The role of KRAS rs61764370 in invasive epithelial ovarian cancer: implications for clinical testing

M. Phelan, Malcolm C. Pike, Paolo Radice, Mary Anne Rossing, Joellen M. Schildkraut, Thomas A. Sellers, Christian F. Singer, Honglin Song, Daniel O. Stram, Rebecca Sutphen, SWE-BRCA Investigators, Kathryn L. Terry, Ya-Yu Tsai, Anne M. van Altena, Ignace Vergote, Robert A. Vierkant, Allison F. Vitonis, Christine Walsh, Shan Wang-Gohrke, Barbara Wappenschmidt, Anna H. Wu, Argyrios Ziogas, Ovarian Cancer Association Consortium, Consortium of Investigators of Modifiers of BRCA1/2, Andrew Berchuck, Harvey A. Risch

Affiliations:

1 Department of Oncology, University of Cambridge, Cambridge, United Kingdom

2 Department of Community and Family Medicine, Duke University Medical Center, Durham, North Carolina, USA

3 Department of Preventive Medicine, Keck School of Medicine and the USC Norris Comprehensive Cancer Center, University of Southern California, Los Angeles, California, USA

4 Ontario Cancer Genetics Network, Cancer Care Ontario and Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, Ontario, Canada

5 Department of Epidemiology, School of Medicine, University of California, Irvine, California, USA

6 Byelorussian Institute for Oncology and Medical Radiology Aleksandrov N.N., Minsk, Belarus

7 Centre for Cancer Genetic Epidemiology, Department of Public Health and Primary Care, University of Cambridge, United Kingdom
8 Breast Cancer Family Registry, Epidemiology and Genetics Research Program, DCCPS, National Cancer Institute, Rockville, Maryland, USA
9 Cancer Risk Program, Departments of Medicine, Epidemiology, and Biostatistics, University of California at San Francisco, San Francisco, California, USA
10 Department of Gynecology and Obstetrics, University Hospital Erlangen, Friedrich-Alexander University Erlangen-Nuremberg, Erlangen, Germany
11 Department of Medicine, Massachusetts General Hospital, Boston, Massachusetts, USA
12 Clinic of Obstetrics and Gynaecology, Hannover Medical School, Hannover, Germany
13 Clinic of Radiation Oncology, Hannover Medical School, Hannover, Germany
14 Division of Cancer Epidemiology and Genetics, National Cancer Institute, National Institutes of Health, Bethesda, Maryland, USA
15 Department of Obstetrics and Gynecology, School of Medicine, University of North Carolina at Chapel Hill, North Carolina, USA
16 Genome Sciences Centre, British Columbia Cancer Agency, Vancouver, British Columbia, Canada
17 Epigenetics Unit, Department of Surgery and Cancer, Imperial College London, London, United Kingdom
18 Department of Obstetrics and Gynecology, Helsinki University Central Hospital, Helsinki, Finland
19 Department of Pathology, University of Helsinki, Helsinki, Finland
20 Molecular Oncology Laboratory, Hospital Clínico San Carlos, Martín Lagos s/n, Madrid 28040, Spain
21 Section of Genetic Oncology, University Hospital of Pisa, Pisa, Italy
Centre for Cancer Genomics and Predictive Medicine, Peter MacCallum Cancer Centre, Melbourne, Victoria, Australia

Department of Pathology, University of Melbourne, Parkville, Victoria, Australia

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

H. Lee Moffitt Cancer Center and Research Institute, Tampa, Florida, USA

The Queensland Institute of Medical Research, Brisbane, QLD, Australia

Division of Epidemiology and Biostatistics, Department of Internal Medicine, University of New Mexico, Albuquerque, New Mexico, USA

Department of Laboratory Medicine and Pathology, Mayo Clinic, Rochester, Minnesota, USA

Obstetrics and Gynecology Epidemiology Center, Brigham and Women's Hospital, Boston, Massachusetts, USA

Genomics Shared Resource, Department of Laboratory Medicine and Pathology, Mayo Clinic College of Medicine, Rochester, Minnesota, USA

Division of Gynaecologic Oncology, Department of Obstetrics and Gynaecology, University Hospitals Leuven, University of Leuven, Belgium

Program in Epidemiology, Fred Hutchinson Cancer Research Center, Seattle, Washington, USA

Clinic of Obstetrics and Gynaecology, Friedrich Schiller University, Jena, Germany

Wessex Clinical Genetics Service, Princess Anne Hospital, Southampton, United Kingdom

Institute of Human Genetics, Friedrich Alexander Universitaet Erlangen-Nuremberg Erlangen, Germany
Centre for Cancer Genetic Epidemiology, Department of Public Health and Primary Care, University of Cambridge, Strangeways Research Laboratory, Worts Causeway, Cambridge, United Kingdom

Division of Hematology and Oncology, Department of Medicine, David Geffen School of Medicine, University of California at Los Angeles, Los Angeles, California, USA.

Department of Gynaecological Oncology, Westmead Hospital, Westmead, NSW, Australia

Westmead Institute for Cancer Research, University of Sydney at Westmead Millennium Institute, Westmead Hospital, NSW, Australia

Department of Health Sciences Research Division of Biostatistics, Mayo Clinic College of Medicine, Rochester, Minnesota, USA

Oncogenetics Unit, Sheba Medical Center, Tel Hashomer, and Sackler School of Medicine, Tel Aviv University, Tel Aviv, Israel

Cancer Genetics Network “Groupe Génétique et Cancer”, Fédération Nationale des Centres de Lutte Contre le Cancer, France

Department of Gynaecological Oncology, University College London, EGA Institute for Women's Health, London, United Kingdom

Department of Pathology and Laboratory Medicine, University of Kansas Medical Center, Kansas City, Kansas, USA

Department of Health Sciences Research Division of Epidemiology, Mayo Clinic College of Medicine, Rochester, MN, USA

Cancer Research Center of Hawaii, University of Hawaii, Honolulu, Hawaii, USA

Women's Cancer Research Institute at the Samuel Oschin Comprehensive Cancer Institute, Cedars-Sinai Medical Center, Los Angeles, California, USA
Genomic Medicine, Department of Clinical Biochemistry, Rigshospitalet, Copenhagen University Hospital, Copenhagen, Denmark

Department of Epidemiology, The Netherlands Cancer Institute, Amsterdam, The Netherlands

Gynecologic Clinic, The Juliane Marie Centre, Rigshospitalet, University of Copenhagen, Copenhagen, Denmark

Department of Viruses, Hormones and Cancer, Institute of Cancer Epidemiology, Danish Cancer Society, Copenhagen, Denmark

Department of Pathology, Molecular Unit, Herlev Hospital, University of Copenhagen, Copenhagen, Denmark

Department of Statistical Science, Duke University, Durham, North Carolina, USA

International Hereditary Cancer Center, Department of Genetics and Pathology, Pomeranian Medical University, Szczecin, Poland

Clinical Genetics Service, Memorial Sloan-Kettering Cancer Center, New York, New York, USA

Section of Medicine, Institute of Cancer Research, Sutton, United Kingdom

Peter MacCallum Cancer Centre, East Melbourne, Victoria, Australia

Department of Population Health Research, Alberta Health Services-Cancer Care, Calgary, Alberta, Canada

Department of Epidemiology, Biostatistics and HTA, Radboud University Nijmegen Medical Centre, Nijmegen, The Netherlands

Vesalius Research Center, VIB and University of Leuven, Belgium

Bayfront Medical Center Obstetrics and Gynecology Residency Program and Women’s Cancer Associates, St. Petersburg, Florida, USA
62 Hereditary Cancer Program, Instituto Catalán de Oncología, Barcelona, Spain

63 Cancer Control Research, British Columbia Cancer Agency, Vancouver, British Columbia, Canada

64 Department of Surgery, Memorial Sloan-Kettering Cancer Center, New York, New York, USA

65 Department of Gynecology, Radboud University Nijmegen Medical Centre, Nijmegen, The Netherlands

66 Cancer Care Ontario, Toronto, Ontario, Canada

67 Immunology and Molecular Oncology Unit, Istituto Oncologico Veneto IOV - IRCCS, Padua, Italy

68 Department of Cancer Prevention & Control, Roswell Park Cancer Institute, Buffalo, New York, USA

69 Women's College Research Institute, University of Toronto, Toronto, Ontario, Canada

70 Department of Medicine, Medical Genetics and Abramson Cancer Center, University of Pennsylvania School of Medicine, Philadelphia, Pennsylvania, USA

71 Department of Pathology, Rigshospitalet, University of Copenhagen, Copenhagen, Denmark

72 University of Texas School of Public Health, Houston, Texas, USA

73 Human Genetics Group, Human Cancer Genetics Programme, Spanish National Cancer Centre, Madrid, Spain

74 Cancer Research UK Clinical Trials Unit, University of Glasgow, Glasgow, Scotland

75 Department of Epidemiology and Biostatistics, Memorial Sloan-Kettering Cancer Center, New York, New York, USA
Unit of Molecular Bases of Genetic Risk and Genetic Testing, Department of Preventive and Predicted Medicine, Fondazione IRCCS Istituto Nazionale Tumori (INT), Milan, Italy

IFOM, Fondazione Istituto FIRC di Oncologia Molecolare, Milan, Italy

Division of Special Gynecology, Medical University of Vienna, Vienna, Austria

University of South Florida College of Medicine, Tampa, Florida, USA

Karolinska University Hospital, Stockholm, Sweden

Department of Obstetrics and Gynecology, University of Ulm, Ulm, Germany

Center of Familial Breast and Ovarian Cancer, Department of Obstetrics and Gynaecology and Center for Integrated Oncology (CIO), University of Cologne, Cologne, Germany

Department of Obstetrics and Gynecology, Duke University Medical Center, Durham, North Carolina, USA

Department of Epidemiology and Public Health, Yale University School of Medicine, New Haven, Connecticut, USA

Correspondence to:

Harvey A. Risch

Department of Epidemiology and Public Health

Yale University School of Public Health, School of Medicine

60 College Street

New Haven, CT 06520-8034 USA

Tel (203) 785-2848

E-mail harvey.risch@yale.edu
TRANSLATIONAL RELEVANCE

An assay for a single nucleotide polymorphism (SNP) in a 3'UTR miRNA binding site of the KRAS gene has recently been commercially marketed as a clinical test to aid epithelial ovarian cancer (EOC) risk assessment in women with family histories of the disease. The justification for use of this assay was based on one published paper which analyzed fewer than 1,000 subjects in total, including only 67 EOC cases carrying BRCA1 mutations or with family histories of EOC. The present report found no association between this SNP and ovarian cancer risk among 8,669 cases of unselected invasive EOC and 10,012 controls, or in 683 cases and 2,044 controls carrying BRCA1 mutations. The results suggest that evaluation of this SNP is not clinically useful for risk prediction in sporadic or familial ovarian cancer.
ABSTRACT

Purpose: An assay for the single nucleotide polymorphism (SNP) rs61764370 has recently been commercially marketed as a clinical test to aid ovarian cancer risk evaluation in women with family histories of the disease. rs61764370 is in a 3'UTR miRNA binding site of the KRAS oncogene, and is a candidate for epithelial ovarian cancer (EOC) susceptibility. However, only one published paper, analyzing fewer than 1,000 subjects in total, has examined this association.

Experimental Design: Risk association was evaluated in 8,669 cases of invasive EOC and 10,012 controls from nineteen studies participating in the Ovarian Cancer Association Consortium, and in 683 cases and 2,044 controls carrying BRCA1 mutations from studies in the Consortium of Investigators of Modifiers of BRCA1/2. Prognosis association was also examined in a subset of five studies with progression-free survival data and eighteen studies with all-cause mortality data.

Results: No evidence of association was observed between genotype and risk of unselected EOC (odds ratio (OR)=1.02, 95% confidence interval (CI)=0.95-1.10), serous EOC (OR=1.08, 95%CI=0.98-1.18), familial EOC (OR=1.09, 95%CI=0.78-1.54), or among women carrying deleterious mutations in BRCA1 (OR=1.09, 95%CI=0.88-1.36). There was little evidence for association with survival time among unselected cases (hazard ratio (HR)=1.10, 95%CI=0.99-1.22), among serous cases (HR=1.12, 95%CI=0.99-1.28), or with progression-free survival in 540 cases treated with carboplatin and paclitaxel (HR=1.18, 95%CI=0.93-1.52).

Conclusions: These data exclude the possibility of an association between rs61764370 and a clinically significant risk of ovarian cancer or of familial ovarian cancer. Use of this SNP for ovarian cancer clinical risk prediction therefore appears unwarranted.
INTRODUCTION

Epithelial ovarian cancer (EOC) is the fifth-most common cancer in women. It generally presents as advanced disease with poor prognosis. Family and twin studies have suggested that inherited genetic variation plays an appreciable part in determining individual risk. However, until recently, knowledge of genetic susceptibility was limited to rare, highly-penetrant alleles in a handful of genes including \textit{BRCA1}, \textit{BRCA2} and the mismatch repair genes (1). In the past two years, genome-wide association studies have identified common susceptibility alleles at four loci at highly stringent levels of statistical significance (P<10^{-8}), but these alleles have small effects on disease risk (per-allele OR<1.3) and explain a small fraction of the genetic component of disease risk (2-4). Many candidate gene studies have identified possible common ovarian cancer susceptibility alleles, but most are likely to represent false-positive associations as none have been reported at the levels of statistical significance required when testing hypotheses with low prior probabilities of association (1).

In July 2010, a single nucleotide polymorphism (SNP), rs61764370, located in the 3’UTR of the \textit{KRAS} oncogene, was reported to be associated with risk of unselected epithelial ovarian cancer (5). The variant was also reported to be associated with a stronger risk in women carrying \textit{BRCA1} mutations, in women not carrying \textit{BRCA1} or \textit{BRCA2} mutations but with a family history of the disease, as well as associated with poorer progression-free survival (5). This SNP was thought to be a strong candidate for cancer risk as it lies in a miRNA binding site, and associations between miRNA mutations or mis-expression and risk of some human cancers have been seen. These observations suggested that miRNAs can function as tumor suppressors or oncogenes (6). An assay to determine genotype at rs61764370 has subsequently been marketed as a commercial test to determine risk in women with a family history of ovarian cancer.
(http://www.miradx.com). However, as with other candidate gene studies, the reported association was not at a level of statistical significance that is regarded as definitive for common susceptibility alleles (7), nor was the magnitude of risk sufficient for this SNP to be acceptable as a useful clinical marker of ovarian cancer risk. The present work therefore sought to: i) replicate the association in a robust manner in multiple study populations genotyped to a high standard with stringent quality assurance procedures; ii) assess the association between genotype at this locus and ovarian cancer risk in women with family histories or who carry deleterious mutations in \textit{BRCA1}; and iii) examine the hypothesis that the SNP is associated with differences in post-diagnosis progression-free survival or all-cause mortality.
METHODS

Study populations. Nineteen ovarian cancer case-control sets and one case series participating in the Ovarian Cancer Association Consortium (OCAC), and one additional case series, contributed data to the analyses (Table 1). Three of the case-control sets were each comprised of a case series matched to controls from the same geographical region: PVM, UK2 and UK-GWAS. Survival time analysis was based on data from eighteen case series including the additional publicly available data for 359 ovarian cancer cases from The Cancer Genome Atlas (http://cancergenome.nih.gov/) that had information on all-cause mortality. The analysis of progression-free survival was based on data from five case series. Finally, data from 683 cases and 2,044 controls enrolled in a stage I project of the Consortium of Investigators of Modifiers of BRCA1/2 (see reference (8) for details of studies participating in CIMBA) were used to examine risk among women carrying deleterious BRCA1 mutations. Each study was approved by a governing research ethics committee and all study subjects provided written informed consent. Clinical and questionnaire data included tumor behavior, histology, stage and grade, age at diagnosis (or at comparable date for controls), family history of ovarian cancer, and ethnicity/race.

Survival-time data were available for cases from eighteen studies (BEL, DOV, UCR, GER, HOP, LAX, MAY, NCO, PVD, RMH, SEA, SOC, SRO, TBO, TCGA, UCI, UKO, USC) and clinical information on chemotherapy, residual disease after surgery and time to progression was collected in five studies (BEL, LAX, MAY, SRO, TCGA). All of the women included in the analysis of progression-free survival (PFS) had at least four cycles of carboplatin and paclitaxel as part of primary treatment. PFS was defined as the time interval between the date of histologic diagnosis and the first confirmed sign of disease recurrence or progression (9).
Genotyping. Genotyping of thirteen case-control sets was performed in a single laboratory using a 5’ nuclease Taqman allelic discrimination assay (Applied Biosystems, Foster City, CA) as part of a 96-SNP Fluidigm multiplex (10 studies) or--with the same batch of Taqman reagents--using the 7900HT Sequence Detection Software (Applied Biosystems) (three studies) (Table 1). Details of OCAC’s quality control (QC) criteria have been described previously (10); they include genotyping of a common set of 95 DNAs (90 CEPH trios and five duplicate samples) and comparison to the genotypes for the same samples as reported by HapMap. However, rs61764370 was not genotyped in the HapMap project. Based on sequence data for 57 individuals of European origin from the 1000Genomes project (http://www.1000genomes.org), a HapMap SNP, rs17388148, was found to be strongly correlated ($r^2=0.97$) with rs61764370. The concordance between the CEPH trio genotype data for rs61764370 and the HapMap genotypes for rs17388148 was 100%. Therefore, data on rs17388148 were obtained from three genome-wide association studies (GWAS), where cases and controls had been genotyped using Illumina genome-wide SNP arrays (1, 2, 4, 8) (Table 1). Neither rs61764370 nor rs17388148 were included on the Illumina arrays used in these GWAS studies, but imputed genotypes were available for rs17388148. These genotypes were provided as the estimated number of rare alleles carried (0 to 2 on a continuous scale). The accuracy of the imputation as calculated by the program MACH of Li and Abecasis (11) for the North American studies (BWH, MAY, NCO, TBO and TOR) was $r^2=0.977$. This high accuracy of the imputation was evidently due to the presence of a nearby SNP (rs12305513, 17kb away) in high LD ($r^2=1$ in HapMap) with rs17388148.

Statistical Analyses. Analyses were restricted to white non-Hispanic women based on self-reported ethnic origin for all of the studies, with the exception of the TCGA, MAY, NCO, TOR,
TBO and UK-GWAS controls. For these studies, genome-wide genotype data were used to estimate intercontinental ancestry and women of less than 90 percent European ancestry were excluded (see methods in reference (3) for details). Cases with borderline (low malignant potential) epithelial ovarian cancer were also excluded, as were 22 cases from TCGA that had been provided to TCGA as part of the MAY case-control study. Departure of genotype frequencies from those expected under Hardy-Weinberg equilibrium was assessed using a chi-square test for each study that was directly genotyped. The association between SNP and disease risk was evaluated using unconditional logistic regression in which number of copies of the minor (infrequent) allele was treated as a continuous variable. This provides an estimate of the per-allele odds ratio (OR) and 95% confidence interval (95% CI). Models adjusted for age categories (<40, 40-49, 50-59, 60-69 and ≥70 years) were also considered. Each case-control set was analyzed individually and the pooled result was obtained by combining the log odds-ratios using standard inverse variance-weighted meta-analytic methods. Analysis of the BRCA1 mutation carrier cohort was carried out using a time-to-event analysis framework that models the association between genotype and ovarian cancer risk as a hazard ratio. Because mutation carriers were not sampled randomly with respect to their disease status, standard methods of survival analysis may lead to biased estimates of associations. Therefore, analyses were carried out by modeling the retrospective likelihood of observed genotype conditional on disease phenotype (see references (8, 12) for details).

Associations between genotype and progression-free survival and all-cause mortality were evaluated using proportional hazards regression. Because the EOC cases were recruited at variable times after diagnosis, regression analysis of all-cause mortality allowed for left truncation, with time at risk starting on date of diagnosis and time under observation beginning at
the time of study entry. This method generates an unbiased estimate of the hazard ratio provided that the proportional hazards assumption is reasonably correct (13). Cause-specific mortality was not available for most studies, so the analysis of all-cause mortality was right-censored at five years after diagnosis in order to minimize the proportion of deaths from causes other than ovarian cancer. The analysis of progression-free survival was adjusted for stage and residual disease, and survival time ended at time of progression or was censored at time of last follow-up.
RESULTS

Details of the nineteen case-control sets used in our analyses are given in Table 1. Genotype data from these sets were available for 8,669 cases and 10,012 controls (Table 2). All studies passed the OCAC criteria for genotyping quality. Genotype frequencies were close to those expected under Hardy Weinberg equilibrium in both cases and controls for the thirteen directly genotyped studies. No evidence was found for association between rs61764370 and invasive EOC in univariate analysis (OR = 1.02, 95% CI 0.95-1.10, P = 0.44), with minimal heterogeneity of risk between studies (P = 0.28). Study specific odds ratios are shown in Figure 1a. When studies with directly genotyped data and with imputed data were analyzed separately, the overall OR in the genotyped studies was 0.96 (95% CI 0.87-1.06, P = 0.42) compared to 1.08 (95% CI 0.97-1.20, P = 0.15) in the imputed data studies. Adjusting for age at diagnosis/interview made little difference to the results (data not shown). No differences in risk were observed when analyses were restricted to cases who provided blood samples within 18 months of diagnosis (n = 6,550, OR = 1.02, 95% CI 0.93-1.10, P = 0.72), cases with serous tumors (Figure 1b, n = 4,706, OR = 1.08, 95% CI 0.98-1.18, P = 0.11), or cases reporting a family history of ovarian cancer in a first-degree relative (from 6 studies) (Figure 1c, n = 249, OR = 1.09, 95% CI 0.78-1.54, P = 0.62). Tests for heterogeneity of risk between studies in all analyses were not statistically significant. A similar result was seen for risk of EOC by genotype among 683 cases and 2,044 controls who were carriers of BRCA1 mutations (HR = 1.09, 95% CI 0.88-1.36, P = 0.40).

Survival-time data were available for 6,002 cases of the 6,826 total from eighteen case series, including 13,696 person-years at risk and 2,044 deaths. Little evidence of association was observed between rs61764370 genotype and all-cause mortality within five years of diagnosis (HR = 1.10, 95% CI 0.99-1.22, P = 0.08), with no evidence of heterogeneity of the hazard ratio.
between studies (P = 0.89). Results of analyses restricted to serous subtype (HR = 1.12, 95% CI 0.99-1.28, P = 0.08) or adjusted for tumor stage and grade (HR = 1.06, 95% CI 0.96-1.18, P = 0.27) were similar. There was also little evidence for association between genotype and progression-free survival in 540 high-grade serous cases known to have been treated with carboplatin and paclitaxel (HR = 1.18, 95% CI 0.93-1.52, P = 0.16).
DISCUSSION

This study provides no evidence to support the previously reported associations between rs61764370 and risk of epithelial ovarian cancer. The relative risk given by Ratner and colleagues for their replication data set of unselected cases was 1.70 (95% CI 1.11-2.63, P = 0.016) (5). The confidence intervals in the present study do not overlap with these. The power of the present study to detect an allele conferring a relative risk of 1.3 under either a dominant or log-additive genetic model with a Type 1 error rate of $10^{-4}$ was greater than 99%, strongly suggesting that the association observed by Ratner and colleagues was a chance finding or possibly due to subtle genotyping errors. This observation is not surprising. Associations with modest P-values that are declared as positive are very likely to be false positives when the prior probability of association is low (14). In genetic association studies, even if evidence exists that a variant has functional effects, the prior probability of association at a relative risk of 1.5 is unlikely to be more than 1:100, and given that only a handful of loci conferring relative risks of more than 1.5 have been found for any cancer, the prior probability is likely to be much less. Based on the methodology of Wacholder and colleagues (14), assuming a prior of 1:100, the probability that the association reported by Ratner and colleagues was a false positive is 86 percent. Under more likely, smaller prior probabilities the false positive probability will approach 100 percent. For familial ovarian cancer, the power of the present study to detect a relative risk of 2.0 was over 95% at a type 1 error rate of 0.05, again suggesting it is unlikely that the present analyses have missed a true association of this magnitude with familial ovarian cancer.

Statistical power to detect an allele with weaker effects is more limited. For example, if the true relative risk were 1.15 under a co-dominant genetic model--similar to the relative risk conferred
by an allele with the biggest risk detected in a recent well-powered lung-cancer GWAS (15)--
power at a type I error rate of 0.001 would be reduced to 70%. A very modest association
between the rs61764370 variant and a slightly increased risk of ovarian cancer cannot therefore
be excluded. Neither has the present study shown much evidence for association between
genotype at this locus and other related phenotypes: EOC risk in carriers of deleterious \textit{BRCA1}
mutations or in women with family histories of EOC, all-cause mortality after diagnosis of EOC,
and progression-free survival in EOC cases treated with carboplatin and paclitaxel.

In summary, the possibility that the minor (infrequent) allele of rs61764340 is associated with an
appreciable risk of epithelial ovarian cancer is excluded. Furthermore, it is debatable whether a
single risk allele, even one conferring a relative risk as high as 2.0, has clinical utility,
particularly in a disease with lifetime risk as low as it is in invasive epithelial ovarian cancer (1
in 70), and even among women with a family history of the disease (16). The marketing of a
commercial assay for rs61764370 for clinical use among unselected cases, or women with family
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FIGURE LEGEND

**Figure 1.** Funnel plots of study-specific odds ratios for association between rs61764370 and ovarian cancer risk. (a) all cases; (b) serous cases; (c) cases with a family history of ovarian cancer in a first-degree relative.
Table 1. Description of participating studies

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*a* Case data included in analysis of all-cause mortality and progression-free survival

*b* Case data included in analysis of all-cause mortality
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<sup>a</sup>Columns labeled 0, 1 and 2 refer to common homozygote, heterozygote and infrequent homozygote, respectively.

<sup>b</sup>Estimated frequency of minor (infrequent) allele: \((f_2 + \frac{1}{2}f_1) / (f_2 + f_1 + f_0)\).

<sup>c</sup>Estimated genotype frequencies based on imputed data.
Figure 1.
REFERENCES


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Clinical Cancer Research

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