Studies biased toward white genomes still predict cancer risk in diverse groups

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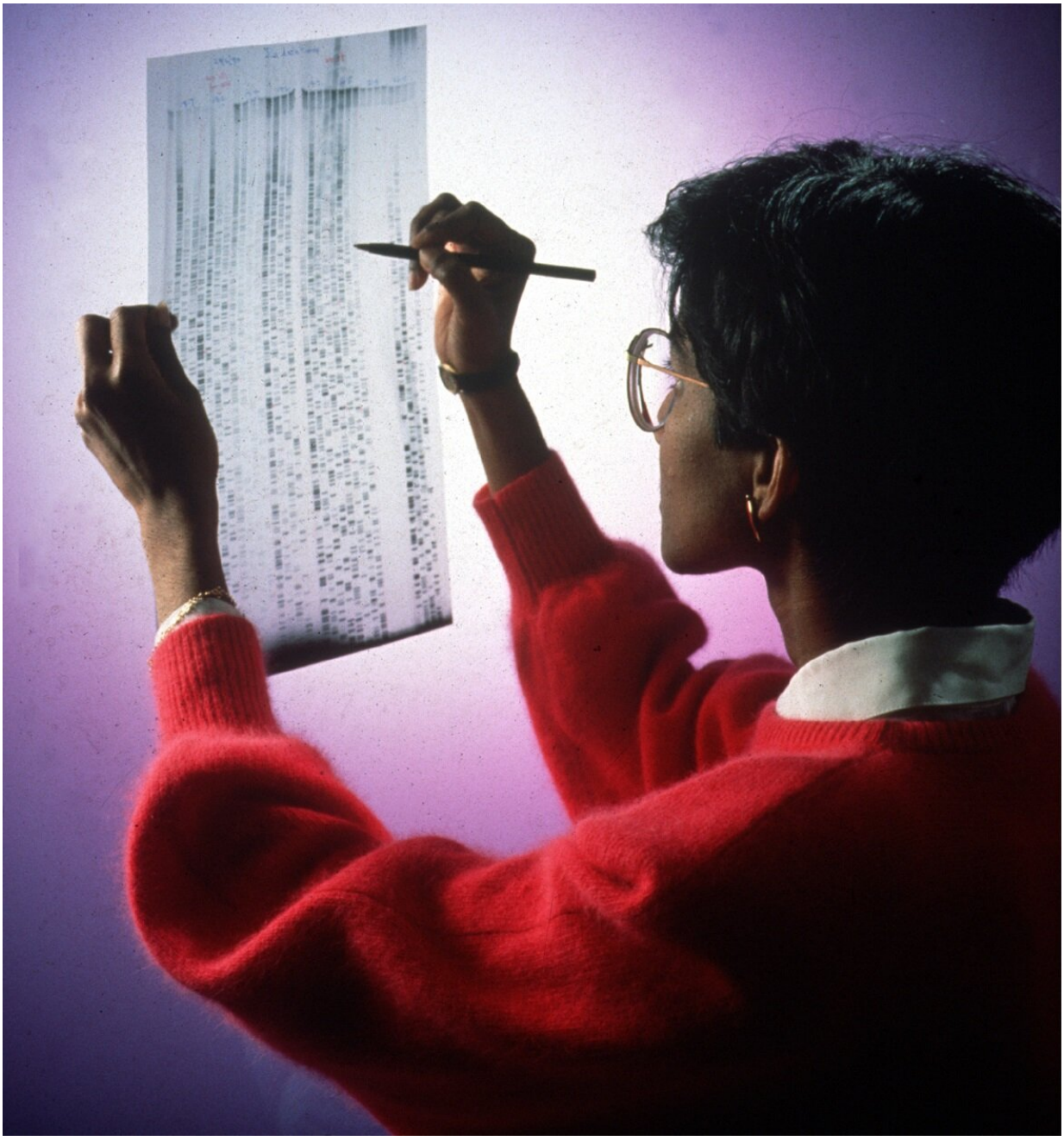

Sequencing DNA. Credit: CSIRO, Wikimedia, CC-BY 3.0 (creativecommons.org/licenses/by/3.0/)

Data sets that are biased by having too many genomes from people with European ancestry can still be applied to other ancestry groups to predict their risk of developing breast and prostate cancer. Lars Fritsche of the University of Michigan and colleagues report these findings in a new study published September 16th in *PLOS Genetics*.

Genome-wide association studies (GWAS) use hundreds or thousands of genomes to find genetic variations linked to specific traits or diseases. Ultimately, geneticists hope to use GWAS results to assign individuals a polygenic risk score (PRS) that predicts their risk of developing a complex disease involving multiple genes, such as diabetes or heart disease, based on which variations they carry. However, most known genetic risk factors, especially for cancer, are based almost exclusively on studies of individuals with European ancestry. Currently, it is unclear if these results can be used to estimate a PRS for people from other groups.

In the new study, researchers used GWAS results from people with European ancestry and data from the UK Biobank to calculate a PRS for breast and prostate cancer for people with African, East Asian, European and South Asian ancestry. They discovered that when they scaled the risk scores within each group, they could identify individuals at higher risk of breast and prostate cancer. The findings suggest it is possible to apply existing European ancestry GWAS results to provide risk scores for people with diverse ancestry.

Of course, this is only a temporary solution. The researchers emphasize that scientists must recruit more diverse participants for GWAS analyses if they hope to realize the full potential of PRS in helping to detect and prevent cancer across ethnic groups.

"Surprisingly, the use of summary statistics from very large, European-based cancer GWAS for PRS construction and their ancestry specific scaling provided meaningful predictors of cancer risk," the researchers add. "While the performance of the breast and prostate cancer PRS was decent across all analyzed ancestry groups, the applicability of such a compromise solution needs to be evaluated on a case-by-case basis."

More information: Fritsche LG, Ma Y, Zhang D, Salvatore M, Lee S, Zhou X, et al. (2021) On cross-ancestry cancer polygenic risk scores. *PLoS Genet* 17(9): e1009670. doi.org/10.1371/journal.pgen.1009670

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