Angiotensin-Converting Enzyme Insertion/Deletion Polymorphism Modulates the Human In Vivo Metabolism of Bradykinin

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Background—Bradykinin is a cardioprotective peptide metabolized by the angiotensin-converting enzyme (ACE). An insertion/deletion (I/D) polymorphism in the ACE gene determines plasma ACE levels. The D allele is associated with cardiovascular disease, which may relate to enhanced angiotensin II production or to increased bradykinin degradation to the inactive metabolite bradykinin 1–5 (BK1–5). Therefore, we determined the effect of the ACE I/D polymorphism on human bradykinin metabolism in vivo.

Methods and Results—Bradykinin (400 ng/min) was infused into the brachial artery of volunteers with ACE I/I, I/D, or D/D genotypes (\(n=9\) each). The bradykinin and BK1–5 levels in forearm venous return were quantified by liquid chromatography–mass spectrometry. Plasma ACE activity was highest in those with the D/D genotype (36.8±6.2 U/mL), intermediate in those with the I/D genotype (25.3±3.3 U/mL), and lowest in those with the I/I genotype (20.3±2.3 U/mL; \(P=0.017\) for effect of number of D alleles). Bradykinin concentrations were 726±242, 469±50, and 545±104 fmol/mL in I/I, I/D, and D/D subjects, respectively (\(P<0.01\)). Bradykinin concentrations were higher in those with the D/D genotype (469±50 fmol/mL) than in those with the I/I or I/D genotypes (726±242 and 25.3±3.3 U/mL, respectively; \(P=0.017\)). Bradykinin concentrations were 726±242, 469±50, and 545±104 fmol/mL in I/I, I/D, and D/D subjects, respectively (\(P<0.01\)). Bradykinin concentrations were higher in those with the D/D genotype (469±50 fmol/mL) than in those with the I/I or I/D genotypes (726±242 and 25.3±3.3 U/mL, respectively; \(P=0.017\)). Bradykinin concentrations were 726±242, 469±50, and 545±104 fmol/mL in I/I, I/D, and D/D subjects, respectively (\(P<0.01\)). Bradykinin concentrations were higher in those with the D/D genotype (469±50 fmol/mL) than in those with the I/I or I/D genotypes (726±242 and 25.3±3.3 U/mL, respectively; \(P=0.017\)).

Conclusions—The ACE D allele has a significant effect on the in vivo degradation of bradykinin in humans. The ratio of BK1–5:bradykinin may serve as a marker for tissue ACE activity. (Circulation. 2000;102:829-832.)

Key Words: bradykinin ■ metalloproteinases ■ metabolism ■ endothelium

Angiotensin-converting enzyme (ACE) catalyzes the conversion of angiotensin I to angiotensin II and the degradation of bradykinin to inactive products.1 An insertion/deletion (I/D) polymorphism in intron 16 of the ACE gene accounts for 50% of the variability of human serum ACE levels.2 The D allele is associated with increased ACE activity and has been linked with cardiovascular disease.3 This link has been attributed to the increased formation of angiotensin II in individuals who carry the D allele.4 A complimentary hypothesis is that cardiovascular morbidity associated with the D allele reflects an increased degradation of cardioprotective bradykinin.

Bradykinin is a potent vasodilator that exerts antiproliferative effects, inhibits thrombin-induced platelet activation, contributes to the cardioprotective effects of ACE inhibitors,5 and stimulates tissue-type plasminogen activator (t-PA) release from vascular endothelium.6 We previously reported that the ACE genotype determines the rate of bradykinin degradation in human sera ex vivo.7 However, serum ACE activity represents only a small fraction of the in vivo activity of this endothelium-bound enzyme.1

Campbell et al8 used the ratio of bradykinin 1–7 (BK1–7) to bradykinin to measure bradykinin degradation by ACE. Recently, we determined the human metabolism of systemic bradykinin in vivo and identified BK1–5 (Arg-Pro-Pro-Gly-Phe-Pro) as a stable, circulating metabolite.9 Whereas BK1–7 represents the product of a single cleavage of bradykinin by ACE, BK1–5 is produced by 2 sequential cleavages at the Pro7-Phe and Phe–Ser bonds. Thus, the ratio of BK1–5:bradykinin in the circulation may reflect the sum of vascular, endothelial, and serum ACE activity. Therefore, we ascertained the effect of ACE genotype on the metabolism of intra-arterially administered bradykinin in the human forearm vasculature.

Methods

Subjects
A total of 27 normotensive volunteers with the ACE I/I, I/D, or D/D genotype (\(n=9\) each) were studied. The protocol was approved by
forearm plasma flow, as reported elsewhere. During the 400 ng/min infusion of bradykinin (Calbiochem; purified and pyrogen-tested by the Vanderbilt Investigational Pharmacy) was infused at 100, 200, and 400 ng/min for 5 minutes each. The forearm blood flow (FBF) response was determined using strain-gauge plethysmography, and net t-PA release was calculated as the product of the arteriovenous t-PA concentration gradient and strain-gauge plethysmography, and net t-PA release was calculated such that vasodilation increased as the number of D alleles present in the D homozygotes, least in D/D homozygotes, as measured by the ratio of BK1–5: bradykinin, was greatest in ACE D homozygotes, least in ACE I homozygotes, correlation. The ACE genotype effect on bradykinin response was determined by repeated-measures ANOVA in which the within-subject variable was bradykinin dose and the between-subject variables were ethnicity and ACE I/D genotype. Differences between I/I and D/D groups were determined using Student’s t test or the Mann-Whitney test, with $\alpha<0.05$ (2-tailed) considered significant.

**Results**

Subject characteristics were similar among the study groups (Table).

Plasma ACE activity increased with number of ACE D alleles (I/I, 20.3±2.3 U/mL; I/D, 25.3±3.3 U/mL; and D/D, 36.8±6.2 U/mL; $P=0.017$; Figure 1A). During a steady-state infusion of bradykinin (400 ng/min), venous bradykinin concentrations were 726±242 fmol/mL in the I/I group, 469±50 fmol/mL in the I/D group, and 545±104 fmol/mL in the D/D group ($P>0.10$ for D allele effect; Figure 1B). The presence of the D allele had a significant effect on the venous concentration of the bradykinin metabolite BK1–5 (1113±290, 1520±318, and 1887±388 fmol/mL for the I/I, I/D, and D/D groups, respectively; $P=0.027$; Figure 1C) and the ratio of BK1–5: bradykinin (1.87±0.35, 3.09±0.40, and 4.31±0.97 for the I/I, I/D, and D/D groups, respectively; $P=0.010$; Figure 1D). Plasma ACE activity correlated with the BK1–5:bradykinin ratio ($r^2=0.16$, $P=0.039$).

Blood samples for kinins were not obtained during bradykinin dose escalation, and the study was not designed to measure the concentration-response for bradykinin or BK1–5. However, bradykinin-induced net t-PA release correlated with total kinin (bradykinin+BK1–5) concentration in venous blood, ($r^2=0.20$, $P=0.027$; Figure 2). No correlation existed between total kinin concentration and FBF ($P>0.10$). ACE I/D genotype did not affect t-PA response to bradykinin ($P>0.10$). Ethnicity and ACE I/D genotype had an interactive effect on the FBF response to bradykinin ($F=4.5$, $P=0.024$), such that vasodilation increased as the number of D alleles increased. ACE I/D genotype effect was most pronounced at submaximal doses (FBF at 100 ng/min: 6.8±1.9, 15.7±5.6, 8.3±0.5, and 14.6±1.6 mL/min per 100 mL of forearm volume for I/I and D/D groups in whites and blacks, respectively; $P=0.026$ for I/I versus D/D).

**Discussion**

This is the first study to report an association between the ACE D allele and increased bradykinin degradation in humans in vivo. Degradation of bradykinin through the ACE pathway, as measured by the ratio of BK1–5:bradykinin, was greatest in ACE D homozygotes, least in ACE I homozygotes.
and intermediate in heterozygotes. Thus, the number of D alleles had a significant effect on bradykinin metabolism. Bradykinin concentrations tended to be highest in the ACE I/I group, but differences were not statistically significant. Although degradation by ACE seems to be diminished in ACE I homozygotes, bradykinin may be degraded via alternative pathways, such as the aminopeptidase P pathway. Additionally, the extremely short half-life of bradykinin (17 s) and the susceptibility to artifactual production during sampling resulted in a large variance in bradykinin concentrations and could have contributed to a type II error.

One potential limitation of the current study was the use of pharmacological concentrations of bradykinin. However, human sera incubations indicate linear bradykinin degradation through micromolar concentrations. A second potential limitation of the present study was the measurement of BK1–5 concentrations under non-steady-state conditions. BK1–5 has a half-life of 80 to 90 minutes in humans. The prolonged half-life of BK1–5 compared with that of bradykinin accounts for the fact that the ratio of metabolite to parent exceeded unity. However, given the relatively low rate of intra-arterial bradykinin infusion (400 ng/min), most BK1–5 produced before blood sampling would have been diluted in the systemic circulation. On the basis of prior systemic infusion studies, we estimate that the resultant intra-arterial concentration of BK1–5 was <100 fmol/mL. Thus, BK1–5 in forearm venous return during intra-arterial bradykinin infusion represented ongoing local metabolism and not prior production of the metabolite.

In the present study, venous kinin concentration correlated significantly with the net t-PA release across the forearm but not with the vasodilator response to bradykinin. Unlike t-PA release, which reflects a specific effect of bradykinin on the

![Figure 1. Plasma ACE activity (A), bradykinin concentration (B), bradykinin metabolite BK1–5 concentration (C), and molar ratio of BK1–5 to bradykinin (D) in forearm venous blood during intrabrachial bradykinin infusion in subjects with ACE I/I, I/D, or D/D genotypes (n=9 in each group).](image)

![Figure 2. Correlation between total forearm venous blood kinin (bradykinin+BK1–5) concentration and net t-PA release (ng/min per 100 mL of forearm volume) across forearm.](image)
endothelial cell, vasodilation depends on both endothelial production of nitric oxide and subsequent vascular smooth muscle relaxation, which is influenced by ethnicity. As such, the ethnic heterogeneity and the small sample size of the study groups may have obscured a relationship between kinin concentrations and the vasodilator response to bradykinin. Nevertheless, the correlation between venous kinin concentration and endothelial t-PA release serves to validate the physiological relevance of these measurements.

The functional significance of the association between ACE I/D genotype and bradykinin metabolism depends on the complex interplay between increased degradation of bradykinin and subsequent B2 receptor upregulation secondary to decreased endogenous bradykinin concentrations. One published study suggests that ACE I/D genotype has no effect on the vasodilator response to infused bradykinin. Our preliminary data indicate that the ACE D allele is associated with an increased vasodilator response to exogenous bradykinin, suggesting that enhanced receptor sensitivity predominates over bradykinin degradation. Studies of the impact of ACE I/D polymorphism on the concentration and effects of endogenous kinins are needed to better define the functional significance of this polymorphism as it relates to cardiovascular risk.

In summary, the present study is the first to demonstrate that ACE I/D polymorphism determines the in vivo metabolism of bradykinin in humans. With the development of sensitive assays for measuring endogenous bradykinin and its metabolite, determination of the ratio of BK1–5:bradykinin may constitute a surrogate marker for vascular ACE activity in humans.

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