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A splicing variant of *TERT* identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer

Alice W. Lee[1], **Ashley Bomkamp**[2], **Elisa V. Bandera**[3], **Allan Jensen**[4], **Susan J. Ramus**[5], **Marc T. Goodman**[6,7], **Mary Anne Rossing**[8,9], **Francesmary Modugno**[10,11,12], **Kirsten B. Moysich**[13], **Jenny Chang-Claude**[14,15], **Anja Rudolph**[14], **Aleksandra Gentry-Maharaj**[16], **Kathryn L. Terry**[17,18], **Simon A. Gayther**[19,20], **Daniel W. Cramer**[17,18], **Jennifer A. Doherty**[21], **Joellen M. Schildkraut**[22], **Susanne K. Kjaer**[4,23], **Roberta B. Ness**[24], **Usha Menon**[16], **Andrew Berchuck**[25], **Bhramar Mukherjee**[2,26], **Lynda Roman**[27], **Paul D. Pharoah**[28,29], **Georgia Chenevix-Trench**[30], **Sara Olson**[31], **Estrid Hogdall**[4,32], **Anna H. Wu**[1], **Malcolm C. Pike**[1,31], **Daniel O. Stram**[1], and **Celeste Leigh Pearce**[1,2] **for the Ovarian Cancer Association Consortium**

[1]Department of Preventive Medicine, University of Southern California Keck School of Medicine, Los Angeles, CA

[2]Department of Epidemiology, University of Michigan School of Public Health, Ann Arbor, MI

[3]Cancer Prevention and Control, Rutgers Cancer Institute of New Jersey, New Brunswick, NJ

[4]Department of Virus, Lifestyle and Genes, Danish Cancer Society Research Center, Copenhagen, Denmark

[5]University of New South Wales, Sydney, Australia

[6]Cancer Prevention and Control, Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center, Los Angeles, CA

[7]Department of Biomedical Sciences, Community and Population Health Research Institute, Cedars-Sinai Medical Center, Los Angeles, CA

[8]Program in Epidemiology, Division of Public Health Sciences, Fred Hutchinson Cancer Research Center, Seattle, WA

[9]Department of Epidemiology, University of Washington, Seattle, WA

[10]Division of Gynecologic Oncology, Department of Obstetrics, Gynecology, and Reproductive Sciences, University of Pittsburgh School of Medicine, Pittsburgh, PA

[11]Department of Epidemiology, University of Pittsburgh Graduate School of Public Health, Pittsburgh, PA

Correspondence to: Celeste Leigh Pearce, PhD, 1415 Washington Heights, SPH Tower Office #4642, Ann Arbor, MI 48109-2029, Tel.: +1-734-764-3835, Fax: +1-734-764-3192, lpearce@umich.edu.

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[12]Womens Cancer Research Program, Magee-Womens Research Institute and University of Pittsburgh Cancer Institute, Pittsburgh, PA

[13]Department of Cancer Prevention and Control, Roswell Park Cancer Institute, Buffalo, NY

[14]Division of Cancer Epidemiology, German Cancer Research Center (DKFZ), Heidelberg, Germany

[15]University Cancer Center Hamburg (UCCH), University Medical Center Hamburg-Eppendorf, Hamburg, Germany

[16]Women's Cancer, Institute for Women's Health, University College London, London, United Kingdom

[17]Obstetrics and Gynecology Center, Brigham and Women's Hospital and Harvard Medical School, Boston, MA

[18]Harvard T.H. Chan School of Public Health, Boston, MA

[19]Center for Cancer Prevention and Translational Genomics, Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center, Los Angeles, CA

[20]Department of Biomedical Sciences, Cedars-Sinai Medical Center, Los Angeles, CA

[21]Department of Epidemiology, The Geisel School of Medicine at Dartmouth, Hanover, NH

[22]Department of Public Health Sciences, The University of Virginia, Charlottesville, VA

[23]Department of Gynecology, Rigshospitalet, University of Copenhagen, Copenhagen, Denmark

[24]University of Texas School of Public Health, Houston, TX

[25]Department of Obstetrics and Gynecology, Duke University Medical Center, Durham, NC

[26]Department of Biostatistics, University of Michigan School of Public Health, Ann Arbor, MI

[27]Department of Obstetrics and Gynecology, University of Southern California Keck School of Medicine, Los Angeles, CA

[28]Department of Public Health and Primary Care, Center for Cancer Genetic Epidemiology, University of Cambridge, Strangeways Research Laboratory, Cambridge, United Kingdom

[29]Department of Oncology, Center for Cancer Genetic Epidemiology, University of Cambridge, Cambridge, United Kingdom

[30]Cancer Division, QIMR Berghofer Medical Research Institute, Brisbane, QLD, Australia

[31]Department of Epidemiology and Biostatistics, Memorial Sloan Kettering Cancer Center, New York, NY

[32]Molecular Unit, Department of Pathology, Herlev Hospital, University of Copenhagen, Copenhagen, Denmark

Abstract

Menopausal estrogen-alone therapy (ET) is a well-established risk factor for serous and endometrioid ovarian cancer. Genetics also plays a role in ovarian cancer, which is partly

attributable to 18 confirmed ovarian cancer susceptibility loci identified by genome-wide association studies. The interplay among these loci, ET use and ovarian cancer risk has yet to be evaluated. We analyzed data from 1,414 serous cases, 337 endometrioid cases and 4,051 controls across 10 case–control studies participating in the Ovarian Cancer Association Consortium (OCAC). Conditional logistic regression was used to determine the association between the confirmed susceptibility variants and risk of serous and endometrioid ovarian cancer among ET users and non-users separately and to test for statistical interaction. A splicing variant in *TERT*, rs10069690, showed a statistically significant interaction with ET use for risk of serous ovarian cancer (p_{int} = 0.013). ET users carrying the T allele had a 51% increased risk of disease (OR = 1.51, 95% CI 1.19–1.91), which was stronger for long-term ET users of 10+ years (OR = 1.85, 95% CI 1.28–2.66, p_{int} = 0.034). Non-users showed essentially no association (OR = 1.08, 95% CI 0.96–1.21). Two additional genomic regions harboring rs7207826 (C allele) and rs56318008 (T allele) also had significant interactions with ET use for the endometrioid histotype (p_{int} = 0.021 and p_{int} = 0.037, respectively). Hence, three confirmed susceptibility variants were identified whose associations with ovarian cancer risk are modified by ET exposure; follow-up is warranted given that these interactions are not adjusted for multiple comparisons. These findings, if validated, may elucidate the mechanism of action of these loci.

Keywords

gene-environment interactions; ovarian cancer; hormone therapy; estrogen; SNPs

Introduction

The etiology of ovarian carcinoma (ovarian cancer) is influenced by several hormonal factors, including menopausal hormone therapy (HT) use. Approximately 5 million women in the United States currently use HT, and according to the National Health and Nutrition Examination Survey (NHANES) in 2010, the most commonly used type of HT among women aged 40 years and older is estrogen-alone therapy (ET).[1,2] ET is a well-established risk factor for serous and endometrioid ovarian cancer.[2–4] Most recently, Lee *et al.* demonstrated that use of ET postmenopausally was associated with a 57% and 82% increased risk of serous and endometrioid ovarian cancer, respectively;[5] the meta-analysis by the Collaborative Group on Epidemiological Studies of Ovarian Cancer showed these histotype effects as well.[2]

Ovarian cancer has also a strong genetic component. A large part is attributable to high-penetrance susceptibility mutations, but common variants identified using genome-wide association studies (GWASs) play important roles as well. There are currently 18 confirmed ovarian cancer common susceptibility loci that explain approximately 3.9% of the disease's excess familial risk.[6–13] Each of these common variants is associated with extremely modest relative risk estimates, but it is possible that interactions between non-genetic and genetic risk factors exist, thereby putting some women at higher risk.

Pearce *et al.* previously examined the interactive effects between six GWAS-identified common variants and five well-accepted non-genetic risk factors: first-degree family history

of ovarian cancer, tubal ligation, parity, oral contraceptive (OC) use and personal history of endometriosis.[14] However, menopausal ET, which has consistently been shown to be associated with risk of serous and endometrioid ovarian cancer,[2,5] was not included in these analyses. Using data from the Ovarian Cancer Association Consortium (OCAC), we have evaluated potential statistical interactions between menopausal ET use and the 18 confirmed ovarian cancer common susceptibility alleles. To our knowledge, this is the first study to investigate the interactions between menopausal ET use and ovarian cancer susceptibility loci on disease risk.

Material and Methods

All studies included in this analysis had approval from ethics committees and written informed consent was obtained from all study participants.

Study populations

A total of 10 case–control studies participating in the OCAC (http://apps.ccge.medschl.cam.ac.uk/consortia/ocac/index.html) were included in this analysis, with seven in the United States and three in Europe. Specific details for each of these studies have been published elsewhere,[15–25] but their main study characteristics are presented in Table 1.

We had a total of 5,403 serous and endometrioid cases and 13,337 controls across the 10 OCAC studies; only serous and endometrioid cases were included as most studies have shown that only these histotypes are significantly associated with ET use.[2,5,26] However, only a proportion of these women had genetic data available, leaving us with 3,855 cases and 9,593 controls. Further exclusions included the following: women who were <50 years of age at reference date, which was typically the date of diagnosis for cases and the date of interview for controls, (871 cases and 2,532 controls), had past diagnoses of cancer (other than non-melanoma skin cancer) (398 cases and 887 controls), had unknown or missing HT information (171 cases and 365 controls) or had used HT in a combined estrogen–progestin form (664 cases and 1,758 controls). Hence, our final dataset included 1,414 serous cases, 337 endometrioid cases and 4,051 controls.

Genotype data

To date, 18 confirmed, genome-wide significant ovarian cancer susceptibility loci ($p \leq .0 \times 10^{-8}$) have been identified.[6–13] However, subsequent fine mapping efforts have shown that in some instances, the originally published best “hit” in the confirmed region was no longer the most strongly associated single nucleotide polymorphism (SNP). Table 2 presents the originally published SNPs and, where applicable, the current best hits, which we used in the analysis presented here.[6]

Details regarding the genetic data have been previously described.[9] Briefly, existing genotype data from three GWASs, their replication efforts, and two large-scale arrays (the Collaborative Oncological Gene–Environment Study (iCOGS) and the Exome chip) were combined with data from the April 2012 release of the 1,000 Genomes Project and imputation using the program IMPUTE2[27] was carried out for all OCAC participants. Subjects from two studies, NCO and NEC, were split into two analytic sets based on the

varying scope of genotype data (genome-wide *vs.* array) available for imputation. This resulted in a total of 12 analytic sets for analysis (see Table 1 footnote).

Exposure and covariate data

Self-completed questionnaires and phone or in-person interviews were used to collect information on HT use and other potential confounding variables including age, OC use, parity, hysterectomy, tubal ligation, endometriosis and education. Given that use of ET increases risk of endometrial cancer in women with intact uteri,[28] the majority of ET users were hysterectomized and hence, their true age at menopause was unknown. We therefore assumed that all women in our analysis had an age at menopause of 50, which is the average age at menopause for women in the Western world.[29]

Given the importance of menopause to ovarian cancer etiology, the effects of ET use prior to menopause when endogenous estrogen levels are naturally high could be inherently different from its effects after menopause.[30] Therefore, we only considered women as ET users if they used ET after age 50 for at least 1 year. Non-users were women who had never used ET after age 50 (including women who only used ET before age 50) or had only used ET after age 50 for less than 1 year as the effect of such short-term use is likely to be minimal. However, a sensitivity analysis was conducted using a true “never” user baseline group, and the results did not change. Duration of postmenopausal ET use was assessed in the following categories: 1 to <5 years, 5 to <10 years and 10+ years.

Statistical analysis

All models were conditioned on analytic set, 5-year age category (50–54, 55–59, 60–64, 65–69, 70–74 and 75+ years), and genetic ancestry (European, Asian, African and other) as determined by the program LAMP (Local Ancestry in Admixed Populations).[31] Women with >90% European ancestry were classified as European, >80% Asian or African ancestry were classified as Asian or African, respectively, and those with mixed ancestry were classified as other.[9] In addition, all models were adjusted for OC use (never [including <1 year of use], 1 to <2 years, 2 to <5 years, 5 to <10 years and 10+ years), parity (never, 1 birth, 2+ births), hysterectomy (yes/no), endometriosis (yes/no), tubal ligation (yes/no) and education (less than high school, high school, some college, college graduate or higher) since they were judged to be potentially important confounders *a priori*. Missing categories were created for women missing any of the covariates so their data could be included in the analysis. Data on hysterectomy status were not available from all sites, but sensitivity analyses showed that hysterectomy status did not substantially impact the estimates for ET or any of the SNPs.

Weighted genetic risk scores, which took into account the 18 confirmed SNPs simultaneously, were calculated by taking the beta coefficients for each SNP’s association with risk of serous and endometrioid ovarian cancer using all OCAC studies in which genotype data was available (43 OCAC studies, which included 18,174 cases and 26,134 controls[9]) and multiplying them by the genotype value (0–2) for each subject (i.e., beta coefficients were derived from a much larger dataset). These values for the 18 SNPs were

then summed to obtain each individual's total risk score, which was then categorized into quartiles according to the distribution in controls for ease of interpretation.

Odds ratios (ORs) and 95% confidence intervals (CIs) were calculated for the main effect association between each SNP or genetic risk score quartile and disease risk using conditional logistic regression. This was done for the serous and endometrioid histotypes separately. Previous analyses that evaluated ET's main effect on risk of serous ovarian cancer showed no difference by grade so all serous cases were combined in our analysis.[5] These genetic associations were further stratified by whether or not ET was used after age 50. Because these gene–environment interaction analyses were primarily focused on understanding disease etiology, we tested for statistical interaction (i.e., departure from a multiplicative model) between the 18 ovarian cancer susceptibility loci or genetic risk score and ET use on risk of serous and endometrioid ovarian cancer using the likelihood ratio test (LRT) comparing models with and without interaction terms.[32] A similar approach was used to analyze the effect of duration categories of ET use for the associations showing a significant interaction with ever/never ET use. For completeness, we also assessed interactions on the additive scale by calculating interaction contrast ratios (ICRs) and 95% CIs for the ICRs; ICR values greater than zero with 95% CIs that excluded zero indicated greater than additive effects.

All p values reported were two-sided and considered significant at $p \leq 0.05$. An adjusted p value that factored in the number of tests for interaction conducted was considered as well. All analyses were performed using STATA release 14.0.

Results

A total of 5,802 women were included in these analyses, with 1,414 serous cases, 337 endometrioid cases and 4,051 controls (Table 1). Approximately 13.6%, 20.0% and 15.1% of the controls, serous cases and endometrioid cases, respectively, reported using ET after age 50. In addition, 18 confirmed ovarian cancer SNPs were investigated here and their characteristics are presented in Table 2. For 9 of the 18 SNPs, their corresponding previously reported best hits are listed as well (Table 2).

Although the main effects of each of the 18 SNPs have been previously published, Table 3 shows their main effects as well as the effects of genetic risk score in quartiles with serous ovarian cancer. There was a statistically significant interaction between ET use and the T allele of rs10069690 on chromosome 5 on risk of serous ovarian cancer that showed departure from both additivity and multiplicativity (ICR = 0.55, 95% CI 0.16–0.94; p_{int} for LRT = 0.013) (Table 3). While the T allele of rs10069690 was associated with a 51% increased risk of serous ovarian cancer among ET users (OR = 1.51, 95% CI 1.19–1.91), there was essentially no risk among non-users (OR = 1.08, 95% CI 0.96–1.21).

Table 4 presents the same information as Table 3, but for the endometrioid histotype. Two statistically significant interactions between the genetic variants rs7207826 and rs56318008 and ET use on risk of disease that showed departure from multiplicativity were observed (p_{int} for LRT = 0.021 and p_{int} for LRT = 0.037, respectively) (Table 4). Rs7207826 (T allele)

on chromosome 17 was positively associated with the endometrioid histotype among non-users of ET (OR = 1.32, 95% CI 1.09–1.61), but showed a decreased risk of disease among ET users (OR = 0.71, 95% CI 0.43–1.18). Similarly, non-users of ET carrying the C allele for rs56318008 on chromosome 1 showed an increased risk of endometrioid ovarian cancer (OR = 1.53, 95% CI 1.21–1.92) whereas ET users showed a decreased risk (OR = 0.82, 95% CI 0.46–1.45). Genetic risk score did not appear to interact with ET use on risk of either histotype (p_{int} for LRT = 0.52 for serous, p_{int} for LRT = 0.25 for endometrioid) (Tables 3 and 4).

For each of the three SNPs that showed a statistically significant interaction with postmenopausal ET use on serous or endometrioid ovarian cancer risk at a $p \leq 0.05$ level on a multiplicative scale, the association between the SNP and risk of disease was assessed by duration of ET use. Rs7207826 and rs56318008 did not have significant interactions with duration for endometrioid ovarian cancer (p_{int} for LRT = 0.18 and p_{int} for LRT = 0.087, respectively). However, rs10069690 did have a significant interaction for serous ovarian cancer (p_{int} for LRT = 0.034); women who carried the T allele and had used ET for 10+ years had close to a twofold increased risk relative to non-users of ET who carried the C (reference) allele (OR = 1.85, 95% CI 1.28–2.66) (Table 5).

With 18 SNPs plus a genetic risk score for two histotypes and three additional duration interactions, we conducted a total of 41 tests for interaction in the analyses presented here. Four of these interactions were considered statistically significant at a $p \leq 0.05$ level. Although this is twice as many interaction associations as would be expected by chance at the $p \leq 0.05$ level, none of the them met a Bonferroni threshold for multiple comparisons of $p = 1.22 \times 10^{-3}$ (0.05/41 tests).

Discussion

We have shown evidence of statistical interactions between postmenopausal ET use and three confirmed ovarian cancer susceptibility alleles with risk of serous and endometrioid ovarian cancer. Although none of the interactions we report here remained significant after adjusting for multiple comparisons, these results may still be relevant as they could contribute to our understanding of the mechanism of action for these loci.

The most significant and biologically plausible interaction identified was rs10069690 for serous ovarian cancer, a SNP whose main effect has only been observed for the serous histotype.[13] Rs10069690 is located in the *TERT-CLPTM1L* region of chromosome 5p15.33, a multi-cancer susceptibility locus that encodes the reverse transcriptase subunit (hTERT) of telomerase, an enzyme known to help maintain telomere length and integrity. Telomere shortening is often associated with genetic instability and hence increased risk of cancer and death, but telomerase has been shown to counteract this process, making the expression of *TERT* important in preventing tumorigenesis. Evidence has suggested that sex steroid hormones, such as estrogen, may be good candidates as physiological regulators of *TERT*.[33] Some findings have shown telomerase activity to be under hormonal control in estrogen-targeted tissues, including the endometrium[34] and the ovary;[35] the expression of *TERT* has been shown to be upregulated by estrogen.[36,37]

Recently, Killedar *et al.* reported rs10069690 as a likely functional SNP since its risk-associated T allele was shown to result in the co-production of full-length hTERT as well as an alternatively spliced transcript, which encodes a catalytically inactive protein that inhibits telomerase activity; this was thought to be due to a dominant negative effect of the protein since telomerase exists as a dimer and its catalytic activity requires both hTERT active sites to be functional.[38] The decreased enzymatic activity may result in shorter telomeres, which could lead to an increased risk of genetic instability and subsequent carcinogenesis. Given the evidence suggesting estrogen's role in the transcriptional regulation of hTERT, the elevated risk of serous ovarian cancer may be attributable to the inhibition of telomerase activity from higher levels of estrogen with prolonged ET use (OR = 1.85, 95% CI 1.28–2.66 for 10+ years).

Cancer cells have also been shown to activate telomerase to stabilize telomeres for continued proliferation and cellular immortalization. However, from this perspective, the inhibition of telomerase associated with rs10069690 would result in cell death of cancer cells and hence a decreased risk of disease particularly among ET users, which is contrary to our findings. Presently, it is unclear whether telomerase activation helps in the uncontrolled cellular proliferation of existing cancer cells or in the preservation of a non-malignant phenotype by maintaining the replicative longevity of ovarian cells.[35] Our results appear to support the latter.

The additional two interactions observed with ET use were rs56318008 and rs7207826 for endometrioid ovarian cancer. Rs56318008 is located near *WNT4*, a gene involved in steroidogenesis[39] and implicated in GWASs for risk of endometriosis,[40] an estrogen-related gynecologic condition strongly associated with the endometrioid histotype.[41] Rs7207826 is located near *SKAP1*, a gene that does not appear to be directly related to female sex hormones and is primarily involved in T cell signaling and the regulation of the lymphocyte function-associated antigen 1 gene (*LFA-1*). It should be noted though that *WNT4* and *SKAP1* have not been shown to be the targets of risk SNPs at these loci.

Although this study is the largest of its kind, it still has a modest sample size in which to attempt to discover interactions. In addition, the self-reported nature of the exposure and covariate data used could be considered a limitation. However, studies have shown high agreement between information collected using interviews *vs.* records for HT use[42] as well as other reproductive factors.[43,44] Our results may be due to chance as these interactions do not survive correction for multiple hypothesis testing, but the fact that these are confirmed susceptibility alleles adds support to our findings. Given the role of estrogen in *TERT* activation and expression, rs10069690 is of particular interest. From a biological standpoint, this SNP appears to affect telomerase activity and hence, telomere maintenance, actions that could promote tumorigenesis if improperly regulated.[38] Although we cannot rule out that the observed interaction may be due to a SNP in the region that is in linkage disequilibrium with rs10069690, the fact that rs10069690 is functional with biological plausibility supporting its interaction with ET use makes it a strong candidate. The other two SNPs implicated in this analysis are intriguing as well in that they are confirmed ovarian cancer susceptibility loci. However, as previously mentioned, the target genes for these SNPs are unknown and hence their relevance remains uncertain at this time.

Our results highlight the complexity of ovarian cancer etiology. In addition, they provide evidence that the roles of ET and the 18 ovarian cancer common variants in ovarian carcinogenesis may be beyond their independent effects. This is the first study, to our knowledge, to suggest potential gene–environment interactions in ovarian cancer in the context of HT use with confirmed susceptibility alleles. These findings, if replicated, may be critical for future risk prediction modeling.

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Abbreviations

CI	confidence interval
COGS	Collaborative Oncological Gene–Environment Study
ET	estrogen-alone therapy
GWAS	genome-wide association study
HT	hormone therapy
ICR	interaction contrast ratio
LAMP	Local Ancestry in Admixed Populations
LRT	likelihood ratio test
NHANES	National Health and Nutrition Examination Survey
OC	oral contraceptive

OCAC	Ovarian Cancer Association Consortium
OR	odds ratio
SNP	single nucleotide polymorphism

References

1. Sprague BL, Trentham-Dietz A, Cronin KA. A sustained decline in postmenopausal hormone use: results from the National Health and Nutrition Examination Survey, 1999–2010. Obstet Gynecol. 2012; 120:595–603. [PubMed: 22914469]
2. Collaborative Group on Epidemiological Studies of Ovarian, C. Beral V, Gaitskell K, et al. Menopausal hormone use and ovarian cancer risk: individual participant meta-analysis of 52 epidemiological studies. Lancet. 2015; 385:1835–42. [PubMed: 25684585]
3. Pearce CL, Chung K, Pike MC, et al. Increased ovarian cancer risk associated with menopausal estrogen therapy is reduced by adding a progestin. Cancer. 2009; 115:531–9. [PubMed: 19127543]
4. Beral V, Million Women Study, C. Bull D, et al. Ovarian cancer and hormone replacement therapy in the Million Women Study. Lancet. 2007; 369:1703–10. [PubMed: 17512855]
5. Lee AW, Ness RB, Roman LD, et al. Association between menopausal estrogen-only therapy and ovarian carcinoma risk. Obstet Gynecol. 2016; 127:828–36. [PubMed: 27054934]
6. Kuchenbaecker KB, Ramus SJ, Tyrer J, et al. Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nat Genet. 2015; 47:164–71. [PubMed: 25581431]
7. Bolton KL, Tyrer J, Song H, et al. Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nat Genet. 2010; 42:880–4. [PubMed: 20852633]
8. Goode EL, Chenevix-Trench G, Song H, et al. A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nat Genet. 2010; 42:874–9. [PubMed: 20852632]
9. Pharoah PD, Tsai YY, Ramus SJ, et al. GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nat Genet. 2013; 45:362–70. 370e361–2. [PubMed: 23535730]
10. Shen H, Fridley BL, Song H, et al. Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nat Commun. 2013; 4:1628. [PubMed: 23535649]
11. Song H, Ramus SJ, Tyrer J, et al. A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nat Genet. 2009; 41:996–1000. [PubMed: 19648919]
12. Permuth-Wey J, Lawrenson K, Shen HC, et al. Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nat Commun. 2013; 4:1627. [PubMed: 23535648]
13. Bojesen SE, Pooley KA, Johnatty SE, et al. Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nat Genet. 2013; 45:371–84. 384e371–2. [PubMed: 23535731]
14. Pearce CL, Rossing MA, Lee AW, et al. Combined and interactive effects of environmental and GWAS-identified risk factors in ovarian cancer. Cancer Epidemiol Biomarkers Prev. 2013; 22:880–90. [PubMed: 23462924]
15. Royar J, Becher H, Chang-Claude J. Low-dose oral contraceptives: protective effect on ovarian cancer risk. Int J Cancer. 2001; 95:370–74. [PubMed: 11668519]
16. Balogun N, Gentry-Maharaj A, Wozniak EL, et al. Recruitment of newly diagnosed ovarian cancer patients proved challenging in a multicentre biobanking study. J Clin Epidemiol. 2011; 64:525–30. [PubMed: 21074968]
17. Lurie G, Terry KL, Wilkens LR, et al. Pooled analysis of the association of PTGS2 rs5275 polymorphism and NSAID use with invasive ovarian carcinoma risk. Cancer Causes Control. 2010; 21:1731–41. [PubMed: 20559705]
18. Ness RB, Dodge RC, Edwards RP, et al. Contraception methods, beyond oral contraceptives and tubal ligation, and risk of ovarian cancer. Ann Epidemiol. 2011; 21:188–96. [PubMed: 21109450]

19. Moorman PG, Calingaert B, Palmieri RT, et al. Hormonal risk factors for ovarian cancer in premenopausal and postmenopausal women. Am J Epidemiol. 2008; 167:1059–69. [PubMed: 18303003]
20. Wu AH, Pearce CL, Tseng CC, et al. Markers of inflammation and risk of ovarian cancer in Los Angeles County. Int J Cancer. 2009; 124:1409–15. [PubMed: 19065661]
21. Terry KL, De Vivo I, Titus-Ernstoff L, et al. Androgen receptor cytosine, adenine, guanine repeats, and haplotypes in relation to ovarian cancer risk. Cancer Res. 2005; 65:5974–81. [PubMed: 15994977]
22. Pike MC, Pearce CL, Peters R, et al. Hormonal factors and the risk of invasive ovarian cancer: a population-based case–control study. Fertil Steril. 2004; 82:186–95. [PubMed: 15237010]
23. Bodelon C, Cushing-Haugen KL, Wicklund KG, et al. Sun exposure and risk of epithelial ovarian cancer. Cancer Causes Control. 2012; 23:1985–94. [PubMed: 23065074]
24. Glud E, Kjaer SK, Thomsen BL, et al. Hormone therapy and the impact of estrogen intake on the risk of ovarian cancer. Arch Intern Med. 2004; 164:2253–9. [PubMed: 15534163]
25. Bandera EV, King M, Chandran U, et al. Phytoestrogen consumption from foods and supplements and epithelial ovarian cancer risk: a population-based case control study. BMC Womens Health. 2011; 11:40. [PubMed: 21943063]
26. Morch LS, Lokkegaard E, Andreasen AH, et al. Hormone therapy and different ovarian cancers: a national cohort study. Am J Epidemiol. 2012; 175:1234–42. [PubMed: 22517811]
27. Howie B, Marchini J, Stephens M. Genotype imputation with thousands of genomes. G3 (Bethesda). 2011; 1:457–70. [PubMed: 22384356]
28. Grady D, Gebretsadik T, Kerlikowske K, et al. Hormone replacement therapy and endometrial cancer risk: a meta-analysis. Obstet Gynecol. 1995; 85:304–313. [PubMed: 7824251]
29. Morabia A, Costanza MC. International variability in ages at menarche, first livebirth, and menopause. World Health Organization Collaborative Study of Neoplasia and Steroid Contraceptives. Am J Epidemiol. 1998; 148:1195–1205. [PubMed: 9867266]
30. Pike MC, Krailo MD, Henderson BE, et al. 'Hormonal' risk factors, 'breast tissue age' and the age-incidence of breast cancer. Nature. 1983; 303:767–70. [PubMed: 6866078]
31. Sankararaman S, Sridhar S, Kimmel G, et al. Estimating local ancestry in admixed populations. Am J Hum Genet. 2008; 82:290–303. [PubMed: 18252211]
32. Rothman KJ, Greenland S, Walker AM. Concepts of interaction. Am J Epidemiol. 1980; 112:467–70. [PubMed: 7424895]
33. Kyo S, Takakura M, Kanaya T, et al. Estrogen activates telomerase. Cancer Res. 1999; 59:5917–21. [PubMed: 10606235]
34. Kyo S, Takakura M, Kohama T, et al. Telomerase activity in human endometrium. Cancer Res. 1997; 57:610–14. [PubMed: 9044835]
35. Liu JP, Li H. Telomerase in the ovary. Reproduction. 2010; 140:215–22. [PubMed: 20562297]
36. Calado RT, Yewdell WT, Wilkerson KL, et al. Sex hormones, acting on the TERT gene, increase telomerase activity in human primary hematopoietic cells. Blood. 2009; 114:2236–43. [PubMed: 19561322]
37. Misiti S, Nanni S, Fontemaggi G, et al. Induction of hTERT expression and telomerase activity by estrogens in human ovary epithelium cells. Mol Cell Biol. 2000; 20:3764–71. [PubMed: 10805720]
38. Killedar A, Stutz MD, Sobinoff AP, et al. A common cancer risk-associated allele in the hTERT locus encodes a dominant negative inhibitor of telomerase. PLoS Genet. 2015; 11:e1005286. [PubMed: 26053551]
39. Franco HL, Dai D, Lee KY, et al. WNT4 is a key regulator of normal postnatal uterine development and progesterone signaling during embryo implantation and decidualization in the mouse. FASEB J. 2011; 25:1176–87. [PubMed: 21163860]
40. Nyholt DR, Low SK, Anderson CA, et al. Genome-wide association meta-analysis identifies new endometriosis risk loci. Nat Genet. 2012; 44:1355–9. [PubMed: 23104006]

41. Pearce CL, Templeman C, Rossing MA, et al. Association between endometriosis and risk of histological subtypes of ovarian cancer: a pooled analysis of case–control studies. Lancet Oncol. 2012; 13:385–94. [PubMed: 22361336]

42. Sandini L, Pentti K, Tuppurainen M, et al. Agreement of self-reported estrogen use with prescription data: an analysis of women from the Kuopio Osteoporosis Risk Factor and Prevention Study. Menopause. 2008; 15:282–9. [PubMed: 17998884]

43. Glass R, Johnson B, Vessey M. Accuracy of recall of histories of oral contraceptive use. Br J Prev Soc Med. 1974; 28:273–5. [PubMed: 4455348]

44. Gentry-Maharaj A, Taylor H, Kalsi J, et al. Validity of self-reported hysterectomy: a prospective cohort study within the UK Collaborative Trial of Ovarian Cancer Screening (UKCTOCS). BMJ Open. 2014; 4:e004421.

What's new?

Menopausal estrogen-alone therapy (ET) is a well-established risk factor for serous and endometrioid ovarian cancer. Genetics also plays a role in ovarian cancer, with 18 ovarian cancer susceptibility loci already confirmed. The interplay among these loci, ET use and ovarian cancer risk has yet to be evaluated. This study identifies three confirmed susceptibility variants whose associations with ovarian cancer risk are modified by ET exposure. Of particular interest is the interaction with rs10069690, a functional variant located in *TERT*. The findings, if validated, may elucidate the mechanism of action of these loci and be critical for future risk prediction modeling.

Table 1

Description of studies included in analysis

Study name	Study abbrev.	Country	Study period	Method of data collection	Number of controls[1]	Number of serous cases[1]	Number of endometrioid cases[1]
Disease of the Ovary and their Evaluation Study[23]	DOV	USA	2002–2009	In-person interview	547 (123)	218 (65)	53 (10)
German Ovarian Cancer Study[15]	GER	Germany	1992–1998	Self-completed questionnaire	232 (39)	66 (11)	11 (4)
Hawaii Ovarian Cancer Study[17]	HAW	USA	1994–2007	In-person interview	229 (28)	68 (13)	23 (6)
Hormones and Ovarian Cancer Prediction[18]	HOP	USA	2003–2008	In-person interview	694 (68)	168 (28)	48 (7)
Malignant Ovarian Cancer Study[24]	MAL	Denmark	1994–1999	In-person or phone interview	363 (47)	96 (11)	17 (2)
North Carolina Ovarian Cancer Study[2,19]	NCO	USA	1999–2008	In-person interview	401 (70)	189 (60)	47 (10)
New England Case-Control Study of Ovarian Cancer[2,21]	NEC	USA	1999–2008	In-person interview	394 (28)	211 (26)	56 (3)
New Jersey Ovarian Cancer Study[25]	NJO	USA	2002–2008	Phone interview	112 (6)	63 (3)	20 (0)
United Kingdom Ovarian Cancer Population Study[16]	UKO	United Kingdom	2006–2007	In-person interview	490 (47)	27 (1)	9 (0)
University of Southern California, Study of Lifestyle and Women's Health[20,22]	USC	USA	1993–2008	In-person interview	589 (95)	308 (65)	53 (9)
				Total	4,051 (551)	1,414 (283)	337 (51)

[1] Number in parentheses indicates the number of postmenopausal ET users.

[2] Subjects were split into two different analytic sets.

Table 2

Characteristics of the 18 SNPs included in the analysis and their previously reported best hits

SNP	Previously published best hit[1]	Chromosome band	Position	Reference allele(s)	Tested allele[2]	Tested allele frequency[3]
rs58722170[6]		1p34.3	38096421	G	C	0.15
rs10069690[13]		5p15.33	1279790	C	T	0.35
chr10:21878831:D	rs1243180[9]	10p12.31	21878831	CCCTTC	–	0.14
rs17329882[6]		4q26	119949960	A	C	0.15
rs1879586	rs12942666[12]	17q21.31	43567337	C	G	0.08
rs56318008[6]		1p36	22470407	C	T	0.20
rs4808075	rs2363956[7]	19p13.11	17390291	T	C	0.16
chr9:136138765:D[6]		9q34.2	136138765	CGCCCACCACTA	–	0.13
rs7207826	rs9303542[9]	17q21.32	46500673	T	C	0.31
rs76837345	rs11782652[9]	8q21.13	82668818	A	G	0.04
rs62274042	rs7651446[9]	3q25.31	156435952	G	A	0.01
rs635634[6]		9q34.2	136155000	C	T	0.14
rs3744763[10]		17q12	36090885	G	A	0.69
chr17:29181220:I[6]		17q11.2	29181220	–	T	0.13
rs6755777	rs2072590[8]	2q31.1	177043226	T	G	0.82
rs117224476	rs3814113[11]	9q22.2	16907967	T	G	0.16
rs1400482	rs10088218[8]	8q24.21	129541931	G	A	0.09
rs116133110[6]		6q22.1	28480635	T	C	0.46

Note: chr10:21878831:D and chr17:29181220:I are listed as rs1449962376 and rs199661266, respectively, in 1000 Genomes. Footnotes next to the SNPs correspond to their published references.

[1] If not specified, the previously published best hit is the same as the current best hit considered.

[2] – Refers to a deletion.

[3] Based on 1000 Genomes for all populations. For chr9:136138765:D (rs587729126), the tested allele frequency was based on the controls in the full OCAC dataset since the SNP is not listed in 1000 Genomes.

Table 3

Association between each of the 18 SNPs and genetic risk score and risk of serous ovarian cancer, stratified by ET use after age 50

	Main effect		No ET use (*N* = 1,131 cases/3,500 controls)		ET use (*N* = 283 cases/551 controls)		
	OR[1,2]	95% CI	OR[1]	95% CI	OR[1]	95% CI	*p* Value for interaction
SNP							
rs58722170	1.25	1.11–1.40	1.21	1.06–1.38	1.41	1.07–1.85	0.31
rs10069690	1.14	1.03–1.26	1.08	0.96–1.21	1.51	1.19–1.91	**0.013**
chr10:21878831:D	1.14	1.03–1.26	1.15	1.03–1.29	1.09	0.86–1.38	0.68
rs17329882	1.14	1.02–1.28	1.17	1.03–1.32	1.05	0.81–1.37	0.47
rs1879586	1.15	1.01–1.30	1.17	1.02–1.34	1.04	0.78–1.37	0.44
rs56318008	1.16	1.03–1.31	1.22	1.06–1.39	0.93	0.698–1.25	0.099
rs4808075	1.18	1.07–1.31	1.20	1.07–1.34	1.13	0.90–1.42	0.64
chr9:136138765:D	1.08	0.93–1.26	1.14	0.96–1.34	0.89	0.63–1.26	0.21
rs7207826	1.17	1.06–1.29	1.19	1.06–1.33	1.06	0.84–1.35	0.39
rs76837345	1.19	0.98–1.44	1.27	1.03–1.57	0.88	0.55–1.39	0.14
rs62274042	1.65	1.36–2.01	1.59	1.28–1.97	1.98	1.24–3.14	0.40
rs635634	1.14	1.01–1.29	1.16	1.01–1.33	1.06	0.80–1.40	0.56
rs3744763	0.89	0.81–0.97	0.89	0.80–0.98	0.88	0.72–1.09	0.97
chr17:29181220:I	0.89	0.80–0.99	0.88	0.78–0.99	0.93	0.72–1.19	0.71
rs6755777	0.98	0.89–1.09	0.98	0.88–1.10	0.99	0.80–1.24	0.94
rs117224476	0.73	0.64–0.84	0.76	0.65–0.88	0.62	0.45–0.85	0.26
rs1400482	0.80	0.69–0.92	0.81	0.69–0.95	0.77	0.54–1.09	0.79
rs116133110	0.86	0.78–0.95	0.87	0.78–0.97	0.83	0.66–1.04	0.69
Risk score quartile							
2nd *vs.* 1st quartile	1.15	0.94–1.41	1.18	0.95–1.48	0.98	0.61–1.59	
3rd *vs.* 1st quartile	1.56	1.29–1.90	1.53	1.24–1.90	1.77	1.12–2.81	0.52
4th *vs.* 1st quartile	2.26	1.87–2.72	2.31	1.88–2.85	2.00	1.30–3.08	

[1]Adjusted for OC use (never (including <1), 1 to <2, 2 to <5, 5 to <10, 10+ years), parity (0, 1, 2+ births), hysterectomy, endometriosis, tubal ligation and education (less than high school, high school graduate, some college, college graduate or more); conditioned on age (50–54, 55–59, 60–64, 65–69, 70–74, 75+), genetic ancestry (European, African, Asian, other) and analytic set.

[2] All SNP main effects show genome-wide significance ($p \leq 5.0 \times 10^{-8}$) in the full OCAC dataset.

Abbreviations: OR, odds ratio; CI, confidence interval.

p Values significant at a ≤0.05 level are indicated in bold.

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Table 4

Association between each of the 18 SNPs and genetic risk score and risk of endometrioid ovarian cancer, stratified by ET use after age 50

	Main effect		No ET use (*N* = 286 cases/3,500 controls)		ET use (*N* = 51 cases/551 controls)		
	OR[1,2]	95% CI	OR[1]	95% CI	OR[1]	95% CI	*p* Value for interaction
SNP							
rs58722170	0.95	0.76–1.20	0.97	0.75–1.25	0.87	0.50–1.52	0.73
rs10069690	0.98	0.81–1.20	0.93	0.75–1.16	1.32	0.82–2.15	0.20
chr10:21878831:D	1.08	0.89–1.30	1.03	0.84–1.27	1.30	0.81–2.08	0.39
rs17329882	1.07	0.87–1.32	1.11	0.88–1.39	0.90	0.52–1.56	0.48
rs1879586	0.97	0.76–1.24	0.99	0.77–1.29	0.83	0.46–1.52	0.59
rs56318008	1.40	1.13–1.74	1.53	1.21–1.92	0.82	0.46–1.45	**0.037**
rs4808075	1.01	0.83–1.22	1.02	0.83–1.25	0.97	0.60–1.56	0.84
chr9:136138765:D	0.99	0.74–1.31	1.03	0.76–1.41	0.74	0.35–1.55	0.41
rs7207826	1.21	1.01–1.45	1.32	1.09–1.61	0.71	0.43–1.18	**0.021**
rs76837345	1.25	0.89–1.75	1.14	0.78–1.68	1.69	0.83–3.46	0.35
rs62274042	1.12	0.75–1.68	1.10	0.70–1.70	1.34	0.47–3.75	0.73
rs635634	1.04	0.83–1.31	1.10	0.86–1.41	0.76	0.41–1.42	0.28
rs3744763	1.06	0.89–1.26	1.07	0.89–1.28	1.00	0.65–1.54	0.79
chr17:29181220:I	0.81	0.66–0.99	0.81	0.65–1.01	0.80	0.49–1.32	0.97
rs6755777	1.01	0.84–1.21	0.98	0.81–1.20	1.14	0.73–1.78	0.56
rs117224476	0.79	0.62–1.02	0.85	0.65–1.11	0.54	0.28–1.06	0.21
rs1400482	0.98	0.76–1.26	0.92	0.70–1.21	1.36	0.73–2.52	0.26
rs116133110	1.04	0.87–1.24	1.08	0.89–1.31	0.85	0.55–1.31	0.32
Risk score quartile							
2nd *vs.* 1st quartile	1.49	1.04–2.14	1.40	0.94–2.09	1.98	0.79–4.94	
3rd *vs.* 1st quartile	1.69	1.18–2.40	1.65	1.12–2.42	2.04	0.80–5.17	0.25
4th *vs.* 1st quartile	1.73	1.22–2.46	1.85	1.27–2.70	1.10	0.42–2.91	

[1]Adjusted for OC use (never (including <1), 1 to <2, 2 to <5, 5 to <10, 10+ years), parity (0, 1, 2+ births), hysterectomy, endometriosis, tubal ligation and education (less than high school, high school graduate, some college, college graduate or more); conditioned on age (50–54, 55–59, 60–64, 65–69, 70–74, 75+), genetic ancestry (European, African, Asian, other) and analytic set.

[2] All SNP main effects show genome-wide significance ($p \leq 5.0 \times 10^{-8}$) in the full OCAC dataset.

Abbreviations: OR, odds ratio; CI, confidence interval.

p Values significant at a ≤0.05 level are indicated in bold.

Table 5

Association between rs10069690 and risk of serous ovarian cancer by duration of ET use after age 50

	1 to <5 years (*N* = 70 cases/193 controls)		5 to <10 years (*N* = 82 cases/168 controls)		10+ years (*N* =131 cases/190 controls)	
SNP	**OR[1]**	**95% CI**	**OR[1]**	**95% CI**	**OR[1]**	**95% CI**
rs10069690	1.41	0.90–2.23	1.21	1.09–2.32	1.85	1.28–2.66
			p Value for interaction = 0.034			

Note: The reference group consists of women who did not use ET after age 50 and carried the C (reference) allele.

[1]Adjusted for OC use (never (including <1), 1 to <2, 2 to <5, 5 to <10, 10+ years), parity (0, 1, 2+ births), hysterectomy, endometriosis, tubal ligation and education (less than high school, high school graduate, some college, college graduate or more); conditioned on age (50–54, 55–59, 60–64, 65–69, 70–74, 75+), genetic ancestry (European, African, Asian, other) and analytic set.

Abbreviations: OR, odds ratio; CI, confidence interval.