



Original Investigation | Genetics and Genomics

Association of Rare Pathogenic DNA Variants for Familial Hypercholesterolemia, Hereditary Breast and Ovarian Cancer Syndrome, and Lynch Syndrome With Disease Risk in Adults According to Family History

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Abstract

IMPORTANCE Pathogenic DNA variants associated with familial hypercholesterolemia, hereditary breast and ovarian cancer syndrome, and Lynch syndrome are widely recognized as clinically important and actionable when identified, leading some clinicians to recommend population-wide genomic screening.

OBJECTIVES To assess the prevalence and clinical importance of pathogenic or likely pathogenic variants associated with each of 3 genomic conditions (familial hypercholesterolemia, hereditary breast and ovarian cancer syndrome, and Lynch syndrome) within the context of contemporary clinical care.

DESIGN, SETTING, AND PARTICIPANTS This cohort study used gene-sequencing data from 49 738 participants in the UK Biobank who were recruited from 22 sites across the UK between March 21, 2006, and October 1, 2010. Inpatient hospital data date back to 1977; cancer registry data, to 1957; and death registry data, to 2006. Statistical analysis was performed from July 22, 2019, to November 15, 2019.

EXPOSURES Pathogenic or likely pathogenic DNA variants classified by a clinical laboratory geneticist.

MAIN OUTCOMES AND MEASURES Composite end point specific to each genomic condition based on atherosclerotic cardiovascular disease events for familial hypercholesterolemia, breast or ovarian cancer for hereditary breast and ovarian cancer syndrome, and colorectal or uterine cancer for Lynch syndrome.

RESULTS Among 49 738 participants (mean [SD] age, 57 [8] years; 27 144 female [55%]), 441 (0.9%) harbored a pathogenic or likely pathogenic variant associated with any of 3 genomic conditions, including 131 (0.3%) for familial hypercholesterolemia, 235 (0.5%) for hereditary breast and ovarian cancer syndrome, and 76 (0.2%) for Lynch syndrome. Presence of these variants was associated with increased risk of disease: for familial hypercholesterolemia, 28 of 131 carriers (21.4%) vs 4663 of 49 607 noncarriers (9.4%) developed atherosclerotic cardiovascular disease; for hereditary breast and ovarian cancer syndrome, 32 of 116 female carriers (27.6%) vs 2080 of 27 028 female noncarriers (7.7%) developed associated cancers; and for Lynch syndrome, 17 of 76 carriers (22.4%) vs 929 of 49 662 noncarriers (1.9%) developed colorectal or uterine cancer. The predicted probability of disease at age 75 years despite contemporary clinical care was 45.3% for carriers of familial hypercholesterolemia, 41.1% for hereditary breast and ovarian cancer syndrome, and 38.3%

(continued)

Key Points

Question What is the prevalence and clinical importance of pathogenic DNA variants in genes associated with familial hypercholesterolemia, hereditary breast and ovarian cancer syndrome, and Lynch syndrome in a national biobank?

Findings In this cohort study of 49 738 participants in the UK Biobank, a pathogenic or likely pathogenic variant associated with the 3 genomic conditions was identified in 0.9% of participants. These individuals had an increased risk of disease identified by gene sequencing that was not found through self-reported family history.

Meaning The findings suggest that some participants in the UK Biobank harbored a pathogenic variant associated with familial hypercholesterolemia, hereditary breast and ovarian cancer syndrome, or Lynch syndrome and may have an increased risk of disease even within the context of routine clinical care; genomic screening efforts may enhance detection and treatment for these individuals.

+ Supplemental content

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Abstract (continued)

for Lynch syndrome. Across the 3 conditions, 39.7% (175 of 441) of the carriers reported a family history of disease vs 23.2% (34 517 of 148 772) of noncarriers.

CONCLUSIONS AND RELEVANCE The findings suggest that approximately 1% of the middle-aged adult population in the UK Biobank harbored a pathogenic variant associated with any of 3 genomic conditions. These variants were associated with an increased risk of disease despite contemporary clinical care and were not reliably detected by family history.

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Introduction

Identification of individuals at high risk for cardiovascular disease or cancer remains a major public health need.¹ Because these diseases have a genetic component, one approach is to use inherited DNA variation to stratify the population. The United States Centers for Disease Control and Prevention has identified 3 tier-1 genomic conditions in which genetic testing to identify carriers of a pathogenic variant may be particularly useful: familial hypercholesterolemia, hereditary breast and ovarian cancer syndrome, and Lynch syndrome.²⁻⁴

Pathogenic variants in any of 9 genes associated with these 3 genomic conditions perturb key driving pathways in disease pathogenesis.⁵⁻⁷ Familial hypercholesterolemia variants accelerate development of atherosclerotic cardiovascular disease by preventing clearance of atherogenic low-density lipoproteins (LDLs) from the circulation.⁸ Those associated with hereditary breast and ovarian cancer syndrome confer increased risk of breast, ovarian, and other malignant tumors by disrupting tumor suppressor genes integral to DNA repair.⁹ Lynch syndrome variants are associated with colorectal, uterine, and other cancers through perturbation of DNA mismatch repair pathways.¹⁰

These genomic conditions remain underdiagnosed and undertreated in current clinical practice; if identified, evidence-based screening or therapies to attenuate risk are available. Such interventions include lipid-lowering therapy, which has been associated with up to a 76% reduced risk for cardiovascular disease among patients with familial hypercholesterolemia^{11,12}; prophylactic mastectomy, which has been associated with up to a 90% reduced risk for breast cancer among patients with hereditary breast and ovarian cancer syndrome¹³; and screening colonoscopies, which have been associated with up to a 62% reduced risk for colorectal cancer among patients with Lynch syndrome.¹⁴

The traditional approach, which is currently recommended by clinical guidelines, has focused on genetic testing for individuals affected by disease and their family members.¹⁵⁻¹⁹ However, this phenotype-first past may give way to a genotype-first future. In this paradigm, population-based genomic screening may identify high-risk individuals before disease onset, enabling targeted screening or prevention.^{20,21}

Population genomic screening has become increasingly feasible because of rapid decreases in the cost of gene sequencing and is already underway or planned in several health care systems and national biobanks.²²⁻²⁴ However, several areas of uncertainty remain. First, the prevalence of pathogenic variants assessed using systematic gene sequencing and clinical-grade variant classification in a large population of otherwise unascertained adults has not been fully characterized. Previous studies have either been small (performing clinical-grade variant classification of up to 1640 individuals, noting a prevalence ranging from 0.9% to 1.5%)^{23,25,26} or restricted to a single disease entity.⁵⁻⁷ Second, contemporary clinical care has expanded efforts to prevent or screen for cardiovascular diseases and cancer; the relative and absolute risks of disease among pathogenic variant carriers within the context of such care warrants further study. Third, whether family history of disease can serve as a reliable proxy for pathogenic variant status and the

incremental risk of a pathogenic variant among individuals stratified by family history has not been fully explored.

We analyzed gene sequencing data from participants of the UK Biobank and used clinical-grade variant classification to assess the prevalence of pathogenic or likely pathogenic variants for the 3 tier-1 genomic conditions. Next, we assessed the association of such variants with family history of disease and the clinical importance of such variants within the context of contemporary clinical care.

Methods

Study Design, Setting, and Participants

This cohort study used data from the UK Biobank, which enrolled more than 500 000 individuals between the ages of 40 and 69 years from 22 sites across the UK between March 21, 2006, and October 1, 2010.^{27,28} Analysis of data from the UK Biobank data was approved by the Mass General Brigham institutional review board in Boston, Massachusetts, and was performed under UK Biobank application #7089. All participants provided electronic informed consent at their initial visit. This study followed the Strengthening the Reporting of Observational Studies in Epidemiology (STROBE) reporting guideline.²⁹

All 49 738 participants with whole exome sequencing data available were included in this analysis. Family history of disease in parents and siblings was reported by participants using a structured assessment tool at the time of enrollment. The LDL cholesterol concentrations and medication lists were assessed at time of enrollment as part of the study protocol, enabling estimation of untreated levels as described previously (eTable 1 in the Supplement).³⁰ At the initial study visit, participants completed questionnaires about health history and lifestyle and underwent physical assessment and phlebotomy.²⁸

Exome Sequencing and Variant Classification

Whole exome sequencing, which enables identification of genetic variants affecting the protein-coding region of each gene, was performed for UK Biobank participants as described previously.³¹⁻³³ Additional details with respect to sequencing and quality control are available in the eMethods in the Supplement. Either of 2 laboratory geneticists (H.M.S. and M.L.), who were certified by the American Board of Medical Genetics and Genomics and who were blinded to any phenotype information, classified the pathogenicity of observed variants in 9 genes known to be associated with any of 3 genomic conditions according to current clinical standards.³⁴ Variants for which classification was not straightforward because of limitations in available evidence were reviewed by both geneticists to arrive at a consensus opinion. These 9 genes included 3 associated with familial hypercholesterolemia (*APOB* [OMIM:107730], *LDLR* [606945], and *PCSK9* [607786]), 2 associated with hereditary breast and ovarian cancer syndrome (*BRCA1* [113705], *BRCA2* [600185]), and 4 associated with Lynch syndrome (*MLH1* [120436], *MSH2* [609309], *MSH6* [600678], and *PMS2* [600259]).

Clinical End Points

Primary end points were composites specific to each genomic condition: coronary artery disease, ischemic stroke, and peripheral artery disease for familial hypercholesterolemia; breast or ovarian cancer for hereditary breast and ovarian cancer syndrome; and colorectal and uterine cancer for Lynch syndrome. Case definitions for each primary end point were defined in the UK Biobank using a combination of self-reported data confirmed by trained health care professionals, hospitalization records, and national procedural, cancer, and death registries. End points were assessed based on hospital inpatient data dating back to 1977, cancer data dating back to 1957, and death registry data available from time of initial enrollment from 2006 onward.³⁵ Additional details with respect to disease ascertainment are available in the eMethods in the Supplement.

Statistical Analysis

Statistical analysis was performed from July 22, 2019, to November 15, 2019. Comparison of baseline characteristics between carriers of pathogenic or likely pathogenic variants and noncarriers was performed with the χ^2 test for categorical variables and analysis of variance for continuous variables. Missing data were excluded. Hazard ratios for disease comparing carriers with noncarriers were calculated using Cox proportional hazards regression models with the covariates of enrollment age, sex, and genetic ancestry, as quantified by the first 4 genetic principal components.³⁶ The age-dependent probability of disease in variant carriers and noncarriers was quantified using a Cox proportional hazards regression model adjusted for sex and the first 4 genetic principal components, with model standardized to the mean of each of the covariates. This model was extended to include family history and, when statistically significant, its interaction with carrier status. Statistical analyses were performed using R software, version 3.5 (R Project for Statistical Computing). Statistical significance was set at $P < .05$, and 2-sided P values were used.

Results

Sequencing of genetic samples from 49 738 participants (mean [SD] age, 57 [8] years; 27 144 female [54.6%]) identified 8777 total variants present in the 9 genes known to be associated with any of the 3 genomic conditions, including 3543 (40.4%) variants in genes associated with familial hypercholesterolemia, 2269 (25.9%) in genes associated with hereditary breast and ovarian cancer syndrome, and 2965 (33.8%) in genes associated with Lynch syndrome. Initial bioinformatic filtering was performed on this list of variants, restricting to those predicted to result in loss of function, rare missense variants (the maximum population allele frequency <0.005 in Genome Aggregation Database, a publicly available genetic variant frequency database),³⁷⁻³⁹ or variants that were previously classified as pathogenic or likely pathogenic in the ClinVar database (**Figure 1**).⁴⁰ This filtering resulted in 3599 candidate variants for subsequent classification, performed according to current clinical criteria by clinical laboratory geneticists blinded to any phenotype information.³⁴ A total of 232 variants met stringent clinical criteria to be classified as pathogenic or likely pathogenic, including 50 associated with familial hypercholesterolemia, 133 with hereditary breast and ovarian cancer syndrome, and 49 associated with Lynch syndrome. Details regarding evidence used to support pathogenicity assertions are provided for each variant in eTable 2 in the [Supplement](#).

A total of 441 individuals harbored any of these 232 pathogenic or likely pathogenic variants, corresponding to a prevalence of 0.89% (95% CI, 0.80%-0.98%). These individuals included 131 (0.26%; 95% CI, 0.22%-0.31%) with a variant associated with familial hypercholesterolemia, 235 participants (0.47%; 95% CI, 0.41%-0.54%) with a variant associated with hereditary breast and ovarian cancer syndrome, and 76 participants (0.15%; 95% CI, 0.12%-0.19%) with a variant associated with Lynch syndrome (eFigure 1 in the [Supplement](#)). Baseline characteristics of carriers and noncarriers of pathogenic or likely pathogenic variants are provided in eTables 3-5 in the [Supplement](#).

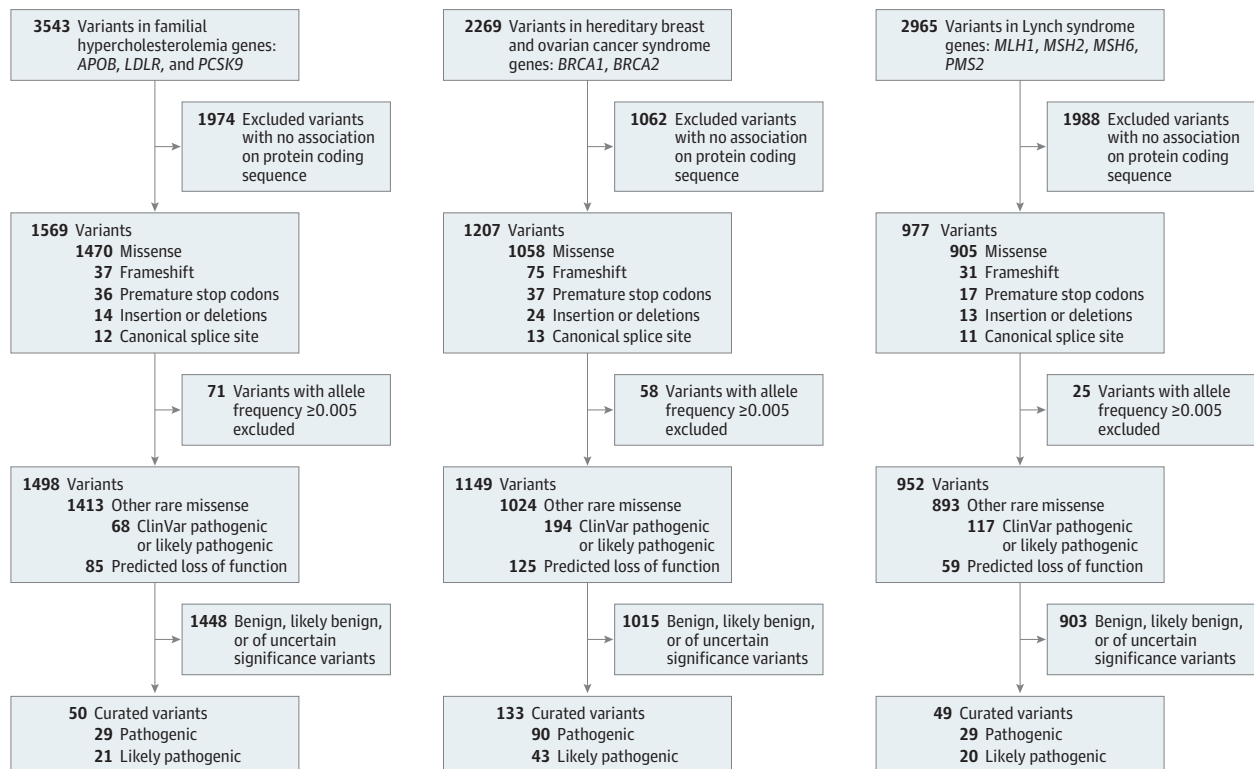
Familial hypercholesterolemia is unique among the 3 genomic conditions because of availability of a circulating biomarker (LDL cholesterol) that might serve as an additional proxy for pathogenic variant carrier status. Both observed LDL cholesterol levels at time of enrollment and estimated untreated LDL cholesterol levels were significantly higher among carriers compared with noncarriers: 24 mg/dL higher (95% CI, 15-33 mg/dL; $P < .001$) for observed values and 53 mg/dL higher (95% CI, 44-62 mg/dL; $P < .001$) for estimated untreated values (to convert LDL cholesterol to millimoles per liter, multiply by 0.0259). However, the broad overlap in LDL cholesterol values between carriers and noncarriers underscores the limitations in the ability to identify variant carriers without access to genetic data (eFigure 2 in the [Supplement](#)).

Individuals who harbored a pathogenic or likely pathogenic variant experienced substantially increased risk of associated diseases. For familial hypercholesterolemia, 28 of 131 carriers (21.4%) vs 4663 of 49 607 noncarriers (9.4%) developed atherosclerotic cardiovascular disease, corresponding

to a 3.03-fold (95% CI, 2.09-4.40) increased risk. For hereditary breast and ovarian cancer syndrome, 32 of 116 female carriers (27.6%) vs 2080 of 27 028 female noncarriers (7.7%) developed associated cancers, corresponding to a 4.11-fold (95% CI, 2.90-5.83) increased risk. For Lynch syndrome, 17 of 76 carriers (22.4%) vs 929 of 49 662 noncarriers (1.9%) developed colorectal or uterine cancer, corresponding to a 12.77-fold increased risk (95% CI, 7.90-20.64). Results stratified by gene end points are given in **Figure 2** and by individual disease end points in eTables 6-9 in the **Supplement**. Risk estimates were similar across the 3 genes associated with familial hypercholesterolemia and 2 genes associated with hereditary breast and ovarian cancer syndrome. For Lynch syndrome, consistent with previous studies,⁴¹⁻⁴⁴ risk was greatest among those with variants in the *MLH1* gene (eTable 9 in the **Supplement**).

Cox proportional hazards regression modeling of cumulative age-specific probabilities of disease reinforced the clinical importance of these increased relative risk estimates. The estimated probability of developing atherosclerotic cardiovascular disease by age 75 years was 34.2% (95% CI, 24.0%-44.5%) in female familial hypercholesterolemia variant carriers vs 12.8% (95% CI, 12.1%-13.4%) in female noncarriers and 60.9% (95% CI, 47.3%-74.6%) in male carriers vs 26.4% (95% CI, 25.4%-27.4%) in male noncarriers. The estimated risk of developing breast or ovarian cancer syndrome by age 75 years in female hereditary breast and ovarian cancer variant carriers was 41.1% (95% CI, 30.2%-52.0%) in female carriers vs 12.2% (95% CI, 11.5%-12.8%) in female noncarriers, whereas the risk of developing male breast cancer by age 75 years was 0.5% (95% CI, 0.2%-0.8%) in male carriers and 0.1% (0.1%-0.2%) in male noncarriers. The estimated risk of developing colorectal or uterine cancer by age 75 years was 40.8% (95% CI, 25.9%-55.7%) in female Lynch syndrome variant carriers vs 4.1% (95% CI, 3.7%-4.5%) in female noncarriers, whereas the risk of developing colorectal cancer by age 75 years was 35.5% (95% CI, 21.7%-49.3%) in male carriers and

Figure 1. Filtration and Classification of Variants Identified by Whole-Exome Sequencing



Variants excluded (allele frequency ≥ 0.005) in the Genome Aggregation Database.³⁷ Predicted loss-of-function variants do not necessarily meet all current standards to be classified as pathogenic or likely pathogenic.

3.4% (95% CI, 3.1%-3.8%) in male noncarriers. Risk estimates appeared similar among male vs female participants, with no evidence of statistical interaction of carrier status by sex for any of the conditions (Figure 3) (eFigure 3 in the Supplement).

A family history of associated diseases as assessed in the UK Biobank by surveys completed at the time of enrollment would have failed to identify most of the individuals harboring a pathogenic or likely pathogenic variant. A first-degree relative with disease was reported by 66.4% (87 of 131) of those carrying a familial hypercholesterolemia variant, 25.5% (60 of 235) of those carrying a hereditary breast and ovarian cancer syndrome variant, and 36.8% (28 of 76) of those carrying a Lynch syndrome variant. Taken together across the 3 genomic conditions, a family history was reported in 175 of 441 carriers (39.7%) vs 34 517 of 148 772 noncarriers (23.3%) (Figure 4).

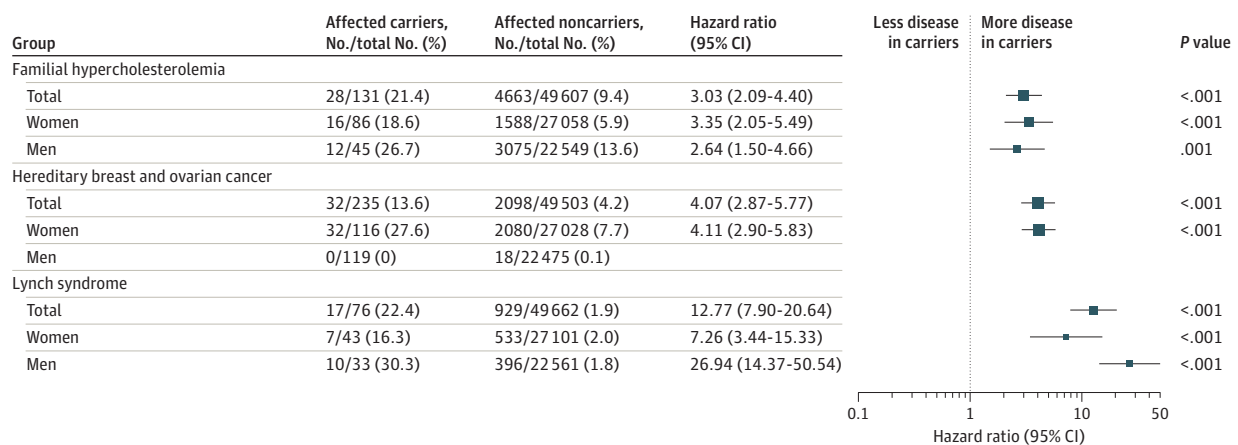
Both family history of disease and pathogenic variant carrier status were independently associated with risk for each of the 3 genomic conditions studied (Figure 5). Within Cox proportional hazards regression models, the relative risk associated with a pathogenic variant was similar for those with and without a family history of disease. For Lynch syndrome, the association of family history with risk of disease was greater among those who reported a family history (eFigure 4 in the Supplement). For example, a woman's risk for developing colorectal cancer or uterine cancer by age 75 years was estimated to be 3.9% (95% CI, 3.5%-4.3%) in a noncarrier without family history and 5.7% (95% CI, 4.7%-6.6%) in a noncarrier with family history and 18.7% (95% CI, 3.9%-33.4%) in a Lynch syndrome variant carrier without family history and 77.3% (95% CI, 58.0%-96.6%) in a variant carrier with family history (eFigure 4 in the Supplement).

The risk estimates presented reflect disease rates despite contemporary clinical practice. Many individuals identified with pathogenic or likely pathogenic variants did not receive recommended measures for screening and prevention of cardiovascular disease and cancer.^{15-17,19,45,46} For example, at the time of enrollment, only 75 of 131 individuals (57.3%) with familial hypercholesterolemia variants reported use of LDL cholesterol-lowering medications, only 12 of 25 female hereditary breast and ovarian cancer syndrome variant carriers younger than 50 years (48.0%) reported having ever undergone mammography screening, and only 4 of 15 of those with Lynch syndrome variants younger than 50 years (26.7%) reported undergoing screening for bowel cancer.

Discussion

In this study, we observed a rare pathogenic or likely pathogenic variant associated with any of 3 genomic conditions (familial hypercholesterolemia, hereditary breast and ovarian cancer syndrome,

Figure 2. Prevalence and Clinical Importance of Pathogenic or Likely Pathogenic Variants for 3 Genomic Conditions



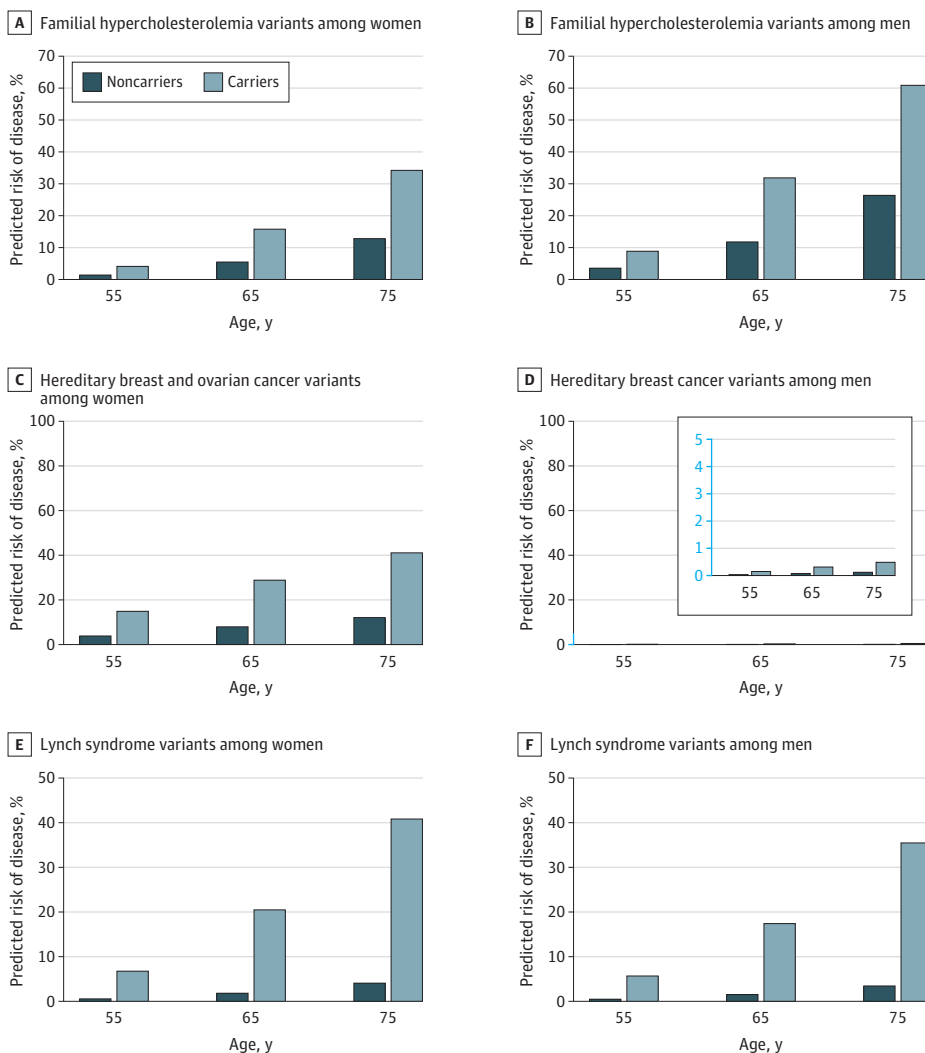
Risk calculated using Cox proportional hazards regression models with covariates of enrollment age, sex, and genetic ancestry as quantified by the first 4 genetic principal components for women, men, and total populations.

and Lynch syndrome) in 441 of 49 738 UK Biobank participants (0.9%). These individuals were at 3.03- to 12.77-fold relative risk for developing associated diseases despite contemporary clinical care, and their conditions were not reliably detected using self-reported family history.

These results build on previous efforts to understand the prevalence and clinical importance of monogenic risk variants in several key ways. First, blinded classification of genetic variants identified using systematic gene sequencing was performed by clinical laboratory geneticists. Second, estimates of increased risk were provided within the context of clinical care, including lipid-lowering therapy, mammography, and endoscopic screening in many participants. Third, all participants provided information about family history of disease in first-degree relatives using a structured survey assessment tool. Fourth, we analyzed a large cohort of individuals from a national biobank.

Although explicit demonstration that population genomic screening improves outcomes in a randomized clinical trial may not be feasible, identification of pathogenic variant carriers before disease onset may provide a clinically actionable opportunity for targeted screening, early therapy, and cascade testing of first-degree relatives.⁴⁷ Previous studies have suggested that population-wide genomic screening of young adults may be cost-effective, particularly if the costs of genetic testing continue to decrease, although this topic warrants additional consideration.⁴⁸ Moreover, although

Figure 3. Predicted Risk of Disease by Ages 55, 65, and 75 Years by Pathogenic or Likely Pathogenic Variant Carrier Status



Risk of disease estimated using a Cox proportional hazards regression model standardized to the mean of the first 4 genetic principal components and sex and stratified by variant carrier status. All $P < .001$.

studies to date have not suggested psychological harm associated with genetic risk disclosure, additional study is needed, particularly across a diverse set of diseases and individuals.^{49,50}

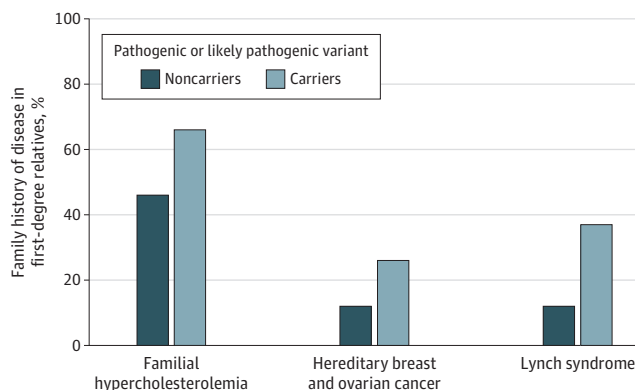
Individuals with high-risk DNA variants may be difficult to reliably identify without direct gene sequencing, even for a condition like familial hypercholesterolemia, which has a measurable circulating biomarker with higher levels in carriers. In this study, family history of disease was reported in only 39.7% of those who harbored a pathogenic or likely pathogenic variant across all 3 genomic conditions, and even when present, clinicians often can not distinguish risk associated with shared DNA vs shared environment. Taken together, these results indicate an important opportunity to increase recognition and guideline-supported care of these individuals.

Representative key challenges to widespread implementation of population-based genomic screening into clinical practice exist. First, even for genes with known disease associations such as those included in this study, rigorous classification of the individual variants using current clinical guidelines is necessary.³⁴ This requires manual curation of evidence, which relies heavily on a given variant co-segregating with disease within a family-based study, absence of presence at an appreciable frequency in diverse population databases of genomic variation, and rare allele frequency in global populations. Within our study, only 232 of 8777 observed genetic variants (2.6%) were ultimately classified as pathogenic or likely pathogenic in blinded review by clinical laboratory geneticists.

Second, few health systems have the necessary personnel and infrastructure to implement genomic medicine. Most current electronic health records do not allow for structured integration of genetic testing results into a patient's medical record, which can lead to inefficiencies and duplicative testing. Moreover, few clinicians have a nuanced understanding of various forms of genetic testing. An instructive recent example involves testing for 3 known pathogenic hereditary breast and ovarian cancer variants by 23andMe (23andMe Inc), a direct-to-consumer genetic testing company. Although each of these 3 variants is associated with disease, this test failed to identify more than 90% of pathogenic variants.⁵¹ Anecdotal evidence suggests that some individuals or clinicians may be falsely reassured by a negative (but not comprehensive) test result.⁵²

Third, carriers of monogenic risk variants may infer that they are predestined to develop disease. However, despite a several-fold increased risk associated with such variants, we estimated that 54.7% of familial hypercholesterolemia variant carriers, 59.0% of hereditary breast and ovarian cancer variant carriers, and 61.7% of Lynch syndrome variant carriers remain unaffected at age 75 years. This observation was consistent with recent results in a US health care system, in which more than 75% of female hereditary breast and ovarian cancer variant carriers remained free of disease well into middle age but was different from other mendelian diseases in which high-risk variants were associated with disease in a nearly 1:1 fashion.⁶ This overlap of disease-associated phenotypes was additionally noted when examining the distributions of LDL cholesterol levels in carriers vs

Figure 4. Family History of Disease in a First-Degree Relative by Presence of a Pathogenic or Likely Pathogenic Variant



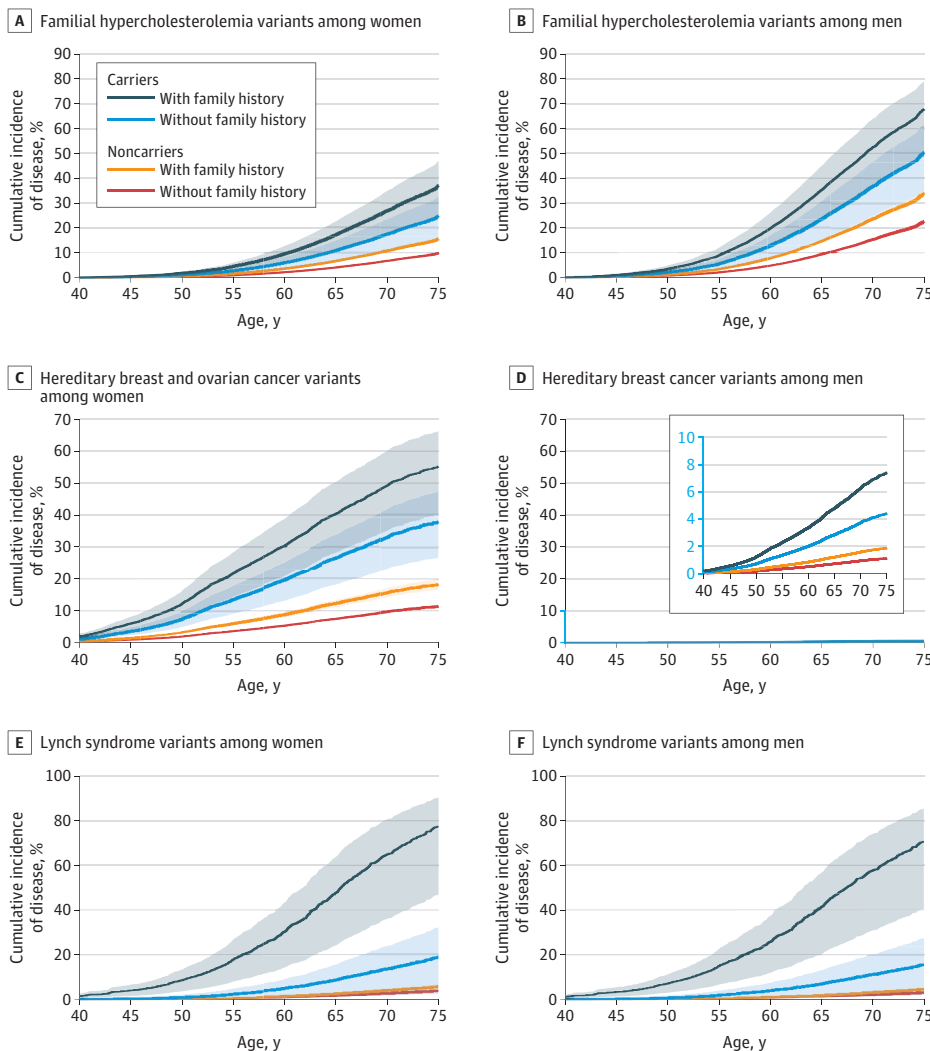
First-degree relative with coronary artery disease for familial hypercholesterolemia, breast cancer for hereditary breast and ovarian cancer syndrome, and colorectal cancer for Lynch syndrome. All $P < .001$ designate statistical significance of differences in means of family history of disease based on variant carrier status.

noncarriers of familial hypercholesterolemia variants; consistent with multiple previous studies,^{5,53,54} we found a substantial right shift but overlapping distributions. Additional efforts are needed to integrate genetic and nongenetic factors into integrated risk estimation tools that better facilitate shared decision-making for patients and their health care teams. Moreover, these observations suggest a potential need to alter the current framework for clinical risk disclosure in which risk is described in a probabilistic manner rather than as pathogenic vs not pathogenic.⁵⁵

Limitations

This study has limitations. First, UK Biobank participants were recruited at age 40 to 69 years, raising the possibility of survivorship or selection bias that limits generalizability to younger patients. Second, disease end points were ascertained through participant self-report, diagnosis codes from inpatient admissions, and national procedure, cancer, and death registries rather than manual review of records by a clinician. Third, participants in research studies tend to be healthier than the general population; recalibration of disease risk models for a given target population may be needed before clinical deployment.^{27,28,31} Fourth, we aggregated all pathogenic and likely pathogenic variants for each monogenic condition together, but even among this group, heterogeneity in risk for each

Figure 5. Age-Dependent Probability of Disease by Pathogenic or Likely Pathogenic Variant Carrier Status and Family History



Results estimated using a Cox proportional hazards regression model standardized to the mean of the first 4 genetic principal components and stratified by sex, variant carrier status, and family history for familial hypercholesterolemia (coronary artery disease, stroke, or peripheral artery disease), hereditary breast and ovarian cancer, and Lynch syndrome (colorectal and uterine cancer). The interaction of family history with carrier status was included in the models for Lynch syndrome variants, in which the interaction term was statistically significant.

specific variant may be present.³⁴ Fifth, we analyzed whole-exome sequencing to identify pathogenic variants, but some classes of genetic variation, including cryptic splice sites, copy number variants, or structural variants, were not reliably detected using this technology.^{32,33} Previous work suggests that such variants account for a relatively small proportion of pathogenic variants, but this topic warrants additional study, particularly as algorithms to detect such variants continue to improve and whole genome sequencing data become available.⁵⁶

Conclusions

The findings suggest that 0.9% of the middle-aged adult population in the UK Biobank harbored a pathogenic variant associated with familial hypercholesterolemia, hereditary breast or ovarian cancer syndrome, or Lynch syndrome. These individuals were at increased risk of disease, even within the context of routine clinical care, and carrier status was not reliably detected based on family history. Population genomic screening efforts may enable identification of these high-risk individuals before disease onset so that established risk mitigation strategies to overcome inherited disease susceptibility can be implemented.

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Author Contributions: Drs Patel and Khera had full access to all of the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis. Drs Patel and Wang contributed equally to this study.

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Acquisition, analysis, or interpretation of data: Patel, Wang, Fahed, Mason-Suares, Brockman, Amr, Machini, Hawley, Witkowski, Koch, Cassa, Ng, Lebo, Khera.

Drafting of the manuscript: Patel, Fahed, Khera.

Critical revision of the manuscript for important intellectual content: All authors.

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Obtained funding: Patel, Philippakis, Cassa, Ng, Khera.

Administrative, technical, or material support: Mason-Suares, Pelletier, Cassa, Ellinor, Lebo.

Supervision: Ellinor, Lebo, Khera.

Conflict of Interest Disclosures: Dr Fahed reported being a consultant and reported holding equity and receiving personal fees from GoodPath outside the submitted work. Dr Philippakis reported receiving personal fees from GV outside the submitted work. Dr Cassa reported receiving grants from the National Institutes of Health during the conduct of the study. Dr Ellinor reported receiving a grant from Bayer AG to the Broad Institute focused on the genetics and therapeutics of cardiovascular diseases and receiving personal fees from serving on advisory boards

or consulting for Bayer AG, Novartis AG, and Quest Diagnostics Inc during the conduct of the study. Dr Kathiresan reported being an employee of Verve Therapeutics and having equity in Catabasis, Maze Therapeutics, San Therapeutics, and Verve Therapeutics; being a member of the scientific advisory boards for Corvidia Therapeutics and Regeneron Genetics Center; reported serving as a consultant for Acceleron, Aegerion, Alnylam, Bayer Healthcare, Blackstone, Color Genomics Inc, Haug Partners, Illumina, Ionis, Leerink Partners, Eli Lilly and Company, MedGenome, Medscape, Merck & Company Inc, Noble Insights, Novartis AG, Novo Nordisk, Novo Ventures, Pfizer, and Quest Diagnostics outside the submitted work; and receiving patents related to a method of identifying and treating a person having a predisposition to or afflicted with cardiometabolic disease and a genetics risk predictor. Dr Ng reported being an employee of IBM Research. Dr Lebo reported receiving grant funding from the National Institutes of Health. Dr Khera reported serving as a consultant and receiving personal fees from Color Genomics, Maze Therapeutics, Medicines Company, Navitor Pharmaceuticals, and Sanofi Pharmaceuticals outside the submitted work; receiving speaking fees from Illumina; receiving grants and personal fees from the Novartis Institute for Biomedical Research; receiving sponsored research agreements from IBM Research and the Novartis Institute for Biomedical Research; receiving grants from the Broad Institute of MIT and Harvard, Massachusetts General Hospital, and the National Human Genome Research Institute (NHGRI) during the conduct of the study; and having a patent related to a genetic risk predictor. No other disclosures were reported.

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SUPPLEMENT.

eMethods. Study Populations, Gene Sequencing, Variant Quality Control, and Variant Classification.

eTable 1. Adjustment of Lipid Levels in the UK Biobank Based on Self-report of Lipid-Lowering Medications

eTable 2. Variant Characteristics and Evidence in Support of Pathogenic or Likely Pathogenic Classifications

eTable 3. Baseline Characteristics of Familial Hypercholesterolemia Variant Carriers and Noncarriers

eTable 4. Baseline Characteristics of Women Hereditary Breast and Ovarian Cancer Syndrome Variant Carriers and Noncarriers

eTable 5. Baseline Characteristics of Lynch Syndrome Variant Carriers and Noncarriers

eTable 6. Familial Hypercholesterolemia, Hazard Ratios for Each Component of the Composite End Point

eTable 7. Hereditary Breast and Ovarian Cancer Syndrome, Hazard Ratios for Primary Cancers

eTable 8. Lynch Syndrome, Hazard Ratios for Primary Cancers

eTable 9. Prevalence and Clinical Importance of Pathogenic or Likely Pathogenic Variants for 3 Genomic Conditions Stratified by Gene

eFigure 1. Frequency of Carriers of Pathogenic or Likely Pathogenic Variants for Each of 3 Genomic Conditions According to Gene

eFigure 2. Observed and Estimated Untreated Low-Density Lipoprotein Cholesterol Levels According to Familial Hypercholesterolemia Variant Status

eFigure 3. Age-Dependent Cumulative Probability of Disease According to Pathogenic or Likely Pathogenic Variant Carrier Status

eFigure 4. Predicted Risk of Disease at Ages 55, 65, and 75 According to Pathogenic or Likely Pathogenic Variant Carrier Status and Family History

eReferences.