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THE DOCTOR WILL TALK TO YOU NOW: A DISCUSSION ON PERSONALISED BREAST CANCER RISK IN THE CLINIC

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ABSTRACT

Primary care providers, typically the first healthcare professionals patients interact with, assess the risk of chronic conditions and collect personal and family medical histories. In line with Singapore's mammography screening recommendations, women aged 40-49 should consider consulting their healthcare provider to discuss the advantages and constraints of screening mammography. If necessary, they may undergo annual mammograms. However, the specific content of these discussions is not detailed. This primer focuses on breast cancer risk factors vis-à-vis commonly used screening tools for other chronic diseases that can aid primary care practitioners in evaluating and addressing breast cancer risk in their patients.

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INTRODUCTION

In contemporary medicine, the transition from standardised healthcare approaches to personalised methodologies represents a significant advancement. This shift hinges on the exploration of individuals' genetic, lifestyle, and environmental factors, offering the prospect of precise and individualised medical interventions. Among these evolving paradigms, personalised risk prediction emerges as a pivotal concept, poised to reshape our strategies for disease prevention, early detection, and patient care.

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SCREENING TO STRATIFY RISK

Personalised health risk assessments are not uncommon. Common conditions and tests that are often part of health screenings for individuals at high risk may include cardiovascular risk (blood pressure measurement, cholesterol level check, electrocardiogram for heart rhythm assessment, and body mass index measurement), diabetes risk (haemoglobin A1c or fasting blood sugar tests), bone health (bone density scan for osteoporosis risk), and cervical cancer risk (Pap smear).[1] Risk stratification focuses on assessing an individual's risk level for selected conditions, which helps guide personalised healthcare decisions. The results of these tests flag potential health problems in individuals before they develop a condition and form an essential part of preventive healthcare.

ROUTINE SCREENING FOR EARLY CANCER DETECTION

Screening for cancers, such as colorectal (through colonoscopy or faecal occult blood tests) and breast malignancies (via mammography), enables the detection of conditions that have already developed, often before symptoms become apparent. Routine screening for these cancers involves routine testing to detect the disease in individuals with the goal of early detection and improved treatment outcomes.

The concept of tailoring screening based on individual risk factors, in addition to age and gender, is already integrated into guidelines established by the National Institute for Health and Care Excellence (NICE) and other organisations.[2] An example of this is the provision of more comprehensive breast cancer screening for women with a family history of the disease.[2]

Personalised risk prediction for breast cancer, also known as breast cancer risk stratification, is not always routinely performed in healthcare settings. However, breast cancer does have certain aspects that make personalised risk prediction particularly relevant.

BREAST CANCER HAS A SIGNIFICANT HERITABLE COMPONENT

In a landmark Nordic twin study, breast cancer was one of the three cancers found to exhibit a significant heritable component (27 percent) among 28 anatomical sites.[3,4] This means that genetics explains a portion of breast cancer risk, but a substantial proportion of risk is attributed to non-genetic factors.[4-6]

HETEROGENEITY IN RISK FACTORS

While cancers of the lung and cervix are associated with primary risk factors such as tobacco smoking and HPV infection respectively, it is less straightforward to pinpoint which women are at elevated risk of developing breast cancer. The heterogeneity of breast cancer risk factors makes it challenging to assess a person's risk accurately using a one-size-fits-all approach, emphasising the need for personalised risk prediction.

Breast cancer risk is influenced by a wide range of factors, including genetics, family history, hormone levels, lifestyle, and environmental exposures.[7-9] Studies have shown that a combination of different risk assessment tools, both genetic and non-genetic, can be valuable in identifying women at high risk of breast cancer.[10,11] Ho et al explored how different risk factors, including family history, genetic predisposition, and non-genetic factors, can be used to stratify women's individual risk of developing breast cancer.[10,11] Results from the analysis involving 7,600 Asian breast cancer patients aged 30 to 75 highlight that each type of risk predictor independently identifies women at high risk of breast cancer. The overlap of high-risk women identified did not show a high degree of overlap. This suggests that a comprehensive risk evaluation for complex diseases such as breast cancer should ideally consider different risk factors in tandem.

Van den Broek et al assessed the clinical utility of combining a first-degree family history of breast cancer and a polygenic risk score (PRS) to inform breast cancer screening decisions for women aged 30 to 50 in the 1985 US birth cohort.[12] They compared various screening strategies based on family history and PRS, and found that using both factors together led to the greatest increase in life years gained (29 percent) and prevented breast cancer deaths (18 percent) for this age group. However, it also resulted in more overdiagnosis and false positives. This suggests that family history and PRS can help tailor screening decisions for high-risk women under 50, but an awareness of potential increases in overdiagnoses and false positives is required.

NON-GENETIC RISK FACTORS

Among questionnaire-based risk assessment tools, the Gail model, also known as the Breast Cancer Risk Assessment Tool, was the most widely used, followed by Tyrer-Cuzick, BRCAPRO, and iCARE-Lit.[9,13-15] Named after its creator, Dr Mitchell Gail, the Gail model is designed to estimate an individual's risk of developing breast cancer over a specified time frame based on various risk factors, including age, family history, personal medical history, and reproductive characteristics.[13] By incorporating these factors, the Gail model provides valuable insights to healthcare professionals and patients, aiding in the identification of individuals who may benefit from enhanced breast cancer screening or risk-reduction strategies.

MAMMOGRAPHIC DENSITY

Differences in breast tissue composition are evident in the varying radiographic appearances of the breast. Darker areas on mammograms indicate the presence of fat tissue, while lighter areas correspond to denser tissue, primarily composed of fibroglandular tissue, which includes the functional parenchyma and supporting stroma elements.[16] Mammographic density (MD) is the proportion of these lighter or dense regions on the mammogram and consistently ranks as one of the most significant risk factors for breast cancer.[17] The level of density results from the interplay of hormonal factors and the genetic control of epithelial cell growth.[18] Women in the highest quartile of MD have a risk three to five times greater than women of similar age in the lowest quartile.[19,20]

In the United States, mammography facilities are federally regulated by the Food and Drug Administration (FDA). In March 2023, the FDA issued a regulation mandating that mammogram reports sent to patients should now include a description of breast density, categorising it as either "not dense" or "dense". This requirement is slated to be in full effect by 10 September 2024, ensuring that all mammogram reports sent to patients in the US include information about breast density.[21]

BREAST CANCER SUSCEPTIBILITY GENES

A large multicentre study examined 34 genes known or suspected to be associated with breast cancer in 60,466 breast cancer patients and 53,461 controls. The authors found that protein-truncating variants in *ATM*, *BRCA1*, *BRCA2*, *CHEK2*, *PALB2*, *BARD1*, *RAD51C*, *RAD51D*, or *TP53* were most useful for incorporation into risk prediction panels for breast cancer.[5] An exome sequencing study comprising 26,368 female cases and 217,673 female controls confirmed the involvement of *ATM*, *BRCA1*, *BRCA2*, *CHEK2*, *PALB2*, *MAP3K1*, and identified another gene, *CDKN2A*, that surpassed exome-wide significance.[4] Suggestive evidence was also found for *LZTR1*, *ATR*, and *BARD1*.[4] The authors noted that the collective impact of coding variants in genes not previously associated with known genes is believed to be modest.

POLYGENIC RISK SCORES

Following on from the identification of well-validated high and moderate-risk genes, recent studies have concentrated on more widespread, lower-penetrance gene variations that, when combined, considerably raise the risk of breast cancer.

Over 10 million single nucleotide polymorphisms (SNPs) are thought to exist in the human genome, making them the most prevalent sort of variation found in DNA sequences.[22] SNPs typically only have a little-known functional impact[23] and frequently explain normal variation across people. However, when an SNP occurs within a gene or in a regulatory region close to a gene, the function of the gene may be impacted, which can aid in the onset of illness.

Numerous of these SNPs have been found to be independently linked to a very little increase in breast cancer risk. BC-associated SNPs are more prevalent in the population compared to the pathogenic variants located in high and moderate-risk genes. However, each individual SNP carries a substantially lower risk of developing BC.[22] Nevertheless, with the identification of over 300 such SNPs to date and their cumulative effects, approximately 30 percent of familial heritability can be ascribed to these recognised SNPs.[24,25]

Arguably, the most well-studied PRS in the breast cancer research community is the 313-SNP breast cancer PRS developed by the Breast Cancer Association Consortium.[26,27] In Mavaddat et al, the development dataset included 94,075 individuals with breast cancer and 75,017 individuals without the condition of European ancestry from 69 different studies.[26] Validation was performed in a separate group consisting of 11,428 breast cancer cases and 18,323 controls from 10 prospective studies, as well as 190,040 women from the UK Biobank, which included 3,215 new breast cancer cases.

For the 313-SNP PRS, the odds ratio for developing breast cancer was 1.61 for every 1 standard deviation increase in risk. The area under the receiver-operator curve (AUC) was 0.630, indicating the model's ability to predict breast cancer. Women in the top 1 percent of risk, as determined by their PRS, had a 32.6 percent lifetime risk of developing breast cancer. In comparison to women in the middle quintile of risk, those in the highest 1 percent had a significantly higher risk of developing estrogen receptor-positive and estrogen receptor-negative breast cancer, with risks increased by 4.37-fold and 2.78-fold, respectively. Conversely, those in the lowest 1 percent of risk had substantially lower risks, with reductions of 0.16-fold and 0.27-fold for developing these two types of breast cancer, respectively.

To examine the effectiveness of the 313-SNP PRS in Asian women, Ho et al used a dataset consisting of 17,262 breast cancer cases and 17,695 controls of Asian descent from 13 case-control studies.[28] Additionally, the authors included data from 10,255 Chinese women in a prospective cohort, which encompassed 413 newly diagnosed breast cancer cases.

When comparing women in the highest 1 percent of PRS distribution to those in the middle quintile of risk, Ho et al observed a roughly 2.7-fold increased risk for the former group, while women in the lowest 1 percent of PRS distribution had a decreased risk of about 0.4-fold for developing breast cancer.[28] Importantly, there was no evidence of variations in PRS performance among Chinese, Malay, and Indian women. This indicates that a PRS originally developed for women of European ancestry is also valuable for predicting breast cancer risk in Asian women, and it can contribute to the development of risk-stratified breast cancer screening programmes in Asia.

HOW DO WE RATE SCREENING TOOLS?

Odds Ratio

An odds ratio (OR) serves as a metric for quantifying the connection between a particular exposure and a resulting outcome.[29] A disease odds ratio (OR) of 2 is typically chosen as a threshold when evaluating the utility of risk factors.[30]

Sensitivity

Sensitivity, also known as the true positive rate, represents the fraction of accurate positive test results among all individuals with a particular condition.[31] In simpler terms, it measures a test or instrument's capability to produce a positive outcome for individuals afflicted with the disease.[32] Sensitivity does not provide insights into individuals who received positive test results despite not actually having the disease.[33]

Specificity

Specificity is the proportion of true negative test results among all individuals who do not have a particular disease or condition.[31] In other words, it represents a test or instrument's ability to deliver results within the normal or negative range for individuals who are free of the disease.[32]

Sensitivity and specificity exhibit an inverse relationship: when sensitivity increases, specificity tends to decrease, and vice versa.[34,35] Tests with high sensitivity are more likely to produce positive results for patients with the disease, while highly specific tests are more likely to return negative results for patients without the disease.[35] To gain a comprehensive understanding of a diagnostic test, it is important to consider both sensitivity and specificity together.[36]

Likelihood Ratios

Likelihood ratios (LRs) provide another statistical method for interpreting diagnostic tests. LRs help healthcare providers assess the extent to which using a specific test will influence the probability of a diagnosis.[31]

A positive likelihood ratio, denoted as LR+, signifies the "probability that a positive test result would occur in a patient with the condition divided by the probability of a positive test result in a patient without the condition".[31] In simpler terms, LR+ represents the true rate of positive test results divided by the rate of false positives.[34]

On the other hand, a negative likelihood ratio, referred to as LR-, quantifies the "probability of a patient testing negative for the condition compared to the probability of a patient testing negative who does not have the condition".[31]

Unlike predictive values and like sensitivity and specificity, likelihood ratios are less influenced by the prevalence of the disease. The formulae for calculating likelihood ratios are provided below[37]:

Positive Likelihood Ratio = Sensitivity/(1 - Specificity)
Negative Likelihood Ratio = (1 - Sensitivity)/Specificity

In most situations, LR+ exceeding 10 are indicative of strong evidence favouring the inclusion of a diagnosis, while LR- below 0.1 are typically indicative of strong evidence favouring the exclusion of a diagnosis.[38]

HOW DO GENETIC BREAST CANCER RISK PREDICTORS COMPARE AMONG THEMSELVES?

Table 1 shows the performance of different breast cancer risk predictors in two large Singaporean studies: the Singapore Breast Cancer Cohort (SGBCC) with controls from the Singapore Multi-Ethnic Cohort (MEC) study), and the Singapore Breast Screening Project (SBSP).[39-41]

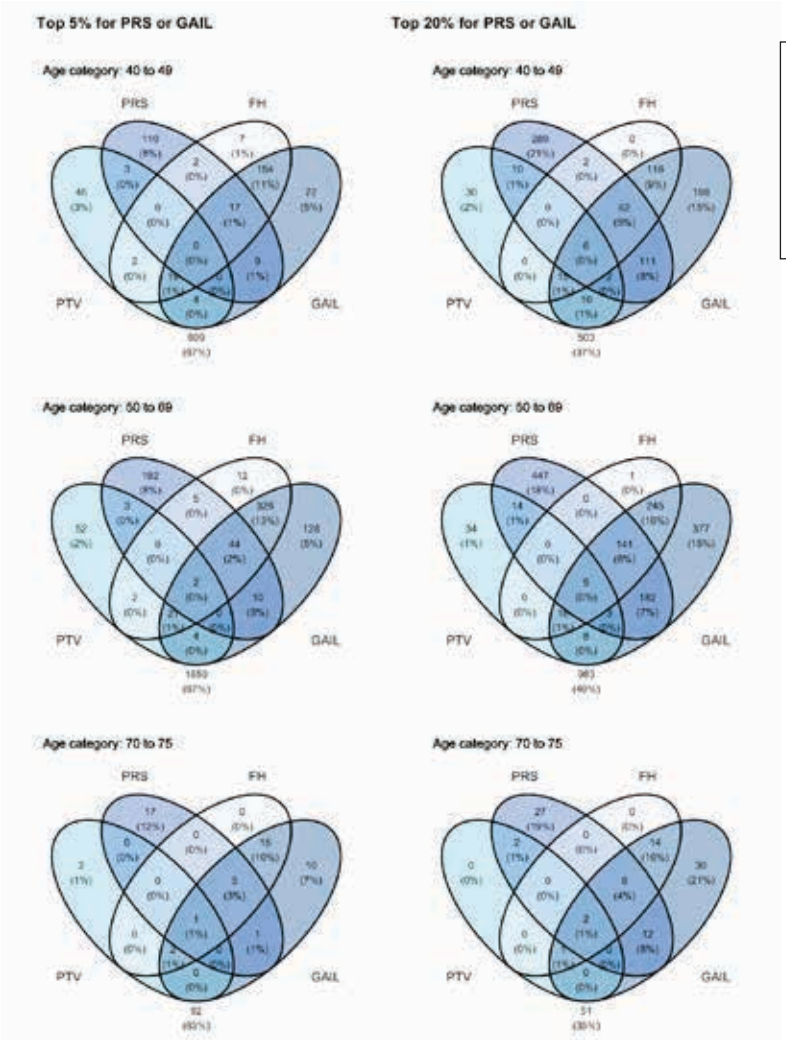
In SBSP, women who self-reported first-degree family history of breast cancer were 3.3 times more likely to develop breast cancer than those who did not. The corresponding sensitivity and specificity values were 7.8 percent and 97.5 percent, respectively.

Carriers of pathogenic variants in any of the nine established breast cancer susceptibility genes (*ATM*, *BRCA1*, *BRCA2*, *CHEK2*, *PALB2*, *BARD1*, *RAD51C*, *RAD51D*, or *TP53*) lead to over 35 times higher risk of developing breast cancer across all age groups. The specificity (1,398/[0+1,398]) is 100 percent. However, the number of true positives comprising pathogenic variant carriers who developed the disease (n=73) is small in comparison to the total number of breast cancer cases in the cohort (with or without pathogenic variants, 1,343). The corresponding sensitivity was 5.4 percent.

As PRS and Gail model risk estimates are in continuous form, a threshold for defining high risk is necessary. When comparing women with the highest PRS and Gail risks (>95th percentile) to the rest of the women in the study population (≤95th percentile), sensitivity and specificity values ranged from 10.4 to 16.6 and 94.1 to 95, respectively. Comparing women with high (>80th percentile) and low risks (≤20th percentile) resulted in higher sensitivity (71.0 to 77.3) but lower specificity (50.0 to 50.4).

The use of multiple risk prediction tools in tandem is important for a comprehensive evaluation of breast cancer risk. **Figure 1** shows the overlap of SGBCC breast cancer patients identified as high-risk by different breast cancer risk factors. Notably, the PRS and Gail risk assessments highlighted distinct groups of women as high-risk, of whom some would have been missed if only one tool had been used. This underscores the need for a multifaceted approach to risk evaluation in the context of breast cancer.

Figure 1. Overlap of breast cancer patients in the Singapore Breast Cancer Cohort (SGBCC) identified as high risk by different breast cancer risk factors. PRS: Polygenic risk score



GAIL : Gail risk score
FH : First-degree family history for breast cancer
PTV : protein-truncating variants in high-risk genes

HOW DO BREAST CANCER RISK PREDICTORS COMPARE TO OTHER SCREENING TESTS?

Table 2 shows the performance of screening tools for breast cancer, diabetes, hypertension, and cardiovascular disease based on published literature. It should be noted that comparing sensitivity, specificity, LR+, and LR- results across different tools or domains should be done cautiously, considering the specific context, methodology, and limitations of each tool.

According to a study by Kerlikowske et al, mammography screening for breast cancer demonstrated high sensitivity (87 percent for 40-49 years, over 90 percent for 50 years and older) and specificity (93-95 percent) for all age groups starting from 40 years.[42] Based on LR+ and LR-, mammography exhibited strong evidence for favouring the inclusion and exclusion of a diagnosis, respectively.

When examining sensitivity and specificity values in the context of screening tests for various chronic conditions, there is considerable diversity in the reported data.[43-47] Specifically, when looking at screening tests for diabetes, such as fasting plasma glucose and haemoglobin A1c (HbA1c), they tend to exhibit a high level of specificity, ranging from 89 to 98 percent. However, the sensitivity values vary considerably, falling between 49 and 82 percent.[43,44]

On the other hand, when considering screening tests for cardiovascular diseases, like total cholesterol (TC) and high-density lipoprotein (HDL) measurements, a different pattern emerges. These tests demonstrate a high level of sensitivity, ranging from 90 to 98 percent, but a more moderate level of specificity, which falls between 37 and 63 percent.[47] Furthermore, in-clinic and home-based blood pressure measurements exhibit a wide range of sensitivity values, spanning from 33 to 88 percent, as well as specificity values that range from 55 to 97 percent.[45,46]

When assessing the effectiveness of breast cancer prediction tools in comparison to established screening methods for chronic conditions, it becomes evident that the LR+ and LR- values closely resemble those seen in blood pressure measurements (refer to **Table 1** and **Table 2**). Focusing solely on LR+ values, breast cancer risk prediction tools exhibit a degree of comparability to screening tests for cardiovascular diseases. While breast cancer risk predictors may lack robust evidence as diagnostic tests, their value emerges in facilitating meaningful discussions regarding individual risk within clinical settings, especially when complemented using mammography screening as an intervention. This underscores the importance of leveraging these tools in practice to enhance patient risk assessment and management. To give perspective, **Table 3** highlights the key differences between breast cancer risk prediction tools and annual health screening tools.

Table 1. Assessment of breast cancer risk predictors.

PTV: Protein truncating variants in at least one of nine genes (*ATM*, *BRCA1*, *BRCA2*, *CHEK2*, *PALB2*, *BARD1*, *RAD51C*, *RAD51D*, or *TP53*)
PRS: 313-SNP breast cancer risk polygenic risk score
Family history: first-degree family history of breast cancer
Gail: Five-year absolute risk calculated from the Gail model
LR+: Positive likelihood ratio
LR-: Negative likelihood ratio
LR+>10 and LR-<0.1 are denoted in bold.

Study	Age (years)	Test	Level	n (%)	Case (%)	OR (95% CI)	Sensitivity (%)	Specificity (%)	LR+	LR-
SGBCC/ MEC[11, 40]	40 to 49 -	PTV	No	2,668 (97%)	1,270 (95%)	1.00 (Reference)				
			Yes	73 (3%)	73 (5%)	Inf	5.4	100	**Inf**	1.0
		PRS	≤95th percentile	2,530 (92%)	1,202 (90%)	1.00 (Reference)				
			>95th percentile	211 (8%)	141 (10%)	2.2 (1.7 to 3.0)	10.5	95	2.1	0.9
			≤20th percentile	419 (36%)	139 (23%)	1.00 (Reference)				
			≥80th percentile	753 (64%)	473 (77%)	3.4 (2.7 to 4.4)	77.3	50	1.5	0.5
	50 to 69	PTV	No	4,371 (98%)	2,376 (97%)	1.00 (Reference)				
			Yes	86 (2%)	84 (3%)	35.3 (11.1 to 214.4)	3.4	99.9	**34.0**	1.0
		PRS	≤95th percentile	4,101 (92%)	2,204 (90%)	1.00 (Reference)				
			>95th percentile	356 (8%)	256 (10%)	2.2 (1.7 to 2.8)	10.4	95	2.1	0.9
			≤20th percentile	696 (37%)	296 (27%)	1.00 (Reference)				
			≥80th percentile	1,196 (63%)	796 (73%)	2.7 (2.2 to 3.3)	72.9	50	1.5	0.5
	70 to 75	PTV	No	242 (98%)	140 (97%)	1.00 (Reference)				
			Yes	5 (2%)	5 (3%)	Inf	3.4	100	**Inf**	1.0
		PRS	≤95th percentile	217 (88%)	121 (83%)	1.00 (Reference)				
			>95th percentile	30 (12%)	24 (17%)	3.2 (1.3 to 8.8)	16.6	94.1	2.8	0.9
			≤20th percentile	41 (37%)	20 (29%)	1.00 (Reference)				
			≥80th percentile	70 (63%)	49 (71%)	2.4 (1.1 to 5.5)	71	50	1.4	0.6
SBSP[8]	50 to 69	Family history	No	23,800 (97%)	309 (92%)	1.00 (Reference)				
			Yes	622 (3%)	26 (8%)	3.3 (2.2 to 4.9)	7.8	97.5	3.1	0.9
		Gail	≤95th percentile	23,200 (95%)	298 (89%)	1.00 (Reference)				
			>95th percentile	1,222 (5%)	37 (11%)	2.4 (1.7 to 3.3)	11	95.1	2.2	0.9
			≤20th percentile	4,886 (50%)	40 (26%)	1.00 (Reference)				
			≥80th percentile	4,885 (50%)	113 (74%)	2.9 (2.0 to 4.2)	73.9	50.4	1.5	0.5

Table 2. Assessment of screening tools for common chronic diseases.

FPG: Fasting Plasma Glucose
HbA1c: haemoglobin A1c
TC: total cholesterol
HDL: high-density lipoprotein
LR+: positive likelihood ratio
LR-: negative likelihood ratio

Test	Reference	Sensitivity (%)	Specificity (%)	LR+	LR-
Breast cancer					
Mammography (age in years)	10.1001/jama.276.1.39[42]				
40-49		87	93-95	**11.7-18.0**	0.2-0.1
50-59		94		**12.6-20.0**	**0.07**
60-69		94		**12.7-19.6**	**0.06**
≥70		91		**12.3-19.0**	**0.09-0.10**
Diabetes					
FPG ≥104 mg/dL	10.1371/journal.pone.024241[43]	82	89	7.8	0.2
FPG ≥126 mg/dl	10.3389/fmed.2023.1016381[44]	49	98	**20**	0.5
HbA1c ≥6.5 percent	10.1371/journal.pone.0242415[43]	50	97.3	**18.5**	0.5
HbA1c ≥6.5 percent	10.3389/fmed.2023.1016381[44]	51	96	**12.8**	0.5
Hypertension					
Blood pressure (clinic)	10.1186/s12872-017-0491-8[45]	33-65	75-97	1.3-**21.7**	0.4-0.9
Blood pressure (clinic)	10.1001/jama.2020.21669[46]	80	55	1.8	0.4
Blood pressure (home)	10.1186/s12872-017-0491-8[45]	68-88	64-80	1.9-4.4	0.2-0.5
Blood pressure (home)	10.1001/jama.2020.21669[46]	84	60	2.1	0.3
Cardiovascular disease					
Euro Task Force (TC)	10.1093/qjmed/92.7.379[47]	98	37	1.6	**0.05**
Sheffield Table (TC)	10.1093/qjmed/92.7.379[47]	90	43	1.6	0.2
Sheffield Table (TC:HDL)	10.1093/qjmed/92.7.379[47]	97	60	2.4	**0.05**
NZ Chart (TC:HDL)	10.1093/qjmed/92.7.379[47]	90	63	2.4	0.2

Table 3. Key differences between breast cancer risk prediction tools and annual health screening tools.

Aspect	Breast cancer risk prediction tools	Annual health screening tools
Purpose	Personal breast cancer risk	Comprehensive health assessment
Timing	Assess long-term risk for developing breast cancer, often for a lifetime (genetic tests) or a specific period (Gail risk score)	Conducted annually
Outcome	Risk score for breast cancer	Data on various health indicators
Invasiveness	Non-invasive; genetic data may be derived from both saliva and blood samples	Generally non-invasive, may include blood draw
Preventive measures	Lifestyle changes, awareness, targeted screening	Early intervention and prevention

CAVEATS OF BREAST CANCER RISK STRATIFICATION

There is a growing recognition of the importance of personalised breast cancer risk assessment.[48-50] Some healthcare systems and breast health clinics are implementing risk stratification programmes, especially for individuals with a family history of breast cancer or other significant risk factors.[48]

Many anticipate that individual risk prediction could enhance cancer screening initiatives by enabling earlier or more frequent screening for individuals with elevated personal risk.[51] For instance, there is a suggestion to provide annual mammograms to women aged 40-50 whose personal scores indicate a moderate or high risk of breast cancer.[51] This approach has the potential to identify additional breast cancer cases but might come at the expense of false positive results, and many cases might still go undetected.[51]

Different rates of participation and adherence among the target population can also significantly reshape the pathways of screening programmes.[52] The effectiveness of screening hinges on the active involvement of both the target population and healthcare providers.[52] While lower compliance may lead to reduced screening and diagnostic expenses, it can also result in a greater disease burden if non-compliant individuals are diagnosed at more advanced and costly-to-treat stages. Additionally, screening efforts may incur elevated costs without yielding improvements in health outcomes if patients identified through screening fail to follow the recommended treatment due to issues with test reliability.

It is also important to note that the adoption of PRS as a risk prediction tool in clinical practice is not yet widespread.[27,53,54] There are still challenges to overcome, including ensuring the accuracy and reliability of PRS, addressing ethical and privacy concerns related to genetic data, and establishing clear guidelines for its use.[55]

A GOOD HEALTH SYSTEM OR A GREAT HEALTH SYSTEM

For general practitioners, who serve as primary healthcare providers, personalised risk prediction holds noteworthy implications. It presents a framework for navigating the intricate landscape of patient health with heightened accuracy and anticipatory insight. Traditional reliance on generic risk assessments is giving way to a new era where each patient's distinct genetic, clinical, and lifestyle attributes can inform medical decisions and recommendations.

The current public involvement efforts primarily emphasise the promotion of the national screening programme and its advantages, offering limited information or direction regarding tests that are not officially recommended (10.1186/s12910-022-00798-5.[56] Effective healthcare conversations between doctors and patients are built on trust and open communication. When patients are informed about all available testing options, they can engage in more informed decision-making with their healthcare providers. In cases where patients have access to comprehensive information, they can engage in more meaningful dialogues with their healthcare providers. These conversations have the potential to foster a stronger doctor-patient bond, with shared decision-making and trust at the core.

Sir William Osler, a renowned physician, underscores the importance of considering multiple factors in medical practice: "The good physician treats the disease; the great physician treats the patient who has the disease." A modified version of the quote that applies to personalised health screening would be that "The good health screener detects the condition; the great health screener detects the individual behind the condition." This adaptation highlights the idea that effective health screening goes beyond identifying specific conditions and considering the unique characteristics, risk factors, and needs of the individual undergoing the screening. It highlights the importance of a personalised approach to health assessment and screening.

CONCLUSION

Adopting a risk-based approach to breast cancer screening represents a significant stride towards personalised and more effective healthcare. By tailoring screening strategies to individual risk profiles, we can optimise the balance between early detection and minimising unnecessary interventions. This approach not only acknowledges the diverse nature of breast cancer risk but also empowers individuals with the knowledge needed to make informed decisions about their health. As we navigate the complexities of breast cancer screening, embracing a risk-based paradigm promises to enhance both the efficiency of healthcare resources and the overall well-being of those undergoing screening. The future of breast cancer screening lies in its ability to adapt to the unique needs of each individual, fostering a more targeted and patient-centric approach to early detection and prevention.

DECLARATION OF CONFLICT OF INTERESTS

The authors declare that they have no conflict of interest in relation to this article.

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LEARNING POINTS

- **There are many breast cancer risk calculators. A personalised risk assessment for breast cancer should ideally comprise a combination of genetic and non-genetic risk calculators.**
- **Each risk predictor has constraints in forecasting disease outcomes, given that a substantial portion of an individual's disease susceptibility arises from factors beyond the scope of what they can assess.**
- **Failing to communicate this limitation effectively may lead to an undue emphasis on the significance of individual risk factors, potentially undercutting the effectiveness of existing screening programmes.**