

A computational genetic model will make it possible to predict increased genetic risk for breast cancer

August 15 2023



Micrograph showing a lymph node invaded by ductal breast carcinoma, with extension of the tumour beyond the lymph node. Credit: Nephron/Wikipedia

Researchers at Tel Aviv University have developed a computational model that makes it possible to predict each woman's genetic risk of developing breast cancer based on her genetic profile. The research was based on a large-scale international study that included genomic data of about a quarter of a million women with and without breast cancer, and applied its findings to about 2,000 Israeli women. The team of researchers explain, "Our method will allow the health system to move to a personalized early detection policy—when those who are identified as being at high risk will be tested from a younger age and more frequently. Focusing the screening tests using the model may save lives and will save health system resources."

The research was conducted by doctoral student Hagai Levi, under the guidance of Prof. Rani Elkon from the Department of Human Molecular Genetics and Biochemistry at the Tel Aviv University School of Medicine, and Prof. Ron Shamir from the Blavatnik School of Computer Science at Tel Aviv University. The research was carried out in collaboration with Prof. Shai Carmi from the Faculty of Medicine at Hebrew University, with Prof. Shay Ben Shachar—Director Of Precision Medicine and Genomics at Clalit Research Institute, and with Dr. Naama Elefant from the Hadassah University Medical Center. The study is published in the *Journal of Medical Genetics*.

Prof. Elkon explains that in 2003, the sequencing of a draft of the human genome was completed, creating new opportunities for improvement in medicine, with an emphasis on personalized medicine. The basic idea was that the better we know how to determine whether a certain person is genetically predisposed to a certain disease, the more we can take appropriate preventive measures.

Prof. Elkon adds that since then, extensive research effort has been invested to identify genetic differences between people which may indicate a genetic susceptibility to specific diseases, especially the

common ones such as cancer, heart disease, diabetes, schizophrenia, and Alzheimer's. Studies of this type, known as Genome-Wide Association Studies (GWAS), compare the genomes of sick and healthy people, and find hundreds of genetic variants whose presence is associated with increased risk of having the disease being studied. Each variant by itself increases the risk to a very small degree, but when a significant number of relevant variants accumulate in the genome of a certain person, their risk of getting sick increases significantly.

The studies assign a "[genetic risk](#) score" to each participant, and in large samples, these scores typically follow a bell distribution: The majority of the population are in the middle, and at the two extremes are people with extremely high or low risk scores of having the same disease. The challenge of medicine is to identify in advance those people who have a high genetic tendency to get sick, especially of diseases that can be prevented or detected in early stages.

The current study was based on the findings of a huge international GWAS study that identified genetic variants associated with breast cancer by analyzing the genetic profiles of approximately 130,000 breast cancer patients from dozens of medical centers in Europe and the United States alongside approximately 100,000 healthy women who served as a control group.

The team of researchers from Tel Aviv University wanted to check if the findings of the international study could be used to reliably predict the risk of breast cancer of Israeli women, using a sample of about 1,000 patients and about 1,000 healthy women, collected by Prof. Gad Rennert from the Carmel Medical Center.

"If a genetic predisposition to breast cancer is discovered in a woman, there is something that can be done. Early detection may save lives," emphasizes Prof. Elkon, and continues, "It is important to note that at

this stage our research focused on Jewish women of Ashkenazi origin, which is the population closest genetically to the participants of the international study on which our model was based."

The researchers built a computational genetic model to predict the risk to the Israeli participants by determining a 'genetic risk score' for each woman and dividing the participants into deciles according to the risk score they received. The findings revealed that women in the top decile of the score calculated by the model have a four times higher chance of getting breast cancer compared to women in the bottom decile. In other words, the genetic risk score has a significant ability to predict the risk of breast cancer among the population examined. The researchers confirmed their findings on another sample of [breast cancer patients](#) collected by physician-researchers in the oncology and genetics departments at the Hadassah Medical Center.

Prof. Elkouf concludes, "Our research revealed that we already have the tools to identify, based on their genetic profile, Israeli women with an increased risk of developing breast [cancer](#). According to the risk score it is possible to recommend that women at high risk of [breast cancer](#) start screening tests for early detection from a younger age, and more frequently. Such a policy may save lives and allow more efficient use of the health system's resources. We hope that the promising results will lead to clinical use of the prediction method we developed and will improve the early detection of this disease. Our research group is now starting a follow-up study, in collaboration with Prof. Rinat Yerushalmi, Director of the Breast Oncology Unit at Beilinson Hospital, which will focus on collecting data and building a genetic model to calculate the risk of the disease for [women](#) of all ethnicities in Israel."

More information: Hagai Levi et al, Evaluation of European-based polygenic risk score for breast cancer in Ashkenazi Jewish women in Israel, *Journal of Medical Genetics* (2023). [DOI:](#)

[10.1136/jmg-2023-109185](https://doi.org/10.1136/jmg-2023-109185)

Provided by Tel-Aviv University

Citation: A computational genetic model will make it possible to predict increased genetic risk for breast cancer (2023, August 15) retrieved 2 May 2024 from <https://medicalxpress.com/news/2023-08-genetic-breast-cancer.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.