

eNOS and *BDKRB2* genotypes affect the antihypertensive responses to enalapril

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Abstract

Purpose The antihypertensive effect of angiotensin-converting enzyme inhibitors (ACEi) is attributed partially to increased nitric oxide bioavailability. It is possible that functional polymorphisms in endothelial nitric oxide synthase (*eNOS*) and bradykinin receptor B2 (*BDKRB2*) genes may affect the antihypertensive response to enalapril.

Methods We evaluated 106 hypertensive patients treated only with enalapril for 60 days. The difference between the mean arterial pressure (MAP) before and after the antihypertensive treatment was defined as Δ MAP. If Δ MAP were below or above the median value, the patients were classified as poor responders (PR) or good responders (GR), respectively. *eNOS* genotypes for the T⁻⁷⁸⁶C, G894T and 4b/

4a polymorphisms were determined and haplotype frequencies were estimated by PHASE and Haplo.stats programs. The C⁻⁵⁸T and BE1 +9/-9 polymorphisms of *BDKRB2* genes and their haplotypes were determined by DNA sequencing. Robust multifactor dimensionality reduction analysis was used to characterize gene–gene interactions.

Results The TC/CC genotypes and the C allele for the *eNOS* T⁻⁷⁸⁶C polymorphism were more frequent in GR than in PR. Furthermore, the TT genotype for the *BDKRB2* C⁻⁵⁸T polymorphism was more frequent in PR than GR. No other significant differences in genotypes or haplotypes were found. However, we found significant gene–gene interactions: the CC genotype for the *BDKRB2* C⁻⁵⁸T polymorphism was associated with response to enalapril depending on *eNOS* T⁻⁷⁸⁶C genotypes.

Conclusions These findings suggest that *eNOS* T⁻⁷⁸⁶C and *BDKRB2* C⁻⁵⁸T polymorphisms may synergically affect the antihypertensive response to enalapril.

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Introduction

Hypertension is a multifactorial disease that represents one of the most important causes of morbidity and mortality worldwide [1]. One of the most used antihypertensive treatments is the angiotensin-converting enzyme (ACE) inhibitor class. The main mechanisms of action for these drugs include decreased formation of the vasoconstrictor angiotensin (Ang) II, and increased levels of the vasodilator bradykinin. The reduction of blood pressure by this class of drugs has an alternative mechanism involving nitric oxide (NO) vasodilation [2–4]. This secondary mechanism seems

to result from increased endothelial nitric oxide synthase (*eNOS*) protein expression and activity [5–8]. However, as it was shown that bradykinin receptor B2 (*BDKRB2*) inhibitors impair ACE inhibitors NO-dependent effects, the increase in NO availability seems to be partially mediated by *BDKRB2* activation [5, 7, 9]. Therefore, it is possible that variations in genes encoding *eNOS* and *BDKRB2* could affect the antihypertensive response to ACE inhibitors.

Three *eNOS* polymorphisms have been widely studied: a T⁷⁸⁶C substitution in the promoter region (rs2070744), a variable number of tandem repeats (VNTR) in intron 4 (the allele 4b has five 27-bp tandem repeats while the allele 4a has four repeats) and G⁸⁹⁴T substitution in exon 7 (rs1799983) resulting in a Glu to Asp substitution at the 298 position in eNOS protein. These polymorphisms have been shown to affect NO production [10–14] and are associated with endogenous NO markers levels in humans [15–17], and with altered risk for hypertension [18–21] and other cardiovascular diseases (CD) [22–25].

Two *BDKRB2* polymorphisms are commonly studied: a C⁵⁸T substitution in the promoter region (rs1799722), and an insertion-deletion in the noncoding exon 1 BE1 +9/-9 (the allele +9 has three 9-bp tandem repeats while the allele -9 has two repeats) [26, 27]. These polymorphisms have been associated with modifications in the transcription rate of the *BDKRB2* gene [26] and were associated with altered risk for developing CD [28–30]. Although it was shown that *eNOS* and *BDKRB2* gene polymorphisms may affect the responses to some drugs that increase NO bioavailability [31–35], no previous studies have examined if these polymorphisms modulate the antihypertensive response to ACE inhibitors.

In the present study, our main objective was to assess whether *eNOS* and *BDKRB2* gene polymorphisms could affect the responses to enalapril in hypertensive patients. In addition, we have also evaluated the combined effect of polymorphisms within genes (in haplotypes) and between genes in the response to enalapril.

Methods

Subjects and study design

This study was approved by the Institutional Review Board at the Faculty of Medicine of Ribeirao Preto, University of Sao Paulo, Brazil, and each subject provided written informed consent. The present work was carried out in accordance with the ethics standards of the Helsinki Declaration. We recruited 106 subjects diagnosed with mild to moderate hypertension from Cardiology Division of the Araçatuba Health Center (Araçatuba, SP, Brazil). All patients were never-treated or underwent a wash-out period for at least

2 weeks. Patients provided complete health history and underwent physical examination and laboratory analysis. Subjects with evidence of severe or secondary hypertension, other concomitant cardiovascular diseases, or respiratory, hepatic, renal, or hematological dysfunction were excluded. Included patients were treated with enalapril, receiving a dose of 10 mg/day (n=48) or 20 mg/day (n=58) for 60 days. A semi-automatic blood pressure monitor (OMRON[®] - HEM-433 INT, Bannockburn, Illinois, USA) was used for blood pressure measurements before and after the use of enalapril. Mean arterial pressure (MAP) was calculated using the averages of three different systolic and diastolic blood pressure measurements, with intervals of 1 minute between each other. The formula used to calculate MAP was $MAP = (SBP + 2 * DBP) / 3$. The responsiveness to enalapril was assessed by the ΔMAP obtained from difference between the MAP before and after treatment with enalapril. According to the response to enalapril, patients were classified as poor responders (PR) or good responders (GR) when their ΔMAP were below or above the median value of the ΔMAP distribution, respectively. After blood pressure measurements, venous blood samples were collected and genomic DNA was extracted by salting-out method and stored at -20 °C until analysis.

Genotyping

Genotypes for the *eNOS* T⁷⁸⁶C (rs2070744) and Glu298Asp (rs1799983) polymorphisms were determined by Taqman Allele Discrimination assay using real-time polymerase chain reaction (PCR). Primers and probes for the T⁷⁸⁶C polymorphism were customized as follows: forward primer 5'-ACCAGGGCATCAAGCTCTTC-3', reverse primer 5'-GCAGGTCAGCAGAGAGACTAG-3' and probes 5'-CAGGGTCAGCC[G/A]GCCA-3'. Primers and probes for the Glu298Asp polymorphism were designed by Applied Biosystems (assay ID: C_3219460-20). Fluorescence was measured on a Chromo 4 Detector (Bio-Rad Laboratories, USA). Genotypes for the *eNOS* VNTR polymorphism were determined by PCR and fragment separation by electrophoresis in 8 % polyacrylamide gels as previously described [32, 36].

The *BDKRB2* C⁵⁸T (rs1799722) and BE1 +9/-9 polymorphisms were determined using PCR amplification followed by DNA sequencing. The forward primer 5'-AACGCCACTGTTTACATCC-3' and reverse primer 5'-ACGACCACAGGGAACTTCT-3' encompassed the polymorphic region as described earlier [37].

Statistical analysis

The clinical and laboratory characteristics of the studied groups were compared by unpaired t test (parametric data),

by Mann Whitney test (non-parametric data), by chi-square test or Fisher's test (categorical variables), where appropriate. Differences in allele and genotypes distributions and deviation from the Hardy-Weinberg equilibrium were tested by chi squared test. A p value <0.05 was considered statistically significant. Given the sample size of this study, we obtained a statistical power of 80 % with an alpha of 0.05, calculated using the PGA Matlab software [38] to detect an odds ratio of 2.5.

eNOS haplotypes were estimated using the program PHASE (version 2.1, <http://www.stat.washington.edu/stephens/software.html>). To further confirm these haplotype estimates, we have also used the Haplo.stats software (version 1.4.4, <http://cran.r-project.org/web/packages/haplo.stats/index.html>), which computes maximum likelihood estimates of haplotype probabilities. The possible haplotypes including genetic variants of the three polymorphisms studied here in the *eNOS* gene (T⁷⁸⁶ C, intron 4 and Glu298Asp) were H1 (T 4b Glu), H2 (T 4a Glu), H3 (T 4b Asp), H4 (T 4a Asp), H5 (C 4b Glu), H6 (C 4a Glu), H7 (C 4b Asp), H8 (C 4a Asp). Only the haplotypes with observed frequencies >2 % were included in subsequent analysis. Additionally, *BDKRB2* haplotypes including two polymorphisms (C⁻⁵⁸T and BE1 +9/-9) were determined by DNA sequencing: H1 (C -9), H2 (T -9), H3 (C +9) and H4 (T +9). As the BE1 +9/-9 polymorphism creates a frame shift in the sequencing results, it was possible to exactly determine which allele of the C⁻⁵⁸T polymorphism was linked to which allele of the BE1 +9/-9 polymorphism.

Differences in haplotype frequencies among groups were further tested using chi squared test, considering $P < 0.00833$ or $P < 0.0125$ as statistically significant (after Bonferroni's correction: $0.05/\text{number of observed haplotypes}$) for *eNOS* or *BDKRB2* haplotypes, respectively.

Multifactor dimensionality reduction (MDR) analysis evaluate all possible combinations of genotypes for their ability to classify them into poor and good responder groups through cross-validation (CV) steps and permutation testing [39, 40]. Here we used the Robust MDR (RMDR; <http://www.epistasis.org/> [41]) approach to characterize the interaction models among all five polymorphisms studied with a threshold $\alpha = 0.05$. We considered the model that had the maximum testing score and CV consistency (CVC) as the best interaction model. Permutation testing was performed to determine the statistical significance of the best model [40].

Results

Clinical and laboratory characteristics of the 106 hypertensive patients studied are shown in Table 1. As expected, both systolic and diastolic blood pressure was lower after

treatment with enalapril ($p < 0.001$). To evaluate if *eNOS* and *BDKRB2* polymorphisms/haplotypes could affect the anti-hypertensive response to enalapril, these patients were grouped according to responsiveness to antihypertensive therapy: poor responders (PR) or good responders (GR) (see Methods section for details).

There were no differences in sex, ethnicity, age, body mass index or any laboratory parameters between PR and GR groups (Table 1; $p > 0.05$). Additionally, blood pressure was lower after treatment with enalapril in both PR and GR groups ($p < 0.001$). However, baseline systolic and diastolic blood pressure and heart rate was higher in GR ($p < 0.05$).

The genotypes distributions for all *eNOS* and *BDKRB2* polymorphisms did not deviate from Hardy-Weinberg equilibrium ($P > 0.05$). Figure 1 shows the results of a single-locus and haplotype analysis for *eNOS* gene. Interestingly, good responders showed higher frequencies of the TC and CC genotypes, and of the C allele for the T⁷⁸⁶ C polymorphism than PR (all $P < 0.05$; and TT vs. TC, $P = 0.0005$, Odds ratio (OR) = 0.35, 95 % confidence interval (CI) = 0.19–0.63; and TT vs. CC, $P = 0.0424$, Odds ratio = 0.38, 95 % CI = 0.14–0.99).

No other significant differences in genotypes/alleles were found with respect to the 4b/4a polymorphism in intron 4 or Glu298Asp in exon 7 (all $p > 0.05$). Additionally, we found that the H7 haplotype (C 4b Asp) is more frequent in GR than in PR patients ($P = 0.0272$; Fig. 1), however this result did not resist to the Bonferroni's correction for multiple comparisons.

The results for *BDKRB2* polymorphisms showed higher frequencies of the TT genotype for the C⁻⁵⁸ T polymorphism in PR compared with GR (all $P < 0.05$, Fig. 2; TT vs. CT, $P = 0.0106$, OR = 3.06, 95 % CI = 1.27–7.35; and TT vs. CT+CC, $P = 0.0175$, OR = 2.69, 95 % CI = 1.16–6.21).

However, no significant differences were seen in the genotype/allele frequencies of BE 1 +9/-9 polymorphisms between groups. We have also not found significant differences in *BDKRB2* haplotype distribution when poor responders and good responders were compared ($P > 0.05$).

When poor and good responders were stratified according to the dose of enalapril used (Table 2 and 3), we found similar results compared to those shown above. Interestingly, despite the reduction in the sample size in each group, we found significant differences in genotype distributions for the *eNOS* T⁷⁸⁶ C polymorphism (Table 2; $P < 0.05$) and for the *BDKRB2* C⁻⁵⁸ T polymorphism (Table 3; $P < 0.05$) between poor and good responders.

When the patients were grouped according to *eNOS* haplotypes or *BDKRB2* haplotypes, we found no significant differences in blood pressure responses to enalapril (Supplementary Fig. 1; $P > 0.05$).

We have also evaluated gene-gene interactions among all the *eNOS* and *BDKRB2* polymorphisms studied. We found a

Table 1 Clinical and laboratory characteristics of hypertensive patients classified as poor or good responders to enalapril

| | All | Poor responders | Good responders |
|---------------------------|-----------|-----------------|---------------------|
| <i>N</i> | 106 | 53 | 53 |
| Sex (% male) | 68 | 75 | 60 |
| Ethnicity (% non-Black) | 85 | 83 | 86 |
| Age (years) | 47±12 | 47±13 | 48±11 |
| BMI (Kg/m ²) | 29.4±5.4 | 30.0±6.0 | 28.8±4.7 |
| Total cholesterol (mg/dL) | 206±43 | 200±38 | 211±48 |
| LDL cholesterol (mg/dL) | 129±38 | 123±24 | 135±48 |
| HDL cholesterol (mg/dL) | 46±14 | 47±19 | 44±8 |
| Triglycerides (mg/dL) | 152±72 | 150±69 | 154±76 |
| Glucose (mg/dL) | 91±13 | 91±16 | 91±10 |
| Creatinine (mg/dL) | 0.91±0.14 | 0.89±0.11 | 0.92±0.17 |
| Potassium (mEq/L) | 4.2±0.3 | 4.2±0.3 | 4.2±0.4 |
| SBP (mm Hg) | | | |
| Baseline | 149±9 | 146±8 | 152±10 [#] |
| After enalapril treatment | 129±9* | 133±8* | 125±9* [#] |
| DBP (mm Hg) | | | |
| Baseline | 93±9 | 89±8 | 97±8 [#] |
| After enalapril treatment | 80±7* | 82±8* | 78±6* [#] |
| HR (beats/min) | | | |
| Baseline | 78±12 | 81±12 | 75±11 [#] |
| After enalapril treatment | 77±11 | 78±12 | 77±9 |

BMI = body mass index; HDL = High-density lipoprotein; LDL = Low-density lipoprotein; SBP = systolic blood pressure; DBP = diastolic blood pressure; HR = heart rate

Values are the mean ± S.D. * $P < 0.001$ vs. baseline; [#] $P < 0.05$ vs. poor responders

significant interaction between the *eNOS* T⁷⁸⁶ C and *BDKRB2* C⁻⁵⁸ T polymorphisms when compared poor and good responders ($p=0.045$; Table 4).

The specific combinations of genotypes classified as better or worse response to enalapril are depicted in Fig. 3. The combination of the CC genotype for the *BDKRB2* C⁻⁵⁸ T polymorphism with the TC genotype for the *eNOS* T⁷⁸⁶ C polymorphism was more frequent in patients that exhibited better response to enalapril treatment. Conversely, the combination of the CC genotype for the *BDKRB2* C⁻⁵⁸ T polymorphism with the TT genotype for the *eNOS* T⁷⁸⁶ C polymorphism was more frequent in the patients that exhibited worse response (Fig. 3).

When poor and good responders were stratified according to the dose of enalapril used, or when dose was treated as an independent variable in MDR analysis, we found similar, but not significant, results compared to those shown above (data not shown). Probably, this is due to the reduction in the sample size in each group in the gene-gene interaction analysis.

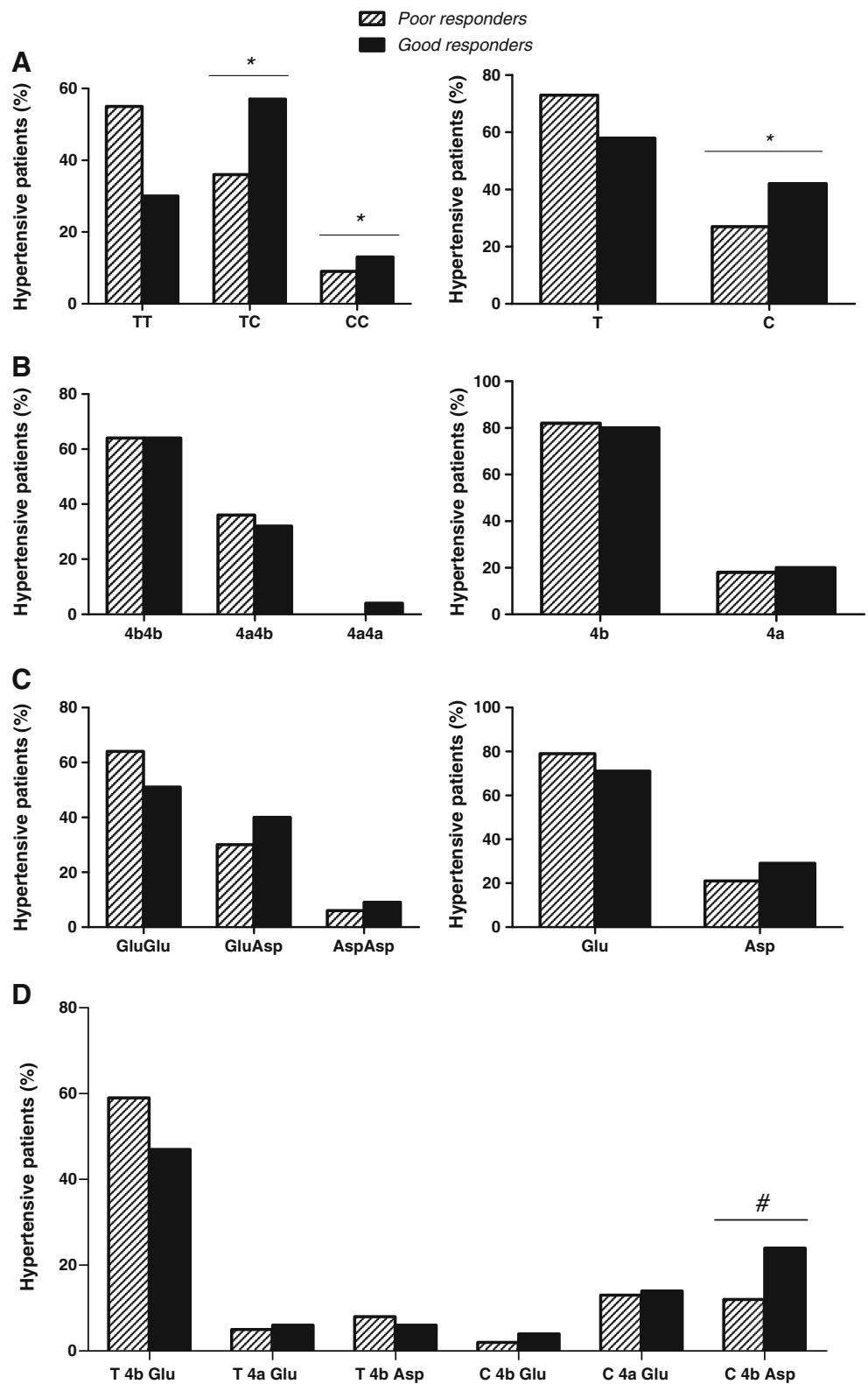
Discussion

To our knowledge, this is the first study to investigate the association between *eNOS* and *BDKRB2* gene

polymorphisms and antihypertensive responses to enalapril. The main findings of this study were that the C allele for *eNOS* T⁷⁸⁶ C polymorphism is associated with better antihypertensive response to enalapril, whereas the TT genotype for *BDKRB2* C⁻⁵⁸ T polymorphism is associated with worse antihypertensive response to enalapril in hypertensive patients. In addition, gene-gene interaction analysis showed that patients with CC genotype for the *BDKRB2* C⁻⁵⁸ T polymorphism were associated with poor or good response depending on the genotype for the *eNOS* T⁷⁸⁶ C polymorphism.

Previous *in vitro* and clinical studies showed that the *eNOS* T⁷⁸⁶ C polymorphism can modify the responses to cardiovascular drugs [32, 33, 42–45]. Endothelial cells with CC genotypes treated with statins showed higher *eNOS* mRNA level than cells with the TT genotype [42]. This effect was attributed to increased transcriptional activity of the *eNOS* gene and mRNA stability, and to decreased expression of the transcriptional repressor factor (RPA-1) in cells carrying the C allele. Consistently, results from a clinical study suggested that individuals with CC genotypes may have increased benefits by atorvastatin treatment as they had increased NO bioavailability and attenuated oxidative stress [33]. Besides that, the anti-inflammatory effects of atorvastatin are modulated by this polymorphism [44]. While treatment with statins reduced the circulating

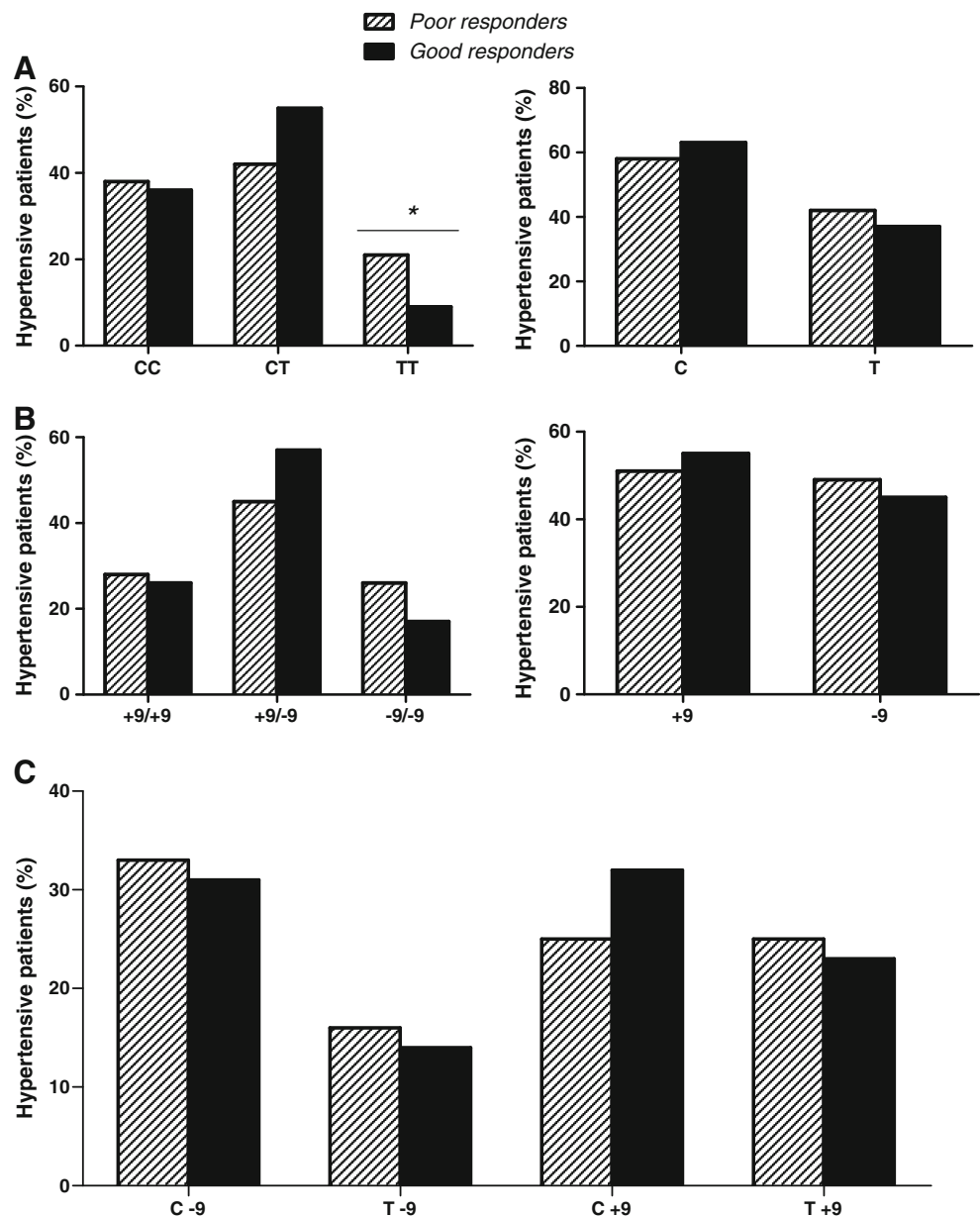
Fig. 1 Genotype, allele and haplotype frequencies distributions (%) for endothelial nitric oxide synthase (*eNOS*) gene polymorphisms in hypertensive patients classified as poor responders (n=53) or good responders (n=53) to enalapril. Panel A: T⁷⁸⁶C polymorphism; Panel B: 4b/4a polymorphism; Panel C: Glu298Asp and Panel D: *eNOS* haplotypes. *P<0.05 vs. reference genotypes/alleles. #P<0.05 vs. all other haplotypes, not statistically significant after Bonferroni's correction for multiple comparisons



concentrations of CD40L, VCAM-1, P-selectin and matrix metalloproteinase-9 in individuals with the CC genotype, no effects were found in these pro-inflammatory mediators in subjects with the TT genotype. Recent findings have

suggested that *eNOS* polymorphisms may also modulate the response to other drugs, such as angiotensin receptor blockers (ARBs) [43]. Olmesartan and the other ARBs produced higher NO release from cells homozygous for C

Fig. 2 Genotype, allele and haplotype frequencies (%) for bradykinin receptor B2 (*BDKRB2*) gene polymorphisms in hypertensive patients classified as poor responders (n=53) or good responders (n=53) to enalapril. Panel A: C⁻⁵⁸T polymorphism; Panel B: BE1 +9/-9 polymorphism and Panel C: B2 receptor haplotypes. *P<0.05 vs. CT genotype



allele endothelial cells compared to cells heterozygous for T⁷⁸⁶C polymorphism. Additionally, the response to phosphodiesterase type 5 (PDE-5) inhibitors was modified by T⁷⁸⁶C polymorphism in the *eNOS* gene [32]. The authors found that C allele apparently improves the responses to sildenafil in postoperative erectile dysfunction patients, as compared to the T allele. Taken together, these consistent findings provide strong evidence supporting the idea that treatment with statins, ARBs, PDE-5 inhibitors and now, enalapril, may be more beneficial in subjects with the C allele.

Interestingly, GR exhibited higher baseline systolic and diastolic blood pressure than PR. These results are in

agreement with previous studies, which also showed that individuals carrying the variant C for the same polymorphism had increased risk of developing cardiovascular diseases, including hypertension [18, 19]. The C allele in the promoter region of the *eNOS* gene is associated with a 50 % decrease of promoter activity [12]. This variant was also associated with decreased NO release by platelets from healthy subjects [46] and lower plasma concentrations of NO metabolites in pre-hypertensive individuals [47].

Conversely, we did not find other significant differences in genotype or allele frequencies with respect to both 4b/4a and Glu298Asp *eNOS* polymorphisms between poor and good responders. Whereas *eNOS* haplotypes had been

Table 2 Genotype, allele and haplotype frequencies for *eNOS* gene in hypertensive patients classified as poor or good responders to enalapril 10 or 20 mg/day

| | | Enalapril 10 mg | | | | Enalapril 20 mg | | | |
|---------------------|-----------------------------|-----------------|--------------|-----------------|---------------------|-----------------|--------------|-----------------|---------------------|
| | | PR (n=24) | GR (n=24) | <i>P</i> -value | OD (CI) | PR (n=29) | GR (n=29) | <i>P</i> -value | OD (CI) |
| T ⁻⁷⁸⁶ C | TT | 50(12) | 33(8) | - | 1.00 (reference) | 59(17) | 28(8) | - | 1.00 (reference) |
| | TC | 42(10) | 58(14) | 0.014 | 0.48 (0.26-0.86) | 31(9) | 55(16) | <0.001 | 0.27 (0.14-0.50) |
| | CC | 8(2) | 8(2) | NS | 0.66 (0.23-1.93) | 10(3) | 17(5) | 0.004 | 0.28 (0.11-0.69) |
| | <i>X</i> ² -test | 6.04 | | 0.049 | | 19.56 | | <0.001 | |
| | T | 71(34) | 63(30) | - | 1.00 (reference) | 74(43) | 55(32) | - | 1.00 (reference) |
| | C | 29(14) | 38(18) | NS | 0.67 (0.37-1.20) | 26(15) | 45(26) | 0.005 | 0.43 (0.24-0.78) |
| Intron 4 | 4b4b | 67(16) | 71(17) | - | 1.00 (reference) | 62(18) | 59(17) | - | 1.00 (reference) |
| | 4b4a | 33(8) | 25(6) | NS | 1.40 (0.75-2.60) | 38(11) | 38(11) | NS | 0.95 (0.54-1.69) |
| | 4a4a | 0(0) | 4(1) | NS | 0.12 (0.01-2.23) | 0(0) | 3(1) | NS | 0.14 (0.01-2.70) |
| | <i>X</i> ² -test | 5.21 | | NS | | 3.07 | | NS | |
| | 4b | 83(40) | 83(40) | - | 1.00 (reference) | 81(47) | 78 (45) | - | 1.00 (reference) |
| | 4a | 17(8) | 17(8) | NS | 1.00 (0.48-2.09) | 19(11) | 22 (13) | NS | 0.83 (0.42-1.66) |
| Exon 7 | GluGlu | 67(16) | 54(13) | - | 1.00 (reference) | 62(18) | 48(14) | - | 1.00 (reference) |
| | GluAsp | 29(7) | 38(9) | NS | 0.62 (0.34-1.12) | 31(9) | 41(12) | NS | 0.59 (0.32-1.07) |
| | AspAsp | 4(1) | 8(2) | NS | 0.40 (0.12-1.41) | 7(2) | 10(3) | NS | 0.54 (0.19-1.53) |
| | <i>X</i> ² -test | 3.93 | | NS | | 3.69 | | NS | |
| | Glu | 81(39) | 73(35) | - | 1.00 (reference) | 78(45) | 69 (40) | - | 1.00 (reference) |
| | Asp | 19(9) | 27(13) | NS | 0.63 (0.33-1.24) | 22(13) | 31 (18) | NS | 0.63 (0.33-1.19) |
| Haplotypes | T 4b Glu | 60(29) | 52(25) | NS | 1.39 (0.79-2.43) | 59(34) | 43(25) | NS | 1.91 (1.09-3.37) |
| | T 4a Glu | 2(1) | 6(3) | NS | 0.32 (0.06-1.63) | 7(4) | 5(3) | NS | 1.43 (0.44-4.67) |
| | T 4b Asp | 8(4) | 4(2) | NS | 2.09 (0.61-7.17) | 9(5) | 7(4) | NS | 1.31 (0.47-3.68) |
| | C 4b Glu | 4(2) | 4(2) | NS | 1.00 (0.24-4.12) | 0(0) | 3(2) | NS | 0.14 (0.01-2.72) |
| | C 4a Glu | 15(7) | 10(5) | NS | 1.59 (0.68-3.73) | 12(7) | 17(10) | NS | 0.67 (0.30-1.48) |
| | C 4b Asp | 10(5) | 23(11) | NS | 0.37 (0.17-0.83) | 14(8) | 24(14) | NS | 0.52 (0.25-1.07) |
| | <i>X</i> ² -test | 10.03 | | NS | | 9.57 | | NS | |

Abbreviations: PR: poor responders; GR: good responders

The frequencies are shown as % (n). OD: Odds ratio. CI: 95 % confidence interval

P were considered significant when <0.05 (genotypes/alleles) or <0.05/6=0.0083 (haplotypes)

Table 3 Genotype, allele and haplotype frequencies for *BDKRB2* gene in hypertensive patients classified as poor or good responders to enalapril 10 or 20 mg/day

| | | Enalapril 10 mg | | | | Enalapril 20 mg | | | |
|-----------------------------|-----------------------------|-----------------|--------------|-----------------|---------------------|-----------------|--------------|-----------------|---------------------|
| | | PR (n=24) | GR (n=24) | <i>P</i> -value | OD (CI) | PR (n=29) | GR (n=29) | <i>P</i> -value | OD (CI) |
| C ⁻⁵⁸ T | CC | 33(8) | 33(8) | - | 1.00 (reference) | 41 (12) | 38 (11) | - | 1.00 (reference) |
| | CT | 46(11) | 58(14) | NS | 0.79 (0.43-1.47) | 38 (11) | 52 (15) | NS | 0.68 (0.37-1.24) |
| | TT | 21(5) | 8(2) | 0.042 | 2.63 (1.02-6.77) | 21 (6) | 10 (3) | NS | 1.95 (0.81-1.67) |
| | <i>X</i> ² -test | 7.21 | | 0.027 | | 6.20 | | 0.045 | |
| | C | 56(27) | 63(30) | - | 1.00 (reference) | 60 (35) | 64 (37) | - | 1.00 (reference) |
| Exon 1 +9/-9 | T | 44(21) | 38(18) | NS | 1.28 (0.73-2.26) | 40 (23) | 36 (21) | NS | 1.19 (0.67-2.10) |
| | +9/+9 | 29(7) | 25(6) | - | 1.00 (reference) | 28 (8) | 28 (8) | - | 1.00 (reference) |
| | +9/-9 | 38(9) | 54(13) | NS | 0.61 (0.31-1.19) | 52 (15) | 59 (17) | NS | 0.88 (0.46-1.68) |
| | -9/-9 | 33(8) | 21(5) | NS | 1.36 (0.63-2.91) | 21 (6) | 14 (4) | M | 1.50 (0.64-3.53) |
| | <i>X</i> ² -test | 5.75 | | NS | | 1.841 | | NS | |
| Haplotypes | +9 | 48(23) | 52(25) | - | 1.00 (reference) | 53 (31) | 57 (33) | - | 1.00 (reference) |
| | - 9 | 52(25) | 48(23) | NS | 1.17 (0.67-2.04) | 47 (27) | 43 (25) | NS | 1.18 (0.67-2.05) |
| | C -9 | 31(15) | 35(17) | NS | 0.83 (0.46-1.51) | 34 (20) | 28 (16) | NS | 1.33 (0.73-2.42) |
| | T -9 | 21(10) | 13(6) | NS | 1.78 (0.84-3.79) | 12 (7) | 16 (9) | NS | 0.72 (0.32-1.60) |
| | C +9 | 25(12) | 27(13) | NS | 0.90 (0.48-1.70) | 26 (15) | 36 (21) | NS | 0.62 (0.34-1.14) |
| <i>X</i> ² -test | T +9 | 23(11) | 25(12) | NS | 0.90 (0.47-1.72) | 28 (16) | 21 (12) | NS | 1.46 (0.76-2.80) |
| | | 2.29 | | NS | | 3.76 | | NS | |

Abbreviations: PR: poor responders; GR: good responders

The frequencies are shown as % (n). OD: *Odds ratio*. CI: 95 % confidence interval

P were considered significant when <0.05 (genotypes/alleles) or <0.05/4=0.0125 (haplotypes)

associated with modulation of pharmacologic treatment in patients with preeclampsia [48] and erectile dysfunction [32], we did not observe associations of haplotypes with the response to enalapril.

In addition to the eNOS gene, the *BDKRB2* gene is other good candidate as predictor of the ACE inhibitor response, because the activation of the bradykinin receptor B2 is related to NO formation pathway [49]. In this regard, our

results suggest that TT carriers of the *BDKRB2* C⁻⁵⁸T polymorphism had worse responses to antihypertensive therapy.

On the other hand, the T allele has been associated with increased *BDKRB2* gene transcription in vitro [26], which is consistent with a protective effect against hypertension exhibited by this genetic variant in Asians and African-Americans [30, 50]. Although the presence of this allele

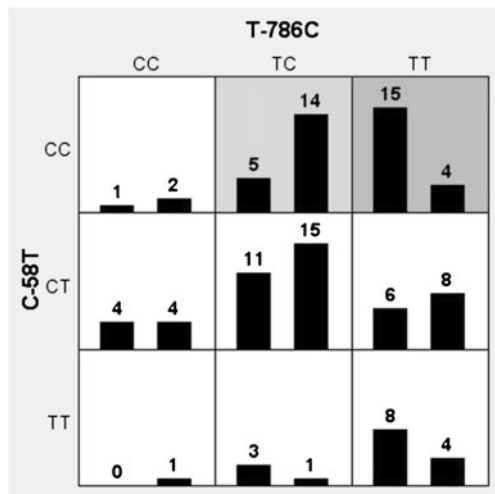


Fig. 3 Robust multifactor dimensionality reduction (RMDR) best model for the interaction between the *eNOS* T⁷⁸⁶C and *BDKRB2* C⁻⁵⁸T polymorphisms in hypertensive patients classified according to response to enalapril. The distributions of poor responders (left bars) and good responders (right bars) are illustrated for each combination of genotypes. The light grey cells are labeled as better response to enalapril, dark grey cells are labeled as worse response to enalapril, and white cells are labeled as unknown

also has been associated with the appearance of ACE inhibitor-related cough in Japanese patients [50, 51], other studies involving different populations did not show any association [52–54].

Our findings showed that TT carriers for the C⁻⁵⁸T polymorphism also had lower baseline systolic and diastolic blood pressure. Altogether, our results suggest that although carriers of C allele may have higher blood pressure levels, they seem to have increased benefits from the treatment with enalapril. We have not found any other association between antihypertensive response to enalapril and BE1 +9/-9 polymorphism or *BDKRB2* haplotypes. These findings are in line with previous results showing that although *eNOS* haplotypes may be

associated with susceptibility to hypertension [24], they are not associated with resistance to antihypertensive therapy [55].

Interactions between *eNOS* and *BDKRB2* genetic variants were also expected, as both proteins are involved in the same physiological pathway described above. While neither the CC genotype nor the C allele for the C⁻⁵⁸T *BDKRB2* polymorphism were significantly associated with the response to enalapril at single-locus analysis, gene-gene interaction analysis showed that the C⁻⁵⁸T CC genotype combined with *eNOS* T⁷⁸⁶C TT genotype was more frequent in poor responders, while the combination of C⁻⁵⁸T CC genotype with *eNOS* TC genotype was more frequent among good responders (Fig. 3). These findings are obscured when single *BDKRB2* genotypes alone are considered, thus highlighting the importance of gene-gene interactions to the genetic component of drug responses (39, 40).

Enalapril had no effects on the circulating concentrations of markers of endogenous NO formation in a previous study [56], although *eNOS* polymorphisms apparently contribute to the responses to enalapril. This is probably explained by the fact that enalapril promotes increased NO formation at tissue levels that are not clearly reflected by the circulating levels markers of NO formation, as previously suggested [56].

As limitations of our study, we should mention the low number of patients included and that we were not able to stratify analysis by race, due to the low number of black subjects. However, given the sample size, we were able to obtain significant results with 80 % statistical power, therefore this study is not underpowered. Ethnicity may be a concern, as there are notable differences in *eNOS* and *BDKRB2* genotypes distributions between white and black subjects [37, 57]. However, there were no inter-ethnic differences between poor and good responders to enalapril in this study. Other issues that have not been addressed in the present study include bradykinin receptor polymorphisms that may predispose to side effects resulting from the use of ACE inhibitors, differences between ACE inhibitors, and other genetic polymorphisms that could affect the responses to these drugs.

In conclusion, our findings suggest that both *eNOS* and *BDKRB2* genotypes may affect the antihypertensive responses to enalapril. The TC and CC genotypes (*eNOS* T⁷⁸⁶C polymorphism) are associated with better antihypertensive responses to enalapril, while the TT genotype of *BDKRB2* gene is associated with worse responses to this ACE inhibitor. Both genes may interact and affect enalapril responses, as CC genotype in *BDKRB2* is associated with good or poor responses depending on the *eNOS* T⁷⁸⁶C genotypes.

Table 4 Robust multifactor dimensionality reduction (RMDR) multi-locus models when compared poor responders (PR) and good responders (GR) to enalapril

| Interaction Models | Training Score | Testing Score | CVC ^a | P |
|---|----------------|---------------|------------------|---------|
| T ⁷⁸⁶ C <i>eNOS</i> | 0.6229 | 0.5099 | 8/10 | 0.7705 |
| T ⁷⁸⁶ C <i>eNOS</i> ; C ⁻⁵⁸ T <i>BDKRB2</i> | 0.6580 | 0.6580 | 10/10 | 0.0450* |
| Intron4 <i>eNOS</i> ; C ⁻⁵⁸ T and BE1+9-9 <i>BDKRB2</i> | 0.6933 | 0.5394 | 9/10 | 0.6060 |
| T ⁷⁸⁶ C and Intron4 <i>eNOS</i> ; C ⁻⁵⁸ T and BE1+9-9 <i>BDKRB2</i> | 0.6429 | 0.4583 | 6/10 | 0.9550 |

^a CVC: Cross Validation Consistency; * P<0.05 statistically significant, after 1.000 permutations

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