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RESEARCH ARTICLE
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Correlation of Angiotensin-converting Enzyme 2 Gene (rs1514283) Polymorphism with the Incidence of COVID-19

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ABSTRACT

It has been a busy year for coronaviruses, with the most recent one causing severe coronavirus illness in 2019 (COVID-19). It is broadly distributed in many human tissues and organs as the potential SARS-CoV-2 receptor angiotensin-converting enzyme 2 (ACE2). ACE2 provides homeostatic modulation of circulation angiotensin II levels by acting as a physiological counterbalance to ACE. They have been linked to COVID-19 disease acquisition, progression, and severity. As a result, we investigated how ACE2 variations and epigenetic variables affect SARS-CoV-2 infection susceptibility and infection outcomes in terms of age, gender, and ethnicity. Debates raged over the etiology of this occurrence. It is important to note that further research is required to demonstrate the efficacy of human recombinant ACE2 and ACE2-derived peptides in fighting SARSCoV-2 variants. Better recognition of a host genetic, as well as the function of the properties of ACE2 variations, would assist in explaining clinical disparities of infection between individuals and contribute to the development of remedies and managing future SARS-CoV-2 epidemics, an essential function for ACE2 in essential hypertension (EH). We wanted to see how ACE2 gene polymorphisms and enzyme activity correlated with COVID-19 incidence in the Iraqi province of Al-Diwaniya. A total of 63 COVID-19 patients and 70 (NT) controls were genotyped using Sequenom Mass-ARRAY RS1000 for ACE2. Participants' ACE2 rs1514283 SNP was linked to COVID-19.

Keywords: *ACE2; COVID-19; hypertension; rs1514283 SNP*

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INTRODUCTION

COVID-19 is a major health hazard, say, physicians. By August 4, 2021, the disease had killed almost 4 million people. SARS-CoV-2 has 85% DNA of SARS-CoV. COVID-19 is SARS 2 (SARS-CoV-2).[1] COVID-19 causes SARS (SARS-CoV-2). SARS-CoV enters a cell via the spike (S) glycoprotein. It unites with the membrane as well as the receptor.[2] The S1/S2 interdomain protease site is thought to be exposed by ACE2's S1 receptor binding protein (RBD) and program death (PD). Proprotein convertase furoate (S1/S2) then cleaves the S protein (TMPRSS2). Somatic S2-fusion peptide injection into the host membrane, to fuse the host membrane, utilizes the S2. The SARS-CoV-2 virus replicates and transcribes RNA.[3] A new infection cycle occurs when new viruses grow within the cell. ACE2 is a 120 kDa ZMP1 member and SARS-CoV-2 is a virus receptor. Collecting-like domain and HEXXH + E consensus zinc-binding domain. The zinc-binding domain (PD) consensus sequence is HEXXH + E which may be open or closed. Ligand has a free path away from the active site,[4] such as testicles (including the adrenal gland), thyroid, heart, and adipose (including the adrenal gland). Acyl cysteine is found in the brain and spinal cord ADP (ACE2). Also, the body has 554 amino acid waste product ACE2.[5]

Due to the metalloproteinase 17 enzyme, these ACP2 protein variations may be anti-inflammatory (ADAM17). SARS-CoV-2 binds to sACE2 and inhibits COVID-19. ACE2 has three main roles: hepatic neutral amino acid absorption is aided by ACE2.[6–9] This gene's variations include protein, transcriptional, and post-transcriptional changes. Scientists are becoming interested in ACE2 single nucleotide polymorphisms (SNPs).[10–12] Several databases found 298 protein-altering variations in human ACE2 (hACE2).[13] COVID-19 symptoms are acute respiratory distress syndrome (ARDS) and death. This mutation may be linked to the differential transmission. For starters, the ACE2 rs1514283 polymorphism must be fully understood as ACE2 mutations[14–18] that may affect SARS-CoV-2 and COVID-19 infection outcomes. Using the enzyme ACE2 in novel therapies is trendy now. The ACE2 peptidase domain is to blame. S1/S2 and TMPRSS2 break the S protein here.[19]

This helps in getting the S2-fusion peptide into the host membrane. After assembling the host membrane, SARS-CoV-2 RNA is released for viral replication and translation. A new infection cycle begins with an entry and exit of a new virus.[20,21] ACE2 is a 120 kDa ZMP type I and is a SARS-CoV-2 virus.[22–29] It has zinc-binding and collecting domains. Its zinc-binding domain is HEXXH + E and may be open or closed. Distant from the active site, such as the thyroid, small intestine, kidneys, and fat (including the fat around the waist), it accepts ligands.[21,30] The ligand binds to ACE2 and disables it: endocrine and liver (ACE2); the brain and spine (ACE2).[11,31] sACE2 is a 554 amino acid digestible byproduct. Anti-inflammatory ACP2 proteins are shed by metalloproteinase 17[9,21] (ADAM17). sACE2 binds SARS-CoV-2 preventing COVID-19. ACE2 has three main roles: it not only protects the heart but also aids in intestine neutral amino acid absorption and regulate blood pressure and blood glucose level.[10,32,33]

The ACE2 gene has SNPs, transcriptional changes, and potential protein mutations. SNPs are variations in the DNA sequence.[22,23,34,35] The human ACE2 protein has 298 protein-altering variants spread across 256 codons. Pneumonia, ARDS, and death are all COVID-19 symptoms.[22–26,36] Researchers in this study suspect ACE2 rs1514283 mutations as a reason. The ACE2 rs1514283 polymorphism needs more research. ACE2 polymorphisms with SARS-CoV-2 and COVID-19 infection risk. These remedies are now being studied and COVID-19 rs1514283 is examined in Al-Diwaniya patients.

MATERIAL AND METHODS

Study design

When it came to this study, which involved participants, the investigators employed a prospective

observational technique. According to the Ethical Committee of Al-Qadisiya University, which is located in the province of Al-Qadisiya, the procedure in the province of Al-Diwaniya was carried out with the agreement of the Ethical Committee of the Faculty of Medicine at Al-Diwaniya University. The Al-Qadisiya University Faculty of Medicine's Ethical Committee is located in the province of Al-Qadisiya, and it is comprised of medical students and faculty members. Participants and their families were invited to submit written informed consent before taking part in the study. Several hours were spent deliberating on the goals and objectives of the study before this choice was reached.

Study population

In this research endeavor, participants were placed in a range of contexts. A total of 133 blood samples were taken from patients at the Diwaniyah Educational Hospital (85 males and 48 females), and each sample was examined for a variety of variables. In this study, blood samples were collected from 62 patients (22 men and 40 women) who were being monitored at Al-Qadisiya University's Faculty of Medicine and provided to 71 healthy persons (45 men and 26 women) who served as a control group for the study. Those who took part in the study ranged in age 32.05 ± 15.9 years and were from various backgrounds. During the steps of the study, each patient underwent routine data collection procedures that included recording their age, weight, BMI, and the polymorphism under investigation, as well as other demographic data.

Living region

This study examined the ACE2 gene polymorphism rs1514283 in all samples, which were dispersed according to dwelling region, to establish if there is a relationship between environmental factors and the frequency of mutations. In order to conduct the demographic research, the study group was classified into two groups based on where they live: in cities and rural areas.

History of respiratory disease

Every sample was checked to see if there were any evidence of respiratory disease in order to further refine the association between the presence of COVID-19 and a single nucleotide mutation in the ACE2 gene. Cases and controls were classified into two subgroups based on whether or not they had a history of previous respiratory disease.

History of hypertension

This study included both hypertensive patients and healthy controls who were categorized as having either positive or negative hypertension for the sake of future data analysis and investigation.

Severity of COVID-19

According to the study's design, the patients with COVID-19 were separated into two groups depending on the severity of their infection status, which were classified as mild and severe, respectively, based on the infection states of the patients.

Genotyping

The blood samples were obtained from each patient and the healthy controls, and they were collected in sodium citrate tubes for further analysis. The plasma separation from the blood samples is carried out by centrifuging them at 3000 x g for 10 min. It was possible to separate genomic DNA from peripheral lymphocytes using a Macherey–Nagel genomic DNA purification kit purchased from the company (Qiagen, Germany). When it came to determining the ACE2 gene rs1514283 polymorphism, the polymerase chain reaction tetra-primer amplification refractory mutation system (ARMS) technique was applied. Real-time polymerase chain reaction (RT-PCR) was employed to corroborate the results.

Primers

As part of this investigation, ARMS-PCR primers were produced for polymorphism rs1514283 in the ACE2 gene, using assistance from the

TABLE 1. Specific primers for ACE2 gene rs1514283 polymorphism.

Primer	Sequence (5'-3')	Product size
Wild type primer	TTAGGTTCATCAACAGCTCCTT	278bp
Mutant type primer	TTAGGTTCATCAACAGCTCCTC	
Common reverse primer	CTACCTCCAAATGCCAATAC	

NCBI-SNP database and the ARMS-PCR primers generation tool, both of which may be obtained from the National Center for Biotechnology Information (NCBI). These primers have been given by Scientific Researcher Co. Ltd., Iraq for your convenience and for individual use only (Table 1).

Statistical analysis

The findings were analyzed by the Statistical Package for Social Sciences (SPSS) program, which was installed on a Windows 11 machine running the SPSS software. The alleles discovered in the wild-type, heterozygote, and mutant groups were compared to one another using a one-way analysis of variance (ANOVA). To determine the relationship between continuous variables and their corresponding discrete variables, the correlation data analysis method was used. It was determined that a p-value greater than 0.05 was statistically significant based on the findings of this inquiry.

RESULTS

Correlation of genotype with the age groups

The study group comprised of different age groups, and there were 18 subgroups based on age (Table 2). The mean age was 32.04 ± 15.9 years (Figure 1). Genotype correlation with the frequency of age did not show a significant relationship.

Correlation of genotype with the sex groups

The collection was according to the distribution of patients and controls in this study (Tables 3 and 4). The study consisted of 62 patients and 71 healthy controls, 85 males and 48 females. The data were analyzed with descriptive statistics to evaluate the correlation between gene polymorphism and sex distribution. There were variable genotypes in each group, and the resulting values indicated no significant correlation between them (Figure 2).

TABLE 2. Genotype correlation with age, weight, and body mass index.

Variable	Mean	Std. Deviation
Age	32.05	15.904
Weight	28.74	2.98
BMI	81.16	11.437

Correlation of genotype with BMI groups

The correlation of BMI with the genotype is given in Table 1 and Figures 3 and 4, and did not show a significant correlation between them.

Correlation of genotype with weight groups

The results did not show a significant correlation between the weight of participants and genotype allele mutation (Tables 5 and 6; Figures 5, 6, 7 and 8).

Correlation of genotype with case and control groups

Results show a significant correlation between genotype and group of cases. CC alleles of polymorphism rs1514283 in the ACE2 gene were correlated with the incidence of this disease (Table 4; Figure 9).

Correlation of genotype with the region of living

The correlation of genotype was clear in the SNP variation of the ACE2 gene. The

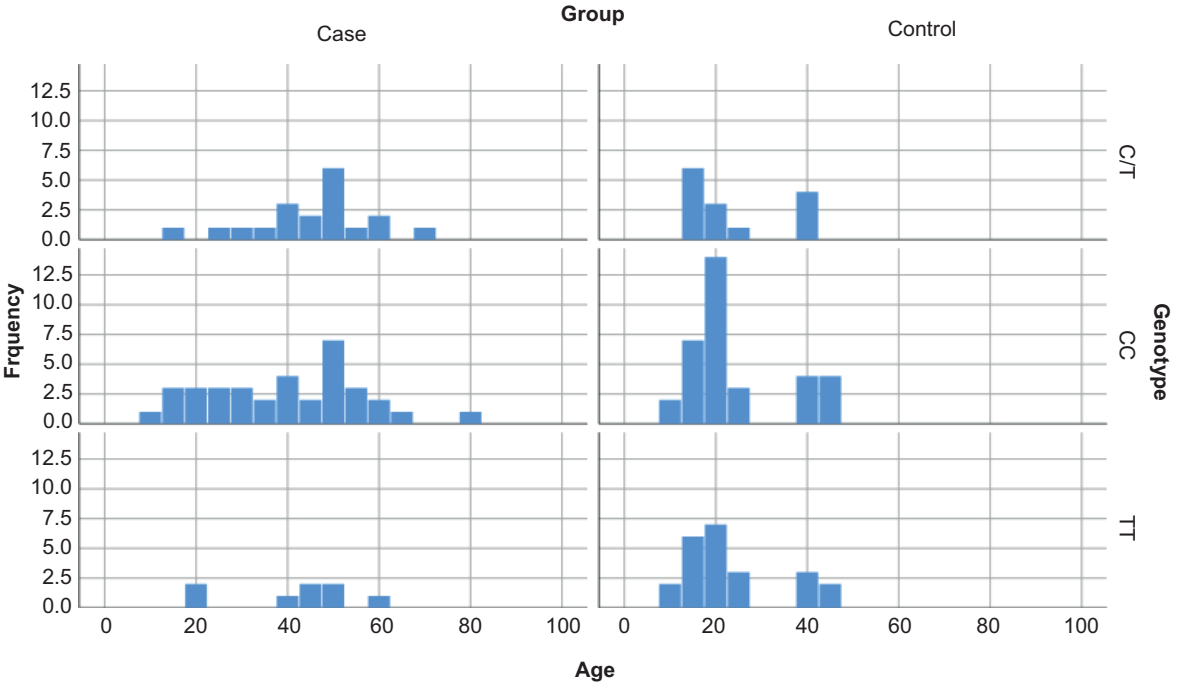

FIGURE 1. Correlation of genotype with age distribution.

TABLE 3. Distribution of sex according to age in each group.

Sex				**Statistics**	**Std. Error**
Age	Female	Mean		30.58	2.170
		95% Confidence interval for mean	Lower bound	26.22	
			Upper bound	34.95	
		5% Trimmed mean		30.01	
		Median		25.00	
		Variance		225.993	
		Std. Deviation		15.033	
		Minimum		10	
		Maximum		62	
		Range		52	
		Interquartile range		25	
		Skewness		0.517	0.343
		Kurtosis		–0.975	0.674

(continues)

TABLE 3. Continued.

Sex				Statistics	Std. Error
	Male	Mean		32.87	1.779
		95% Confidence interval for mean	Lower bound	29.33	
			Upper bound	36.41	
		5% Trimmed mean		32.11	
		Median		31.00	
		Variance		269.138	
		Std. Deviation		16.405	
		Minimum		10	
		Maximum		80	
		Range		70	
		Interquartile range		28	
		Skewness		0.422	0.261
		Kurtosis		–0.678	0.517

TABLE 4. Genotype and sex groups.

Sex				Genotype			
				C/T	CC	TT	Total
Female	Group	Case	Count	7	13	2	22
			% within Group	31.8%	59.1%	9.1%	100.0%
		Control	Count	5	10	11	26
			% within Group	19.2%	38.5%	42.3%	100.0%
	Total		Count	12	23	13	48
			% within Group	25.0%	47.9%	27.1%	100.0%
Male	Group	Case	Count	12	22	6	40
			% within Group	30.0%	55.0%	15.0%	100.0%
		Control	Count	9	24	12	45
			% within Group	20.0%	53.3%	26.7%	100.0%
	Total		Count	21	46	18	85
			% within Group	24.7%	54.1%	21.2%	100.0%

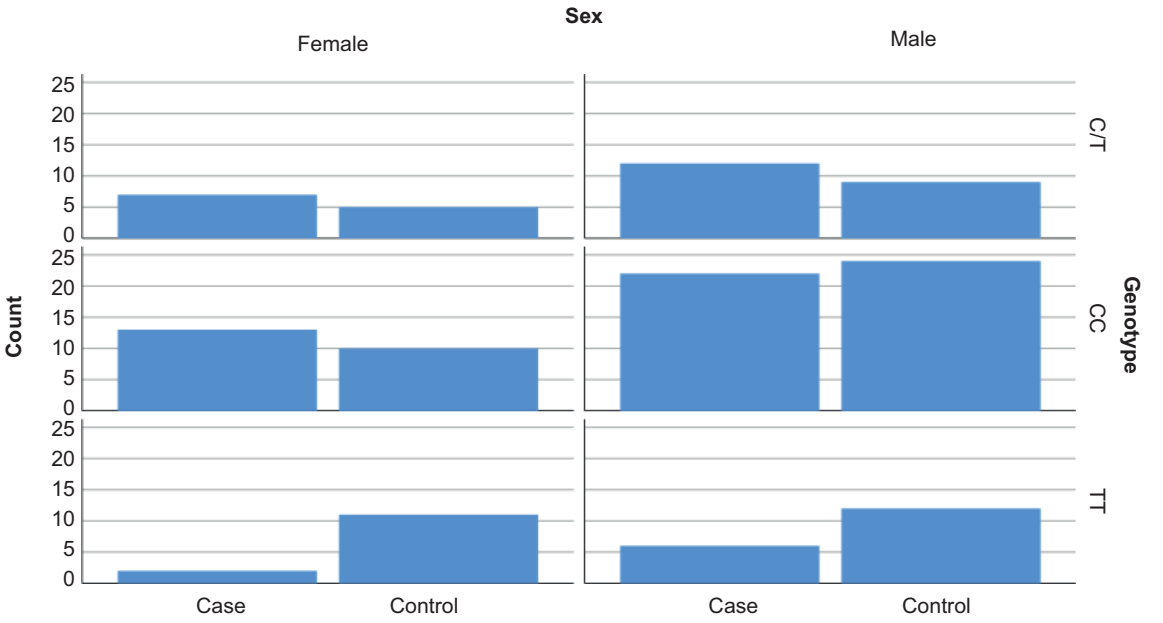

FIGURE 2. Distribution of genotype in the sex.

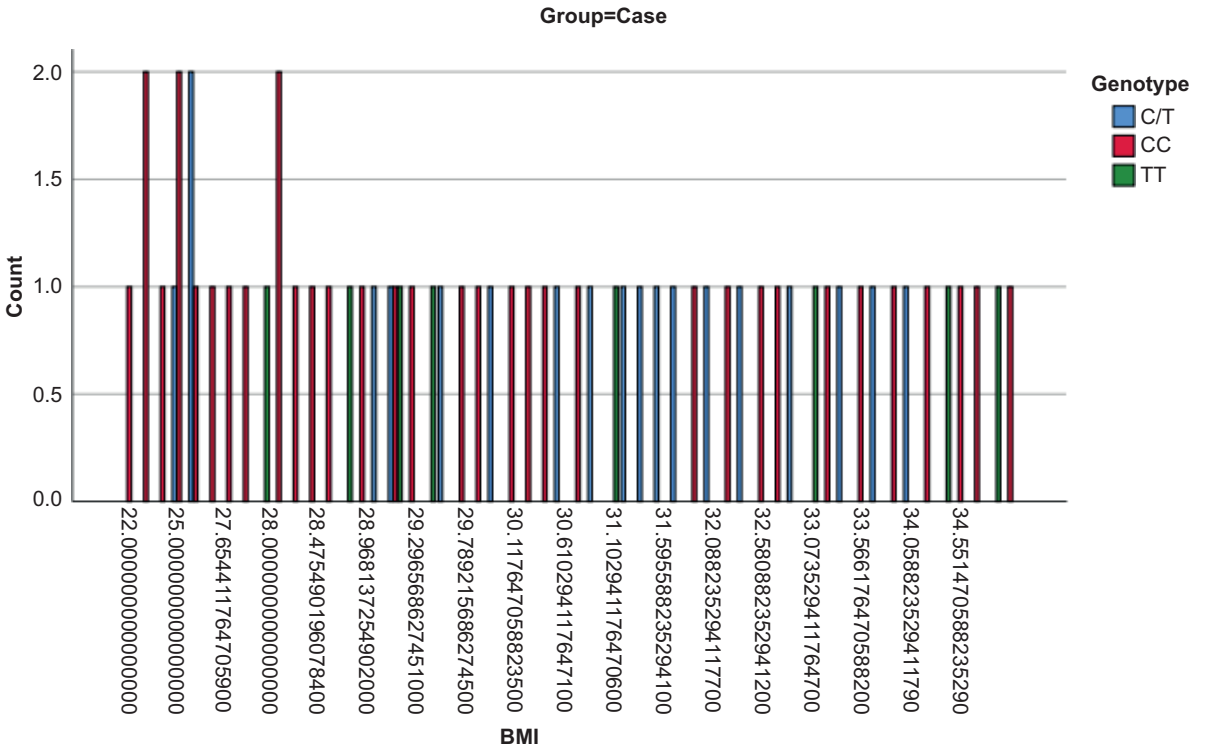

FIGURE 3. Genotype and BMI in the case group.

J Popul Ther Clin Pharmacol Vol 29(1):e122–e141; 8 June 2022.

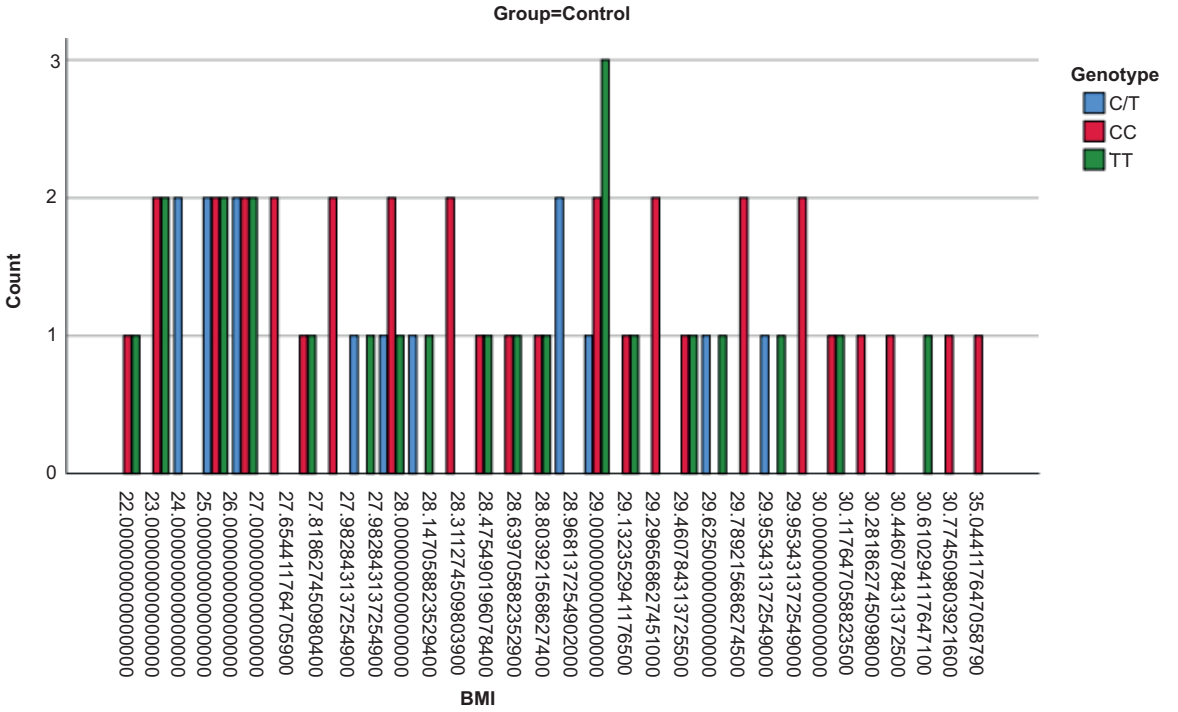

FIGURE 4. Genotype and BMI in the control group.

TABLE 5. Correlation of genotype with weight groups.

		Genotype			Total
		C/T	CC	TT	
Weight	62	0	3	2	5
	63	0	4	1	5
	67	6	8	2	16
	71	0	3	2	5
	73	0	5	1	6
	74	2	3	1	6
	75	1	3	2	6
	77	2	3	1	6
	78	3	6	3	12
	81	2	1	2	5
	85	3	1	1	5
	87	5	4	2	11
	88	1	5	0	6
	89	0	4	2	6
	90	4	0	2	6
	91	2	1	2	5
	95	1	3	2	6
	98	1	7	2	10
	103	0	5	1	6
Total		33	69	31	133

J Popul Ther Clin Pharmacol Vol 29(1):e122–e141; 8 June 2022.

TABLE 6. Significancy of data analysis.

Group		Value	df	Asymptotic significance (2-sided)
Case	Pearson chi-square	42.464[a]	36	0.212
	Likelihood ratio	52.664	36	0.036
	Number of valid cases	62		
Control	Pearson chi-square	39.698[b]	36	0.309
	Likelihood ratio	48.819	36	0.075
	Number of valid cases	71[c]		

[a]*53 cells (93.0%) have an expected count of less than 5. The minimum expected count is 1.17.*
[b]*57 cells (100.0%) have an expected count of less than 5. The minimum expected count is 0.26.*
[c]*57 cells (100.0%) have an expected count of less than 5. The minimum expected count is 0.39.*

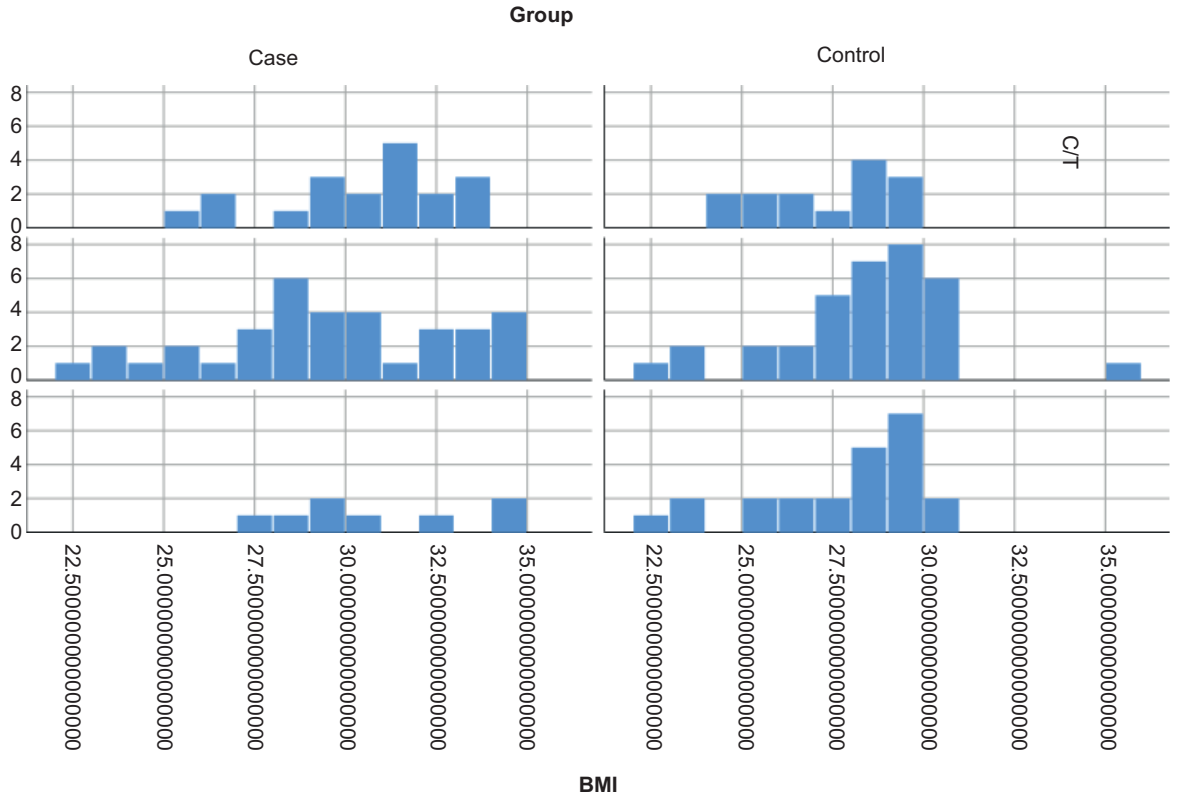

FIGURE 5. Frequency of BMI in the genotypes of groups.

correlation shows variation in alleles mutation in the city rather than in the countryside (Table 7; Figure 10).

Correlation of genotype with hypertension of participants

A significant correlation is shown between cases of hypertension and genotype alterations. While there is no significance shown regarding the sex (Tables 8 and 9; Figure 11).

Correlation of genotype with history of respiratory disease of participants

A significant correlation between cases of hypertension and genotype alterations is shown in Table 10 and Figure 12.

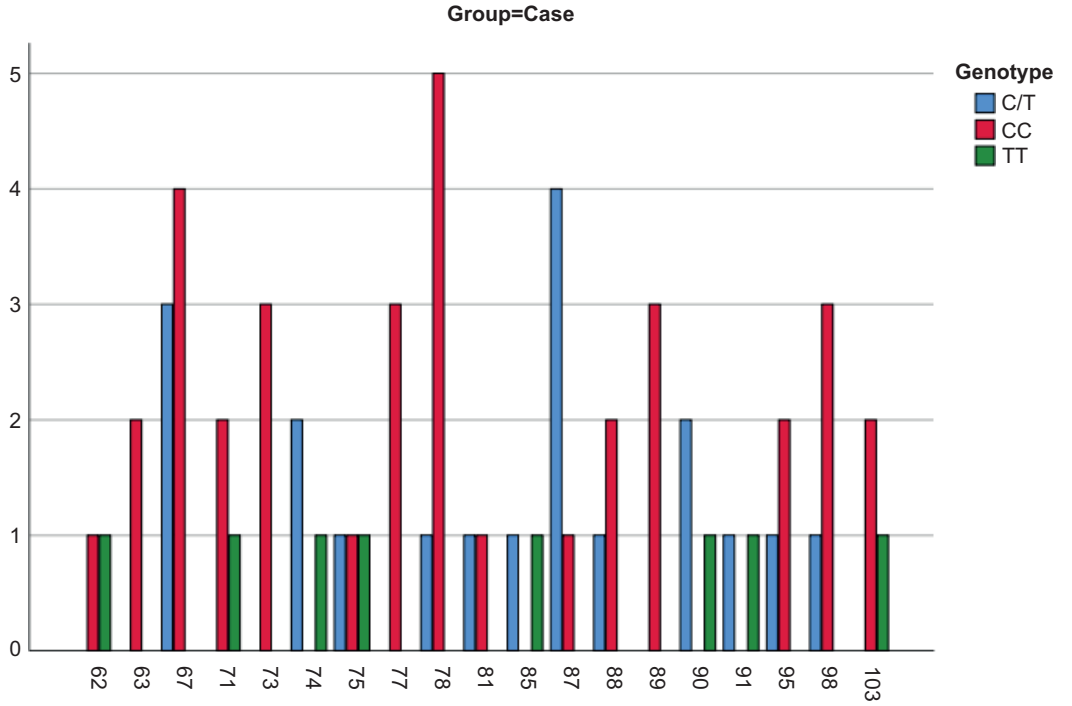

FIGURE 6. Correlation of genotype with weight of the case group.

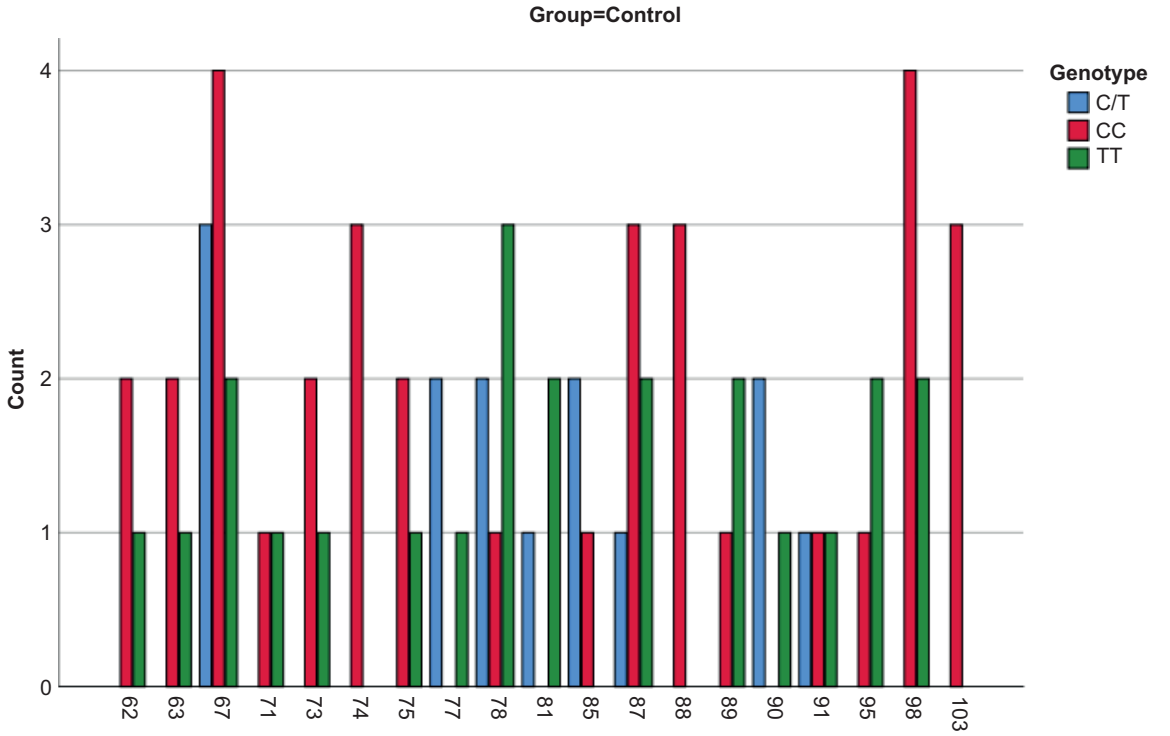

FIGURE 7. Correlation of genotype with weight of the control group.

J Popul Ther Clin Pharmacol Vol 29(1):e122–e141; 8 June 2022.

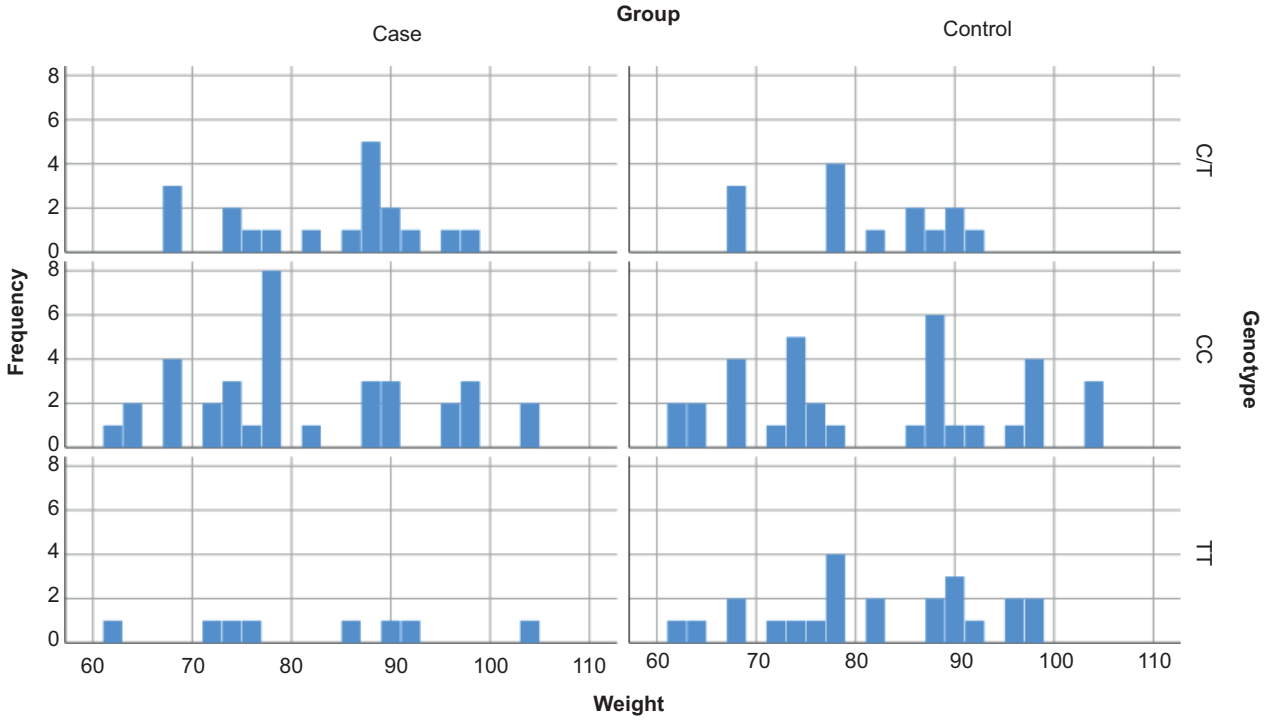

FIGURE 8. Frequency of weight in the genotype of each group.

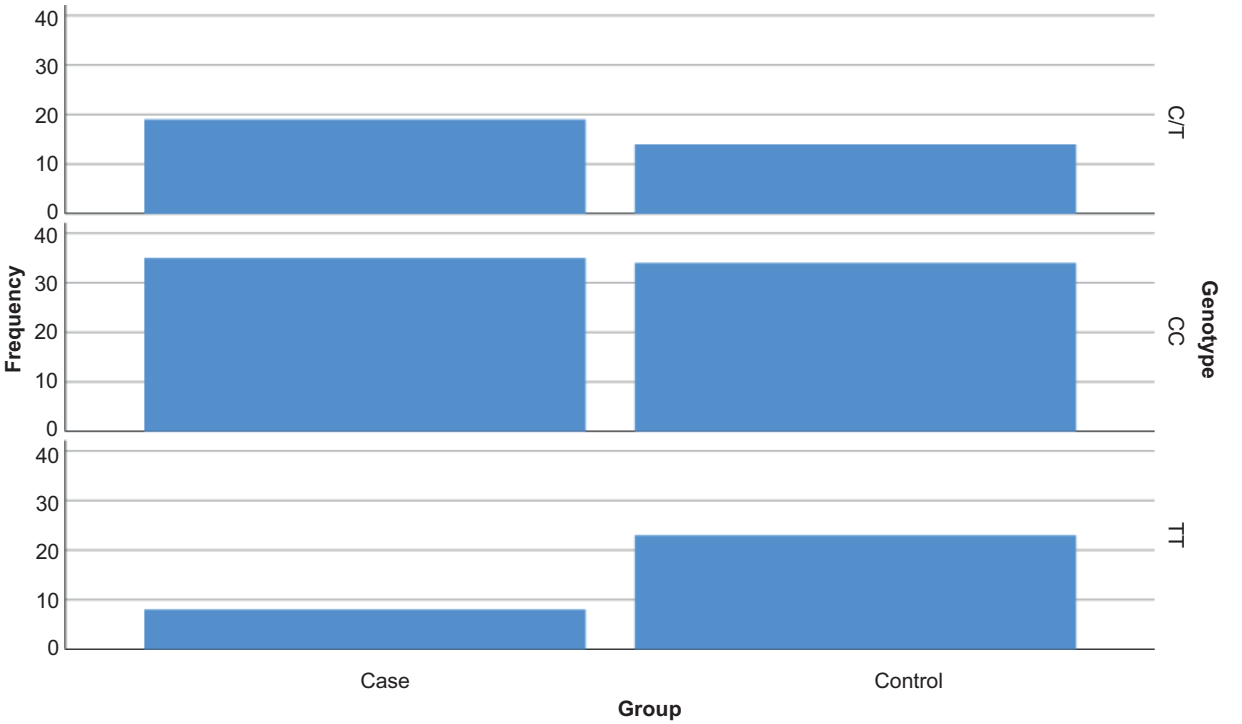

FIGURE 9. Correlation of genotype with case and control groups.

J Popul Ther Clin Pharmacol Vol 29(1):e122–e141; 8 June 2022.

TABLE 7. Genotype and the region of living.

Group				Region		Total
				City	Countryside	
Case	Genotype	C/T	Count	11	8	19
			% within region	28.2%	34.8%	30.6%
		CC	Count	23	12	35
			% within region	59.0%	52.2%	56.5%
		TT	Count	5	3	8
			% within region	12.8%	13.0%	12.9%
	Total		Count	39	23	62
			% within region	100.0%	100.0%	100.0%
Control	Genotype	C/T	Count	6	8	14
			% within region	20.0%	19.5%	19.7%
		CC	Count	16	18	34
			% within region	53.3%	43.9%	47.9%
		TT	Count	8	15	23
			% within region	26.7%	36.6%	32.4%
	Total		Count	30	41	71
			% within region	100.0%	100.0%	100.0%
Total	Genotype	C/T	Count	17	16	33
			% within region	24.6%	25.0%	24.8%
		CC	Count	39	30	69
			% within region	56.5%	46.9%	51.9%
		TT	Count	13	18	31
			% within region	18.8%	28.1%	23.3%
	Total		Count	69	64	133
			% within region	100.0%	100.0%	100.0%

Correlation of genotype with COVID-19 severity disease

Results show a significant correlation between the severity of COVID-19 with alteration of alleles in the SNP of ACE2 (Table 11; Figure 13).

DISCUSSION

This study investigates ACE2 rs1514283 SNP variants and epigenetic factors to improve our understanding of the COVID-19 disease. Specifically, we were interested in learning how the history of respiratory disease, the severity of COVID-19, gender, BMI, weight, and age affects the susceptibility of individuals to SARS-CoV-2 disease and its outcomes in relation to one's overall susceptibility, as well as how these factors interact with one another. Also, we investigated how they influence the overall outcome of the disease.[26] Some of the COVID-19 genetic variations that are currently available in the research investigation and is based on the rs1514283 SNP of the ACE2 gene, as well as those that are in the development stage and are based on other genes, were also covered in detail.[25]

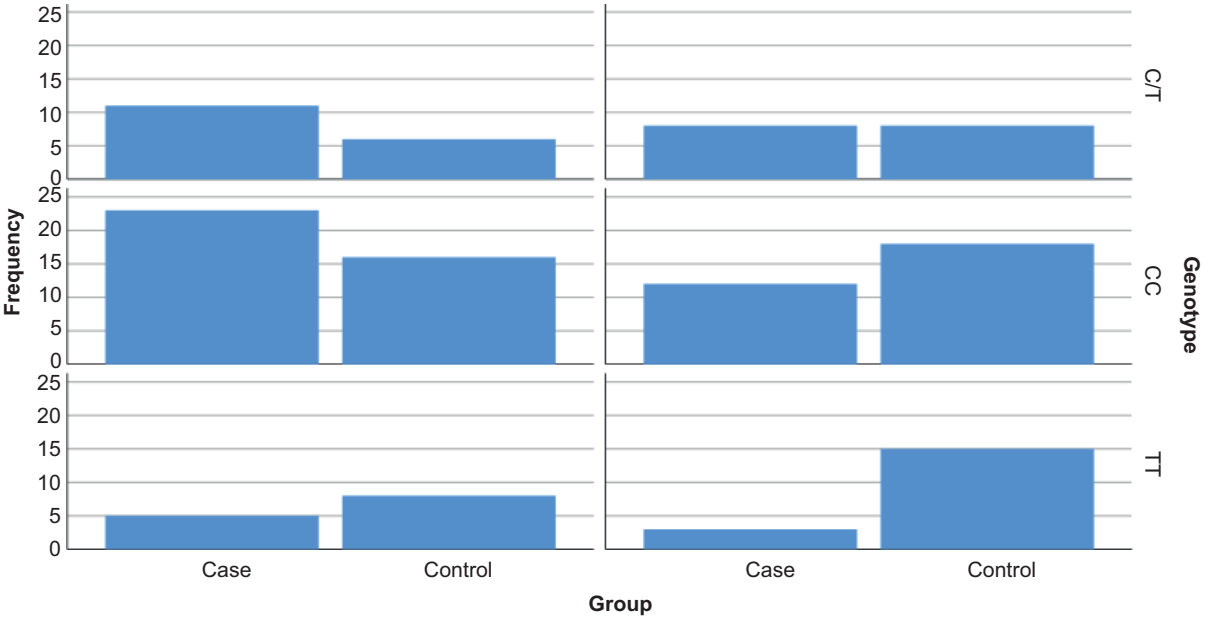

FIGURE 10. Genotype and the region of living.

TABLE 8. Correlation of genotype with hypertension of participants.

Group				Hypertension		Total
				Negative	Positive	
Case	Genotype	C/T	Count	4	15	19
			% within hypertension	25.0%	32.6%	30.6%
		CC	Count	9	26	35
			% within hypertension	56.3%	56.5%	56.5%
		TT	Count	3	5	8
			% within hypertension	18.8%	10.9%	12.9%
	Total		Count	16	46	62
			% within hypertension	100.0%	100.0%	100.0%
Control	Genotype	C/T	Count	9	5	14
			% within hypertension	19.6%	20.0%	19.7%
		CC	Count	22	12	34
			% within hypertension	47.8%	48.0%	47.9%
		TT	Count	15	8	23
			% within hypertension	32.6%	32.0%	32.4%
	Total		Count	46	25	71
			% within hypertension	100.0%	100.0%	100.0%

(continues)

TABLE 8. Continued.

Group				Hypertension		Total
				Negative	Positive	
Total	Genotype	C/T	Count	13	20	33
			% within hypertension	21.0%	28.2%	24.8%
		CC	Count	31	38	69
			% within hypertension	50.0%	53.5%	51.9%
		TT	Count	18	13	31
			% within hypertension	29.0%	18.3%	23.3%
	Total		Count	62	71	133
			% within hypertension	100.0%	100.0%	100.0%

TABLE 9. Correlation of genotype with hypertension of male and female groups.

Sex				Hypertension		Total
				Negative	Positive	
Female	Genotype	C/T	Count	4	8	12
			% within hypertension	18.2%	30.8%	25.0%
		CC	Count	9	14	23
			% within hypertension	40.9%	53.8%	47.9%
		TT	Count	9	4	13
			% within hypertension	40.9%	15.4%	27.1%
	Total		Count	22	26	48
			% within hypertension	100.0%	100.0%	100.0%
Male	Genotype	C/T	Count	9	12	21
			% within hypertension	22.5%	26.7%	24.7%
		CC	Count	22	24	46
			% within hypertension	55.0%	53.3%	54.1%
		TT	Count	9	9	18
			% within hypertension	22.5%	20.0%	21.2%
	Total		Count	40	45	85
			% within hypertension	100.0%	100.0%	100.0%
Total	Genotype	C/T	Count	13	20	33
			% within hypertension	21.0%	28.2%	24.8%
		CC	Count	31	38	69
			% within hypertension	50.0%	53.5%	51.9%
		TT	Count	18	13	31
			% within hypertension	29.0%	18.3%	23.3%
	Total		Count	62	71	133
			% within hypertension	100.0%	100.0%	100.0%

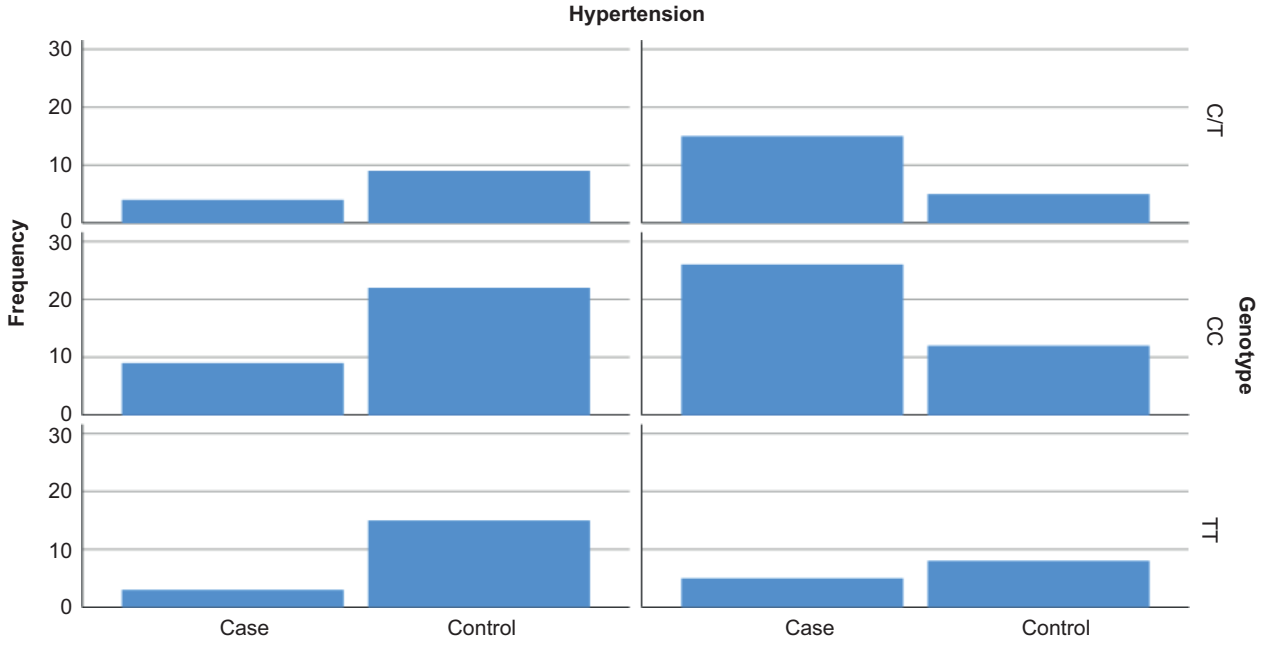

FIGURE 11. Correlation of genotype with hypertension of participants.

As a result of the presence of SARS-CoV-2, changes in the ACE2 rs1514283 SNP at the binding interface, among other factors, may have an impact on the virus's expression and affinity for SARS-CoV-2. To compare allele frequencies and expression patterns between two different populations, the ACE2 rs1514283 SNP was investigated in different populations. According to our findings, some variations in the prevalence of COVID-19 and rates of mortality that have been observed between two populations may be explained by these variants.[31]

It has resulted in many different publications, including one in Nature, that some variants of the ACE2 variant-S1 proteins have increased affinity, but the findings have not been confirmed by systems biology studies, even though some variants have been reported to increase the affinity in several different publications. Our study includes one immediate follow-up to determine the role played by population-specific rs1514283 SNP of ACE2 and host factor in the susceptibility of humans to SARS-CoV-2 are required. As a result of the publication of this finding, these will be conducted as soon as possible.[22,23]

Also important is the promotion of the use of multidisciplinary tools and cutting-edge "omics" technologies to define a comprehensive extent of interindividual differences in immune response and subsequent susceptibility affected by genetic polymorphism. Meanwhile, we should conduct a large-scale sequencing project in severely diseased patients in each population, with a particular emphasis on ACE2 rs1514283 SNP sequencing, while we wait for this to happen. The findings of this research should allow them in identifying highly specific sensitive markers for different populations within each population.[27]

Polymorphic variants in the rs1514283 SNP ACE2 gene, which have been linked to a number of infections such as cardiomyopathy, type 2 diabetes, and hypertension are associated with a poor prognosis in the COVID-19 study population, may be responsible for these diseases, according to the researchers. Overexpression of the ACE2 gene investigated by rs1514283 SNP is particularly noteworthy, according to the findings, because it may explain why older populations, including children,

TABLE 10. Correlation of genotype with history of respiratory disease of participants.

Group				History of respiratory disease		Total
				Absence	Presence	
Case	Genotype	C/T	Count	4	15	19
			% within history of respiratory disease	26.7%	31.9%	30.6%
		CC	Count	10	25	35
			% within history of respiratory disease	66.7%	53.2%	56.5%
		TT	Count	1	7	8
			% within history of respiratory disease	6.7%	14.9%	12.9%
	Total		Count	15	47	62
			% within history of respiratory disease	100.0%	100.0%	100.0%
Control	Genotype	C/T	Count	8	6	14
			% within history of respiratory disease	16.0%	28.6%	19.7%
		CC	Count	25	9	34
			% within history of respiratory disease	50.0%	42.9%	47.9%
		TT	Count	17	6	23
			% within history of respiratory disease	34.0%	28.6%	32.4%
	Total		Count	50	21	71
			% within history of respiratory disease	100.0%	100.0%	100.0%
Total	Genotype	C/T	Count	12	21	33
			% within history of respiratory disease	18.5%	30.9%	24.8%
		CC	Count	35	34	69
			% within history of respiratory disease	53.8%	50.0%	51.9%
		TT	Count	18	13	31
			% within history of respiratory disease	27.7%	19.1%	23.3%
	Total		Count	65	68	133
			% within history of respiratory disease	100.0%	100.0%	100.0%

are greatly susceptible to SARS-CoV-2 disease when compared to younger individuals.[28]

As a result of having lower levels of sACE2 andvitamin D in their blood, previous research has suggested that they are less protected from ARDS. Because it is believed that promoting specific DNA methylation of the ACE2 gene may reduce susceptibility to infection and severity of disease in the elderly, early zinc and vitamin D supplementation, in particular, may be beneficial. Our study investigates the correlation of severity of infection as a marker for analysis.[21,37]

According to the correlation of history of respiratory disease with the severity of COVID-19, this study discussed the age-related inflammation that has been shown to reduce the expression of ACE2 in type II pneumocytes and infection of damaged alveolar epithelia, both of which are detrimental to lung function; therefore, it has been demonstrated

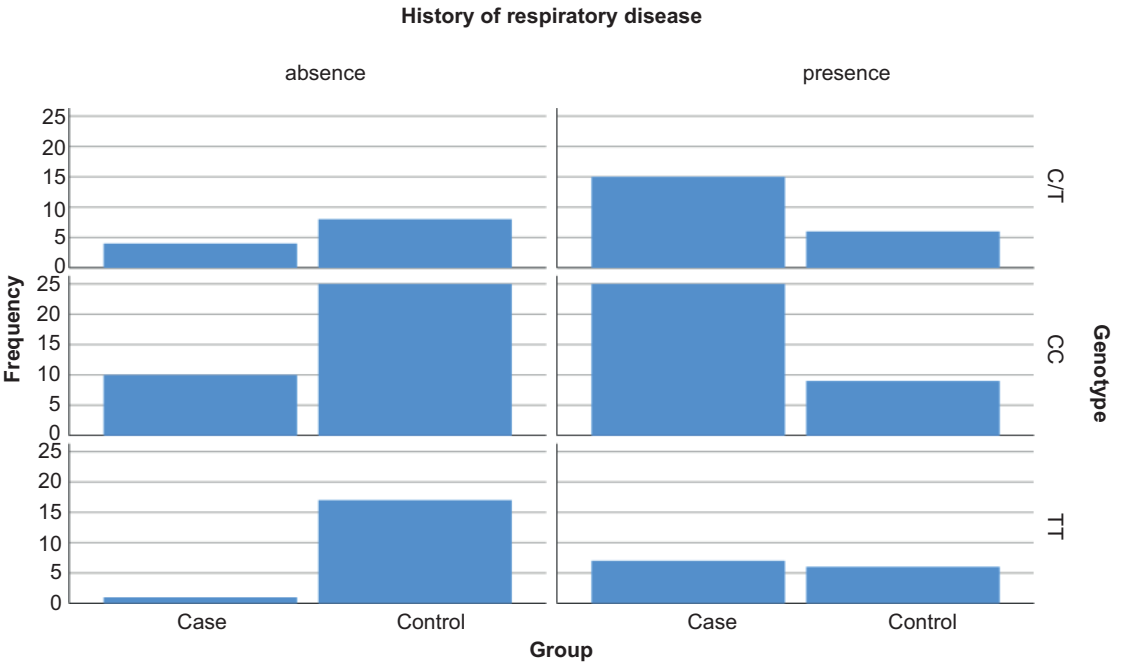

FIGURE 12. Correlation of genotype with history of respiratory disease of participants.

TABLE 11. Correlation of genotype with COVID-19 severity disease.

Group				COVID-19 Severity		
				Moderate	Severe	Total
Case	Genotype	C/T	Count	6	13	19
			% within COVID-19 severity	28.6%	31.7%	30.6%
		CC	Count	11	24	35
			% within COVID-19 severity	52.4%	58.5%	56.5%
		TT	Count	4	4	8
			% within COVID-19 severity	19.0%	9.8%	12.9%
	Total		Count	21	41	62
			% within COVID-19 severity	100.0%	100.0%	100.0%

that decreasing age-related inflammation improves lung function.[24,38]

CONCLUSIONS

The finding in this study refers to the accurate correlation between the ACE2 rs1514283 SNP and the incidence of COVID-19 in this population. These ACE2 rs1514283 SNP variants and epigenetic factors help improve our understanding of the COVID-19 disease. In particular, we were interested in findings on how a person's susceptibility to SARS-CoV-2 infection is influenced by their history of respiratory disease, the severity of COVID-19

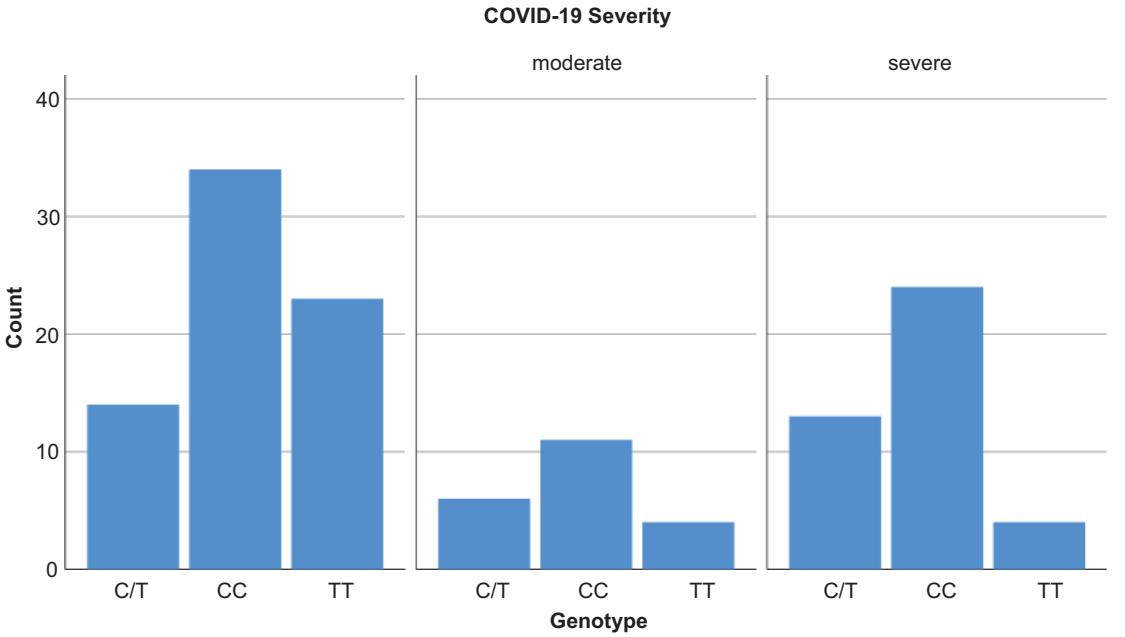

FIGURE 13. Correlation of genotype with COVID-19 severity disease.

infection, their gender, BMI, weight, and age. We concluded that the severity of COVID-19 and the area of residence were related to allele mutations of ACE2 rs1514283 SNP.

ETHICAL APPROVAL

The study protocol was approved by the Iraqi Ethical Committee at the Departments of Microbiology, College of Medicine, University of Al-Qadisiyah, Iraq.

CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

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