Identification of the Interleukin-6 Polymorphism (-174) in the Saliva of Hemodialysis Patients

ABSTRACT

Background: Chronic Kidney Disease is prevalent in the general population and is associated with high morbidity and mortality and its pathogenic mechanisms are related to pro-inflammatory cytokines, such as Interleukin 6 (IL-6). It is known that polymorphisms associated with IL-6 can trigger a different immune response in the individual and therefore be a determining factor in the progression of the disease. The idea of using saliva as an analysis matrix for diagnostic methods suggests that the methodology may be viable due to the easy way collection of these fluids and the amount of information in saliva molecular constituents.
Aims: To identify the relationship between IL-6 polymorphism (-174) in dialysis patients using saliva.
Methodology:40 individuals were assessed, divided into a test group: 24 on hemodialysis; and a control group: 16 healthy individuals. Saliva samples were collected, DNA was extracted, and genotyping was performed using Real Time-Polymerase Chain Reaction (RT-PCR).
Results: The genotype frequency identified was 6.2% GC, 81.2% GG and 12.6% CC for the test group and 33.3% GC, 62.5% GG and 4.2% CC (p=0.1054).
Conclusion: Given the results obtained, it is feasible to verify the presence of the IL-6 (-174) polymorphism in saliva, but it was not possible to correlate hemodialysis patients with the polymorphism studied.

Key words: *Interleukin-6; Chronic kidney disease; Polymorphism; IL-6 polymorphism*

1. INTRODUCTION

Chronic Kidney Disease (CKD) is defined as an abnormality of the structure or function of the kidneys, present for more than three months with implications for the health of individuals, and therefore comprises a myriad of kidney diseases with a wide range of clinical and morphological characteristics [1].

CKD is considered a public health problem around the world [2]. According to the latest Brazilian Dialysis Census (2022), the increase in the prevalence of hemodialysis patients (758 patients per million) was significant. The incidence, although lower than in 2021, remained high - 224 patients per million - especially when compared to the estimates of the Latin American Society of Nephrology and the European Registry. The most frequent causes of CKD are hypertension, diabetes, glomerulonephritis, and polycystic kidney, among other less frequent ones [3].

CKD is progressive and irreversible, implying the limitation of glomerular filtration, causing uremia, and generating an accumulation of substances in the blood, which should have been filtered by the kidneys and subsequently excreted. Uremia causes immunodeficiency due to the increase in toxic substances in the bloodstream, so patients have a suppressed immune and humoral response [4]. In addition, it can cause various systemic changes such as cardiovascular alterations, anemia, hemostatic problems and lymphocytopenia [5,6]. Thus, CKD has a complicated interrelationship with other diseases [2].

The rate of progression of CKD varies between patients and is largely determined by genetic factors. Genetic mutations can result in disturbances in the function of the corresponding proteins, which will favor the development of kidney disease. One example is single nucleotide polymorphisms (SNPs) in genes that encode proteins with the ability to protect kidney tissue from permanent damage, and when present may be the basis of differences in susceptibility to disease progression between patients [7].

Koshino et al. showed that circulating levels of Interleukin-6 (IL-6) may be associated with a drop in renal function in patients with CKD and that the dosage of IL-6 in plasma and its changes over one year may be important in the prognosis for cardiovascular disease and progression of CKD in patients with type II diabetes at high cardiovascular risk. [8]. Therefore, this study aimed to identify IL-6 polymorphisms in saliva samples from patients with chronic kidney disease on hemodialysis.

2. MATERIALS AND METHODS

The study was approved by the Santo Amaro University Research Ethics Committee - protocol number: 1.113.922.

Forty patients were selected, 16 were healthy and 24 undergoing hemodialysis at the Medirim Hemodialysis Sector in the municipality of Cariacica/ES- Brazil. All study participants were informed of the study's objectives and signed an informed consent form, which had previously been approved by the ethics committee.

The inclusion criteria were hemodialysis patients who agreed with the study objectives and signed a consent form. Patients who did not agree with the objectives of the study and who refused to sign the consent form were excluded from the study, as were pregnant and breastfeeding women and patients seropositive for HIV, hepatitis B (HBV), and C (HCV).

Saliva samples were collected using the Salivette®tubes method (dry cotton swab in a plastic tube).The samples (containing at least 5mL) were placed in collection tubes, following all the manufacturer's guidelines. The samples were frozen at -20° C for subsequent IL-6 genotyping.

Genomic DNA was extracted using the QIAampDNA Kits extraction kit according to the manufacturer's instructions. Allelic discrimination assays were used to genotype the rs1800795 SNPs in the IL-6 gene (position -174), and amplification and reading were carried out using the Real-Time PCR technique(StepOne™ Real-Time PCR System - Applied Biosystems). The products were digested by 1U per reaction with 25 µl of NlaIII (CATGk) at 37° C to detect the G allele and the C allele. Three possible genotypes can be detected at position -174 in the IL-6 promoter gene, defined as high (G/G), medium (G/C) or low (C/C). The following primers was used to amplify the genomic DNA samples (Invitrogen Life Technologies) (-174): 5' -TTGTCAAGACATGCCAAGTGCT-3' (forward primer) and 5'-GCCTCAGAGACATCTCCAGTCC-3' (reverse primer).

2.1 Statiscal Analysis

For statistical analysis, SPSS software version 13.0 was used (SPSS, Chicago, Ill). The χ^2 test was performed on categorical data.The significance level for all tests was set at 5%.

3. RESULTS

The results obtained from the analysis of the distribution of IL-6 genotypes among healthy individuals were 81.2% for the GG genotype, 12.6% for CC and 6.2% for GC. The distribution among hemodialysis patients was 62.5% for GG, 33.3% for GC and 4.2% for CC(Table 1). No statistical difference was found in either group (*P*-value = 0.1054).

Table 1: Distribution of IL-6 genotypes in healthy individuals and those on hemodialysis

Genotype	Health		Hemodialysis		*P*-value
	n	%	*n*	%	
GG	13	81.2	15	62.5	0.1054
GC	01	6.2	08	33.3	
CC	02	12.6	01	4.2	

In terms of allele distribution, 84.3% of healthy individuals had the G allele and 15.7% had the C allele. 79.1% of hemodialysis patients had the G allele and 20.9% had the C allele(Table 2). No statistical difference was found (*P*-value = 0.5587).

Table 2: Distribution of IL-6 alleles in healthy individuals and on hemodialysis

Allele	Health		Hemodialysis		*P*-value
	n	%	*n*	%	
G	27	84.3	38	79.1	0.5587
C	05	15.7	10	20.9	

4. DISCUSSION

Some studies have linked genetic polymorphisms as a risk factor associated with CKD and different related pathologies [2]. According to the justification that genetic factors influence the susceptibility and progression of CKD [7], and the IL-6 single nucleotide polymorphism [SNP) is related to various diseases and complications related to CKD [9-11]. This study was designed to verify a possible relationship between the IL-6 polymorphism (-174 G/C) and chronic kidney disease.

A predominance of the GG genotype was found for both healthy patients and hemodialysis patients, but there was no statistical difference between the groups analyzed. A literature review with meta-analysis showed that the IL-6 -174 G/C polymorphism has no significant correlation with susceptibility to the risk of end-stage renal disease, which suggests that the IL-6 polymorphism has no influence on the progression of CKD [12] corroborating the results of this study. Even so, further studies are needed as there are few studies in the literature relating IL-6 polymorphism to CKD.

In this study, it was possible to see a predominance of the G allele (84.3%). In hemodialysis group, the Callele (20.9%) was higher in comparison with G allele (15.7%) in health group. Lorente et al. associated the presence of the G allele with the amplification of the inflammatory response in patients with sepsis. That is, patients with the GG and GC genotypes had higher circulating levels of IL-6. The same authors associated the allele with a worse prognosis and increased mortality in sepsis patients [13]. Other authors have linked the G allele with increased levels of IL-6 and, consequently, deterioration of the clinical picture and greater disease susceptibility [10,14]. However, some studies place the C allele as a determinant of a worse prognosis or increased risk [15,16]. This is probably due to the genetic variability of the different populations analyzed since genetics varies from population to population.

However, the population analyzed in our study was unable to establish a statistical difference in the comparison between the C allele and the G allele, indicating no relationship between the polymorphism and CKD in this population.

Although we were unable to demonstrate that the IL-6 polymorphism did not correlate with CKD, few studies have attempted to relate CKD to the IL-6 polymorphism, so there is a need for further studies to establish whether this relationship can be established.

In addition, studies show that polymorphism has a significant influence on diabetes, which acts as one of the main etiological factors of CKD [9,10,17]and can be considered an important biomarker for treatment management. There are also studies linking the risk of cardiovascular disease with IL-6 polymorphism [18]. Hypertension, the underlying disease of CKD, may also be related to an increased risk in the presence of higher IL-6 levels. Some studies have tried to establish this relationship with the risk of hypertension. However, there are still no consistent conclusions [19,20].

5. CONCLUSION

Given the results obtained, it was possible to verify the presence of the IL-6 polymorphism (-174) in saliva, nonetheless it was not possible to determine the altered expression of the cytokine (due to the presence of the G allele).

CONSENT AND ETHICAL APPROVAL

The participants were informed about the purpose and methodology of the study and signed a consent form that had been previously approved by the Ethics Committee (45478615.1.0000.0081).

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