iCARE-Lit model (excluding use of OCs given missing data in PBCCG) performance was similar [our model: AUC = 59.8 (58.2–61.4), E/O = 1.20 (1.13–1.27) vs. iCARE-Lit < 50: AUC = 60.7 (59.0–62.3), E/O = 1.20 (1.13–1.27)].

Table 4 Expected over observed (E/O) ratio and 95% confidence interval (CI) by decile of relative or absolute risk score among 19 cohorts within the PBCCG in testing dataset (*N* = 261,130, breast cancer cases = 3,226)

Decile	E/O (95% CI)	
	By linear predictor decile[a,b]	By absolute risk decile[b]
1	1.40 (1.39–1.42)	0.59 (0.58–0.60)
2	1.19 (1.18–1.20)	0.69 (0.68–0.70)
3	1.19 (1.18–1.19)	0.93 (0.92–0.94)
4	1.22 (1.21–1.23)	0.98 (0.98–0.99)
5	1.32 (1.31–1.33)	1.02 (1.01–1.02)
6	1.12 (1.12–1.13)	1.04 (1.04–1.05)
7	1.12 (1.11–1.13)	1.23 (1.22–1.24)
8	1.11 (1.10–1.11)	1.35 (1.34–1.36)
9	1.20 (1.20–1.21)	1.41 (1.41–1.42)
10	1.15 (1.14–1.15)	1.48 (1.48–1.49)

[a] Linear predictor = $\log_e$ relative risk for individual calculated by the prediction model

[b] Decile of relative risk and absolute risk scores determined by distribution in training dataset

Invasive BC model

There were 7,914 invasive BC cases within the PBCCG cohorts (Table S8). Among those with known estrogen receptor (ER) status, most (75%) had ER + BC (Table S9). The relative risk model included all variables selected in the in situ + invasive model plus alcohol consumption. Following meta-analysis, HR estimates were similar to those in the in situ + invasive model. Though current alcohol was selected into the model as a significant predictor for the full cohort using our procedure (see Supplemental Methods), the HR was not significant in the full cohort after meta-analysis accounting for all cohorts [aHR (95% CI) drinks/week = 1.01 (0.99–1.02)] (Table S10). Alcohol intake remained modestly significantly associated with risk in the complete case model [aHR (95% CI) drinks/week = 1.01 (1.00–1.02)] (Table S10).

Five-year absolute risk of invasive BC ranged from 0.00018% to 5.67%. The invasive-only model overestimated risk more than the in situ + invasive model [average E/O = 1.45 (95% CI = 1.39–1.50)]. Risk was underestimated in the lowest deciles of absolute risk to a lesser degree than in the in situ + invasive model, though risk was highly overestimated in upper risk deciles [e.g., in the 10 th decile of absolute risk, the model predicted 87% more cases than observed (Table S11, Figure S2 A)]. Relative risk was well-calibrated (Figure S2B).

Among women < 50 years of age, discrimination and average calibration were similar for our model and the iCARE-Lit model [our model: AUC = 58.2% (56.3–60%), E/O = 1.49 vs. iCARE-Lit < 50: AUC = 59.3% (57.4–61.1%), E/O = 1.49]. While the iCARE-Lit model was better calibrated in lower risk deciles, overestimation was higher in upper risk deciles [e.g., E/O in decile 10 iCARE-Lit = 2.17 (2.14–2.20) vs. our model = 1.66 (1.64–1.68)].

Model by ER status

Availability of ER-status of cases by cohort is provided in Table S12. Due to limited case numbers for ER-negative BC, we conducted a sensitivity analysis for ER-positive BC only. Variables selected for the ER-positive BC specific model were the same as those chosen in our overall model (Table S13), with a similar contribution to risk for age at menarche, height, parity, BMI, and BMI in young adulthood. Family history of BC and personal history of BBD were weaker risk factors in the ER-positive

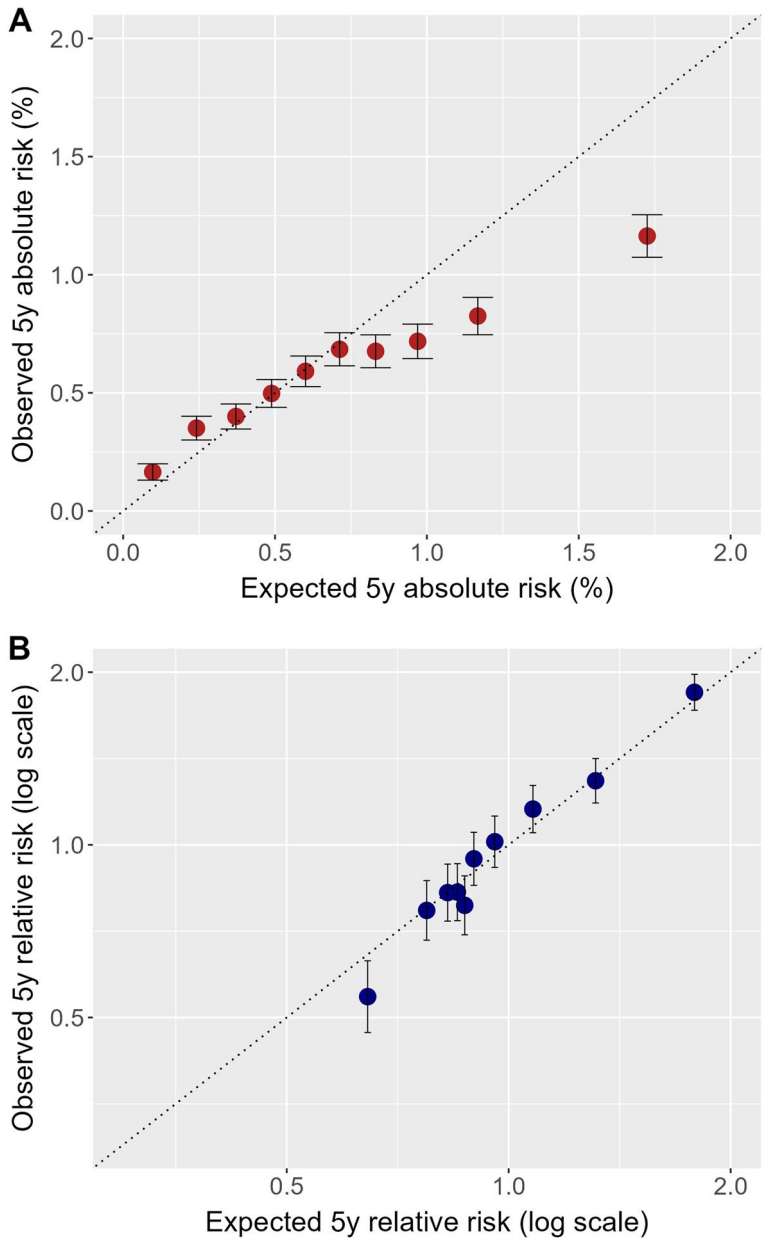


Fig. 1 Calibration for the risk model among 19 cohorts within the PBCCG. E/O within the testing dataset (*N* = 261,130, breast cancer cases = 3,226), for (**A**) absolute risk of BC a by decile of absolute risk in the training dataset and (**B**) relative risk of BC in the testing dataset, by decile of relative risk in the training dataset (log scale)

specific model (Table S13). The ER-positive set overestimated BC risk [E/O overall ER-positive = 2.43 (2.30–2.56)] (Table S14, Figure S3), which may in part to the large amount of missingness for ER-status. Discrimination of the ER-positive model was similar to the overall invasive model [ER-positive: AUC by linear predictor = 58.0% (56.5–59.5%), AUC by absolute risk = 62.2% (60.8–63.6%)].

Discussion

By pooling data from 19 international cohorts, we built an absolute risk prediction model for premenopausal BC informed by the largest set of data on premenopausal women to date. Our model tended to overestimate risk and discrimination remained modest, with performance similar to existing models for overall BC. Other cohorts, which have fewer premenopausal women and/or limited follow-up time compared to PBCCG, are unlikely to

produce better risk predictions using similar variables. To improve premenopausal BC risk prediction, it will be essential to incorporate additional known risk factors (e.g., OC use, polygenic risk score, and mammographic density), to increase granularity of data on existing variables, to test the contribution of novel risk factors such as early life environmental exposures, and to account for gene-environment interactions.

The variables selected in our premenopausal BC risk model matched those included in models for overall BC risk [14, 15, 17, 26]. It is important to note that, while our model included both ER-positive and ER-negative cases, given the much higher proportion of ER + cases, this subtype dominates our results. The strongest risk factors in our model were personal history of BBD and first-degree family history of BC, both of which had HRs consistent with previous models [14, 15, 29]. Personal history of BBD was associated with a 55% increased risk of premenopausal BC in this population, similar to values reported in the Gail model (HR for one biopsy if < 50 years = 1.70) [14], the Tyrer-Cuzick Model (HR for prior biopsy among women < 50 years = 1.26–2.0, depending on biopsy findings) [15], and the iCARE-Lit model (HR for history of BBD = 1.68 for women) [26]. Current estimates for the contribution of family history to overall BC risk vary across the literature, with some using detailed pedigrees [15, 17], and others using simple first-degree family history [39]. We found that first-degree family history of BC was associated with a 72% higher risk of premenopausal BC in this cohort, which is lower than estimates given for iCARE-Lit (< 50 model, aHR = 2.5) [29]. When modeling risk of ER + BC specifically, history of BBD and family history had a lower hazard ratio than in our overall model [aHR BBD = 1.21 (0.61–2.41), aHR family history = 1.67 (1.49–1.87)] suggesting these factors were potentially influenced by risk of ER-negative BC.

Similarities in reproductive factors between our model and existing risk prediction models include inverse associations of age at menarche and parity with premenopausal BC risk. Interestingly, age at first birth was not selected in our model, although a younger age at first birth has been associated with lower risk in cohorts of majority postmenopausal women [14, 15, 29, 40]. The lack of predictive value may be explained by the lag time required after pregnancy to experience the benefit of decreased BC risk following birth; for example, in the PBCCG, pregnancy was positively associated with BC risk up until 24 years after birth [41]. Based on variations in data collection methods across cohorts, we were unable to assess recency of last birth, which may be a more important predictor of risk within premenopausal women [41]. While some studies have reported an inverse association between breastfeeding and risk of premenopausal BC [21, 42–44], breastfeeding was not selected in our model. Heterogeneity across molecular subtypes may have contributed to the lack of selection, as stronger protective associations have been reported for triple negative BC [43], and for luminal Bsubtypes [44]. It is also possible that our results were biased by the high percentage of missingness by design in PBCCG cohorts for breastfeeding.

Our finding that BMI in young adulthood contributed to risk prediction aligns with data suggesting stronger inverse associations between young adult BMI and BC among premenopausal (vs. postmenopausal) women [45–47]. The inverse association between adulthood BMI and premenopausal BC found here follows the paradoxical relationship that is well-established in the literature [47]. While studies have shown increased BC risk among premenopausal women with short-term weight gain [22], and earlier age at BC diagnosis overall with increased annual adulthood weight gain [48], short-term weight change was not selected into our model. Lack of an observed association may be explained by the small average change over four years (+ 0.5 kg), and a narrow distribution of weight changes, precluding our ability to assess more extreme alterations. Further, because the linear interpolation method assumes constancy of weight change over questionnaire cycles, projected values may have been too small.

Our finding that alcohol consumption was selected as a predictor of invasive BC risk but not overall BC aligns with results from a study in the UK Biobank that found alcohol was not a risk factor for ductal carcinoma in situ [49]. Given that intake after in situ BC diagnosis has been associated with development of invasive BC [50], it is plausible that alcohol may play a role in later stages of BC development. However, the exclusion of this variable in our final model may simply be due to chance.

We did not assess the potential contribution of OC use and smoking to risk prediction due to limited detailed information available on these variables in the harmonized dataset, beyond ever vs. never use for OCs and current smoking status, though both remain of interest. A recent meta-analysis found no association for ever vs. never OC use and premenopausal BC risk [51]; however, studies have shown increased premenopausal BC risk for current OC users [52], or recent (< 5 years ago) users [53]. Evaluation is complicated by evidence that the association between OC use and BC differs across molecular subtypes [54], and the wide variation of types and dosages of OCs used across age groups, birth cohorts, and countries. Smoking has been shown to be associated with increased risk of BC only when incorporating information on duration, intensity, and years of quitting smoking [55–57], and, timing of initiation before first childbirth

[57, 58]. In the future, detailed data collection for active and passive [59, 60] smoking and OC use should be prioritized.

Given the small absolute risk of premenopausal BC for most women, the assignment of appropriate population-based incidence rates is essential to accurate risk prediction. We attempted to account for geographic, age, and birth-cohort differences using data collected on invasive BC incidence rates from GCO data [36]. Despite this, absolute risks were overestimated, especially among those with higher risk profiles. While the estimation was imperfect due to our assignment of invasive BC incidence rates to 1,673 in situ BC cases in our cohort, when predicting risk for invasive BC only, estimation was not improved. While this can be explained in part by differences in model specification, which disallows a direct comparison between models, the lack of improvement in the invasive-only model may be indicative of non-representative incidence rates, perhaps due to within-country heterogeneity and varied quality of data for different birth cohorts.

Prior validation of established risk prediction models in the BCN Generations Study demonstrated AUCs based on relative risk scores similar to that of our model [Gail model (AUC = 54.6%), Tyrer-Cuzick model (AUC = 57.0%), and iCARE-Lit < 50y (AUC = 58.8%)] [26]. While the addition of polygenic risk score (PRS), pathogenic variants, and mammographic density have been shown to enhance risk prediction in existing models [61], we did not have data to test these in PBCCG.

Though this is the largest study of premenopausal BC risk modeling to date, there are several limitations to note. First, the PBCCG is still overwhelmingly represented by majority White, Western European and North American Studies, and findings cannot be generalized to diverse populations. The large amount of missing data by design complicated model building and calibration; while we used selection methods and generalized meta-analysis to obtain the most informative set of variables and beta coefficients for our model, coefficient estimates may be biased due to missing data. While the harmonization of menopausal status information was carefully considered in the creation of the PBCCG, it is possible that we have misclassified some individuals missing explicit information on menopausal status, limiting the performance of our risk prediction model.

Overall, the similarity of our model performance to the iCARE-Lit model demonstrates the difficulties of predicting premenopausal BC risk using variables readily obtained from cohort questionnaires and medical records, even with substantial case numbers. The addition of genetic information and breast density may be a first step toward improving risk prediction. However, PRS and RR estimates for BC due to associated variants were developed using data from majority postmenopausal women. Given that interactions between age and PRS, while minimal, have been shown [62], moving forward, it will be important to consider how germline variation uniquely influences premenopausal BC risk. Ultimately, further research into the mechanisms driving premenopausal BC development is necessary to improve clinical risk prediction in younger women.

Conclusions

Here we developed and internally validated the first risk prediction model for premenopausal breast cancer, using questionnaire-based data from over 780,000 women. Our model performed similarly to a literature-derived model for women < 50 years of age, with performance statistics similar to those of existing risk prediction models (developed among primarily postmenopausal women). This indicates that additional variables and/or a deeper level of detail of questionnaire-based variables are needed to better predict premenopausal BC risk.

Abbreviations

BC	Breast cancer
PBCCG	Premenopausal Breast Cancer Collaborative Group
BBD	Benign breast disease
HR	Hazard ratio
CI	Confidence interval
AUC	Area under the curve
E/O	Expected to observed ratio

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s13058-025-02031-8.

Supplementary Material 1: Figure 1. Calibration for the risk model among 19 cohorts within the PBCCG in subset of cohorts with complete covariate data. E/O within the testing dataset, N=141,979, breast cancer cases=1,927) for: (A) absolute risk of BC in testing dataset by decile of absolute risk in the training dataset (B) relative risk of BC in the testing dataset, by decile of relative risk in the training dataset.

Supplementary Material 2: Figure 2. Invasive-only BC model calibration among 19 cohorts within the PBCCG. Observed vs. expected in testing dataset (N=261,130, breast cancer cases=2,640): (A) absolute risk of BC in testing dataset by decile of absolute risk in the training dataset (B) relative risk of BC in the testing dataset, by decile of relative risk in the training dataset.

Supplementary Material 3: Figure 3. ER-positive BC model calibration among 16 cohorts within the PBCCG. Observed vs. expected in testing dataset (Breast cancer cases=1,390): (A) absolute risk of BC in testing dataset by decile of absolute risk in the training dataset (B) relative risk of BC in the testing dataset, by decile of relative risk in the training dataset.

Supplementary Material 4.

Supplementary Material 5.

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Authors' contributions

KDB wrote the manuscript text. KDB and MEJ conducted the statistical analyses. AHE, BR, and RMT conceptualized the idea and KDB, AHE, BR, RMT, and PK developed the methodology. MJS, DPS, KMO and MEJ supplied the harmonized dataset. All authors reviewed the manuscript.

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Data availability

PBCCG data is housed at the Coordinating Centers (Institute of Cancer Research (ICR), London, and The National Institute of Environmental Health Sciences (NIEHS) and the harmonized dataset cannot be transferred to other institutions. Those seeking to conduct an analysis in PBCCG may put in a formal proposal to the Consortium leaders via email and reasonable requests will be considered. Data usage agreements will be required.

Declarations

Ethics approval and consent to participate

Approval from institutional review boards and individual consent for all cohorts in the PBCCG conformed to each study's ethics review requirements.

Consent for publication

The authors give their consent for publication.

Competing interests

The authors declare no competing interests.

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