CYP3A5 polymorphisms and their effects on tacrolimus exposure in an ethnically diverse South African renal transplant population

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Background. Tacrolimus forms the cornerstone for immunosuppression in solid-organ transplantation. It has a narrow therapeutic window with wide inter- and intra-patient variability (IPV). Cytochrome P-450 3A5 (CYP3A5) is the main enzyme involved in tacrolimus metabolism, and rs776746A>G is the most frequently studied polymorphism in the *CYP3A5* gene. The rs776746A>G (i.e. *CYP3A5*3*) single-nucleotide polymorphism in *CYP3A5* alters tacrolimus predose trough concentration (C_0) and may also affect IPV, which may lead to immune- and/or drug-mediated allograft injury. *CYP3A5*3* may result in absent (**3/*3*), partial (**1/*3*) or normal (**1/*1*) *CYP3A5* expression. The effect of *CYP3A5*3* on tacrolimus exposure and variability has not been examined in South African (SA) transplant recipients.

Objectives. To determine the frequencies and effect of *CYP3A5* and adenosine triphosphate-binding cassette subfamily B member 1 (*ABCB1*) polymorphisms on tacrolimus C_0/dose ratios in different ethnic groups attending a tertiary renal transplant clinic in SA, and other factors that may explain inter- and IPV in tacrolimus C_0.

Methods. All consenting stable renal transplant recipients on tacrolimus at the Livingstone Hospital Renal Unit in Port Elizabeth, SA, were included. Tacrolimus concentrations were obtained using a microparticle enzyme immunoassay method (ARCHITECT analyser, Abbott Laboratories). Polymerase chain reaction/restriction fragment length polymorphism was used to genotype for *CYP3A5*3* and **6* allelic variants.

Results. There were 43 participants (35% black African, 44% mixed ancestry and 21% white), with a mean age of 44.5 years, median duration post-transplant of 47 months and median (interquartile range) creatinine and estimated glomerular filtration rate levels of 118 (92 - 140) µmol/L and 62 (49 - 76) mL/min at study inclusion. The mean tacrolimus C_0 in the study was 6.7 ng/mL, with no difference across the different ethnic groups. However, the mean total daily dose of tacrolimus required was 9.1 mg (0.12 mg/kg), 7.2 mg (0.09 mg/kg) and 4.3 mg (0.06 mg/kg) in black, mixed-ancestry and white patients, respectively (p=0.017). The frequencies for *CYP3A5* expressors (i.e. *CYP3A5*1/*1 + CYP3A5*1/*3* genotypes) were 72%, 100%, 76% and 12% for all patients combined and black, mixed-ancestry and white patients, respectively. The frequencies for *CYP3A5* non-expressors (i.e. *CYP3A5*3/*3* genotypes) were 0%, 24% and 88% among the black, mixed-ancestry and white patients, respectively. None of the patients carried the *CYP3A5*6* allele. *CYP3A5*1/*1* and *CYP3A5*1/*3* genotype carriers required a two-fold increase in dose compared with the non-expressor genotype carriers, *CYP3A5*3/*3* (p<0.05). *CYP3A5*3/*3* carriers also demonstrated higher IPV than *CYP3A5*1/*1* and **1/*3* carriers (18.1% v. 14.2%; p=0.125).

Conclusions. Compared with global transplant populations, SA renal transplant recipients demonstrated a very high rate of *CYP3A5* expression, with a significant impact on tacrolimus pharmacokinetics. Genetic variation in *CYP3A5* expression affects tacrolimus dosing requirements, and knowing the *CYP3A5* genotype of transplant patients may allow better dose prediction compared with current standard dosing recommendations in a multi-ethnic population. Overall, black African patients required higher doses of tacrolimus than their white counterparts. While further prospective studies are needed to better evaluate dosing algorithms, it would appear that the starting dose of tacrolimus should be higher in black and mixed-race patients.

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Tacrolimus is a calcineurin inhibitor frequently used in transplantation to prevent allograft rejection.[1,2] Its use has been associated with improved graft survival, and it currently forms the cornerstone of immunosuppressive therapy in solid-organ transplantation.[3] There is a shortage of donors, especially cadaveric donors, on an international and local level. Maintaining graft function is therefore of the utmost importance to protect a limited resource in medicine.[4,5]

Tacrolimus has a narrow therapeutic window and wide pharmacokinetic variability in transplant recipients.[1,6,7] In clinical practice, this translates into marked inter- and intra-patient variability (IPV) in measured tacrolimus predose trough concentrations (C_0),

which makes selection of the appropriate dose difficult for transplant physicians.[1] Tacrolimus IPV, which is defined as fluctuations of measured tacrolimus C_0 in an individual over a given period of time, is an independent predictor for worsening graft function.[8,9] Variability in tacrolimus C_0 may result in subtherapeutic levels, leading to inferior graft outcomes from immune-mediated allograft injury with allograft rejection.[10] On the other hand, high tacrolimus C_0 may also lead to an adverse side-effect profile and renal toxicity.[11,12]

While various non-pharmacogenetic factors such as poor adherence, high-fat meals, grapefruit intake, drug-drug interactions and circadian rhythms may explain some of this variability,[1,13] much attention has been given in the past two decades to pharmacogenomics and the cytochrome pathway.[14] Tacrolimus is predominantly a substrate for metabolism by cytochrome P-450 3A5 (CYP3A5) and is dependent on cellular transport by P-glycoprotein (P-gp), coded for by the adenosine triphosphate (ATP)-binding cassette subfamily B member 1 (*ABCB1*) gene. Single-nucleotide polymorphisms (SNPs) in the *CYP3A5*, *CYP3A4* and *ABCB1* genes affect tacrolimus C_0 and the dose required through variability in metabolism and absorption, respectively.[15,16]

The CYP450 enzymes are membrane-bound proteins found in the endoplasmic reticulum that facilitate metabolism of a wide variety of drugs.[1] CYP3A5 is the major enzyme involved in the metabolism of tacrolimus, while CYP3A4 plays a minor role.[17,18] The rs776746A>G (i.e. *CYP3A5*3*) SNP in *CYP3A5* abolishes CYP3A5 enzyme activity and has been reported to alter tacrolimus C_0. *CYP3A5* may result in absent (**3/*3*), partial (**1/*3*) or normal (**1/*1*) CYP3A5 expression.[15-17] A second allele (*CYP3A5*6*) resulting from a splicing variant at 14690G>A also produces a non-functional CYP3A5 enzyme.[1,18]

Transplant recipients with normal or partial expression of CYP3A5 require higher tacrolimus doses than non-expressors to achieve similar therapeutic tacrolimus C_0.[15,17,19] Other enzymes may also influence inter- and IPV in tacrolimus dosing, namely P450 oxidoreductase (POR), nuclear receptor perioxisome proliferator-activated receptor alpha (PPAR-α) and CYP2C8.[1,19]

The *ABCB1* gene encodes P-gp, which functions as an ATP-dependent efflux pump that protects intestinal cells from harmful substances. The absorption of certain drugs from the gut is therefore inversely proportional to P-gp expression. Polymorphisms in *ABCB1* alter expression of P-gp, which in turn can affect tacrolimus C_0 by altering drug absorption from the intestine. An SNP in exon 26 (3435 C>T) in the *ABCB1* gene has been widely studied for its effects on many drugs.[1,16,20] The *ABCB1* 3435T allele is associated with reduced expression of *ABCB1*.[20,21] The role of SNPs in *ABCB1* on tacrolimus C_0 and dosing is currently controversial, and several studies have shown conflicting results pointing towards a minor role.[15,19,22]

Objectives

The frequencies of SNPs of *CYP3A5* and *ABCB1* and their effect on tacrolimus C_0/dose ratios have been described internationally, but not in South African (SA) renal transplant recipients.[15,23-25] We therefore set out to determine the frequencies and effect of *CYP3A5* and *ABCB1* polymorphisms on tacrolimus C_0/dose ratios in different ethnic groups attending a tertiary renal transplant clinic at Livingstone Hospital, Port Elizabeth, SA, and to determine other factors that may explain inter- and IPV in tacrolimus C_0.

Methods

Study participants and sample collection

A cohort of stable renal transplant recipients at least 12 months post transplant was invited to participate in the study. Stable was defined as having had no major intercurrent illness during the preceding 12 months. Ethics approval for genetic testing was obtained from the Walter Sisulu University Ethics Committee (ref. no. 017/2016). The study was a retrospective cohort study, and information was obtained from four quarterly periods prior to the inclusion date. Data were collected on relevant demographic and clinical measures. Self-reported ethnicity was included in our data collection tool and categorised as black African, mixed ancestry and white.

All consenting patients aged >18 years who were using tacrolimus as part of their immunosuppression were included. Five millilitres of venous whole blood was taken in ethylenediaminetetra-acetic acid-containing blood tubes and stored at –20ºC. Repeated tacrolimus C_0 and dosages were obtained retrospectively from case notes. Data collected included body weight, age, level of education, type of immunosuppression used, perceived medication adherence, type of transplant, months post-transplant, ethnicity (self-reported) and the aetiology of chronic kidney disease. Five recipients who were positive for HIV were excluded from the study because of potential drug interactions. Two other patients were excluded because they were also using medications known to affect tacrolimus C_0, such as antifungal agents, rifampicin, verapamil, macrolide antibiotics and antiepileptics.

Analytical methods

Tacrolimus C_0 (ng/mL) was obtained by means of a microparticle enzyme immunoassay method using the ARCHITECT analyser (Abbott Laboratories, USA). DNA was extracted using the QIAamp DNA Mini Kit (Qiagen, Germany), following the manufacturer's instructions. Polymerase chain reaction (PCR)-restriction fragment length polymorphism (RFLP) was used to genotype *CYP3A5*3* and **6* and *ABCB1*. Each PCR reaction contained the following reagents: 0.40 μM of each of the forward and reverse primers (Inqaba Biotechnical Industries, SA), 100 ng of genomic DNA, 1 × Green GoTaq Flexi Reaction Buffer (Promega, USA), 0.2 mM deoxyribonucleotide triphosphate (Promega), 2.5 mM magnesium chloride (Promega) and 0.5 U GoTaq Flexi DNA Polymerase (Promega), and was made up to a volume of 25 μL with sterile deionised water.

PCR and RFLP conditions are summarised in Table 1.

Statistical analysis

Categorical variables were summarised as frequencies and percentages. Continuous variables were summarised as means and standard deviations (SDs). Student's *t*-test or analysis of variance was used to compare continuous tacrolimus measures (dosage, level and C_0 dose/kg) variables between two groups and three groups, respectively. Linear mixed-effects models were used to analyse the change in repeated variables (tacrolimus dose, C_0/dose, creatinine and estimated glomerular filtration rate (eGFR)) associated with increasing time. IPV in tacrolimus was expressed as a coefficient of variation using the following formula: $CV\% = (\sigma/\mu) \times 100$

A p-value <0.05 was considered statistically significant. Statistical analysis was carried out using Stata statistical software, version 15.1 (StataCorp, USA).

Results

Study participants

There were 43 study participants, of whom 18 (42%) received a kidney from a related living donor, with the rest receiving cadaveric transplants. All the patients were stable during the study period with no major illnesses reported. Baseline demographics and clinical characteristics are shown in Table 2. All the participants were non-

Table 1. List of primers and polymerase chain reaction cycling conditions for mutation detection

SNP	Primer (5′ - 3′)	T_a, ext	Thermal cycling conditions	Restriction enzyme
*CYP3A5*3*	F: CATCAGTTAGTAGACAGATGA	51°C, 30 s	94°C, 3 min	SspI,
	R: GGTCCAAACAGGGAAGAAATA		94°C, 30 s	12 - 16 h
			51 °C, 30 s	
			72 °C, 30 s	
			72°C, 10 min	
*CYP3A5*6*	F: GTGGGGTGTTGAZAGCTAAAG	55°C, 30 s	94°C, 3 min	DdeI,
	R: TGGAAGATGATTCAGCAGATAGT		94°C, 30 s	12 - 16 h
			55 °C, 30 s	
			72 °C, 1 min	
			72°C, 10 min	
ABCB1 (1236 C>T)	F: ACTCTTGTTTTCAGCTGCTTG	54°C, 30 s	94°C, 3 min	MboI,
	R: GAGTCACTGCCTAATGTAAGTCTCT		94°C,30 s	12 - 16 h
			54 °C, 30 s	
			72 °C, 50 s	
			72°C, 10 min	

SNP = single-nucleotide polymorphism; *CYP3A5* = cytochrome P-450 3A5 gene; *ABCB1* = adenosine triphosphate-binding cassette subfamily B member 1 gene; F = forward primer; R = reverse primer; T_a = annealing temperature; ext = extension time.

Table 2. Baseline demographics and clinical characteristics of the population studied (*N*=43)

Characteristic	
Age (years), mean (SD)	45 (12)
Males, *n* (%)	25 (58)
Cadaveric transplants, *n* (%)	25 (58)
Living related donor transplants, *n* (%)	18 (42)
Months post transplant, median (IQR)	47 (24 - 110)
Indication for transplant, *n* (%)	
Hypertension	23 (54)
ADPKD	6 (14)
Glomerulonephritis	5 (12)
CAKUT	4 (9)
Diabetic nephropathy	1 (2)
Other*	4 (9)
Weight (kg), mean (SD)	75 (14)
Ethnicity, *n* (%)	
Black African	15 (35)
Mixed ancestry	19 (44)
White	9 (21)
HIV status negative, *n* (%)	43 (100)
Baseline immunosuppression, *n* (%)	
Prednisone	43 (100)
Azathioprine	10 (23)
MMF	30 (70)
Tacrolimus	43 (100)
NODAT, *n* (%)	13 (30)
Males	10 (77)
Females	3 (23)

SD = standard deviation; IQR = interquartile range; ADPKD = autosomal dominant polycystic kidney disease; CAKUT = congenital abnormalities of the kidney and urinary tract; MMF = mycophenolate mofetil; NODAT = new-onset diabetes after transplantation.
*Includes acute tubular necrosis, urological strictures and unknown causes.

smokers. Self-reported ethnic groups were black African (*n*=15), mixed ancestry (*n*=19) and white (*n*=9).

New-onset diabetes after transplantation (NODAT) was more common in males, with a prevalence of 10/13 (77%) v. 23% in females. Patients with NODAT had a higher mean serum creatinine level than those without NODAT (132 μmol/L v. 117 μmol/L; *p*=0.253) and were more likely to have autosomal dominant polycystic kidney disease (ADPKD), with NODAT developing in 67% of those with ADPKD v. 24% of the others.

Indication for transplantation

Hypertension (54%) was the leading indication for transplantation, followed by ADPKD (14%), glomerulonephritis (12%) and congenital abnormalities of the kidney and urinary tract (9%). Other causes included acute tubular necrosis, urological strictures and unknown aetiologies.

Tacrolimus dose and C_0 over the study period

Table 3 shows the mean tacrolimus C_0 and dosing requirements during the study period. Mean tacrolimus C_0 (6.7 ng/mL) and dose (7.3 mg/d) did not change significantly over the study period. The mean (SD) creatinine level was 121.5 (39) μmol/L, with an absolute increase over the study period of 8.9 μmol/L (*p*=0.004). The mean (SD) eGFR was 62 (18) mL/min/1.72 m^2 and remained unchanged over the study period (*p*=0.616).

Table 4 shows the frequency and distribution of genotypes across ethnic groups. Among those who could be genotyped (39 of the 43 participants), homozygous *CYP3A5*1/*1* frequency was highest in black Africans (64%), followed by patients of mixed ancestry (41%), while the genotype was not observed among white patients; the inverse was true for the non-expressor *CYP3A5*3/*3* genotype, with frequencies of 0%, 24% and 88% among black Africans, patients of mixed ancestry and whites, respectively. Overall, 72% of the study population were *CYP3A5* expressors (*CYP3A5*1/*1* + **1/*3*). *CYP3A5*6* was not observed in the study population.

The *ABCB1* 3435C>T SNP genotypes also showed differences among the different race groups, with the exception that the T/T genotype appeared less frequently in black Africans (0%) than in patients of mixed ancestry (11%) and whites (33%). Two participants could not have the *ABCB1* gene typed.

Effect of ethnicity on tacrolimus C_0 and dose

The mean (SD) tacrolimus dose for each ethnic group was as follows: black African 9.1 (4.2) mg, mixed ancestry 7.2 (4.1) mg, and white 4.3 (2.2) mg (Table 5). This translates into a weight-based

Table 3. Patient pharmacokinetic and clinical characteristics during the study period, by quarter

Characteristic	Q1	Q2	Q3	Q4	Mean	Coefficient	95% CI	*p*-value*
Tacro dose (mg/d), mean (SD)	7.2 (4.2)	7.3 (4.2)	7.3 (4.2)	7.3 (4.2)	7.3 (4.1)	–0.028	–0.068 - 0.0126	0.177
Tacro C_0 (ng/mL), mean (SD)	6.6 (1.4)	6.7 (1.5)	6.5(1.5)	6.9 (1.7)	6.7(1.2)	–0.057	–0.209 - 0.094	0.459
Tacro C_0/dose (ng.mL^{-1}/mg)	0.92	0.92	0.89	0.95	0.92			
Tacro C_0/dose (ng.mL^{-1}/mg.kg^{-1}) (SD)	98 (68)	99 (77)	96 (75)	106 (86)	100 (75)	–2.281	–5.192 - 0.6300	0.125
Creatinine (μmol/L), median (IQR)	117.8 (35.4)	119.7 (35.9)	122.7 (40.5)	126.7 (51.5)	121.51 (39.0)	–3.082	–5.200 - –0.964	0.004
eGFR (mL/min/1.72 m^2), median (IQR)	62 (18)	62 (22)	62 (19)	60 (189)	62 (18)	0.266	–0.775 - 1.308	0.616

Q = quarter; Tacro = tacrolimus; CI = confidence interval; SD = standard deviation; C_0 = predose trough concentration; IQR = interquartile range; eGFR = estimated glomerular filtration rate.
*p<0.05 indicates significant change in repeated measures over time.

Table 4. Frequency and distribution of genotypes across ethnic groups

Genotype	Total (*N*=43)	Black African (*N*=15)	Mixed ancestry (*N*=19)	White (*N*=9)
CYP3A5, *n* (%)*				
**1/*1* (AA)	16 (41)	9 (64)	7 (41)	0
**1/*3* (AG)	12 (31)	5 (36)	6 (35)	1 (12)
**3/*3* (GG)	11 (28)	0	4 (24)	7 (88)
N/R	4	1	2	1
ABCB1, *n* (%)*				
C/C	23 (56)	10 (71)	9 (50)	4 (44)
C/T	13 (32)	4 (29)	7 (39)	2 (22)
T/T	5 (12)	0	2 (11)	3 (33)
N/R	2	1	1	0

CYP3A5 = cytochrome P-450 3A5 gene; *ABCB1* = adenosine triphosphate-binding cassette subfamily B member 1 gene; N/R = no result.
**CYP3A5* and *ABCB1* carrier frequency was determined only for those patients who could be genotyped.

Table 5. Effect of ethnicity on tacrolimus C_0 and dose

Clinical characteristics	Race	Q1	Q2	Q3	Q4	*p*-value	Mean (SD)
Tacrolimus dose (mg), mean (SD)	Black African	8.9 (3.6)	9.2 (4.2)	9.2 (4.2)	9.2 (4.2)	0.171	9.1 (4.1)
	Mixed ancestry	7.2 (4.1)	7.2 (4.1)	7.2 (4.1)	7.2 (4.1)	*	7.2 (4.1)
	White	4.3 (2.2)	4.3 (2.2)	4.3 (2.2)	4.3 (2.2)	*	4.3 (2.2)
	p-value	0.017	0.017	0.017	0.016		0.017
Tacrolimus C_0 (ng/mL), mean (SD)	Black African	7.0 (1.8)	6.8 (1.6)	7.1 (1.4)	6.8 (1.5)	0.998	6.9 (1.6)
	Mixed ancestry	6.7 (1.5)	6.3 (1.5)	6.5 (1.6)	6.5 (1.4)	0.708	6.5 (1.5)
	White	7.1 (2.2)	6.1 (1.3)	6.1 (1.6)	6.4 (1.3)	0.376	6.5 (1.6)
	p-value	0.890	0.524	0.300	0.770		0.519

C_0 = predose trough concentration; Q = quarter; SD = standard deviation.
*Statistical testing not justified owing to lack of change in repeated measures over time.

Table 6. Effects of polymorphisms in *CYP3A5* and *ABCB1* on tacrolimus C_0

		Tacrolimus C_0 (ng/mL), mean (SD)					
Genotype	Allelic status	Q1	Q2	Q3	Q4	Mean	*p*-value
*CYP3A5*1/*1*	A/A	6.3 (0.8)	6.5 (1.7)	6.5 (1.7)	6.53 (1.5)	6.5 (1.3)	0.783
*CYP3A5*1/*3*	G/A	7.0 (1.5)	6.8 (1.6)	6.5 (1.2)	7.3 (2.1)	6.9 (1.6)	0.669
*CYP3A5*3/*3*	G/G	6.2 (1.2)	6.3 (1.4)	6.2 (1.3)	6.7 (1.4)	6.4 (1.3)	0.263
ABCB1	C/C	6.5 (1.1)	6.5 (1.4)	6.6 (1.6)	7.0 (1.7)	6.7 (1.4)	0.181
	C/T	6.6 (1.6)	6.6 (1.3)	5.9 (1.1)	6.9 (1.9)	6.5 (1.5)	0.877
	T/T	7.5 (2.0)	7.7 (2.7)	7.3 (1.6)	6.7 (1.6)	7.3 (2.0)	0.297

C_0 = predose trough concentration; Q = quarter; *CYP3A5* = cytochrome P-450 3A5 gene; *ABCB1* = adenosine triphosphate-binding cassette subfamily B member 1 gene.

dose for black, mixed-ancestry and white study participants of 0.12, 0.09 and 0.06 mg/kg, respectively, which differed significantly between ethnic groups (p=0.017). Overall, there was no significant change in tacrolimus C_0 over time when observed in each ethnic group.

Effect of genotype on tacrolimus C_0

Table 6 shows the effect of *CYP3A5* and *ABCB1* SNPs on tacrolimus C_0 over the four quarters during the study period. Overall, there was no significant change in tacrolimus C_0 over time when analysed per genotype.

Effect of genotype on tacrolimus dose requirements

The distribution of *CYP3A5* expressor status (i.e. *CYP3A5*1/*1* + **1/*3*) in patients who could be genotyped was 100%, 75% and 12.5% among black African, mixed-ancestry and white participants, respectively. *CYP3A5*1/*1* and *CYP3A5*1/*3* genotypes were associated with a two-fold increase in required tacrolimus dose ($p<0.05$). The mean (SD) total daily dose per genotype was 9 (0.12) mg/kg, 5 (0.07) mg/kg and 3 (0.04) mg/kg for *CYP3A5*1/*1, *1/*3* and **3/*3*, respectively.

CYP3A5 genotypes had mean (SD) C_0/dose ratios of 54 (16), 95 (57) and 170 (94) for *CYP3A5*1/*1*, **1/*3* and **3/*3*, respectively ($p<0.001$). The C_0/dose ratio per *CYP3A5* genotype over time can be seen in Fig. 1. *ABCB1* genotypes had the following C_0/dose ratios (mean (SD)): 78 (53) for C/C, 142 (104) for C/T and 103 (66) for T/T ($p=0.015$ for C/C v. C/T and $p=0.347$ for C/C v. T/T). The mean (SD) total daily dose per *ABCB1* genotype was 6 (0.09) mg/kg, 3 (0.05) mg/kg and 5 (0.07) mg/kg for C/C, C/T and T/T, respectively.

Fig. 1 demonstrates the C_0/dose for tacrolimus by genotype during the study period, while Figs 2 and 3 demonstrate the effect of *CYP3A5* and *ABCB1* genotype on tacrolimus C_0/dose ratios per participant, respectively.

IPV during the study period

Tacrolimus C_0 varied among individual transplant recipients. Fig. 4 shows tacrolimus levels for each individual in the cohort over the four study quarters.

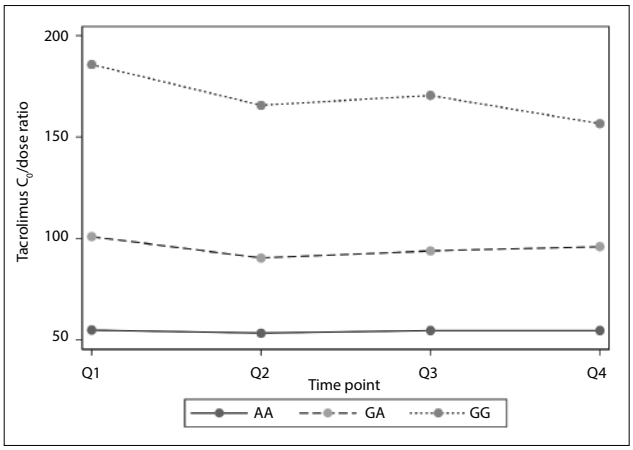

Fig. 1. Effect of CYP3A5 *on C_0/dose ratio during study period. (*CYP3A5 *= cytochrome P-450 3A5 gene; C_0 = predose trough concentration; Q = quarter.)*

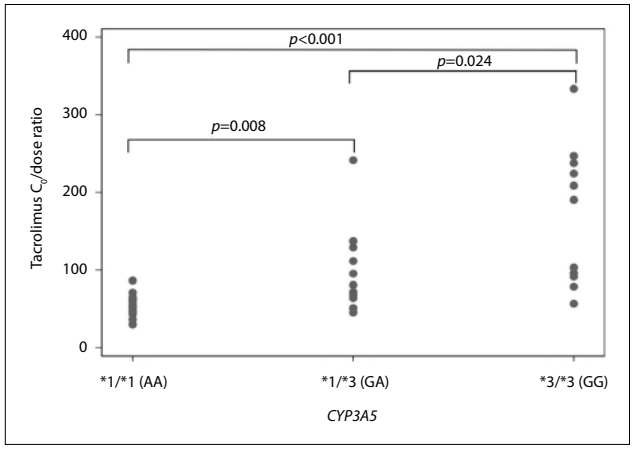

Fig. 2. Effect of CYP3A5 *on tacrolimus C_0/dose ratio in the study population. (*CYP3A5 *= cytochrome P-450 3A5 gene; C_0 = predose trough concentration.)*

Fig. 5 shows the distribution of tacrolimus IPV in the study cohort during the study period. Figs 6 and 7 show IPV by genotype and ethnicity, respectively. IPV was divided into two groups using the median (interquartile range) IPV of 14.4% (10.5 - 19.0) as a cut-

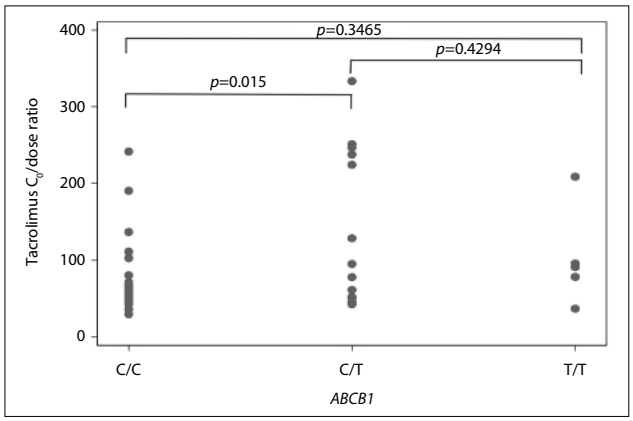

Fig. 3. Effect of ABCB1 *on tacrolimus C_0/dose ratio. (*ABCB1 *= ATP-binding cassette subfamily B member 1 gene; C_0 = predose trough concentration.)*

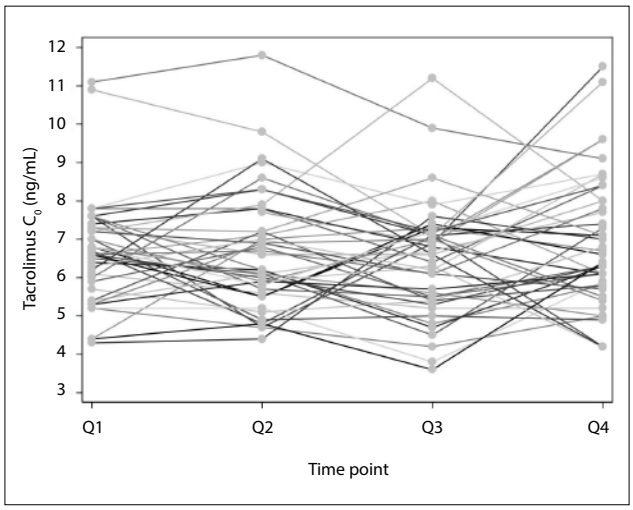

Fig. 4. Tacrolimus C_0 per patient over the study period. (C_0 = predose trough concentration; Q = quarter.)

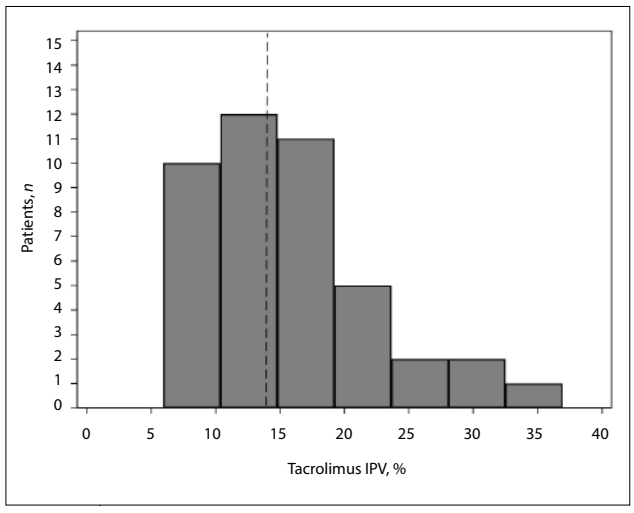

*Fig. 5. Tacrolimus IPV among study participants over the study period (*N*=39). The median (14.4%) is shown by the dotted line. (IPV = intra-patient variability.)*

off. IPV ≥14.4% was classified as high and <14.4% as low. *CYP3A5* expressors *(*1/*1 + *1/*3*, *n*=28) had a lower IPV than *CYP3A5* non-expressors *(*3/*3*, *n*=11) with a mean (SD) IPV of 14.2% (6.6) v. 18.1% (7.5), respectively (*p*=0.125). Similarly, white participants had a higher IPV than those of black African and mixed ancestry (*p*=0.041). Creatinine did not differ between high- and low-IPV groups (*p*=0.757).

Discussion

This was an observational study examining tacrolimus C_0 in stable renal transplant recipients attending a transplant clinic in Port Elizabeth, SA. Patients in the immediate post-transplant period were excluded because variations in tacrolimus levels often occur due to drug interactions such as high prednisone exposure, fluid shifts, and individual physician preferences to obtain therapeutic C_0.[9]

Over time, the mean tacrolimus C_0 and dose did not change among the different genotypes studied. There was a slight rise in serum creatinine over the study period, but eGFR remained unchanged.

In this cohort, *CYP3A5* expression varied markedly by ethnic group. Black African participants were much more likely to be *CYP3A5*1/*1* and **1/*3* carriers reflecting full or partial expression of *CYP3A5* compared with white participants. Conversely, no black African participant was a *CYP3A5* non-expressor (*CYP3A5*3/*3*), while 88% of white participants were homozygous *CYP3A5* non-expressors, with none having normal expression of *CYP3A5*. Black African participants required a 2.1-fold higher dose to maintain therapeutic tacrolimus C_0 compared with white participants. This is consistent with a previous study by Macphee *et al.*[14] Previous studies have also shown that white patients were more likely than black patients to present with *CYP3A5*3/*3* genotypes.[24,25] Haufroid *et al.*[23] also demonstrated an allele effect of *CYP3A5*1/*1*, with a 2.3-fold increase in daily dose requirements to maintain therapeutic tacrolimus C_0 compared with *CYP3A5*3/*3*.

The dose of tacrolimus required to achieve similar tacrolimus C_0 was clearly affected by *CYP3A5* genotype. Participants with the *CYP3A5*3/*3* non-expressor genotype achieved over three times the tacrolimus C_0/dose ratio compared with those with normal expression (*CYP3A5*1/*1*). Similarly, participants with the *CYP3A5*1/*1* genotype required a twofold increase in tacrolimus dose compared with those with the *CYP3A5*3/*3* genotype in order to maintain therapeutic tacrolimus C_0. This finding has major economic implications for SA, where until recently no cheaper generic formulations of tacrolimus have been available and where tacrolimus drug costs form a substantial part of the cost of transplantation.[4,26]

Participants of mixed ancestry had more variable expression of CYP3A5 than black Africans or whites. Black African and white ethnicity therefore appear to be a good proxy for CYP3A5 expression and non-expression, respectively, and could potentially allow reasonable prediction of dosing requirements in these population groups, while CYP3A5 genotyping could be reserved for patients of mixed ancestry, among whom there is a much wider spread in enzyme expression. Accurate prediction of dosing through this combination of ethnic profiling and genotyping could both be cost-effective and lead to improved graft outcomes by rapidly achieving appropriate tacrolimus C_0, although further prospective studies would be needed to confirm this. In a recently published randomised controlled trial of pharmacogenetic adaptation of the tacrolimus starting dose according to CYP3A5 expression, genotyping did not lead to a higher percentage of participants reaching the desired outcome compared with the standard weight-based dose, and did not improve clinical outcomes.[25] However, the ethnic distribution in that study was markedly skewed towards white patients (78%), among whom non-expressor status is much more common and likely to lessen the effect of pharmacogenetic adaptation. In our cohort, 72% of participants were CYP3A5 expressors or partial expressors. In another study, *CYP3A5*1/*1* genotype carriers were found to have more rejection episodes than heterozygous carriers (*CYP3A5*1/*3*) and homozygous non-expressor genotype carriers (*CYP3A5*3/*3*).[27] Studies with a more equal ethnic distribution are needed to further assess genotype-based dosing. Similar studies by Thervet *et al.*[28] and Shuker *et al.*[25] showed that genotype-based dosing was associated with fewer dose modifications and a shorter time to reach the target tacrolimus C_0. However, genotype-based dosing did not improve clinical outcomes.[25,28]

Black African participants predominantly expressed the *ABCB1* C/C and C/T genotypes, with no expression of the T/T genotype. However, overall expression of the *ABCB1* genotype was more evenly distributed among the different ethnic groups than that of *CYP3A5*, and there was no clear polarising effect of ethnicity on *ABCB1* expression. There was a decrease in the achieved tacrolimus C_0/dose ratio among participants carrying the C/C genotype compared with C/T and T/T. This is probably due to increased expression of P-gp, which reduces net absorption of tacrolimus at the intestinal level. These findings are also consistent with those of Helal *et al.*,[21] who demonstrated that participants expressing the C/C genotype had a lower tacrolimus C_0/dose ratio compared with other genotypes of *ABCB1*. Previous studies have not consistently demonstrated an effect of the *ABCB1* SNP on tacrolimus C_0/dosing.

Variability of tacrolimus C_0 strongly correlates with a negative effect on graft outcomes.[9,10] Studies have shown that a tacrolimus SD of C_0 of >2 is associated with increased late acute rejection, and that patients with higher IPV have a 1.4 times increased risk of allograft injury or rejection.[29] High variability in tacrolimus C_0 has also been shown to correlate with poorer overall graft function.[10,13,29,30] Although most of our study participants had therapeutic tacrolimus C_0, significant intra- and IPV was present in 14.4% (see Fig. 6). This is somewhat lower than the figure reported by Shuker *et al.*[13] in their large study of 808 renal transplant recipients, in which the median IPV was 16.2%, and may reflect the high proportion of *CYP3A5* expressors in our study (72%). In an excellent review of the subject,[13] these authors noted that CYP3A5 non-expression was associated with increased tacrolimus IPV in one small Korean study where the expressor genotype was present in 55% of the cohort,[31] but not in three larger studies,[29,32,33] where the prevalence of the CYP3A5 expressor genotype in the population studied was very much lower at between 9% and 45%. Similar to the Korean study, the prevalence of the CYP3A5 expressor genotype in our cohort was much higher at 72% and is comparable to the previously reported allele frequency of 85% in healthy SA black Africans.[34] The increase in IPV of tacrolimus C_0 in *CYP3A5* non-expressors has been postulated to be due to their increased reliance on CYP3A4 for tacrolimus metabolism and the fact that *CYP3A4* is more prone to induction and inhibition.[35] Similarly, CYP3A5 non-expressors were shown to be more prone to the inhibitory effects of fluconazole on tacrolimus metabolism owing to the fact that fluconazole relies predominantly on CYP3A4 for metabolism.[36] Knowing the *CYP3A5* expressor status of an individual therefore also has relevance in determining the risk of drug-drug interactions in transplant recipients, who not infrequently require treatment with drugs that interfere with CYP450 metabolism.

CYP3A5 SNPs only explain 40 - 50% of tacrolimus variability among patients.[1] Other factors such as food ingestion, type of assay used, diarrhoea, drug-drug interactions, haematocrit and compliance issues may also play a role.[13,24] Non-adherence to tacrolimus is

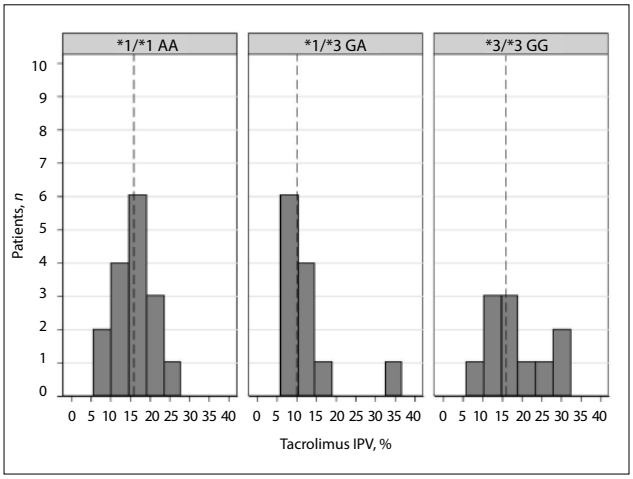

Fig. 6. Effect of the CYP3A5 *genotype on tacrolimus IPV. The median is shown by the dotted line. (*CYP3A5 *= cytochrome P-450 3A5 gene; IPV = intra-patient variability.)*

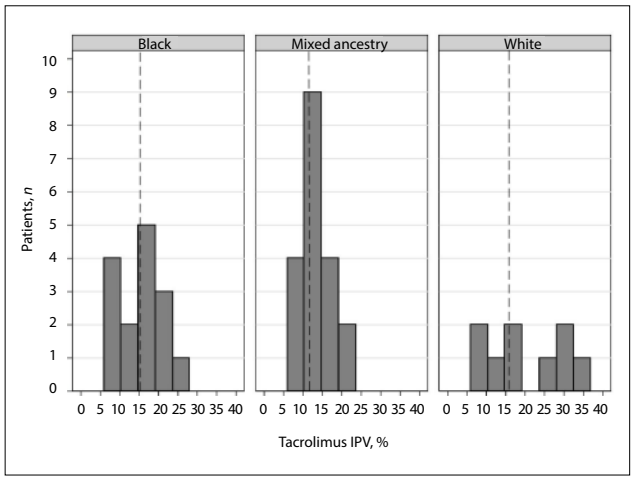

Fig. 7. Tacrolimus IPV for the different ethnic groups studied. The median is shown by the dotted line. (IPV = intra-patient variability.)

probably the most common reason for tacrolimus inter- and IPV. All our study participants reported good adherence during the 1-year study period, with non-adherence being assessed clinically if the tacrolimus C_0 fell out of the therapeutic range.

Study limitations

The present study has several limitations. The fact that it was conducted at a single centre and had a relatively small sample size compared with other studies may affect some aspects of the findings, and translation of our results may not be feasible for other centres. The duration of follow-up (1 year) was short compared with other studies, where durations were up to 10 years, and longer follow-up may further describe the gene effect on creatinine over time. Other enzymes that may explain tacrolimus variability, such as CYP2C8, POR and the nuclear receptor PPAR-α, were not investigated owing to cost limitations. Linkage disequilibrium may be present among genes. Gene interactions may play an important role, and further study is needed to assess this effect.

Conclusions

This study confirms the previously described effects of *CYP3A5* SNPs on tacrolimus C_0 and dosing requirements. Furthermore, it appears to support the notion that CYP3A5 non-expression may be associated with increased IPV in tacrolimus C_0. With the exception of patients of mixed ancestry, black African and white ethnicity should serve as a proxy for *CYP3A5* expression and non-expression, respectively, in SA patients, necessitating higher and lower starting doses of tacrolimus, respectively, prior to therapeutic drug level monitoring being available. While a genotype-based tacrolimus dosing algorithm could still be beneficial in predicting an appropriate starting or switching dose of tacrolimus in a multi-ethnic population such as ours, this could be restricted to patients of mixed ancestry in order to reduce costs. Finally, the high frequency of the *CYP3A5*1/*1* and **1/*3* expressor genotype has important cost implications for the provision of tacrolimus-based immunosuppression in SA. Since tacrolimus is also used in the treatment of various autoimmune diseases, this may well have wider applicability outside of transplantation medicine.

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Author contributions. WKM, lead investigator and MMed student: responsible for protocol development, data collection and write-up of thesis. RF, consultant nephrologist: supervisor for MMed project. Provided expert input with regard to kidney transplants and immunosuppression. CD, Professor of Pharmacogenomics, University of Cape Town: co-supervisor for MMed project. Provided expert input into pharmacogenomics including DNA extraction and genotyping of cytochrome enzymes. KM, statistician: provided expert input into statistical analysis of results obtained from the study. JE, consultant nephrologist: co-supervisor for MMed project. ZB, consultant nephrologist, University of Cape Town: expert opinion. DM, pharmacogenomics, University of Cape Town: assisted with DNA extraction and genotyping of blood samples.

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Conflicts of interest. None.

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