ORIGINAL ARTICLES

ISCHEMIC HEART DISEASE

The involvement of the renin-angiotensin system gene polymorphisms in coronary heart disease

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\textbf{Introduction and objectives.} Previous studies angiotensin-converting enzyme gene insertion/deletion polymorphism ACE (I/D), angiotensinogen gene polymorphism, and angiotensin II AT1 receptor polymorphism in relation to coronary heart disease controversial results. This study was designed to analyze the association between these gene polymorphisms and the first coronary event in individuals residing on Grand Canary Island, Spain.

\textbf{Patients and method.} Case-control study. Case subjects (n=304) were recruited at the first coronary event; age-matched controls (n=315) were randomly selected from the Grand Canary population. Participants were examined for the usual risk factors. Blood samples were obtained for biochemical analyses and DNA extraction. Genotyping was performed by PCR and restriction analysis.

\textbf{Results.} Neither ACE (I/D) nor AT1 receptor polymorphism was associated with coronary heart disease, whereas the frequency distribution of AGT M235T genotypes among patients and control subjects (TT: 29% and 19%; MT: 48% and 50%; MM: 22% and 31%, respectively) was statistically different (P=.003). Multiple logistic regression analysis identified the TT genotype of the angiotensinogen gene (OR=1.9; 95% CI 1.1-3.4), diabetes (OR=4.4; 95% CI 2.0-9.4) and hypertension (OR=2.1; 95% CI, 1.3-3.3) as risk factors predicting the coronary event.

\textbf{Conclusions.} Our results provide no evidence of an association between ACE (I/D) or AT1 receptor polymorphism and coronary heart disease. However, homozygosity for the T allele of the angiotensinogen gene, diabetes and hypertension independently place individuals at higher risk of experiencing a coronary event on Grand Canary Island.

INTRODUCTION

Cardiovascular diseases—especially coronary artery disease—are the main cause of death in developed countries and their relation with certain risk factors like arterial hypertension, dyslipidemia, smoking, or diabetes mellitus is well-known. It also is known that a family history of ischemic heart disease is a powerful independent coronary risk factor; this illustrates the multifactorial nature of the disease, in which environmental factors and genetic factors interact.1

New molecular biology techniques applied to genetic diagnosis make it possible to study the mechanisms underlying individual and familial predisposition to suffering certain diseases. Specifically, in relation to coronary artery disease, the genetic markers linked to the renin-angiotensin-aldosterone system (RAAS) have received special attention, not only because of their well-known effects on vascular homeostasis,2,3 but also the promise of the use of angiotensin-converting enzyme inhibitor (ACEI) to reduce morbidity and mortality in ischemic heart disease.4,5

The findings that relate RAAS genes to ischemic heart disease are recent and several polymorphisms in different genes of this system have been described.6,8 I/D polymorphism of the gene that codes for ACE consists of the presence (I) or absence (D) of 287 base pairs in intron 16 of the gene.6 The D allele is accompanied by higher plasma and tissue concentrations of ACE activity than the I allele,6,9 which could provide a pathophysiological explanation for the higher incidence of myocardial infarction and coronary artery disease in individuals with the DD genotype.10 Various studies have tried to confirm these observations, with debatable results.11-14

The angiotensinogen gene, a second component of the RAAS, has been related with the progression of heart disease. A polymorphism in exon 2 of the gene, consisting of the substitution of methionine by treonine in position 235 of the coded protein (M235T),15 has been associated with higher angiotensinogen concentrations,16 higher blood pressure,17 and even the development of pre-eclampsia.18 A study made in Spain by our group has reported an association between the TT genotype and increased risk of coronary artery disease, independently of the presence of arterial hypertension.19

A third component of the RAAS is the gene of the AT1 receptor (AT1R) of angiotensin II. Most of the effects of angiotensin II are mediated through AT1R.8 A polymorphism of receptor AT1 (A1166C) has been identified in region 3' of the gene that corresponds with an A#-?C substitution in messenger RNA. The association between this polymorphism and coronary artery disease has been analyzed by different groups.20,21

In this study we examined the classic risk factors and various gene polymorphisms of the RAAS that may explain the high incidence of coronary artery disease in the Canary Islands.22

PATIENTS AND METHOD

Subjects

A study was made of cases and controls adjusted for age who met the following requirements: age over 18 years, Canary Island origin (born in the Canary Islands into a family with at least three previous generations of Canary Islanders) and absence of cardiovascular antecedents, contagious infectious diseases, and parental drug use.

The cases (n=304; mean age 56±10 years; 237 men) were selected consecutively in 1996-1998 after suffering a first coronary event (angina or acute myocardial infarction), which was diagnosed by clinical and electrocardiographic criteria and confirmed by coronary angiography.

The controls (n=315; mean age 54±10 years; 223 men) were selected from the census lists of different municipalities of Gran Canaria Island and the sample was stratified by a multi-stage conglomerate. In this group, the presence of previous cardiovascular events was excluded by a clinical examination.

All subjects completed a questionnaire with a trained nurse (AAP) that included demographic data: age, place of birth, habitat, hypertension, diabetes mellitus, smoking, alcohol use, physical activity, and use of oral contraceptives or hormonal replacement therapy by women. Blood pressure measurements were made in triplicate using a semiautomatic monitor (Omron Hem 705 CP), which has been homologated and validated by the British Society of Arterial Hypertension.23 Arterial hypertension was defined as 140/90 mm Hg or more. The body mass index (BMI) was calculated as weight/height² and obesity was defined as a BMI over 26. Smokers were defined as anyone who had smoked...
in the last year. Several blood samples were obtained, after a 12 h fast, for biochemical determinations and DNA extraction and at least 2 urine samples were obtained for albuminuria determination.

**Laboratory methods**

Plasma concentrations of glucose, creatinine, total cholesterol, HDL-C, and triglycerides were determined by enzymatic-colorimetric methods. The LDL-C was calculated using the Friedewald formula. Lp(a) was analyzed by immunoturbidimetry (Boehringer, Mannheim). Homocysteine was determined by polarized fluorescence immunoanalysis, which had a variation in the intra-assay coefficient of 1.9% (Abbott, Diagnostic Division). Microalbuminuria was measured by immunoturbidimetric analysis (Boehringer, Mannheim).

The genomic DNA used for the genetic determinations was extracted from leukocytes using a standardized procedure. The I/D genotypes of ACE were determined following the procedure described by Rigat24 in 1992. Briefly, a reaction was made with 10 pmol of each primer in a final volume of 25 µl. DNA was amplified 30 cycles with denaturation at 94°C for a minute, ringed at 58°C for a minute and extension at 72°C for 2 min. PCR generated a fragment with 190 base pairs (bp) in the case of deletion, and a 490-bp fragment in the case of the insertion.

Since the D allele is amplified in mainly heterozygotic samples,25 each sample of the DD genotype of ACE was reamplified in a second round of PCR with specific primers for insertion.13 An amplification protocol described previously26 was used and ID and II samples were used as amplification controls. Our rate of DD false positives was only 1.2% compared with 4-5% described in other published studies.

The M235T polymorphism of AGT was analyzed by the mismatch method described previously,15 with some modification. Genomic DNA was amplified by initial denaturation at 94°C followed by 30 cycles at 94°C for one minute, at 66°C for one minute, and at 72°C for one minute and a final extension at 72°C for 2 min. The 10 µl of amplified product was digested overnight at 37°C with 0.3 units of SfaNI. A total of 579 subjects for which a serology library and gene library were available were gene typed for the A1166C polymorphism of the AT1R gene. Genotypes A1166C in region 3 ´UTR of gene AT1R were determined following the protocol described by Nakauchi, et al.27 Amplification yielded a 201-bp product. The mutated product (A1166C) generated 171-bp and 30-bp fragments when cut with HaeIII. The products were developed with an ethidium bromide stain after electrophoretic fractionation through agarose gels (Figure 1).

**Statistical analysis**

The SPSS statistical program version 8.0 for Windows was used for data analysis. Differences were considered statistically significant if \( P < .05 \). All continuous variables were expressed as mean ± standard deviation. The Student t test was applied to independent samples to compare means between two groups and \( \chi^2 \) analysis was used to compare differences in the distribution of genotypes and other coronary risk factors, including sex, arterial hypertension, diabetes mellitus, smoking and alcohol use, and habitat and sedentary life style between patients and the control group.

The Kolmogorov-Smirnov test was used to estimate the normal distribution of variables. The odds ratio (OR) and 95% confidence intervals (CI) were calculated to estimate the risk of coronary artery disease associated with categorized continuous variables (age <50
or >50 years; BMI <26 or = 6; alcohol use <30 or = 30 g/day; systolic blood pressure <90 or = 140 mm Hg; diastolic blood pressure <90 mm Hg; total cholesterol = 200 or >200 mg/dl; LDL-C = 160 or >160 mg/dl; triglycerides = 150 or >150 mg/dl; total cholesterol/HDL-C ratio = 5 or >; Lp(a) = 30 or >30 mg/dl; glycemia = 126 or >126 mg/dl; creatinine <1 or = 1 mg/dl; homocysteine = 15 or >15 µmol/l, and microalbuminuria <30 or = 30 mg/g creatinine) and for discrete variables: diabetes yes/no, rural/urban habitat, hypertension yes/no, sex, smoking yes/no and sedentary life style yes/no. The Hardy-Weinberg equilibrium for the frequencies of ACE, AGT and AT1R genotypes was tested by $\chi^2$ analysis. The OR and 95% CI were calculated to estimate the relative risk of coronary artery disease associated with the ACE (I/D), AGT M235T, and AT1R (A1166C) polymorphisms. Finally, the independent variables with predictive capacity for coronary artery disease were determined by logistic regression analysis.

RESULTS

Univariate analysis

Study of patients, life style, and cardiovascular risk factors

This study included 619 patients selected at random (460 men and 159 women), ranging in age from 25 to 80 years. All the patients completed the study protocol. In Table 1 the main characteristics of the population, separated by cases and controls, are described. Male sex, urban habitat, smoking, arterial hypertension, and diabetes were significantly more frequent factors in the group with coronary artery disease. The control group had significantly higher HDL-C values. The groups did not differ significantly in age, BMI, systolic blood pressure, or albuminuria. Nevertheless, the diastolic blood pressure, total cholesterol, and LDL-C were lower in patients than in the control group, which probably reflects the use of antihypertensive and lipid-lowering medication as routine treatment. Coronary patients had a significant increase in the total cholesterol/HDL-C ratio and plasma Lp(a). Paradoxically, plasma homocysteine concentrations were higher in the control group than in patients, although both values were within the range of normality.

Distribution of the ACE, AGT, and AT1R genotypes between cases and controls

For the ACE (I/D), AGT M235T, and AT1R (A1166C) polymorphisms, it was confirmed that the proportion of genotypes fit the Hardy-Weinberg equilibrium.

The distribution of the frequencies of the ACE, AGT, and AT1R genotypes for the polymorphisms mentioned is described in Table 2. In our population, the frequency of the ACE DD genotype was higher (Table 3) than the frequency reported for populations of diverse ethnic origin, including other Caucasian populations. Nevertheless, the frequency of the DD genotype was not significantly greater among coronary
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Examination of the distribution of frequencies in the AGT M235T polymorphism revealed a significant difference ($\chi^2=11.60; P=.003$) between coronary patients and controls. The frequency of the TT homozygote was significantly higher ($\chi^2=9.08; P=.002$) in cases than in controls. There were no differences in the distribution of the frequencies of AT1R polymorphisms between patients and the control group. The risk (OR) of coronary artery disease among individuals with the genotypes analyzed are shown in Figure 2. The analyses adjusted for age revealed no significant changes for the ACE (I/D) and AT1R (A1166C) polymorphism. Nevertheless, the risk associated with TT homozygosis was 1.78 (95% CI, 1.06–2.59; $P<.05$), whereas participants with the MM genotype had an OR of 0.63 (95% CI, 0.43–0.90; $P<.05$). No significant differences between heterozygotic subjects were observed.

**TABLE 2. Distribution of the ACE, AGT, and AT1R genotypes**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Controls</th>
<th>Cases</th>
<th>$\chi^2$</th>
<th>$P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACE genotype</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DD</td>
<td>137 (43.5)</td>
<td>128 (42.7)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ID</td>
<td>132 (41.9)</td>
<td>140 (46.7)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>II</td>
<td>46 (14.6)</td>
<td>32 (10.6)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>315</td>
<td>300</td>
<td>2.69</td>
<td>.26</td>
</tr>
<tr>
<td>AGT genotype</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TT</td>
<td>59 (18.7)</td>
<td>87 (29.1)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>MT</td>
<td>157 (49.9)</td>
<td>145 (48.5)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>MM</td>
<td>99 (31.4)</td>
<td>67 (22.4)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>315</td>
<td>299</td>
<td>11.61</td>
<td>.003</td>
</tr>
<tr>
<td>AT1R genotype</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>150 (49.7)</td>
<td>133 (48.0)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>AC</td>
<td>126 (41.7)</td>
<td>122 (44.0)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CC</td>
<td>26 (8.6)</td>
<td>22 (7.9)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>302</td>
<td>277</td>
<td>.34</td>
<td>.844</td>
</tr>
</tbody>
</table>

The figures in parenthesis indicate the percentage of the total.

**TABLE 3. Distribution of ACE genotypes in different countries**

<table>
<thead>
<tr>
<th>Region</th>
<th>Control group (n)</th>
<th>DD (%)</th>
<th>ID (%)</th>
<th>II (%)</th>
<th>Author and bibliographic reference</th>
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<tr>
<td>Japan</td>
<td>76</td>
<td>18.3</td>
<td>48.9</td>
<td>32.8</td>
<td>Mizuiri et al(^{32})</td>
</tr>
<tr>
<td>South Asia*</td>
<td>442</td>
<td>18.3</td>
<td>41.8</td>
<td>39.8</td>
<td>Sagnella et al(^{31})</td>
</tr>
<tr>
<td>Chile</td>
<td>117</td>
<td>18.5</td>
<td>49.0</td>
<td>32.5</td>
<td>Jalil et al(^{28})</td>
</tr>
<tr>
<td>Australia</td>
<td>51</td>
<td>22.0</td>
<td>53.0</td>
<td>25.0</td>
<td>Smith et al(^{33})</td>
</tr>
<tr>
<td>France</td>
<td>157</td>
<td>30.6</td>
<td>44.0</td>
<td>25.4</td>
<td>Marre et al(^{29})</td>
</tr>
<tr>
<td>U.S.A.</td>
<td>2,340</td>
<td>30.9</td>
<td>49.2</td>
<td>19.9</td>
<td>Lindpaintner et al(^{13})</td>
</tr>
<tr>
<td>Germany</td>
<td>234</td>
<td>33.0</td>
<td>50.0</td>
<td>17.0</td>
<td>Schmidt et al(^{30})</td>
</tr>
<tr>
<td>Gran Canaria</td>
<td>315</td>
<td>43.5</td>
<td>41.9</td>
<td>14.6</td>
<td>Este estudio</td>
</tr>
</tbody>
</table>

*The study of Sagnella, et al. Includes different ethnic groups.

**Multivariate analysis**

Step by step analysis of multiple logistic regression identified individuals at risk of presenting a coronary event. Two vectors of variables were established, one using the genotypes and the other with traditional coronary risk factors. Using 50% as the cut-off point, the model correctly classified 78% of the participants and 76% of coronary patients. The sensitivity of the model was 74% and the specificity was 80%.

In multiple logistic regression analysis adjusted for different risk factors, the TT genotype presented an OR of 1.9 (95% CI, 1.06–3.40; $P=.03$). The highest estima-
ted risks corresponded to diabetes (OR=4.4; 95% CI, 2.0-9.4; \(P<.001\)), total cholesterol/HDL-C ratio (OR=4.0; 95% CI, 2.4-6.8; \(P<.001\)), smoking (OR=2.7; 95% CI, 1.7-4.3; \(P<.001\)), alcohol use (OR=2.2; 95% CI, 1.2-4.2; \(P=.02\)), and hypertension (OR=2.1; 95% CI, 1.3-3.3; \(P=.001\)). There was no statistical evidence indicating that any genotype of ACE (I/D) or AT1R (A1166C) polymorphism could improve the capacity to predict a coronary event with respect to the traditional predictive factors cited above.

**DISCUSSION**

The basis of genetic approaches to complex diseases has been reviewed by Risch in 1996, and other authors. Together with the problems derived from sample size and ethnic diversity, there is a certain tendency to publish studies in which a positive association has been demonstrated, a bias that makes it difficult to analyze association studies. An additional characteristic of our study was that it minimized the effect of the selection bias and loss of patients—due to early mortality—since it was a consecutive population studied during the acute phase of the coronary event.

Cambien, et al., were the first to describe the association between the DD genotype of the ACE gene and myocardial infarction, finding a more marked association between subjects with a low coronary risk profile according to classic risk factors. In other studies, the DD genotype has been related with coronary artery disease, coronary restenosis, and a family history of myocardial infarction. In contrast, no evidence was obtained that the genetic variations in the I/D polymorphism of the ACE gene influence the incidence of coronary artery disease in our population in a relevant way. Similarly, in the prospective study of Lindpaintner in 1995, no significant association was found between this polymorphism and ischemic heart disease, although a lower frequency of coronary events in II homozygotes was appreciated. We are found a higher than expected frequency of the DD genotype in both the patients who had suffered a coronary episode and the control population, compared with previous studies, including the study made in Spain by Espinosa, et al., who found the DD genotype in 33.9% of the control population.

The TT genotype of the angiotensinogen gene was present in 19% of our control population, compared with only 15% in most Western populations. Our results demonstrated a strong association between this polymorphism and the risk of coronary artery disease. Thus, TT homozygotes had a risk that was approximately two-fold, whereas the M235T homozygotes had a lower risk of coronary artery disease. Although studies of association suggest a role of the AGT gene in hypertensive disease, the link between the AGT gene and essential hypertension initially described by Jeunenai-
Spanish population, could have special interest with respect to the application of more aggressive preventive measures in this subpopulation.

CONCLUSIONS

The CC genotype of the AT1 receptor of angiotensin II and the DD genotype of angiotensin-converting enzyme did not behave like predictors of coronary artery disease. Nevertheless, TT homozygosis of the angiotensinogen gene predisposed independently to the appearance of a first coronary episode in the Canary Island population.

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REFERENCES


