Plasma estrogen levels, estrogen receptor gene variation, and ischemic arterial disease in postmenopausal women: the three-city prospective cohort study.
Valérie Scarabin-Carré, Sylvie Brailly-Tabard, Marie-Laure Ancelin, Cécilia Maubare, Anne Guiochon-Mantel, Marianne Canonico, Pierre-Yves Scarabin

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**Abstract:**

Background: In older postmenopausal women, high levels of endogenous estrogen have been related to adverse health outcomes including ischemic arterial disease (IAD). Whether estrogen receptor alpha (ESR1) and beta (ESR2) polymorphisms modulate the effects of estradiol on IAD has not been investigated.

Methods: In the Three-City prospective cohort study among subjects over 65 years, we used a case-cohort design in which plasma levels of 17β-estradiol were measured. After exclusion of postmenopausal women using hormone therapy, a random subcohort of 533 women and 105 incident cases of first IAD events over 4-year of follow-up were analyzed. Five common polymorphisms of ESR1 and ESR2 were genotyped. Hazard ratios (HRs) of IAD for 1-standard deviation increase in estradiol levels by genotypes were estimated from Cox models after adjustment for cardiovascular risk factors and correction for multiple testing. We also investigated the role of haemostatis and inflammation as potential mediators.

Results: Neither estradiol nor IAD risk were significantly associated with estrogen receptor polymorphisms. Overall, IAD risk increased with estradiol (HR: 1.40, 95%CI: 1.11-1.77). Stratified analysis by genotypes showed that estradiol was positively related to IAD risk in women with ESR1 rs9340799-AA genotype but not in women with AG/GG genotype (HR: 1.62, 95%CI: 1.22-2.17 and HR: 1.03, 95%CI: 0.81-1.30, respectively; p for interaction<0.05). Additional adjustment for haemostatic variables reduced the HR by about one third in women carrying rs9340799-AA genotype (HR: 1.41, 95%CI: 1.06-1.90).
Conclusion: ESR1 rs9340799 genotype may modify IAD risk related to high endogenous estradiol levels in older postmenopausal women. Hypercoagulability may act as a mediator.

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**Opposed Reviewers:**
Dear Editor,

Please find enclosed our article entitled “Plasma estradiol, estrogen receptor gene variation and ischemic arterial disease in postmenopausal women: the Three-City prospective Cohort Study” submitted for publication as an original article. In this paper, we found that \textit{ESRI rs9340799} genotype may modify IAD risk related to high endogenous estradiol levels in older postmenopausal women and hypercoagulability may act as a mediator.

Best regards,

Valérie Scarabin-Carré
Plasma estradiol levels, estrogen receptor polymorphisms and ischemic arterial disease in postmenopausal women

Plasma estradiol, estrogen receptor gene variation and ischemic arterial disease in postmenopausal women: the Three-City prospective Cohort Study

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Plasma estradiol levels, estrogen receptor polymorphisms and ischemic arterial disease in postmenopausal women

ABSTRACT:

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Conclusion: ESR1 rs9340799 genotype may modify IAD risk related to high endogenous estradiol levels in older postmenopausal women. Hypercoagulability may act as a mediator.
INTRODUCTION

Few epidemiologic studies have been conducted to assess the association between circulating levels of endogenous estradiol and the risk of chronic diseases in postmenopausal women (1). Despite an important estrogen deficiency in postmenopausal women, high plasma estradiol levels have been related to several adverse health outcomes including breast cancer (2), dementia (3), frailty (4) and all-cause mortality (5). In addition, previous data reported a positive relation of endogenous estrogens with coronary heart disease (CHD) (6, 7) and stroke (8) but these associations were not independent of traditional cardiovascular risk factors such as diabetes and body mass index (BMI). In a recent study, we found that high plasma level of endogenous estradiol was an independent predictor of ischemic arterial disease (IAD) in older postmenopausal women (9).

Estrogens exert their actions via two distinct types of estrogen receptors (ER): ER-α and ER-β, encoded by the estrogen receptor α gene (ESR1) located on chromosome 6 and the estrogen receptor β gene (ESR2) located on chromosome 14, respectively. ERs are expressed in many tissues especially in vascular endothelial and smooth muscle cells of cerebral and coronary arteries and may play a role in the development of cardiovascular disease (10, 11). Previous studies suggested that the rs2234693 and rs9340799 single nucleotide polymorphism might influence the expression of ESR1 (12) and affect the function of estrogen on arterial disease including CHD and stroke (13, 14). However, a recent meta-analysis concluded to a lack of association between ESR1 polymorphisms and CHD (15). Conflicting results about the association of ESR1 polymorphisms with the risk of stroke have been also reported (16, 17). Similarly, data on association of ESR2 polymorphisms (including rs1256049 and rs1271572) with the risk of CHD or stroke have not been consistent (18, 19).

Despite the potential role of estrogens and their receptors in the development of IAD, no study has evaluated whether ER polymorphisms could modulate the effects of estradiol on IAD. Therefore, we investigated the risk of CHD and ischemic stroke related to plasma estradiol levels by ESR1 and ESR2 polymorphisms in a cohort study among postmenopausal women over 65 years, who did not use hormone therapy. In addition, since estradiol is known to be associated with haemostatic and
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94 inflammation parameters (20, 21), their role was evaluated as potential mediators in the association of
95 both estradiol and ER polymorphisms with IAD risk.

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METHODS

Population study

The Three-City (3C) study is a large ongoing French prospective cohort designed to evaluate the risk of dementia, CHD and stroke, in subjects over 65 years. The study was approved by the Ethics Committee of the University Hospital of Kremlin-Bicêtre and a written informed consent was obtained for all participants. A detailed methodology of the study has been previously described (22). Briefly, 3,649 men and 5,645 women, not institutionalized, registered on electoral rolls in 3 French cities (Bordeaux, Dijon and Montpellier), were recruited between 1999 and 2001. Baseline data were collected for each participant by trained psychologists or nurses using standardized questionnaires during a face-to-face interview. Moreover, each subject underwent a clinical examination to measure blood pressure, weight and height.

Baseline covariates

Information on sociodemographic characteristics, education, medical history, medication use, smoking status and consumption of alcohol were systematically collected at baseline. Women were classified as current hormone therapy users if they used hormone therapy at any time during the 3 months before the inclusion. BMI was calculated as weight in kilograms divided by height in meters squared. Hypertension status was defined as a high blood pressure measurement (systolic blood pressure ≥140mmHg and/or diastolic blood pressure ≥90mm Hg) or antihypertensive treatment at inclusion. Participants were categorized as diabetic if their fasting blood glucose level exceeded 1.26g/L (or 7mmol/L) or if they used current treatment for diabetes at baseline. Hypercholesterolemia was considered present if the fasting blood total cholesterol level was above 2.40g/L or if the subjects...
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were treated for hypercholesterolemia. Smoking status was studied in three categories (never, past and current).

Follow-up and event ascertainment

Every 2 years after inclusion, the participants have been reexamined for the detection of dementia and IAD events. For this study, we focused on data collected over the 4-year follow-up. IAD consisted of either CHD or ischemic stroke during the follow-up. These events were adjudicated within an independent group of experts using medical documentation. CHD was defined as a hospitalization for either stable or unstable angina pectoris, coronary dilatation, artery by-pass, myocardial infarction, or CHD death. Non-fatal CHD were ascertained using hospital charts and practitioners’ reports. CHD deaths were validated by reviewing hospital records, medical data obtained from family physicians or specialists and proxy interviews (coded I210 to 219, I251 to 259, I461 and R960 according to 10th version of the International Classification Disease) as described (23). Stroke events were defined as a rapid onset of a neurological deficit lasting more than 24 hours and confirmed by a lesion compatible with an acute stroke on computed tomography or magnetic resonance imaging of the brain. Ischemic or hemorrhagic stroke events were classified by a review of brain imaging. Our study focused on IAD and hemorrhagic stroke events were therefore excluded. For subjects who presented with both CHD and ischemic stroke during follow-up, we used the first cardiovascular event that occurred.

Case-cohort study

A case-cohort study was designed from the 3C study to investigate the association of blood biomarkers with cardiovascular risk and dementia (24). The case-cohort study design was described firstly by Prentice (25) and consists of a random sample of the original cohort together with all incidents cases of this cohort. In practice, after exclusion of men (n=1,264), current users of hormone therapy (n=120), women with a personal history of CHD or stroke at baseline (n=86) and lost for
follow-up (n=16), the subcohort included 537 women (522 non-cases and 15 cases) to which 91 incident cases of IAD outside the subcohort were added. The detailed flowchart has been described (9). Data on all ER polymorphisms were missing for 5 subjects. The final sample therefore consisted of 623 women, 518 non-cases and 105 incident cases of a first IAD event including 67 CHD and 38 ischemic strokes.

Blood collection and laboratory methods

At baseline, blood samples were collected for more than 90% of the full cohort. Plasma samples were available for all the subjects included in the case-cohort study. EDTA plasmas were obtained after one centrifugation at 3,000g and immediately stored at -80°C in 1-mL plastic tubes.

Plasma total estradiol was measured with a sensitive direct radioimmunoassay (RIA) using an Orion Diagnostica device (Spectria, Espoo, Finland). The minimum detectable concentration was 2pg/mL (7.3pmol/L). The intraassay and interassay coefficient of variation (CV) were 17.6% and 18.1% respectively, for total estradiol concentrations of 3.2pg/mL (12pmol/L) and were 2.8% and 5.8% respectively, for total estradiol concentrations of 24pg/mL (88pmol/L).

DNA was extracted from white blood cells (Puregene Kit, Qiagen, France) and stored at-80°C. Genotyping of ER polymorphisms was performed by Kbiosciences (Hoddesdon Herts, UK) using their competitive allele specific polymerase chain reaction (PCR) single-nucleotide polymorphism (SNP) genotyping system (KASPar). Fluorescence scanning in a BMG Labtech Pherastar scanner analyzed the amplified PCR products and the results were interpreted with KlusterCaller 1.1 software. The error rate for the KASPar assay system is less than 0.3%. The two most commonly studied ESR1 polymorphisms were investigated: rs2234693 and rs9340799 (otherwise known as PvuII and XbaI), which are located at position 397 and 351 of intron 1, respectively. Three ESR2 polymorphisms were genotyped: rs1256049 (otherwise known as RsaI), rs4986938 (otherwise known as AluI) and rs1271572, which are located in position 1082 of exon 5, in position 1730 of the 3’-untranslated region of exon 8 and in the promoter region, respectively. The selection of these polymorphisms was based
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on previously published associations with risk of CHD and stroke (15, 17, 18) and possible functional significance (12, 26, 27).

Laboratory methods for haemostatic variables and CRP have been described (20, 24, 28, 29). Briefly, fibrinogen was measured in citrated plasmas by the kinetic method of Clauss and von Willebrand factor and fibrin D-dimer by ELISAs. Thrombin generation was measured by the calibrated automated thrombography. We used peak height (highest value of thrombin generated), and endogenous thrombin potential (ETP; total quantity of thrombin generated) in our analyses. High-sensitivity serum C-reactive protein (hs-CRP) was measured using a particle-enhanced turbidimetric immunoassay.

Statistical analyses

Chi-square tests were used to compare the distribution of ER genotypes with those predicted under the Hardy-Weinberg equilibrium in the subcohort. Pairwise linkage disequilibrium between the different polymorphisms was analyzed by using Thesias software in the subcohort (30).

Baseline characteristics of all subjects in the subcohort are presented as frequencies for categorical variables and arithmetic means with standard deviations for continuous variables that presented a normal distribution. Variables with a positive skewed distribution were log-transformed and values were expressed as geometric means and interquartile ranges. Baseline characteristics of subjects in the subcohort were compared by rs9340799 genotypes using χ² tests and 2-tailed Student’s t-tests. Mean levels of total estradiol were compared by ER polymorphisms in women of the subcohort using ANOVA tests adjusted for study center and traditional cardiovascular risk factors including BMI, diabetes, hypertension, hypercholesterolemia and smoking status. In addition, Pearson’s correlations were estimated between haemostatic variables and estradiol by ER genotype in the subcohort.
The association of both estradiol levels and ER polymorphisms with IAD risk and their interactions were investigated using weighted Cox proportional-hazards models adapted for the case-cohort design by the method of Barlow (31, 32). Because age is sharply associated with IAD risk, age as time-scale was used as recommended (33). The proportional hazards assumption was checked for each model. Additive, dominant and recessive models were initially examined to determine which genetic model best described the data. Therefore, results are presented assuming a genotype model in dominant model with a 2-level categorical variable. The hazard ratios (HRs) and 95% confidence intervals (95%CI) by ER genotypes were estimated for 1-standard deviation increase in the log-transformed estradiol distribution. Estradiol x ER genotypes interaction terms were introduced into statistical models. The HRs for IAD were adjusted for study center and traditional cardiovascular risk factors including BMI, diabetes, hypertension, hypercholesterolemia and smoking status. In addition, given that five SNPs were investigated, Bonferroni correction for multiple comparisons was used. The HRs for IAD were further adjusted for haemostatic and inflammation markers including fibrinogen, thrombin generation, von Willebrand factor, fibrin D-dimer and hs-CRP, to evaluate the part of the excess risk explained by these variables. Of note, data on haemostatic and inflammation variables were missing for 25 subjects.

For each ER polymorphism, the risk of IAD was also investigated by tertiles of estradiol distribution and the low tertile was chosen as the reference group. Tests for linear trend across the 3 categories of estradiol levels were used to investigate the significance of the variables, after having evaluated the linearity of the associations. To assess the linearity of the relation of estradiol levels with IAD risk, we used tests based on the difference in the log-likelihood between two models of prediction (one with 2 dummy variables corresponding to the tertiles of the estradiol levels and the other including the qualitative ordinal variable in 3 categories). All tests were non-significant and we did not reject the hypothesis of linearity.

Finally, a separate analysis was performed for CHD and ischemic stroke, including the first arterial event. Similarly to analyses on IAD risk, the HRs of CHD and ischemic stroke in relation to estradiol levels were estimated by ER polymorphisms with a multivariate Cox model.
Statistical analyses were performed with the Statistical Analysis System software version 9.2 (SAS Institute Inc, Cary, NC).
RESULTS

Baseline characteristics are described for 533 women in the whole subcohort and according to rs9340799 genotype (table 1). The distribution of ESRI rs9340799 polymorphisms in the subcohort was similar to those expected in Caucasian subjects, as follows: 45.6%, 42.9%, and 11.5% for AA, AG and GG respectively. No significant difference was detected among traditional cardiovascular risk factors between women with rs9340799-AA genotype and those with rs9340799-AG/GG genotype. Mean levels of total estradiol were similar across rs9340799 genotypes. There was no significant association between estradiol levels and other ER polymorphisms (data not shown).

The genotypic frequencies of ER polymorphisms were in agreement with the Hardy–Weinberg equilibrium. The two ESRI polymorphisms were in strong linkage disequilibrium and so were the three ESR2 polymorphisms (all D’ ranged from 0.90 to 1.00).

No significant association was found between IAD risk and the different ER polymorphisms (data not shown). After adjustment for traditional cardiovascular risk factors, plasma estradiol levels were positively associated with IAD risk in the whole population sample (HR: 1.40 for 1-SD log estradiol change, 95% CI: 1.11-1.77). Adjusted HR for IAD events and 95% CI in relation to estradiol levels by ER polymorphisms are given in table 2 before and after Bonferroni correction. With regard to ESRI rs9340799 polymorphism, the risk of IAD was positively associated with total estradiol in women with AA genotype but not in women with AG/GG genotype (HR: 1.62, 95% CI: 1.22-2.17 and HR: 1.03, 95% CI: 0.81-1.30, respectively; p for interaction<0.05). In women with AA genotype, high levels of estradiol increased significantly the risk of IAD compared to the lowest estradiol levels (HR: 3.78, 95% CI: 1.59-8.99 for the higher tertile vs the lower tertile, p for linear trend<0.01). After Bonferroni correction for multiple testing, the estradiol x rs9340799 genotype interaction remained significant. Similar associations were observed for rs2234693 polymorphism, although the interaction between estradiol levels and rs2234693 polymorphism was not significant. No significant interaction was detected between estradiol levels and ER-β polymorphisms on IAD risk.
Estradiol was positively correlated to fibrinogen (r=0.21, p<0.01), peak height of thrombin generation (r=0.10, p=0.13) and hs-CRP (r=0.38, p<0.01) in women with rs9340799-AA genotype. After additional adjustment for haemostatic variables, the HR for IAD risk in women with AA genotype (HR:1.58 for 1-SD log estradiol change, 95%CI:1.21-2.05) was reduced to 1.41 (95%CI:1.06-1.90), suggesting that hypercoagulability explained 29% of the excess risk of IAD. Adjustment for hs-CRP alone or combined with haemostatic variables made no substantial change to the results (data not shown).

When the analyses were stratified by type of arterial events, total estradiol was positively associated with CHD risk in women with rs9340799-AA genotype, but not in women with rs9340799-AG/GG genotype (adjusted and corrected HR: 1.93, 95% CI: 1.28-2.91 and HR: 1.01, 95% CI: 0.76-1.35, respectively; p for interaction<0.05). No significant interaction was found between rs9340799 genotype and estradiol for the risk of ischemic stroke.
DISCUSSION

In this prospective study, neither estradiol levels nor IAD risk were significantly associated with ER polymorphisms in older postmenopausal women. However, we found that genetic variations in ESR1 modified the risk of IAD related to high endogenous estradiol levels. Plasma estradiol levels were positively associated with IAD risk in women carrying rs9340799-AA genotype but not in women carrying rs9340799-AG/GG genotype. The excess risk of IAD in women with AA genotype was partially explained by hypercoagulability. No interaction between estradiol levels and other ER polymorphisms was observed in relation with the risk of IAD.

Many studies have investigated the association of ER polymorphisms with the risk of IAD but previous data led to conflicting results. The reasons for such discrepancies include differences in study population, design and analysis, together with a strong heterogeneity in quality of investigations (15). Importantly, while the effect of ER polymorphisms on IAD may be different for women and men, few data were stratified by sex. Furthermore, use of hormone therapy and/or menopause status were not taken into account in most studies among women and ultimately, only few studies focused on postmenopausal women. A population-based prospective cohort study including 3,488 older postmenopausal women showed a positive association of ESR1 rs2234693-T/rs9340799-A haplotype with the risk of myocardial infarction (34). However, although the results were adjusted for use of hormone therapy, no data were given among women not using estrogens. Consistently, another study excluding women using hormone therapy, reported an increased risk of stroke in women carrying ESR1 rs2234693-TT (17). By contrast, a Japanese case-control study including highly selected postmenopausal women reported that the ESR1 rs2234693-CC and rs9340799-GG genotypes were more common in women with coronary artery disease than in controls (35). With regard to ESR2 polymorphisms, the Women’s Health Study showed that rs1256049-G and rs1271572-T alleles increased CHD risk but not stroke risk, whereas rs4986938 polymorphism was associated with neither CHD nor stroke (18). Most other investigations among postmenopausal women failed to detect an association of either CHD or stroke risk with ESR1 and ESR2 polymorphisms (16, 19, 36-38).
Therefore, our data are consistent with these null findings which are also supported by a meta-analysis (15).

Few studies investigated the interaction between estradiol and ER polymorphisms in relation to health outcomes in postmenopausal women. Interestingly, a Dutch case-cohort study showed that the positive association between estradiol and breast cancer risk was more pronounced among women with rs2234693-CT/T TT genotype than among those with rs2234693-CC genotype (39). This result may be relevant to our finding because both rs2234693 and rs9340799 are in linkage disequilibrium. To our knowledge, the 3C study is the first to show that ESR1 polymorphisms may modulate the association between plasma estradiol levels and IAD risk. As previously described, plasma estradiol levels were positively associated with IAD risk in the whole population irrespective of ER genotypes (9). Adjustment for traditional cardiovascular risk factors yielded similar results suggesting no major mediator role of obesity, diabetes, hypercholesterolemia, hypertension and smoking status. Therefore, we can hypothesize that the relation between estradiol an IAD risk among women with rs9340799-AA genotype could be driven by other mechanisms involved in atherothrombosis such as inflammation and hypercoagulability. Both estradiol levels and IAD risk are known to be positively associated with CRP in postmenopausal women (21, 29, 40). Moreover, one study reported that the rs2234693-T allele carriers exhibited an enhanced inflammatory response compared to the CC homozygous (41). Of note, while rs2234693 and rs9340799 polymorphisms are in linkage disequilibrium, inflammation could be similarly increased in women with rs9340799-AA genotype as those with rs2234693-TT genotype. Nevertheless, in our study, the additional adjustment for hs-CRP did not change the results, suggesting that the inflammation did not explain the excess of IAD risk. Alternatively, given that high estradiol levels and IAD risk are known to be associated with hypercoagulability (20, 24, 28, 42), the association between estradiol and IAD risk could also be mediated through haemostatic variables. Interestingly, a nested case-control study in the Women’s Health Initiative trials reported an increased response of plasmin-antiplasmin to hormone therapy in women with rs9340799-AA genotype compared to women with rs9340799-AG or rs9340799-GG genotypes (38). Although exogenous and endogenous estrogens might have different metabolic and vascular effects, it can be suggested that
endogenous estradiol levels play a role in the thrombotic component of IAD through blood coagulation and fibrinolysis activation. In our study, hypercoagulability explained a part of the relation between estradiol and IAD risk in women with rs9340799-AA genotype. Further adjustment for hs-CRP did not change the results, suggesting that changes in coagulation pathway play a more important role in the development of IAD than inflammation. Other unmeasured haemostatic variables could also be involved in the association of IAD risk with estradiol in women with rs9340799-AA genotype and further data on clotting factors are required.

Increased IAD risk in women with elevated estradiol levels and carrying rs9340799-AA genotype does not necessarily imply that relationship is causal. First, our findings could be due to the chance. Second, studied genetic variants may be highly correlated with other variants within ESR1 or nearby genes that are themselves “causal” in the development of IAD, suggesting that the ER polymorphisms are not the only factor that determines the effect of estrogen on IAD. Few studies support the functional importance of ESR1 polymorphisms altering the quantity or the quality of ER-α transcripts or resulting proteins and the underlying mechanisms related to a direct effect of ER polymorphism in vascular biology remain to be clarified (12, 27, 43).

The strengths of our study include the prospective population-based and multicenter cohort design with a high participation rate during the 4 years of follow-up. Moreover, baseline data were collected by a direct interview and high-quality methods of ascertainment of cardiovascular risk factors and disease outcome were used. In addition, estradiol measurements and genotyping were conducted without knowledge of the case or non-case status, using validated methodology. Furthermore, our genetic-association study cannot be influenced by stratification population or heterogeneity because most participants were Caucasian.

Our study has several limitations. Firstly, the small number of incident cases may result in a lack of statistical power, especially for subgroup analyses by CHD or stroke event. In addition, multiple comparisons by different polymorphisms could result in falsely positive findings. However, our results remained significant after Bonferroni correction for multiple testing. Secondly, our
population study included older women who were aged 73 years on average and mostly Caucasian. Our data cannot therefore be generalized to younger postmenopausal women or other ethnicities. With regard to the sex steroid hormones assays, especially at low levels of estradiol in postmenopausal women, conventional RIAs with preceding purification steps would provide more reliable and accurate measurements of plasma estradiol as compared with direct RIA (44). However, measurement error related to direct RIA would bias our analysis toward the null hypothesis, resulting in a potential underestimation of the true associations (1). On the other hand, the blood concentration of estrogens does not necessarily reflect the biologically active forms at the tissue level, as they are dependent on the local enzyme activity and the binding on the protein transporters such as sex hormone binding globulin.

In conclusion, ESR1 rs9340799-AA genotype may increase IAD risk related to high endogenous estradiol levels in older postmenopausal women and hypercoagulability may explain a part of this excess of risk. These innovative results have the potential to improve the stratification of IAD risk in postmenopausal women whose IAD risk may depend upon both plasma estradiol levels and ESR1 genotype and their interaction. However, further investigations with larger sample size are needed to replicate these findings and to assess the interaction between estradiol levels and ESR1 genetics polymorphism on CHD and stroke risk separately.

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Plasma estradiol levels, estrogen receptor polymorphisms and ischemic arterial disease in postmenopausal women
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Table legends:

Table 1. Baseline characteristics of participants in subcohort of 3C study by ESRI rs9340799 genotype

Table 2. Hazard Ratios of IAD events in relation to 1 SD log increase of estradiol levels by ER polymorphisms among 623 postmenopausal women of 3C case-cohort study
Table 1. Baseline characteristics of participants in subcohort of 3C study by ESR1 rs9340799 genotype

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>All subjects (n=533)</th>
<th>ESR1 rs9340799 Genotype**</th>
<th>p value*</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(n=241)</td>
<td>(n=288)</td>
<td></td>
</tr>
<tr>
<td>Age, mean (SD), y</td>
<td>74.4 (5.3)</td>
<td>74.8 (5.2)</td>
<td>74.1 (5.4)</td>
</tr>
<tr>
<td>BMI, mean (SD), kg/m²</td>
<td>25.7 (4.8)</td>
<td>25.8 (4.7)</td>
<td>25.7 (4.9)</td>
</tr>
<tr>
<td>Hypertension, n (%)</td>
<td>407 (76.4)</td>
<td>186 (45.9)</td>
<td>219 (54.1)</td>
</tr>
<tr>
<td>Diabetes, n (%)</td>
<td>38 (7.2)</td>
<td>17 (44.7)</td>
<td>21 (55.3)</td>
</tr>
<tr>
<td>Hypercholesterolemia, n (%)</td>
<td>338 (63.4)</td>
<td>160 (47.6)</td>
<td>176 (52.4)</td>
</tr>
<tr>
<td>Smoking, n (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Never</td>
<td>435 (81.6)</td>
<td>202 (46.8)</td>
<td>230 (53.2)</td>
</tr>
<tr>
<td>Past</td>
<td>73 (13.7)</td>
<td>27 (37.5)</td>
<td>45 (62.5)</td>
</tr>
<tr>
<td>Current</td>
<td>25 (4.7)</td>
<td>12 (48.0)</td>
<td>13 (52.0)</td>
</tr>
<tr>
<td>Total Estradiol, GM (IQR), pg/mL</td>
<td>5.24 (3.51-8.00)</td>
<td>5.23 (3.57-7.90)</td>
<td>5.28 (3.15-8.33)</td>
</tr>
</tbody>
</table>

* p value obtained from t-tests or χ² tests for all characteristics except for total estradiol (ANOVA adjusted for study center, BMI, diabetes, hypertension, hypercholesterolemia and smoking status )

** 4 missing values

GM: Geometric Mean; IQR: Interquartile Range
Plasma estradiol levels, estrogen receptor polymorphisms and ischemic arterial disease in postmenopausal women

Table 2. Hazard Ratios of IAD events in relation to 1 SD log increase of estradiol levels by ER polymorphisms among 623 postmenopausal women of 3C case-cohort study

<table>
<thead>
<tr>
<th>No. of Events</th>
<th>Marginal p</th>
<th>Corrected p</th>
<th>Marginal p</th>
<th>Corrected p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total Estradiol, pg/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>For 1 SD log</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T1 &lt; 4.21</td>
<td>1.52 (1.06-2.18)</td>
<td>0.02</td>
<td>0.11</td>
<td>74</td>
</tr>
<tr>
<td>T2 [4.21-7.27]</td>
<td>3.39 (1.02-11.29)</td>
<td>0.04</td>
<td>0.22</td>
<td>20</td>
</tr>
<tr>
<td>T3 ≥ 7.27</td>
<td>3.09 (0.98-9.82)</td>
<td>0.13</td>
<td>1.00</td>
<td>26</td>
</tr>
<tr>
<td>rs2234693*</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total Estradiol, pg/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>For 1 SD log</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T1 &lt; 4.21</td>
<td>1.62 (1.22-2.17)</td>
<td>&lt;0.01</td>
<td>&lt;0.05</td>
<td>56</td>
</tr>
<tr>
<td>T2 [4.21-7.27]</td>
<td>3.14 (1.33-7.45)</td>
<td>0.01</td>
<td>0.54</td>
<td>21</td>
</tr>
<tr>
<td>T3 ≥ 7.27</td>
<td>3.78 (1.59-8.99)</td>
<td>0.13</td>
<td>1.00</td>
<td>17</td>
</tr>
<tr>
<td>rs9340799*</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total Estradiol, pg/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>For 1 SD log</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T1 &lt; 4.21</td>
<td>1.22 (1.01-1.48)</td>
<td>0.04</td>
<td>0.20</td>
<td>5</td>
</tr>
<tr>
<td>T2 [4.21-7.27]</td>
<td>1.79 (1.06-3.02)</td>
<td>0.01</td>
<td>0.50</td>
<td>3</td>
</tr>
<tr>
<td>T3 ≥ 7.27</td>
<td>1.60 (0.91-2.82)</td>
<td>0.01</td>
<td>0.50</td>
<td>1</td>
</tr>
<tr>
<td>rs1256049*</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total Estradiol, pg/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>For 1 SD log</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T1 &lt; 4.21</td>
<td>1.85 (1.17-2.94)</td>
<td>&lt;0.01</td>
<td>&lt;0.05</td>
<td>84</td>
</tr>
<tr>
<td>T2 [4.21-7.27]</td>
<td>22.47 (2.20-229.87)</td>
<td>0.01</td>
<td>0.75</td>
<td>25</td>
</tr>
<tr>
<td>T3 ≥ 7.27</td>
<td>9.65 (0.91-102.43)</td>
<td>0.01</td>
<td>0.50</td>
<td>30</td>
</tr>
<tr>
<td>rs4986938*</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total Estradiol, pg/mL</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>For 1 SD log</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>T1 &lt; 4.21</td>
<td>3.68 (1.95-6.87)</td>
<td>0.09</td>
<td>0.47</td>
<td>67</td>
</tr>
<tr>
<td>T2 [4.21-7.27]</td>
<td>1.96 (0.85-4.51)</td>
<td>0.01</td>
<td>0.50</td>
<td>16</td>
</tr>
<tr>
<td>T3 ≥ 7.27</td>
<td>1.74 (0.68-4.44)</td>
<td>0.01</td>
<td>0.50</td>
<td>14</td>
</tr>
</tbody>
</table>

* 12 missed values for rs2234693, 5 for rs9340799, 8 for rs1256049, 7 for rs4986938 and 13 for rs1271572
** Including 67 CHD and 39 stroke events
† P value for continuous variable and p for trend for variable in tertiles
λ P value after Bonferroni correction
Model adjusted for study center, BMI, diabetes, hypertension, hypercholesterolemia and smoking status
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