Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors


Abstract

Background: Many epithelial ovarian cancer (EOC) risk factors relate to hormone exposure and elevated estrogen levels are associated with obesity in postmenopausal women. Therefore, we hypothesized that gene–environment interactions related to hormone-related risk factors could differ between obese and non-obese women.

Methods: We considered interactions between 11,441 SNPs within 80 candidate genes related to hormone biosynthesis and metabolism and insulin-like growth factors with six hormone-related factors (oral contraceptive use, parity, endometriosis, tubal ligation, hormone replacement therapy, and estrogen use) and assessed whether these interactions differed between obese and non-obese women. Interactions were assessed using logistic regression models and data from 14 case-control studies (6,247 cases; 10,379 controls). Histotype-specific analyses were also completed.

Results: SNPs in the following candidate genes showed notable interaction: IGF1R (rs41497346, estrogen plus progesterone therapy, histology = all, $P = 4.9 \times 10^{-4}$) and ESR1 (rs12661437, endometriosis, histology = all, $P = 1.5 \times 10^{-3}$). The most notable obesity–gene–hormone risk factor interaction was within INSR (rs113759408, parity, histology = endometrioid, $P = 8.8 \times 10^{-4}$).

Conclusions: We have demonstrated the feasibility of assessing multifactor interactions in large genetic epidemiology studies. Follow-up studies are necessary to assess the robustness of our findings for ESR1, CYP11A1, IGF1R, CYP11B1, INSR, and IGFBP2. Future work is needed to develop powerful statistical methods able to detect these complex interactions.

Impact: Assessment of multifactor interaction is feasible, and, here, suggests that the relationship between genetic variants within candidate genes and hormone-related risk factors may vary EOC susceptibility. Cancer Epidemiol Biomarkers Prev; 25(5); 780–90. ©2016 AACR.
Introduction

Little research has been conducted to determine multifactor gene–environment interaction at the candidate gene or genome-wide level despite the emerging evidence to show that these types of complex relationships do exist (1–3). In addition to the lack of studies assessing complex interactions in cancer risk, only a limited number of studies have assessed gene–environment (GE) interactions by histologic subtype, as genetic and environmental risk factors have been found to differ by the histology. Recently, consortia have been established to give the large sample size needed to detect SNPs with small effects, providing the ability to study GE interactions. In April 2005, the Ovarian Cancer Association Consortium (OCAC) was formed; the largest international consortium conducting genetic epidemiology studies for epithelial ovarian cancer (EOC; ref. 4). This international effort comprises more than 40 different genetic epidemiologic studies, with the focus on assessing single SNP associations with EOC.

To date, OCAC has identified 18 confirmed novel susceptibility loci that are associated with EOC risk (5–12). In addition to finding new risk loci, GWAS also confirm the biologic distinction of the various EOC histologies. For example, risk alleles in 8p24 and 13p13 associate almost exclusively with serous EOC (8, 13), yet those in 2q31 and 17q12 are also associated with other subtypes (8, 14). However, it is hypothesized that the known risk loci are likely to represent only a fraction of the common risk alleles for EOC and that numerous undetected common variant loci still remain to be discovered (15).

In addition to genetic susceptibility loci, there are several confirmed EOC environmental risk factors. Similar to other hormone-related cancers in women, many of these risk factors related to hormone exposure, including obesity (risk; refs. 16–19), history of endometriosis (risk; ref. 20), estrogen use menopausal hormonal therapy (MHT; risk; ref. 21), estrogen plus progesterone MHT (risk; ref. 21), oral contraceptive use (protective effect that increases with time of use; ref. 22), parity (protective effect increases with number of live births; refs. 23, 24), tubal ligation (protective; ref. 25), and breast feeding (protective; refs. 26, 27).

Similar to genetic risk factors, environmental risk factors also differ by histology (28); for example, endometriosis is associated with risk of only clear cell, low-grade serous, and endometrioid EOC (20, 29). The vast majority of epidemiologic studies of EOC risk have focused on marginal effects of genetic and environmental factors. A recent study by OCAC investigators assessed GE interactions across six known genetic risk loci (30). While this study looked at GE by histotype, this study did not investigate a three-way interaction involving obesity.

Obesity is associated with an increase in insulin levels, resulting in an increase in insulin-like growth factor 1 (IGF1) activity (31, 32). Increased levels of adiposity also lead to increased aromatase activity, and thus to an increase in estrogen levels (31, 33–35). After menopause, adipose tissue is the major source of estrogen in women. In breast cancer, evidence suggests that increased estrogen levels might underlie the association between BMI, breast cancer risk and MHT (31). It has been found that in postmenopausal women, the association between breast cancer and BMI is stronger in women who have never received MHT, compared with women who have used MHT (36). Similarly, a recent meta-analysis (2012) found that use of MHT attenuated the effect of BMI on EOC risk (17). A recent OCAC study found that high BMI was associated with increased risk of EOC in 15 case–control studies (16). In addition to finding an association between BMI and EOC risk, they found that this association was more pronounced in borderline serous, invasive endometrioid, and invasive mucinous histotypes. However, they found that MHT did not attenuate the effect of BMI on EOC risk when the analyses were restricted to postmenopausal women. In addition, they also found no association of BMI with risk of ovarian cancer in the most common serous histotype (16). On the basis of these data, we hypothesize that GE effects could differ between obese and non-obese women.

On the basis of the complex relationship between hormone exposure, obesity, growth factors/insulin levels, and genetic factors we hypothesize that GE effects could be histology dependent and differ between obese and non-obese women. This hypothesis is illustrated in Supplementary Fig. S1. In this candidate gene study, we sought to detect both two-way and multifactor obesity–GE interactions for EOC risk. Overall, we assessed 11,441 SNPs located within 80 candidate genes related to hormone biosynthesis and metabolism in addition to those in insulin-like growth factors (IGF). The case–control analyses were run separately for case groups that involve (i) all EOC invasive cases; (ii) high-grade serous (HGS) invasive cases; and (iii) endometrioid (ENDO) invasive cases. Candidate gene analyses specific to the less common histotypes were excluded due to the difficulty of assessing three-way interactions.

Materials and Methods

Study participants

Supplementary Tables S1 and 2 summarize the characteristics of the 14 OCAC studies used to assess GE interactions (37–49). The 14 studies included in this analysis were part of the Collaborative Oncological Gene Environment Consortium (COGS)
study in which approximately 200,000 SNPs were genotyped in breast, ovarian and prostate cancers. Each OCAC study included in the analyses had to contribute at least 50 ovarian cancer cases and 50 controls, with controls further required to be sampled from the same population as the cases. Thus, 6,247 invasive cases and 10,379 controls of European descent were included in this analysis. GE interactions have been explored in these studies previously (28) and are described in further detail therein. Each study provided information on age at diagnosis or enrollment, BMI and other reproductive and lifestyle factors as well as information regarding tumor histology (serous, endometrioid, clear cell, mixed, other), tumor behavior (invasive or borderline), and tumor grade (well differentiated, moderately differentiated, poorly differentiated, undifferentiated). All patients provided informed consent, including for passive and active follow-up, using protocols approved by the appropriate Institutional Review Board. Table 1 describes the clinical features of EOC cases (6,247 all EOC, 3,019 HGS, 961 ENDO) and controls (N = 10,379).

Environmental and genetic risk factors

Young adult BMI. To quantify obesity, we used BMI calculated in early adulthood (18–29 years of age) as opposed to BMI at diagnosis as early adulthood BMI would better approximate subjects obesity levels integrated over a lifetime (18, 50), and thus exposure to estrogen derived from adipose tissue. Measurement of weight in early adulthood was conducted in 9 of the 14 studies used for the GE analyses (16); and, therefore, the three-way BMI–GE interaction analyses were limited to these 9 studies. Five studies reported weight at age 18 (DOV, HAW, HOP, POL, UCI), two studies reported weight "in your 20s" (MAL, USC), and two studies reported weight at age 20 (AUS, GER). The calculated BMIs were classified according World Health Organization (WHO) standards: (<18.5 "underweight"; 18.5–24.9 "normal weight"; 25–29.9 "overweight"; 30–34.9 "class I obesity"; 35–39.9 "class II obesity"; ≥40 "class III obesity"; ref.51). From these WHO standards, the subjects BMI were further categorized into two groups for GE analyses: (i) underweight or normal weight individuals with BMI less than 25 and (ii) overweight or obese individuals BMI greater than 25.

Hormone-related environmental factors. The GE analyses included seven hormone-related environmental factors: oral contraceptive use, parity, breast feeding, tubal ligation status, endometriosis, estrogen MHT, and estrogen plus progesterone MHT. To facilitate testing for multifactor interactions, each environmental factor was dichotomized to ensure reasonable sample sizes in the various groups. Oral contraceptive use (years) was divided into (<1 year; ≥1 year), parity (0 full births; ≥ 1 full birth), breast feeding was separated into (ever/never), estrogen MHT and estrogen plus progesterone MHT were categorized as (never/ever), while endometriosis and tubal ligation were included in terms of yes/no status.

Genetic markers. We searched the literature to determine a set of candidate genes related to steroid biosynthesis, estrogen signaling, and IGFB, as we hypothesize that genetic variants within these candidate genes modify EOC risk and that these effects are modified by hormone-related risk factors and obesity (52–54), and identified a list of 80 candidate genes (Supplementary Table S3). Using the National Center for Biotechnology Information (NCBI) website, SNPs were selected within 20 Kb of the first or last exon, as this was expected to sufficiently cover the promoter regions of most genes, as well as SNPs in LD with variation in the gene region (55). Because of power limitations for testing multifactor GE interactions, SNPs were excluded from the analysis if the minor allele frequency (MAF) was less than 10%. This approach extracted 11,441 candidate gene SNPs. The candidate gene SNPs were imputed using the 1000 Genomes project (56), from an original set of >200,000 genotyped SNPs from the COGS custom Illumina SNP array (57, 58). Details on the number of imputed SNPs for each candidate gene are included in (Supplementary Table S3).

Statistical analysis

The study population was restricted to individuals of European descent based on LAMP analyses (59) with complete covariate information, and only invasive EOC cases were considered. For
analyses involving the MHTs, either estrogen use or estrogen plus progesterone (EPP) use, the cases and controls were further restricted to postmenopausal women. For both the GE and BMI-GE (or GEE) analyses, the presence or absence of the environmental factors were coded as either 0 or 1. Separate analyses were conducted for case groups that included: (i) all invasive EOC cases, (ii) HGS cases, and (iii) ENDO cases. Analyses were adjusted for age of diagnosis (enrollment), study site, and the first 5 principal component scores from a principal component analysis to adjust for population substructure. With the goal to determine GE effects and not general genetic association, assessment of significance was restricted to the highest level interaction effects (as opposed to “omnibus” tests for both main and interaction effects; ref. 60).

The following logistic regression model was used to assess GE interaction for each SNP. For $i = 1, \ldots, n$ let

$$
\logit(P (D_i = 1 | G_i, E_k, Z_i)) = \beta_0 + \beta_c G_i + \beta_k E_k + \beta_{cE} G_i E_k + \beta_{cZ} G_i Z_i + \beta_{kZ} E_k Z_i.
$$

where $D_i$ represents that disease status (case = 1, control = 0) for subject $i$, $G_i$ represents the number of minor alleles observed for subject $i$ for SNP $j$, $E_k$ represents the presence or absence of environmental factor $k$ for subject $i$, and $Z_i$ represents a vector of covariates for subject $i$ to account for potential confounding, and each $\beta_{cE}$ represents a corresponding interaction regression coefficient. For each SNP $j$ and environmental factor $k$, we tested the null hypothesis of no GE interaction versus an alternative hypothesis that a GE interaction is present (i.e., null hypothesis: $\beta_{cE} = 0$ vs. alternative hypothesis: $\beta_{cE} \neq 0$). The hypothesis was tested with the likelihood ratio test statistic

$$
D = -2 \ln \left( \frac{\text{likelihood for reduced (null) model}}{\text{likelihood for full (alternative) model}} \right) \sim \chi^2_1.
$$

Similarly, to test whether GE interactions could be modified by BMI, we considered the following logistic regression model. For $i = 1, \ldots, n$ let

$$
\logit(P (D_i = 1 | G_i, E_k, Z_i)) = \beta_0 + \beta_c G_i + \beta_k E_1 + \beta_{cE} G_i E_1 + \beta_{cZ} G_i Z_i + \beta_{kZ} E_1 Z_i.
$$

where $E_1$ represents the BMI status (low/high) at young adulthood of subject $i$, $E_2$ represents the presence of absence of the second environmental factor for subject $i$, and $Z_i$ represents a vector of covariates for subject $i$ that account for potential confounding, and each $\beta$ represents a corresponding regression coefficient. To test whether GE interactions differ between non-obese and obese individuals, we test the null hypothesis of no GE interaction versus an alternative hypothesis of GE interaction is present (i.e., null hypothesis $\beta_{cE} = 0$ vs. alternative hypothesis $\beta_{cE} \neq 0$). This hypothesis was tested using a likelihood ratio test statistic $D = -2 \ln \left( \frac{\text{likelihood for reduced (null) model}}{\text{likelihood for full (alternative) model}} \right) \sim \chi^2_1$.

**Results**

**GE interaction**

In total, the GE analyses were run across 11,441 candidate gene SNPs, and included 91,528 GE combinations (11,441 SNPs x 7 Environmental Factors + BMI]). And these analyses were run across 3 separate case groups (All, HGS, ENDO). However, the imputed SNPs were in high linkage disequilibrium (LD), and the analyses across case groups were also highly correlated. The SimpleM method was used to estimate the effective number of independent SNPs tested within each gene (ref.61; Supplementary Table S3) and, in total, the analyses were estimated to involve independent 2,336 SNPs. Using the estimated effective number of independent tests, the Bonferroni correction for the number of total candidate gene SNPs was $0.05/2,336 = 2.1 \times 10^{-5}$, while adjusting for the total number of independent GE combinations gives $0.05/(2,336 \times 8) = 2.7 \times 10^{-6}$, respectively. Several SNP–environment interactions were significant using the former threshold, however using the latter strict threshold, no significant GE was detected. SNPs with GE interaction $P < 10^{-4}$ are presented in Table 2.

**Table 2.** Association with $P < 10^{-4}$ for GE and BMI-GE analyses

<table>
<thead>
<tr>
<th>Analysis</th>
<th>Histology</th>
<th>Environment</th>
<th>Gene</th>
<th>SNP</th>
<th>MAF</th>
<th>N cases</th>
<th>N controls</th>
<th>Interaction</th>
<th>$P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>GE All</td>
<td>EPP MHT</td>
<td>IGF1R</td>
<td>rs41497346</td>
<td>0.28</td>
<td>2,870</td>
<td>5,051</td>
<td>-0.57</td>
<td>4.92 x 10^{-5}</td>
<td></td>
</tr>
<tr>
<td>GE All</td>
<td>EPP MHT</td>
<td>ESR1</td>
<td>rs12661437</td>
<td>0.34</td>
<td>5,333</td>
<td>9,306</td>
<td>0.53</td>
<td>1.47 x 10^{-5}</td>
<td></td>
</tr>
<tr>
<td>GE END0</td>
<td>Estrogen MHT</td>
<td>HS271B2</td>
<td>rs2955362</td>
<td>0.23</td>
<td>405</td>
<td>9,054</td>
<td>-1.12</td>
<td>3.44 x 10^{-3}</td>
<td></td>
</tr>
<tr>
<td>GE HGS</td>
<td>Endometriosis</td>
<td>CYP1A1</td>
<td>rs9944175</td>
<td>0.24</td>
<td>2,578</td>
<td>9,306</td>
<td>-0.87</td>
<td>4.13 x 10^{-4}</td>
<td></td>
</tr>
<tr>
<td>GE END0</td>
<td>Endometriosis</td>
<td>AKR1C3</td>
<td>rs61856340</td>
<td>0.10</td>
<td>405</td>
<td>9,054</td>
<td>-1.47</td>
<td>5.30 x 10^{-5}</td>
<td></td>
</tr>
<tr>
<td>GE END0</td>
<td>Endometriosis</td>
<td>CYP1B2</td>
<td>rs28526467</td>
<td>0.43</td>
<td>815</td>
<td>9,054</td>
<td>-1.09</td>
<td>6.83 x 10^{-5}</td>
<td></td>
</tr>
<tr>
<td>GE END0</td>
<td>OC Use</td>
<td>PRL</td>
<td>rs7283669</td>
<td>0.10</td>
<td>945</td>
<td>10,323</td>
<td>-0.82</td>
<td>7.09 x 10^{-5}</td>
<td></td>
</tr>
<tr>
<td>BMT-GE EMD</td>
<td>Parity</td>
<td>INS</td>
<td>rs802954</td>
<td>0.37</td>
<td>778</td>
<td>8,284</td>
<td>-2.56</td>
<td>8.35 x 10^{-4}</td>
<td></td>
</tr>
<tr>
<td>BMT-GE EMD</td>
<td>Parity</td>
<td>IGFBP2</td>
<td>rs869654</td>
<td>0.11</td>
<td>4,954</td>
<td>8,284</td>
<td>-2.54</td>
<td>1.43 x 10^{-5}</td>
<td></td>
</tr>
<tr>
<td>BMT-GE EMD</td>
<td>HGS OC</td>
<td>Use</td>
<td>rs31759408</td>
<td>0.17</td>
<td>2,296</td>
<td>8,250</td>
<td>1.49</td>
<td>2.18 x 10^{-5}</td>
<td></td>
</tr>
</tbody>
</table>

Note: Results highlighted in green or red in Figs. 1 and 3. More detailed summaries of these top hits are shown in Supplementary Tables S4 and S5.
risk in patients with no endometriosis and increased risk in patients with endometriosis. The marginal OR estimate of rs12661437 was 0.95 ($P = 0.17$). However, when women with no endometriosis history, the presence of a rs12661437 minor allele decreased risk for EOC (OR = 0.92); while within women with a history of endometriosis, the rs12661437 minor allele provided increased risk (OR = 1.59). Subtype-specific analyses for rs12661437 also found qualitatively similar effect sizes across all histologies (Supplementary Table S4). Rs12661437 lies in an intron near the 5′ end of ESR1.

When restricting the cases to HGS, the most notable interaction was for CYP11A1 (rs9944175, endometriosis, histology = HGS, OR = 0.42, $P = 4.1 \times 10^{-3}$; Fig. 2E and F). The marginal OR estimate for HGS EOC risk of rs9944175 was 1.06 ($P = 0.26$). However, for women with no history of endometriosis, the estimated effect of one rs9944175 minor allele increased HGS EOC risk (OR = 1.11) but decreased HGS EOC risk in women with a history of endometriosis (OR = 0.47). This SNP showed no statistically significant interaction for the ENDO histology (OR = 0.69, $P = 0.18$). rs9944175 lies within 20 Kb of the 3′ end of CYP11AI.

**Multifactor or BMI–GE interactions**

For each gene, SNPs with notable BMI–GE interaction results ($P < 10^{-5}$) and their estimated interaction effects are presented (Supplementary Table S5). Figure 3 provides an image map that highlights three-way interaction tests of obesity, lifestyle, and reproductive factors, and candidate genes with at least on SNP $P$ value less than: $P = 10^{-5}$, $P = 10^{-3}$, and $P = 10^{-5}$. This image map groups the candidate genes alphabetically and according to their involvement in the production of hormones hypothesized to influence EOC risk (ref.62; Androgen, Estrogen, Progesterone, Gonadotropins, Insulin-related). No statistically significant SNPs were detected after Bonferroni correction for the effective number of candidate gene SNPs ($P < 2.1 \times 10^{-5}$). A stricter threshold that adjusts for effective number of candidate gene SNPs by 7 environmental factors in the BMI-GE analyses was $P < 3.1 \times 10^{-6}$.

The most statistically significant SNP for the BMI-GE analyses lies in INSR (rs8102954, parity, histology = ENDO, BMI-GE OR = 0.074, $P = 8.83 \times 10^{-6}$; Figs. 4A and B). Within the low-BMI group, the estimated SNP–Parity interaction of one rs8102954 minor allele for the ENDO cases was negligible (OR GE low BMI = 1.4, $P = 0.15$); while within high-BMI women the estimated GE effect is (OR GE high BMI = 0.10, $P = 0.0021$). The BMI–GE interaction effect was not significant for analyses with case groups that included all histology and high-grade serous cases. rs8102954 lies in an exon region near the 3′ end on INSR.

For case–controls analyses involving all histologies, the most notable BMI–GE interaction was IGFBP2 (rs869564, parity, histology = All, BMI–GE OR = 0.096, $P = 1.43 \times 10^{-5}$; Fig. 4C and D). For low-BMI women, the estimated SNP–parity interaction effect of one rs869564 minor allele was negligible (OR GE low BMI = 0.48); however, within high-BMI women, the estimated GE interaction effect was (OR GE high BMI = 0.11, $P = 4.14 \times 10^{-5}$). The three-way BMI–GE interaction effect was significant for the HGS cases (BMI–GE OR = 0.077, $P = 1.23 \times 10^{-5}$), but not the analyses involving the ENDO cases (BMI–GE OR = 0.18). Rs869564 resides in an exon region on the 3′ end of IGFBP2.

For HGS cases, the most statistically significant SNP for the BMI-GE analyses lies in CYP11B1 (rs113759408, oral contraceptive use, histology = HGS, BMI–GE OR = 0.072, $P = 2.2 \times 10^{-5}$; Figs. 4E and F). Within the low-BMI women group, the estimated SNP–OC use interaction effect of one rs113759408 minor allele for HGS cases was negligible (OR GE low BMI = 0.90, $P = 0.41$), while within high-BMI women, the estimated GE effect is large (OR GE high BMI = 4.52, $P = 0.0028$). The BMI–GE interaction effect was not statistically significant for the ENDO histology (BMI-GE OR = 2.11, $P = 0.24$). Rs113759408 lies in an intronic region in the middle of CYP11B1.

**Discussion**

In this article, we investigated both GE and multifactor obesity–GE interactions in epithelial ovarian cancer (EOC) risk. We used 14 case–control studies within the Collaborative Ovarian Cancer Association Consortium (COGS) and Ovarian Cancer Association Consortium (OCAC) that provided more than 6,000 cases and 10,000 controls. Our main hypothesis was that some EOC risk due to SNPs could be explained by interactions with environmental factors. Similar to breast and endometrial cancers, many EOC risk factors relate to hormone exposure and increased levels of estrogen has been associated with obesity.
postmenopausal women. Therefore, we hypothesized that GE interactions dealing with hormone-related risk factors could differ between obese and non-obese women. None of the tests of GE interaction and multi-factor obesity–GE interaction were significant at genome-wide level ($P = 5 \times 10^{-8}$).

The most statistically significant GE interaction result was IGF1R (rs41497346, estrogen plus progesterone MHT, histology = All, OR = 0.56, $P = 4.9 \times 10^{-6}$). Rs41497346 lies in an intronic region near the 3' end of IGF1R, and is in the same LD block as several SNPs hypothesized to have marginal risk in breast cancer.
High expression levels of IGFIR were reported by Tang and colleagues (64) in tumor tissue samples from 25 of 36 patients with EOC. Estrogen use is associated with increased IGFIR expression, while progesterone was associated with decreased IGFIR expression in breast cancer cells (65). Variation within the gene ESR1 was also found to be involved in an interaction involving endometriosis in analyses of all histologies (rs12661437, intronic SNP near 5’ end of gene. \( P = 1.5 \times 10^{-5} \)), where the minor allele decreased EOC risk in patients with no endometriosis and increased risk in patients with endometriosis. Subtype-specific analyses for rs12661437 also found qualitatively similar effect sizes across all histologies. Variation near ESR1 (rs2295190) has been reported to be associated with EOC risk (66); however, the SNPs are in low LD \( (r^2 = 0.001) \).

For the BMI–GE interaction analyses, the most statistically significant results were INSR (rs8102954, parity, histology = ENDO, BMI–GE OR = 0.074, \( P = 8.83 \times 10^{-9} \); Fig. 4A and B) and IGFBP2 (rs869564, parity, histology = All, BMI–GE OR = 0.996, \( P = 1.43 \times 10^{-5} \); Figs. 4C and D). No genetic polymorphisms within INSR and IGFBP2 have been associated previously with ovarian cancer risk. Nevertheless, considerable research exists on the role of insulin receptors and cancer as studies have shown that insulin receptors may be involved in the regulation of ovarian cancer cell growth (67) and that increased levels of insulin have been associated with breast and endometrium cancers for which these tumorigenic properties can be modified by insulin receptors (31). Similarly, the role of IGFs have been extensive studied for their role in carcinogenesis (68). Specifically, IGFBP2 has been linked ovarian cancer by promoting cancer cell invasion (69), while common variants in IGFI, IGFBP1 and IGFBP3, have been associated with ovarian (70) and endometrial cancers (71). IGFBP2 has also been linked to other hormone-related cancers (72–74).

For the high-grade serous cases, the most statistically significant SNP for the BMI-GE analyses lies in CYP11B1 (rs113759408, oral contraceptive use, histology = HGS, BMI-GE estimate = 1.49, \( P = 2.2 \times 10^{-5} \); Figs. 4E and F). Polymorphism rs113759408 lies in an intronic region in the middle of CYP11B1 (between exons 3 and 4), the gene that encodes for steroid 11β-hydroxylase. Mutations in this gene cause congenital adrenal hyperplasia (OMIM #202010). No research has been published showing a link between EOC risk and variants within this gene. However, genetic variation in CYP11B1 has been reported to be associated with breast cancer risk from a prediction model involving SNP rs4541 in exon 7 of CYP11B1 (75) and the association with serum hormone levels in breast cancer patients (76).

We chose to restrict our analyses to SNPs located within 80 candidate gene and 8 established ovarian cancer reproductive or lifestyle factors. An earlier study investigated two-way interactions between 6 established SNP risk loci and 5 established environmental risk factors (30). Similar to our study results, their two-way interaction analyses were not strong enough to rule out the role of chance. While these initial findings suggest that GE interactions play a modest role in EOC risk, genome-wide studies are necessary to fully examine the potential interplay between SNPs and environmental factors.

For the obesity–GE analyses, a strength of this study was the use of young adult BMI (low, high) as opposed to BMI at diagnosis, as young adult BMI may serve as an indicator of obesity integrated over a life-time and adipose-based estrogen exposure (18, 50). While a biologic rationale exists for higher order interactions, very little literature has focused on multi-factor interactions, perhaps due to the challenge of necessary power to detect these higher order interactions. Therefore, a limitation of the multi-factor GE interaction analyses were modest sample sizes: especially for less well-documented environmental factors and histology-specific analyses (Supplementary Table S7).

In conclusion, we have demonstrated the feasibility of assessing multi-factor interactions in large genetic epidemiology studies. Future work is needed to develop powerful statistical methods able to detect these complex interactions, as they may provide additional information regarding the genetic etiology of ovarian and other hormone-related cancers. Follow-up studies are necessary to assess the robustness of our notable findings in ESR1, CYP11A1, IGFIR, CYP11B1, INSR, and IGFBP2. To further follow-up our investigation of multi-factor GE interactions, we will explore other potential modifiers of GE risk, such as BRCA mutation status, and assess BMI-GE in other hormone-related cancers, such as breast, prostate, and endometrial.
Disclosure of Potential Conflicts of Interest
M.T. Goodman is a consultant/advisory board member for Johnson and Johnson. No potential conflicts of interest were disclosed by the other authors.

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Figure 4.
Locus zoom plots and estimated BMI–GE interaction effects of top results for INSR-Parity-BMI (Histology ENDO; A and B), IGFBP2-Parity-BMI (Histology all; C and D), and CYP11B1-OC Use-BMI (Histology HGS; E and F). The vertical black lines represent 95% CIs for estimated ORs.
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): J.L. Usset, J.P. Tyrer, W. Sieb, M.C. Larson, K.B. Moysich, H. Yang, P. Pharaoh, B.L. Fridley


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