



Lack of association between *ACE I/D*, *NOS3 VNTR* polymorphisms and drug toxicity of tacrolimus treated post-renal transplantation patients

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ARTICLE INFO

Article Type:
Original

Article History:

Received: 30 August 2019

Accepted: 30 October 2019

Published online: 5 December 2019

Keywords:

Tacrolimus

ACE I/D

NOS3 VNTR

Transplantation

Polymorphisms

End-stage renal disease

Calcineurin inhibitors

ABSTRACT

Introduction: Tacrolimus is the most commonly used calcineurin inhibitor for renal transplant individuals. Genetic factors play a major role in allografts by affecting blood pressure regulation, vascular proliferation and inflammatory responses.

Objectives: The aim of this study was to evaluate a possible role of the *ACE I/D* and *NOS3 VNTR* polymorphisms in kidney transplantation patients treated with tacrolimus in the south Indian population.

Patients and Methods: This study included 50 kidney transplant individuals and 100 unrelated healthy individuals from the general population as control. The genotyping was performed by polymerase chain reaction and electrophoresis. Genotypes were compared among cases and controls applying χ^2 test. The difference in C/D ratios was compared using Mann–Whitney U test or Kruskal–Wallis test.

Results: The *ACE ID* polymorphisms in different models [genetic ($P=0.723$), dominant ($P=0.148$) and recessive ($P=0.652$)] or allele model ($P=0.455$) did not differ significantly between the groups. Similarly, there was no significant difference for the *NOS3 VNTR* genotypes in genetic model (bb vs ba $P=0.118$; bb vs aa $P=0.446$), dominant model (bb vs ba+aa $P=0.099$) and allelic model (b vs a $P=0.103$). No significant difference was observed for *ACE ID* and *NOS3 VNTR* genotypes between the toxicity and non-toxicity groups. Furthermore, no significant association was observed for daily dose and concentration dose ratio for the studied polymorphisms.

Conclusion: The present study revealed no significant association between cases and controls as well as toxicity and non-toxicity groups. Furthermore, there was no association between genotypes and daily dose and dose concentration.

Implication for health policy/practice/research/medical education:

To evaluate a possible role of the *ACE I/D* and *NOS3 VNTR* polymorphisms in the kidney transplantation patients treated with tacrolimus in south Indian population, we conducted a study on 50 kidney transplant individuals. Our study revealed the absence of a significant association between cases and controls as well as toxicity and non-toxicity groups. Furthermore, the association between genotypes and daily dose and dose concentration was also not observed.

Please cite this paper as: AS. Lack of association between *ACE I/D*, *NOS3 VNTR* polymorphisms and drug toxicity of tacrolimus treated post-renal transplantation patients. J Nephroarmacol. 2020;9(2):e19. DOI: 10.34172/npj.2020.19.

Introduction

End-stage renal disease (ESRD) is a major health problem, associated with morbidity and mortality. The renal transplantation option is the best therapy, far superior to dialysis in patients with ESRD (1). Tacrolimus is the most commonly used calcineurin inhibitor for renal transplant individuals. However, the graft function is multifactorial

which includes, primary disease, immunosuppressive regimen, metabolic and cardiovascular conditions, episodes of acute rejection and donor and recipient ages (2). Furthermore, the genetic factors also play a major role in the allografts by affecting blood pressure regulation, vascular proliferation and inflammatory responses (3). Further studies have also confirmed the

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associations of genetic variation with immunosuppressant pharmacokinetics, toxicity, and outcomes after transplantation (4-6).

Among the different pathways which regulate the allografts, the renin angiotensin aldosterone system (RAAS) is an independent factor for progression of renal attrition and ESRD (7). Therefore, genetic polymorphism of RAAS might be the most important mediator of renal allograft among transplanted individuals. Further, the RAAS activity is regulated by an angiotensin-converting enzyme (ACE) gene by converting angiotensin I into vasoactive and aldosterone stimulating peptide angiotensin II (8). Among the several polymorphisms of ACE gene, the ACE insertion/deletion (I/D) gene polymorphism is found to be more frequently associated with renal allograft survival after renal transplantation. In past years, several studies have investigated the association between ACE I/D polymorphism and renal transplantation yielding inconsistent results (9-11). Similarly, the endothelial nitric oxide synthase gene polymorphisms affect the renal rejection through the endothelial nitric oxide synthase activity and endothelial dysfunction. Among the several functional polymorphisms of NOS3 gene, the VNTR polymorphisms can alter renal function (12). Recent studies conducted in Iranian kidney transplant recipients and chronic allograft nephropathy in Turkey population have found, no significant association between the allele/genotype and acute rejection (13, 14). So far, no studies have shown the association of ACE I/D and NOS3 VNTR polymorphisms with renal rejection in our population. Therefore, the present study aimed to investigate the possible correlation between ACE I/D and NOS3 VNTR polymorphisms with renal transplantation individuals treated with tacrolimus.

Objectives

The aim of this study was to evaluate a possible role of the ACE I/D and NOS3 VNTR polymorphisms in kidney transplantation patients treated with tacrolimus in the south Indian population.

Patients and Methods

Study patients

The present study investigated fifty individuals of post-renal transplantation patients (male 76%; female 34% and age was 35.0 ± 13.23) treated with tacrolimus based immunosuppressive as the outpatient and inpatient wings of the Nephrology Department of Sri Ramachandra Institute of Higher Education and Research, and hundred unrelated healthy individuals from general population as the control subjects (male 64%; female 36% and age was 53.9 ± 12.9 years). For all transplant individuals, the tacrolimus levels in blood were measured using the chemiluminescent microparticle immunoassay (CMIA) method. The trough C_0 (ng/mL) level, was revised by dose and patient's body weight. Moreover, based on the

tacrolimus toxicity the subjects were divided into two groups such as toxicity (18%) and non-toxicity groups (82%).

Genotyping

Human genomic DNA was extracted from peripheral blood specimens by phenol chloroform extraction and ethanol precipitation method(15). The polymerase chain reaction (PCR) and electrophoresis were used to detect the ACE gene insertion deletion (16) and NOS3 VNTR polymorphism (12). All homozygous deletion of ACE gene were further subjected to a second PCR amplification with insertion-specific primers to prevent mistyping of heterozygous genotypes (17).

Ethical issues

Human rights were respected under the Helsinki Declaration 1975, as revised in 1983. The study protocol was approved by the Institutional Ethics Committee of Sri Ramachandra Institute of Higher Education and Research, Chennai, India. Informed consent was obtained from all the study participants before collecting the blood samples.

Statistical analysis

The direct gene-counting method was adapted to calculate allele frequencies. The distribution of genotypes was tested for Hardy-Weinberg equilibrium using the χ^2 goodness-of-fit test. A χ^2 test was carried out to check the association between cases vs controls. Odds ratios (ORs) and 95% CIs were calculated. The SPSS (version 16.0; SPSS, Chicago, IL) was applied to evaluate the association amongst the genetic variants and P values <0.05 were considered to be statistically significant. The tacrolimus C/D ratios are expressed as median \pm SD range. The difference in C/D ratios was compared using Mann-Whitney U test or Kruskal-Wallis test among groups.

Results

Association analysis between the ACE ID, NOS3 VNTR polymorphism and subjects

For this study were genotyped 50 kidney transplanted individuals treated with tacrolimus and 100 unrelated healthy individuals were genotyped. Of the studied 100 control subjects the II, ID and DD were 40 (40%), 41 (41%) and 19 (19.0%), respectively, and of the studied 50 renal post-transplantation patients treated with tacrolimus were II 14 (28%), ID 28 (56%) and DD 8 (16%). For NOS3 VNTR the observed genotyped frequencies of controls were bb 75 (75.0%), bb 21 (21 %) and aa 3 (3 %). For the renal transplantation cases bb were 31(62.0%), ba were 16 (32.0%) and aa were 4(4.0%) (Table 1). The genotype frequencies of kidney transplanted individuals treated with tacrolimus and control group were in accordance with the HWE for both polymorphisms. The ACE ID polymorphisms in different models (genetic ($P=0.723$), dominant ($P=0.148$) and recessive ($P=0.652$)) or allele

Table 1. Association between the studied subjects and ACE ID, NOS3 VNTR polymorphism

	Genotype	Control	Case	OR (95% CI)	P value (df=1)	P value (df=2)
		n=100 (%)	n=50 (%)			
ACE ID	II	40 (40)	14 (28)	Reference		
	ID	41 (41)	28 (56)	1.95 (0.89-4.23)	0.088	
	DD	19 (19)	8 (16)	1.20 (0.43-3.35)	0.723	
	ID+DD	60 (60)	36 (72)	1.71 (0.82-3.57)	0.148	0.209
	DD	19 (19)	8 (16)	Reference		
	II+ID	81	42 (84)	1.23 (0.49-3.04)	0.652	
	HWE-p	0.155	0.334			
	MAF	39.5	44			
NOS3 VNTR	I	121 (60.5)	56 (56)	Reference		
	D	79 (39.5)	44 (44)	1.20 (0.74-1.95)	0.455	
	bb	75 (75)	31 (62)	Reference		
	ba	21 (21)	16 (32)	1.84 (0.85-3.99)	0.118	
	aa	4 (4)	3 (6)	1.81 (0.38-8.58)	0.446	
	ba+aa	25 (25)	19 (38)	1.83 (0.88-3.81)	0.099	0.256
	aa	4 (4)	3 (6)	Reference		
	bb+ba	96 (96)	47 (94)	0.65 (0.140-3.03)	0.584	
HWE-p	0.125	0.632				
MAF	14.5	22				
	a	171 (85.5)	78 (78)	Reference		
	b	29 (14.5)	22 (22)	1.66 (0.89-3.07)	0.103	

* χ^2 p value. OR: odds ratio; CI: confidence interval.

model ($P=0.455$) did not differ significantly between the groups. Similarly, there was no significant difference for the NOS3 VNTR genotypes between the control and case in genetic model (bb vs ba $P=0.118$; bb vs aa $P=0.446$), dominant model (bb vs ba+aa $P=0.099$) and allelic model (b vs a $P=0.103$).

Drug toxicity among kidney transplanted individuals and genotypes

The genotype distribution of ACE ID and NOS3 VNTR polymorphisms between the non-toxicity and toxicity

groups are presented in Table 2. There was no significant difference for ACE ID genotypes between the toxicity and non-toxicity groups in genetic (II vs ID OR=0.80,95% CI = (0.16-3.95); II vs DD OR=0.52,95% CI = (0.04-6.09)), dominant (II vs ID +DD OR=0.73,95% CI = (0.15-3.45)) and allelic models (I vs D OR=0.77, 95% CI = (0.27-2.19)) (Table 2). Furthermore, the other studied NOS3 VNTR polymorphisms also revealed the absence of significant association between the non-toxicity and toxicity groups in genetic ($P=0.703$), dominant ($P=0.75$) and allelic models ($P=0.546$) (Table 2). These results suggest that

Table 2. Association between toxicity and non-toxicity among the kidney transplantation patients

Gene	Genotypes	No Toxicity	Toxicity	OR (95% CI)	P value df=1	P value df=2
		n=41 (%)	n=9 (%)			
ACE ID	II	11 (26.8)	3 (33.3)	Reference		
	ID	23 (56.1)	5 (55.5)	0.80 (0.16-3.95)	0.781	
	DD	7 (17.0)	1 (11.1)	0.52 (0.04-6.09)	0.601	
	ID+DD	30 (73.1)	6 (66.6)	0.73 (0.15-3.45)	0.693	0.871
	I	45 (54.9)	11 (61.1)	Reference		
	D	37 (45.1)	7 (38.9)	0.77 (0.27-2.19)	0.629	
NOS3 VNTR	bb	25 (60.9)	6 (66.6)	Reference		
	ba	13 (31.7)	3 (33.3)	0.96 (0.20-4.48)	0.96	
	aa	3 (7.3)	0 (0)			0.703
	ba+aa	16 (39.0)	3 (33.3)	0.78 (0.17-3.57)	0.75	
	b	63 (76.8)	15 (83.3)	Reference		
	a	19 (23.2)	3 (16.7)	0.66 (0.17-2.53)	0.546	

both ACE ID and NOS3 VNTR polymorphisms were are not susceptible genes for drug toxicity among the kidney transplanted patients treated with tacrolimus.

Effect of ACE ID and NOS3 VNTR genetic polymorphisms on tacrolimus daily requirements and concentration/dose ratio

The distribution of ACE ID and NOS3 VNTR polymorphisms between the tacrolimus daily dose and concentration dose ratio of renal transplant patients is documented in Table 3. The daily dose required for II genotype was more than the other ID and DD genotype. Contradictory to this, the concentration dose ratio was more for DD genotype compared to other II and ID genotypes. However, there was no significant association between daily dose ($P=0.910$) and concentration dose ratio ($P=0.461$). For NOS 3 VNTR polymorphisms, a high dose is required for aa genotype when compared to bb and ba. However, the concentration dose ratio for bb is very high when compared to the ba and aa. However, no significant difference was observed for daily dose ($P=0.515$) and concentration dose ratio ($P=0.884$; Table 3).

Discussion

Genetic polymorphisms regulating RAAS, in organ transplant recipients might affect kidney function as independent factor (18). In the present study, the association between ACE I/D, NOS3 VNTR gene polymorphisms and kidney transplant patients treated with tacrolimus was analyzed. There was no significant association between the cases and the controls as well as toxicity and non-toxicity groups.

Several studies have investigated the relationship between ACE I/D gene polymorphism and patient survival after kidney transplantation. However, these studies have yielded inconclusive results. In a genome-wide association study, O'Brien et al recognized two variants which had genome-wide significance for long-term graft survival and allograft function in kidney transplant recipients (19). Another study by Akcay et al suggested the DD variant of the ACE gene polymorphism might be associated with increased risk of developing chronic allograft dysfunction (20). A very recent meta-analysis study also

observed the significant association between allograft rejections, allograft function and ACEI/D polymorphism. Furthermore, they suggested that the early identification of ACE I/D genotype can significantly improve the outcome of patients(3). Similarly, the other meta-analysis also revealed that the ACE D allele and DD genotype to be associated with renal allograft survival after renal transplantation (21). In contradictory to this study, Azmandian et al in 2015 found that donor and recipient ACE-DD genotype might not be a risk factor for acute renal allograft rejection. Similarly, the present study also revealed the absence of significant association between cases and controls.

Several studies have discussed the role of nitric oxide and allograft rejection in liver, heart, kidney, and pancreatic islet cell transplant (22-25). Further studies have also proved a significant increase in serum NO levels during episodes of rejection in renal transplant recipients (24,26). Furthermore, in the past decades, several association studies were conducted between the NOS3 gene polymorphisms and chronic allograft nephropathy. Yilmaz et al in 2009 (14) and Viklicky et al in 2002 (27) studied G894T polymorphisms of NOS3 gene and revealed its influence is long-term renal allograft outcome and did not consider it as a risk factor for chronic allograft failure. In 2005 Sezer et al found that bb allele of the NOS3 gene was associated with an anti-inflammatory state and may predict renal outcome in transplant patients(28). Variant eNOS gene polymorphism, which produced decreased eNOS activity, was linked to worse remote graft function (29). Azarpira et al in 2013 revealed that the NOS 3 gene polymorphisms did not alter the risk of acute rejection after a renal transplant (13). Similarly, another study also found the absence of association between NOS3 gene and chronic renal transplant dysfunction (20). Even the current study results were also being in accordance with previous reports.

ACE, which is a key enzyme in the RAS system, catalyzes the conversion of angiotensin I to II in the liver and kidney. Evidence suggests that polymorphisms of the ACE gene may play an important role in pharmacokinetics and pharmacodynamics of tacrolimus (30). However, studies conducted on the association between ACE gene polymorphisms and renal dysfunction in adult recipients

Table 3. The effect of ACE ID and NOS3 VNTR genetic polymorphisms on tacrolimus daily requirements and concentration/ dose ratio at 3 month post-transplantation

Genotype	Daily Dose (mg/kg/d)	P value	Concentration dose ratio (ng/mL)/(mg/kg/d)	P value
	Mean \pm SD		Mean \pm SD	
ACE II	2.71 \pm 8.3		3.20 \pm 1.62	
ID	2.75 \pm 1.04		3.27 \pm 1.87	
DD	2.57 \pm 0.98	0.910	4.27 \pm 3.0	0.461
NOS3 bb	2.74 \pm 0.96		3.38 \pm 2.36	
ba	2.63 \pm 1.02		3.40 \pm 1.32	
aa	3.33 \pm 0.58	0.515	2.78 \pm 0.76	0.884

who received tacrolimus yielded inconsistent results. Chen et al study in the Chinese population where 90 consecutive de novo liver graft recipients who underwent living-donor liver transplantation were studied revealed the absence of significant association between its genotypes and the disposition of tacrolimus (31). Another study on post-transplantation diabetes mellitus in Korean kidney transplanted individuals also showed the absence of significant association between ACE polymorphisms and tacrolimus, however, the effect of AGT polymorphisms on post-transplantation diabetes mellitus remained significant (32). However, a study from cosmopolitan city in south India revealed the DD genotype and D allele of ACE gene polymorphism to be associated with post-transplantation diabetes mellitus (33). The present study, though from the south Indian population, failed to observe such association between tacrolimus dose or concentration and post-renal transplantation patients.

Conclusion

In conclusion, the present study revealed the absence of a significant association between cases and controls as well as toxicity and non-toxicity groups. Furthermore, the association between genotypes and daily dose and dose concentration was also not observed. However, further studies are warranted with large number of patients to find the proper impact of genetic polymorphisms on tacrolimus.

Limitations of the study

The main limitations of this study were the retrospective design from a single center and a limited number of patients. Further, the confounding effect of that which may have affected tacrolimus pharmacokinetics was not examined. Finally, the data of the donor individuals were not collected for comparisons.

Acknowledgments

The authors would like to thank Sri Ramachandra Institute of Higher Education and Research for providing necessary facilities and the subjects.

Authors' contribution

RE; the concept, design, manuscript preparation and final revision. KK & SS; performing experiments and data collection and writing proposal. GR; statistical analysis, manuscript editing, and manuscript review. SFDP; genetic data analysis, experiment design. JM; data collection and manuscript editing.

Conflicts of interest

The authors declare that they have no conflicts of interest.

Ethical considerations

Ethical issues (including plagiarism, data fabrication,

double publication) have been completely observed by the authors.

Funding/Support

None.

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