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Interleukin-10 Genetic Polymorphisms and Risk of COVID-19 in Yaounde, Cameroon: A Case Control Study

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Abstract

Severe acute respiratory syndrome coronavirus 2 is the causative agent of the COVID-19 disease. Host susceptibility might be as a result of Single Nucleotide Polymorphisms (SNP) observed on genes that encode for cytokines in the immune system, thereby impacting the immune response. This study was aimed at investigating the association between the Single Nucleotide Polymorphisms (SNPs) within IL-10 (rs1800896 and rs1800871) with COVID-19 susceptibility in Yaounde, Cameroon. A case-control study was performed on 240 conveniently collected blood samples, spotted on Whartman N° 3-filter paper from which DNA was extracted by the chelex-100 DNA extraction method. Genotyping of the IL-10 SNPs was done using the Polymerase Chain Reaction and Restriction Fragment Length Polymorphism (PCR-RFLP). The Chi squared test (X^2) was used to establish associations and a p-value of <0.05 was considered statistically significant. The most predominant genotype and allele for rs1800896 and rs1800871, was the heterozygous genotype AG and wildtype allele A (212/240, 88.33%; 50.83%), and the heterozygous genotype TC and wildtype allele T (138/240, 57.50%; 59.58%) respectively. No statistically significant association was found in the gene and genotype frequencies of IL-10 (rs1800896 and rs1800871) between the COVID-19 infected group and healthy controls. Individuals possessing wildtype allele, T for rs1800871 were at increased risk of presenting clinical features of COVID-19 (OR=3.152; P=0.014). In conclusion, an association was found between the SNP of IL-10 (rs1800871) and the manifestation of COVID-19 clinical features. However, no association was found between the SNPs of IL-10 (rs1800896 and IL-10 rs1800871) and risk of COVID-19.

Keywords: Interleukin-10, COVID-19, Susceptibility, Gene Polymorphism, Immune Response

Introduction

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the causative agent of the Coronavirus disease (1). SARS-CoV-2 is an enveloped, positive-sense, single-stranded RNA virus that uses envelope spike glycol protein projections to enter human airway cells (2,3). Being of the *Sarbecovirus* subgenus, it is the 7th Coronavirus that is reported to have caused infections in humans among the following; SARS-CoV, MERS-CoV, HKUI, NL63, OC43 and 229E. The first two (SARS-CoV and MERS-CoV) caused various fatal and respiratory diseases while the others (HKU1, NL63, OC43

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and 229E) have been associated with only minor symptoms (4). According to a situational analysis and review on the global burden of SARS-CoV-2, the disease has been a major public health burden in the world (5). A total of 774 469 939 confirmed cases had been reported globally with over 7 026 465 deaths. In the WHO African region, a total of 12 596 186 confirmed COVID-19 cases and 257 971 deaths were reported with a case fatality rate of 2.1% in 2024. In Cameroon, a total of 125 379 confirmed COVID-19 cases were recorded with 123 280 recoveries and 1974 deaths (case fatality rate: 1.6%) (6). Many countries had shown increasingly slow COVID-19 transmission results by forming a strong collaboration among all sectors and designing effective prevention and control strategies which included staying home, social/physical distancing, quarantine, testing of suspected patients, isolation and managing of the confirmed cases (5).

It has been understood that viral infection drives an intense inflammatory response, which gives way to severe lung injury that may require intensive care unit admission, mechanical ventilation and increases the risk of multi-organ failure and death (7). From emergence of COVID-19 till date, its infection and severity has been heterogenous, driven by various immunologic complications which stem from macrophage activation, cytokine storm and or acute respiratory distress syndrome (8). Although comorbidities including chronic lung disease, cardiovascular disease and hypertension, diabetes, obesity and cancers, old age and male sex (9,10) as well as ethnicity (11) have been identified, host genetics has also been proposed as a risk factor of COVID-19 infections or severe courses of SARS-CoV-2 through genome-wide association studies (GWAS), whole-exon sequencing (WES) and candidate gene studies by COVID-19 Host Genetics Initiative (HGI) (9,10). SARS-CoV-2 is capable of inducing a cytokine storm which has been advocated as a key pathogenetic factor in COVID-19 (12). Studies have also shown that there is an increased level of numerous inflammatory cytokines in COVID-19 infected patients among which is IL-10, (MCP-1) (12).

IL-10 is a cytokine secreted by most immune system cells in response to antigen which regulates the inflammatory response inhibiting the synthesis of other cytokines, for example IL-2, IL-3, interferon-gamma (IFN-g), and granulocyte-macrophage colony-stimulating factor (GM-CSF) by T helper cells (13). It is the founding member of the IL-10 cytokine family, which includes IL-19, IL-20, IL-22, IL-24, and IL-26 (14). IL-10 can control viral infections and related tissue damages through stimulating the secretion of immune factors, controlling the phagocytosis and antigen presentation. On the other hand, IL-10 improves the innate and adaptive immunity (15). Mutations in IL-10 expression have been linked to polymorphisms in the promoter region that span at least 5 kb upstream of the transcription start point and known to contain at least 27 polymorphic sites (16). IL-10 polymorphisms in this promoter region of the IL-10 gene can affect the expression of IL-10 cytokine which leads to changes in inflammatory processes (15). An earlier study on IL-10 genetic polymorphism had reported an association of SNP with higher IL-10 serum levels and an increased risk of pneumonia severity (8). The narrative that these IL-10 gene polymorphisms decrease the expression of IL10 and are implicated in susceptibility to pulmonary infection and inflammation, such as tuberculosis (PTBC) and ARDS, specifically in the adult and elderly is not distorted (15). It has been shown that polymorphisms in pro-inflammatory and anti-inflammatory cytokines gene are related to the susceptibility and severity to the chronic inflammatory diseases such as chronic periodontitis and chronic hepatitis B virus infection (15). However, few studies have been done on the association of the SNPs in IL-10 with COVID-19 host susceptibility. Therefore, our study aimed at detecting the IL-10 SNPs, -1082: A/G and -819: T/C, and COVID-19 host susceptibility in Yaounde, Cameroon.

Materials and Methods

Study Setting and Location

This study was carried out in Yaoundé, the capital of the Centre Region in Cameroon (3°51′ N 11°29′ E) the second largest city of Cameroon with a population of more than 4 million. It has a surface area of about 180 km² and an elevation of 726 meters above sea level. It is surrounded by 7 hills with an average annual rainfall of 1628.3mm per year. Yaoundé is cosmopolitan city that is located within the Congo-Guinean phytogeographic zone characterized by a typical equatorial climate with two rainy seasons extending from March to June and from September to November (3,17,18).

Study Population and Sampling

A total of 240 archived samples were used in this study, including 120 COVID–19 infected patients and 120 healthy individuals as a case–control study after obtaining their informed consent. Inclusion criteria were: positive for COVID–19 after diagnosis for case group and a negative COVID–19 test for the control group, with individuals in both groups exposed to the virus. The samples used in this study were collected thus; Nasopharyngeal swabs were collected from study participants and a COVID–19 Antigen Test (RDT) (LOT N°: QCO3021003C/Sub: C–2) was carried out to confirm diagnosis. Positive results were later confirmed by a returning Real Time Polymerase Chain Reaction (qPCR) test results. Venus blood samples were also collected from study participants, from which dried blood spots were made using the Whartman N° 3-filter paper and sealed in sterile individual zip lock bags with silica gels crystals and stored at room temperature for further Molecular analysis as previously described (3).

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DNA Extraction and Genotyping

Genomic DNA was extracted from dried blood spots on Whartman No3 filter papers using Chelex-100 method as previously described (3,19). The amplification of the IL-10 gene at -1082 and 819 loci: A/G rs1800896 and T/C rs1800871 respectively was performed using a T3 Thermocycler (Biometra, UK), as previously described (15). The primer sequences used to amplify the genes were -1082F:5′-CCAGATATCTGAAGAAGTCCTG-3′ and -1082R: 5′-CTCTTACCTATCCCTACTTCC-3′, 819F:5′-CCAGATATCTGAAGAAGTCCTG-3′ and 819R: 5′-TGGGGGAAGTGGGTAAGAGT-3′, respectively. A total reaction mixture of 20µl, consisting of 7 µl of nuclease free water, 10µl of One Taq® Hot Start 2X Master Mix with standard buffer (New England Biolabs, MA, USA.), 0.5 µl of each primer (10 pmol) and 2 µl of DNA template made up the master mix. The PCR protocol was as follows: pre-denaturation (95°C for 2mins), denaturation (94°C for 30secs), annealing (50.6°C for 30secs), elongation (72°C for 45secs), amplified for 30 cycles and a final elongation of 72°C for 7minutes to terminate all reactions. The amplicons after amplification if not immediately used was stored at 4° C. The PCR products were then digested with MnlI and MslI (RseI) (New England Biolabs) respectively at 37°C for 18 h overnight as previously described (15). The products of digestion were run on 2% agarose gel stained with Ethidium bromide and visualized under UV light (Table 1).

Statistical Analysis

Data from this study were transcribed from laboratory worksheet records unto Microsoft Excel, version 2016. Allelic frequencies of the IL-10 gene were obtained using the Hardy-Weinberg formula. Data were analyzed using the IBM SPSS biostatistics version 20.0 software (SPSS, Chicago, IL). Descriptive statistics, percentage rate and frequencies were used to describe the socio-demographic and clinical data. Chi Square test (X^2 test) was used to establish associations between variables. Where the number of expected observations was less than 5, the Fisher's test was used. Unadjusted Odds Ratios (ORs) were calculated with 95% Confidence Intervals (CI). A $p < 0.05$ was considered significant in all comparisons (3,18,20).

Results

Distribution of Demographic Characteristics of the Study Population

Out of the 240 samples used in this study, 118 (49.17%) were women and 122 (50.83%) were men. In the COVID–19 infected group, 64 were male (53.33%) and 56 were female (46.67%) and on the other hand, in the control group 54 individuals were male (45.00%) and 66 were female (55.00%). Again, based on the clinical features of the disease, in the symptomatic group, 46 were male (35.33%), and 58 were female (55.77%) and on the other hand, in the asymptomatic group, 72 individuals were male (60.00%) and 64 were female (40.00%). The mean age was 35.15±14.79 years, that of the patients was 34.64±15.17 years, and controls were 36.19±14.79 years (Table 2).

Genotype and Allele Frequency of the IL10 1082: A/G rs1800896 and 819: T/C rs1800871 Gene Polymorphisms

Results from genotyping were as follows: the IL10 1082: A/G rs1800896 single nucleotide polymorphism revealed the distribution of AA (12, 10.00%), AG (102, 85.00%) and GG (6, 5.00%) in the COVID–19 infected group and AA (4, 3.33%), AG (110, 91.67%) and GG (6, 5.00%) in the control group. The IL10 819: T/C rs1800871 single nucleotide polymorphism revealed the distribution of TT (38, 30.00%), TC (72, 60.00%), and CC (10, 8.33%) in the COVID–19 infected group and TT (36, 30.00%), TC (66, 55.00%), and CC (18, 15.00%) in the controls group (Table 3).

Table 1: Restriction enzymes to digest IL10 1082: A/G rs1800896 and 819: T/C rs1800871 SNPs and band sizes.

IL-10 Gene reference SNP	Amplicon size(bp)	Restriction enzyme	Digested Amplicon size (bp)	Alleles and Genotypes
-1082 (A/G; rs1800896)	199	MnlI	A: 134 and 65	Alleles: A and G
			G: 112, 65 and 22	Genotypes: AA, AG, and GG
-819 (T/C; rs1800871)	559	MslI (RseI)	T:559	Alleles: T and C
			C: 443 and 116	Genotypes: TT, TC and CC

Table 2: Demographic Distribution of Study Population.

Variables		Population N=240	COVID-19 N=120	Controls N=120	Symptomatic N=104	Asymptomatic N=136
Age		35.15±14.79	34.64±15.17	36.19±14.79	36.15±15.12	34.59±14.80
(Mean ± SD)						
Gender	**Male**	122(50.83%)	64(53.33%)	54(45.00%)	46(44.23%)	72(60.00%)
	Female	118(49.17%)	56(46.67%)	66(55.00%)	58(55.77%)	64(40.00%)

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Table 3: Association between IL-10 gene polymorphisms (rs1800896 and rs1800871) and susceptibility to COVID-19

IL-10 Polymorphisms -1082 (rs1800896, A/G) Genotypes	COVID-19 N=120	Control N=120	OR	95%CI	P value
AA	12(10.00%)	4(3.33%)	3.222	1.008-10.294	0.067
AG	102(85.00%)	110(91.67%)	0.515	0.227-1.168	0.158
GG	6(5.00%)	6(5.00%)	1	0.313-3.193	1
Alleles					
A	126(52.50%)	118(49.17%)	1	0.313-3.193	1
G	114(47.50%)	122(50.83%)	0.31	0.097-0.992	0.067
-819 (rs1800871, T/C)					
Genotypes					
TT	38(31.67%)	36(30.00%)	1.081	0.625-1.871	0.889
TC	72(60.00%)	66(55.00%)	1.227	0.735-2.049	0.514
CC	10(8.33%)	18(15.00%)	0.515	0.227-1.168	0.158
Alleles					
T	148(15.00%)	138(57.50%)	0.472	0.094-2.382	0.158
C	92(85.00%)	102(42.50%)	0.972	0.109-8.702	0.673

SNP= Single Nucleotide Polymorphism, OR= Odds Ratio, CI= confidence interval, P- value=statistical significance level

Table 4: Association between IL-10 gene polymorphisms (rs1800896 and rs1800871) and COVID-19 Clinical Features

IL-10 Polymorphisms	Symptomatic N=104	Asymptomatic N=136	OR	95%CI	P value
-1082 (rs1800896, A/G)					
AA	8(7.69%)	8(5.88%)	1.333	0.483-3.679	0.609
AG	92(88.46%)	120(88.24%)	1.022	0.461-2.267	1
GG	4(3.85%)	8(5.88%)	0.64	0.187-2.186	1
Allele					
A	108(51.92%)	136(50.00%)	1.563	0.313-3.193	0.56
G	100(48.08%)	136(50.00%)	0.75	0.271-2.069	0.609
-819 (rs1800871, T/C)					
TT	30(31.67%)	44(32.35%)	0.848	0.486-1.478	0.889
TC	68(60.00%)	70(51.47%)	1.781	1.053-3.013	**0.035***
CC	6(8.33%)	22(16.18%)	0.317	0.124-0.814	**0.014***
Allele					
T	128(61.54%)	158(58.09%)	3.152	1.229-8.087	**0.014***
C	80(38.46%)	114(41.91%)	1.102	0.109-8.702	0.777

SNP= Single Nucleotide Polymorphism, OR= Odds Ratio, CI= confidence interval, P- value=statistical significance level

Table 5: Association between IL-10 gene polymorphisms (rs1800896 and rs1800871) Haplotypes and susceptibility to COVID-19

Haplotypes	COVID-19 2n=240	Controls 2n=240	OR	95% CI	P-Value
A-T	71(29.58%)	63(26.25%)	1.893	0.926-3.868	0.111
A-C	82(22.50%)	56(23.33%)	0.925	0.535-1.599	0.888
G-T	98(20.83%)	65(27.08%)	1	0.520-1.923	1
G-C	76(27.08%)	56(23.33%)	0.74	0.432-1.269	0.338

OR= Odds Ratio, CI= confidence interval, P- value=statistical significance level

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Table 6: Association between IL-10 gene polymorphisms (rs1800896 and rs1800871) Haplotypes and COVID-19 Clinical Features

Haplotypes	Symptomatic 2n=208	Asymptomatic 2n=272	OR	95% CI	P-Value
A-T	61(29.33%)	73(26.84%)	2.437	1.125-5.280	**0.021***
A-C	46(22.12%)	64(23.53%)	1.005	0.578-1.747	1
G-T	58(27.88%)	71(26.10%)	1.819	0.909-3.641	0.095
G-C	43(20.67%)	64(23.53%)	0.776	0.452-1.334	0.407

OR= Odds Ratio, CI= confidence interval, P- value=statistical significance level

From the genotyping results of this study, no statistical significance was found between the COVID-19 infected and the healthy controls for SNPs of IL10 1082: rs1800896 and 819: rs1800871 (Tables 3). Statistical significance was observed in the gene and genotype frequencies for the SNP of IL-10 819: T/C rs1800871 and clinical features of COVID-19 between the symptomatic and asymptomatic groups (Table 4).

No statistically significant difference was found between the haplotypes of the IL-10 SNP of IL-10 819: T/C rs1800871 and COVID-19 clinical features (Table 5). A statistical significance between the symptomatic and asymptomatic groups was observed, when the wildtype allele (A) and (T) for IL-10 rs1800896 and IL-10 rs1800871 respectively were combined amongst study participants, and participants possessing the resultant genotype (A-T) were 2.4 times likely to present with clinical features of COVID-19 (GC; OR=2.437, P=0.021) (Table 6).

Discussion

This study aimed at detecting the genetic polymorphisms within IL10 1082: A/G rs1800896 and 819: T/C rs1800871 and to establish a possible association with susceptibility to COVID-19 in Yaounde, Cameroon. Genome-wide studies have investigated the association between SNPs, which is the most common type of DNA sequence variations and susceptibility to various diseases (21) as they are involved in the pathways that play a key role in the attachment of the SARS-COV-2 to the host cells, in the host resistance, susceptibility to and severity of the disease (22). Host genetic background is a crucial factor which regulates cytokine responses, and this may be linked with inflammation, viral clearance, or disease progression. Several studies have demonstrated significant association of SNPs present in immune genes with increased susceptibility to diseases and infections (3,20). The association between single nucleotide polymorphisms and various clinical diseases such as colorectal cancer, gastric cancer, and autoimmune diseases or infectious diseases including HBV, HCV and COVID-19 infections have been studied and proved in several different surveys (3,23). IL-10 is a cytokine secreted by most immune system cells in response to antigen which regulates the inflammatory response inhibiting the synthesis of other cytokines, for example IL-2, IL-3, interferon-gamma (IFN-g), and granulocyte-macrophage colony-stimulating factor (GM-CSF) by T helper cells (13). IL-10 polymorphisms in the promoter region of the IL-10 gene can affect the expression of IL-10 cytokine which leads to changes in inflammatory processes (15). These polymorphisms include functional single nucleotide polymorphisms (SNPs) located in the 50-flanking promoter region at –1082 (G to A substitution i.e., rs1800896), 819 (C to T substitution i.e., rs1800871)) and –592 (C to A substitution i.e., rs1800872) have been reported to regulate IL10 gene transcription and expression and the secretion of IL10 consequentially (16). Literature as shown that IL-10 gene polymorphisms at the locus rs1800896 that limit the expression of IL-10 are linked with susceptibility to pulmonary infection and inflammation, such as tuberculosis (PTBC) and ARDS, specifically in the adult and elderly (24). There have also been reports of a link between SNPs in the IL10 gene and respiratory viral infectious diseases and this cytokine is thought to be a critical molecule in COVID-19 development (25).

Results from our study, showed the A alleles at rs1800896 locus of IL-10 gene to be most prevalent in the COVID 19 group than in the healthy controls, with a frequency of 52.50% and 49.17% respectively. On the contrary, the G allele was most prevalent in the healthy controls (50.83%). The heterozygous genotype, AG was found to be most predominant in our study population (85% for cases and 91.6% for controls). These results are different from a study carried by (8), where the A allele had a prevalence of 35% whereas that of the G allele was 65%. In another study carried out by (26) amongst Egyptian women with polycystic ovary syndrome (PCOS), they found the G allele (65%) to be more prevalent than the A allele (35%). The GG genotype (46%) in the same study was rather more prevalent that the AA (16%) and AG (38%) genotypes. The T allele at the rs1800871 locus of IL-10 gene was most prevalent (61.67% than the C allele (38.33%) at the same locus. TC genotype was found to be prevalent (60.00%) than TT (31.67%) and the CC (8.38%) genotypes. Interestingly these does not tie with the frequency distribution in a study carried by Oktariana *et al*., on the distributions of -819 IL-10 promoter gene polymorphisms among Leprosy patients with the frequency distribution of the T allele most predominant (27). These differences and similarities observed could be due to uncontrolled urbanization and major changes in lifestyle which has led to reduced physical activity and unhealthy

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diets, and thus contribute to development of mutations within the population. Also, the differences observed could be attributed to ethnicity and environmental conditions.

The G to A polymorphism at rs1800896 controls how the IL10 gene is expressed. It has been reported that individuals with the GG genotype have higher levels of IL-10 transcription and circulating levels of IL-10 than individuals with the AA genotype(25). IL-10 has been demonstrated to control viral infections and related tissue damages through stimulating the secretion of immune factors, controlling the phagocytosis and antigen presentation. While on the other hand, IL-10 improves the innate and adaptive immunity (15). Mutations in IL-10 expression have been linked to polymorphisms in the promoter region that span at least 5 kb upstream of the transcription start point and known to contain at least 27 polymorphic sites (16). It has been shown that polymorphisms in pro-inflammatory and anti-inflammatory cytokines gene are related to the susceptibility and severity to the chronic inflammatory diseases such as chronic periodontitis and chronic hepatitis B virus infection (15). Results from this study, showed no association between the SNP of IL10 rs1800896 and rs1800871 and COVID-19. These findings are contrary to a study carried out in 2021 by Oktariana *et al*., among leprosy patients in Indonesia (27). In a recent study carried out in Iran on different SARS-CoV-2 variants to examine the genetic susceptibility of the host to COVID-19 mortality, to ascertain if IL10 rs1800871, rs1800872, and rs1800896 polymorphisms are connected to the vulnerability to COVID-19 mortality according to different SARS-CoV-2 variants, the alleles and their genotypes were investigated (25) and in patients with COVID-19, the allele T for the IL10 rs1800872 as minor allele frequency MAF was directly correlated with death, meanwhile the MAF for IL10 rs1800872 in recovered patients was lower than in the deceased ones. In patients with COVID-19, the allele C (0.36) for the IL10 rs1800871 as MAF was directly correlated with death and the MAF for IL10 rs1800871 in recovered patients was lower than in the deceased ones (25). In this study, the COVID-19 mortality rate was associated with the IL-10 rs1800896 GG and AG genotypes in the Delta and Omicron BA.4 variants. The IL-10 rs1800871 CC genotype in the Alpha variant and CT genotype in the Delta variant had a relationship with COVID-19 mortality; nonetheless, there was no association between the rs1800871 polymorphism with the Omicron BA.5 variant in the current study. Contrarily to this, another study in Mexico showed that the IL-10 rs1800871 and rs1800872 polymorphisms among 193 COVID-19 patients were not linked to the severity of the disease (25). Nevertheless, there was no association between rs1800896 polymorphism with the Alpha variant. Rizvi *et al*, indicated that AG genotypes was correlated with COVID-19 severity (8). Ethnic differences may be a plausible explanation for the lack of an association between IL-22 (rs1179251) polymorphisms and COVID-19 as compared to other studies (3).

IL-10 has an immune regulatory function and has shown to inhibit production by dendritic cells and macrophages of many inflammatory molecules such as IL-12, major histocompatibility complex (MHC) and other costimulatory molecules. As such IL-10 is able to suppress pro-inflammatory cytokine in HIV, HBV, influenza virus, dengue, and other virus infection like COVID-19 in the beginning stage of the viral infection (28). Results from this study shows a statistically significant difference in the rs1800871 locus of IL-10 gene with clinical features of COVID-19 between the symptomatic and asymptomatic groups. The T allele was found to be an increased risk (OR= 3.152; P=0.014) to COVID-19 clinical features. Results also shows that, individuals possessing the CC genotype for the IL10 rs1800871 SNP, where at decreased risk to COVID-19 clinical features (OR=0.317; P=0.014). These results are contrary to a study on IL22 rs1179251 SNP and COVID-19 population of Yaounde (3). IL10 1082: A/G rs1800896 and 819: T/C rs1800871 haplotypes showed statistical significance between the symptomatic and asymptomatic groups when the wildtype allele (A) for rs1800896 and that of rs1800871 (T) for IL-22 rs1179251 were combined amongst study participants with participants possessing the resultant genotype (A-T), at increased risk to present the clinical features of COVID-19 (GC; OR=2.437, P=0.021). It has been shown that, the primary function of IL-10 during infection is to inhibit the host immune response to pathogens and microbiota, thereby mitigating tissue damage and immunopathology (29). IL-10 has an immune regulatory function and has shown to inhibit production by dendritic cells and macrophages of many inflammatory molecules such as IL-12, MHC and other costimulatory molecules. As such IL-10 is able to suppress pro-inflammatory cytokine in HIV, HBV, influenza virus, dengue, and other virus infection like COVID-19 in the beginning stage of the viral infection (28). Interestingly, the influence of some of the genetic factors may have a geographic distribution. In other words, one specific SNP may predispose individuals in a given ethnic group, whereas in a different group, it may neither predispose to nor protect against COVID-19 clinical features (3,30).

Conclusion

In summary, an association was found between the SNPs of IL10 819: T/C and COVID-19 clinical features. An association was also found between the haplotypes of the IL10 1082: A/G rs1800896 and 819: T/C rs1800871 and COVID-19 clinical features. However, the limitation of a relatively small sample size should be taken into consideration for lack of associations with COVID-19. Thus, a further study with larger sample size should be conducted to better conclude our findings.

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Authors Contributions

Conceptualization, WFM, CFT, TNT; **Methodology**, WFM, TNT, CFT, PMN, JPCK, PAN; **Sample collection**, CFT, PMN, RBL, AMN, LNN, WONT; **Data analysis**, CFT, WONT, TNT; **Molecular analysis**, CFT, TNT, GNN, DBK, LFA; **Writing of original manuscript**, TNT, CFT. All authors contributed in the revision of the manuscript and approved the final version prior to submission.

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Conflicts of Interest

The authors declare no conflicts of Interest.

Institutional Review Board Statement

The study was conducted according to the guidelines of the Declaration of Helsinki, and was approved by the Cameroonian Regional Ethics Committee for Research in Human Health (CRECRHH) under the ethical clearance document number 2173/CRERSHC/2021 on the 21st July, 2021.

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