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The relationship between COVID-19, depressive disorder, and anxiety: a bidirectional Mendelian randomization study

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Background: Previous clinical studies have found that negative mental states such as depression and anxiety are closely related to COVID-19 infection. We used Mendelian randomization (MR) to explore the relationship between depression, anxiety, and COVID-19 infection.

Methods: Our data were based on publicly available GWAS databases. The COVID-19 samples were obtained from the COVID-19 Host Genetics Initiative (HGI). The depression samples were obtained from the Psychiatric Genomics Consortium (PGC). The anxiety samples were derived from the Finngen database. We used inverse-variance weighting (IVW) as the primary analysis method, with weighted median, MR Egger, and multivariate MRI adjustment.

Results: There was no causal effect of different COVID-19 infection statuses on depression and anxiety as determined by MR analysis. In addition, in the reverse MR analysis, we found a significant causal effect of anxiety on severe symptoms after COVID-19 infection. The results of the MR Egger regression, weighted median, and weighted mode methods were consistent with the IVW method. Based on sensitivity analyses, horizontal pleiotropy was unlikely to influence the final results.

Conclusion: Our findings indicate that anxiety is a risk factor for severe symptoms following COVID-19 infection. However, the mechanism of interaction between the two needs further investigation.

KEYWORDS

COVID-19, anxiety, depression, Mendelian randomization, GWAS

1. Introduction

From 2019 to 2022, COVID-19 spread worldwide, causing severe public health issues on a global scale. It is an infectious disease caused by the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), with an estimated 2.75 billion persons at risk of infection (1). Despite the end of the pandemic, many patients have been found to have acute SARS-CoV-2 sequelae, also known as long COVID or post-COVID-19 syndrome (2). The World Health Organization (WHO) defines it as a condition in which individuals who have been diagnosed or may have been infected with SARS-CoV-2 in the past have persistent symptoms within 3 months of onset that persist for at least 2 months and cannot be explained by an alternative diagnosis (3).

The main symptoms of COVID-19 sequelae include shortness of breath, cognitive dysfunction, fatigue, anxiety, and depression (4). Compared to the latest WHO incidence

rates for common mental health disorders, the incidence of depression in patients with COVID-19 was three times higher (15.97%) than in the general population; The prevalence of anxiety disorders is four times higher than in the general population (15.15% higher than in the general population) (5).

Depression is a prevalent mental illness that affects many individuals. In clinical practice, the most common symptoms are a depressed mood, a lack of interest, and impaired cognitive function (6). According to the most recent data, there are approximately 264 million patients worldwide (7). Major depressive disorder (MDD) can even lead to suicide and death. Depression has arisen as a risk factor for numerous illnesses. Many studies have shown that there is a significant increase in the incidence of depression in people infected with COVID-19 (8). Clinical studies have suggested that anxiety and depression are risk factors for COVID-19 infection and will lead to a longer recovery period after COVID-19 infection (9, 10). Due to the negative effects of social isolation and disruptions in health services on people's mental health and wellbeing, researchers believe that the increase in depression following COVID-19 infection is likely to be comparable to the increase following other previous pandemics, such as SARS (severe acute respiratory syndrome) and MERS (Middle East respiratory syndrome coronavirus) (4, 11).

Genetic factors significantly influence the susceptibility to and the severity of a wide range of infectious diseases and psychiatric disorders. Several recent studies have found the same genetic factor linking psychiatric disorders and infectious diseases. The presence of numerous SNP sites on the HLA gene associated with psychiatric disorders and mutations in these sites may affect the immune response to foreign antigens, which may account for the increased incidence of infections and inflammation in patients with schizophrenia and bipolar disorder and their parents (12). A large Danish genomic study identified 90 SNPs associated with mental disorders and susceptibility, most notably rs6447952 (13). Chen analyzed GWAS data from populations with psychiatric disorders and COVID-19 infections utilizing polygenic risk scores and found that genetic susceptibility to psychiatric disorders correlated with the risk of COVID-19 and severe COVID-19 (14).

Mendelian randomization (MR) is an epidemiological research technique that uses genetic variants as instrumental variables to infer the causality of a risk factor because it employs genetic variants as instrumental variables (15, 16). Mendelian randomization is independent of environmental factors and self-selected lifestyle choices (17). When the sample size is adequate, and the genetic variant is not associated with potential confounders, the quasi-random assignment of that variant outside of the exposure level ought to produce groups with nearly identical characteristics on average. MR analysis is now widely used to analyze causal relationships between diseases and risk factors, e.g., between gut microbes and disease, between two different diseases, and between metabolites and disease (18). Therefore, we used Mendelian randomization to determine whether COVID-19 as the exposure and depression/anxiety as the outcome were directly causally related.

2. Materials and methods

2.1. Design of experiment

We hereby briefly describe the design of the bidirectional MR between COVID-19 and depression/anxiety. Using pooled data from genome-wide association studies (GWAS), we performed two MR analyses to examine bidirectional associations between various COVID-19 statuses and depression/anxiety. Reverse MR analyses used depression/anxiety as exposure and distinct COVID-19 statuses as outcomes. Figure 1 depicts the fundamental hypotheses of MR. Using three guiding principles, this study hypothesizes the following (17, 19, 20):

- (1) There is a substantial association between genetic variation and exposure.
- (2) Genetic mutations are unrelated to other confounding variables.
- (3) Only exposure is associated with genetic variation and outcome.

Based on summary statistics available to the public, this research did not require ethical approval.

2.2. Data sources

We attempted to perform MR analysis using the COVID-19 GWAS data. The COVID-19 dataset was obtained from the COVID-19 Host Genetics Initiative (HGI). GWAS provided us with the association between COVID-19 and COVID-19 genetic associations of phenotypes. The GWAS yielded three phenotypes: (1) COVID-19 patients and the general population (38,984 cases and 1,644,784 controls); (2) hospitalized COVID-19 patients and the general population (3,159 cases and 7,206 controls); and (3) patients with severe respiratory confirmed COVID-19 and the general population (5,101 cases and 1,383,241 controls) (21). Depression data were obtained from the Psychiatric Genomics Consortium (PGC), which currently contains 807,553 individuals (246,363 cases and 561,190 controls) (22, 23). The data on patients with anxiety disorders were obtained from the Finngen database (40,191 cases and 277,526 controls). To exclude the influence of ethnicity, we chose a cohort of European populations. Details and sources of the data are given in Table 1.

2.3. Screen of instrumental variable (IV) for MR analysis

In order to obtain appropriate instrumental variables from different GWAS data, we first selected genome-wide significant SNPs ($p < 5 \times 10^{-8}$) (24). To ensure linkage disequilibrium of instrumental variables, we chose kb = 10,000, r² < 0.001 as a condition. Finally, in order to evaluate the tool strength, we made sure the F > 10 ones were used as instrumental variables (25, 26). We then harmonized the exposure and outcome datasets



TABLE 1 Specific information and sources of GWAS data.

Phenotype	Trait contains ID		Source
COVID-19	Very severe respiratory confirmed COVID-19	Very severe respiratory confirmed COVID-19 A2_ALL_eur_leave_23andme	
	Hospitalized COVID-19	B2_ALL_eur_leave_23andme	
	COVID-19	C2_ALL_eur_leave_23andme	
Depression	Major depression	mdd2019edinburgh	https://pgc.unc.edu/for-researchers
Anxiety	Anxiety disorders (more control exclusions)	Psychiatric endpoints from Katri Räikkönen	https://r9.finngen.fi/

to obtain genetic instrument effects on the outcome and to remove palindromic SNPs.

2.4. Statistical analysis

Using a random-effects inverse variance weighting (IVW) method, we estimated the bidirectional causality between COVID-19 status and depression/anxiety. The IVW method presupposes that all MR assumptions are legitimate. However, IV influenced the results through other pathways, indicating that horizontal pleiotropic effects may exist and that estimates of IVW causality may be biased. Therefore, we conducted sensitivity analyses utilizing the MR Egger and weighted median methodologies, allowing us to estimate causality accurately even in the presence of invalid SNPs.

As MR relies on the three central IV assumptions of the primary analysis (Figure 1), we hereby describe the methods used to evaluate or demonstrate the validity of these assumptions. The correlation hypothesis calculates r^2 , which indicates the proportion of the exposure variable's variation that can be explained by genetic variation. We calculated the *f*-statistics to evaluate the instrumental intensity of the relationship between IV and interest exposure risk. *F* represents weak instrumental vigor. MR Egger regression intercepts and their respective 95% confidence intervals (CIs) were utilized to examine the extent to which directional pleiotropy, which precludes limiting assumptions, leads to bias in arbitrary estimates. Moreover, horizontal pleiotropy was evaluated using the Mendelian

randomized pleiotropy residuals and outliers (MR-PRESSO) global test, and the outlier SNPs were excluded using the MR-PRESSO outlier test. Additionally, after removing the peripheral IV, we examined whether there was a statistically significant difference between the new IV and the previous one. Using Cochran's Q statistic and funnel diagrams, we also examined the IVW and MR Egger methods for heterogeneity. Then, various sensitivity analyses (such as leave-one-out and individual SNP analyses) were conducted to determine whether individual SNPs affected primary causality. Using odds ratios (OR) and 95% confidence intervals (CIs), we estimated causality for binary outcomes. We presented causal estimates, p-values, and their standard errors for both binary and continuous outcomes. Each p-value is bilateral. All analyses were conducted utilizing the R (version 4.3.0, www.r-project.org) TwoSampleMR and Mendelian randomization packages.

3. Results

3.1. Screening of genetic tools

We obtained 51 SNPs as instrumental variables in depression, 54 in anxiety, 29 in very severe respiratory confirmed COVID-19, 33 in COVID-19 hospitalization COVID-19 SNPs, and 15 SNPs in COVID-19 infection, which met the generally accepted genomewide significance threshold ($p < 5 \times 10^{-8}$, $r^2 < 0.001$, kb = 10,000) for exposure. However, anxiety was adjusted to a significance threshold of $p < 5 \times 10^{-6}$ because only a few SNPs were acquired. Detailed data are provided in Supplementary material 1.

TABLE 2 Association of different COVID-19 statuses with depression in MR analysis.

Exposures	Outcome	Method	NSNP	В	SE	PVAL
Very severe respiratory confirmed COVID-19	Depression	MR Egger	25	-0.004750305	0.014698014	0.749468684
		Weighted median	25	-0.003462482	0.009228979	0.707530372
		Inverse variance weighted	25	-0.007485112	0.008077615	0.354108922
		Simple mode	25	0.000260369	0.016283651	0.987374874
		Weighted mode	25	-0.004118848	0.009492068	0.668218554
Hospitalized COVID-19		MR Egger	30	-0.014133196	0.019894181	0.48332025
		Weighted median	30	-0.005353026	0.014435836	0.710775237
		Inverse variance weighted	30	-0.007569588	0.010585632	0.474558809
		Simple mode	30	-0.015398662	0.024174515	0.529135197
		Weighted mode	30	-0.00839524	0.015219947	0.585451845
COVID-19		MR Egger	13	0.082818581	0.052502673	0.143004122
		Weighted median	13	0.015392815	0.033484634	0.645733096
		Inverse variance weighted	13	0.008645516	0.032104582	0.787704783
		Simple mode	13	-0.006519406	0.045052035	0.887343158
		Weighted mode	13	0.021868586	0.033654926	0.528071848

TABLE 3 Association of different COVID-19 statuses with anxiety in MR analysis.

Exposures	Outcome	Method	NSNP	В	SE	PVAL
Very severe respiratory confirmed COVID-19	Anxiety	MR Egger	11	0.10405562	0.075761299	0.202848524
		Weighted median	11	0.00313751	0.032409234	0.922877973
		Inverse variance weighted	11	-0.001468431	0.024205732	0.951626322
		Simple mode	11	-0.025030973	0.051538129	0.637660477
		Weighted mode	11	0.024661144	0.036202126	0.511206489
Hospitalized COVID-19		MR Egger	31	0.005487875	0.037303033	0.884058454
		Weighted median	31	-0.019340422	0.032976124	0.557541073
		Inverse variance weighted	31	-0.004411899	0.020924363	0.833004451
		Simple mode	31	-0.06280267	0.060541055	0.307859095
		Weighted mode	31	-0.022371918	0.032397031	0.495154045
COVID-19		MR Egger	12	0.160125115	0.152084869	0.317177605
		Weighted median	12	-0.027206087	0.094539137	0.773518271
		Inverse variance weighted	12	0.028543326	0.080379876	0.722510653
		Simple mode	12	0.128634762	0.170710516	0.46695675
		Weighted mode	12	0.106043511	0.117072928	0.384458108

3.2. Causal effects of COVID-19 infection on anxiety and depression

As shown in Tables 2, 3 and Figure 2, the IVW results indicated no significant correlation between the genetically predicted COVID-19 infection profiles and depression and anxiety. For example, very severe respiratory confirmed COVID-19 showed no significant association with anxiety (OR, 0.99; 95% CI, 0.95– 1.04; P = 0.95) and depression (OR, 0.99; 95% CI, 0.97–1.01; P = 0.35). Similarly, COVID-19 requiring hospitalization exhibited no significant relation to anxiety (OR, 0.83; 95% CI, 0.96– 1.04; P = 0.83) and depression (OR, 0.99; 95% CI, 0.97–1.01; P = 0.47), while COVID-19 infection also presented with no significant association with anxiety (OR, 0.83; 95% CI, 0.96– 1.04; P = 0.83) and depression (OR, 1.01; 95% CI, 0.95–1.07; P = 0.79). Further analyses using MR Egger regression, weighted median, and weighted mode methods continued to show no causal association between different COVID-19 infection statuses and depression/anxiety. Detailed information can be found in Supplementary material 2.

exposure	outcome	method		NSNP Pvalue
Very severe respiratory confirmed covid		MR Egger Weighted median Inverse variance weighted Simple mode Weighted mode	P ■ 4	 25 0.749468684 25 0.707530372 25 0.354108922 25 0.987374874 25 0.668218554
Hospitalized covid	depression	Weighted mode MR Egger		30 0.48332025 30 0.710775237 30 0.474558809 30 0.529135197 30 0.585451845 13 0.143004122
Covid		Weighted median Inverse variance weighted Simple mode Weighted mode	0.7 1	13 0.645733096 13 0.787704783 13 0.887343158 13 0.528071848 1.5
Very severe respiratory		MR Egger Weighted median		11 0.202848524 11 0.922877973 11 0.951626322
confirmed covid		nverse variance weighted Simple mode Weighted mode MR Egger Weighted median		11 0.637660477 11 0.511206489 31 0.884058454 31 0.557541073
Hospitalized covid	anxiety	nverse variance weighted Simple mode Weighted mode MR Egger		31 0.833004451 31 0.307859095 31 0.495154045 12 0.317177605
Covid		Weighted median nverse variance weighted Simple mode Weighted mode		12 0.773518271 12 0.46695675 12 0.384458108
FIGURE 2 MR analysis of dep	ression and anxi	0 ety as outcomes using different infections	0.5 1 of COVID-19 as exposure.	2

3.3. Causal effects of anxiety and depression on COVID-19 infection

We further validated the relationship between different COVID-19 infection statuses and depression/anxiety using directional MR. As shown in Table 4 and Figure 3, the results differ from previous ones in that we found a possible correlation between anxiety and severe illness after COVID-19 infection. We set depression and anxiety as the exposure factors and different COVID-19 infection statuses as outcomes. Depression for very severe respiratory confirmed COVID-19 (OR, 0.82; 95% CI, 0.67–1.01; P = 0.06), depression for hospitalized COVID-19 (OR, 0.91; 95% CI, 0.81–1.04; P = 0.16), and depression for COVID-19 (OR, 1.00; 95% CI, 0.95–1.05; P = 0.86). Anxiety for very severe

respiratory confirmed COVID-19 (OR, 1.12; 95% CI, 1.00–1.24; P = 0.05), anxiety for hospitalized COVID-19 (OR, 1.03; 95% CI, 0.96–1.11; P = 0.40), and anxiety for COVID-19 (OR, 1.00; 95% CI, 0.98–1.03; P = 0.74).

4. Discussion

In this study, we explored whether there is a causal relationship between COVID-19 infection and anxiety/depression. As described in the results, we found that there does not appear to be a highly significant causal link between COVID-19 infection and anxiety/depression. Only anxiety disorders were causally associated with severe reactions after COVID-19 infection, and anxiety

Exposures	Outcome	Method	NSNP	В	SE	PVAL
Depression	Very severe respiratory confirmed COVID-19	MR Egger	46	0.598459	0.570471	0.299878
		Weighted median	46	-0.06259	0.129955	0.630088
		Inverse variance weighted	46	-0.19771	0.105107	0.059962
		Simple mode	46	-0.24836	0.311976	0.430156
		Weighted mode	46	0.200381	0.2996	0.507021
Anxiety	-	MR Egger	49	0.006646308	0.139774233	0.962276119
		Weighted median	49	0.086616086	0.075381972	0.250543946
		Inverse variance weighted	49	0.109121703	0.055551695	0.049492166
		Simple mode	49	0.011127597	0.145311095	0.93927776
		Weighted mode	49	0.056740439	0.110460996	0.609839692
Depression	Hospitalized COVID-19	MR Egger	46	0.495696	0.333149	0.143907
		Weighted median	46	-0.09427	0.082273	0.251845
		Inverse variance weighted	46	-0.08681	0.061954	0.161135
		Simple mode	46	-0.01787	0.178002	0.920477
		Weighted mode	46	-0.05624	0.176718	0.751766
Anxiety		MR Egger	49	-0.040552251	0.097312214	0.678778072
		Weighted median	49	0.08425579	0.045937605	0.066633892
		Inverse variance weighted	49	0.031754872	0.037417872	0.396073183
		Simple mode	49	0.133054135	0.104330645	0.208336838
		Weighted mode	49	0.104582907	0.078908792	0.191324383
Depression	COVID-19	MR Egger	47	0.05368	0.140077	0.703362
		Weighted median	47	0.008824	0.034224	0.796528
		Inverse variance weighted	47	-0.0046	0.025446	0.856553
		Simple mode	47	-0.0099	0.075865	0.896783
		Weighted mode	47	0.006712	0.068608	0.922493
Anxiety		MR Egger	51	0.012916928	0.040546914	0.751408466
		Weighted median	51	0.012513017	0.020452191	0.540658208
		Inverse variance weighted	51	0.004884418	0.014890149	0.742888848
		Simple mode	51	0.046435184	0.042932531	0.284625993
		Weighted mode	51	0.042550178	0.038202593	0.270689266

TABLE 4 Association of anxiety/depression with different COVID-19 statuses in MR analysis.

disorders may be a risk factor for severe illness after COVID-19 infection.

Previous observational clinical studies have found that more than 50% of the infected patients have depression or anxietylike symptoms after COVID-19 infection, and anxiety and depression are also the typical symptoms of COVID-19 sequelae considered by the WHO (27, 28). In addition, researchers from the United Kingdom discovered that those infected with COVID-19 who were hospitalized were 49% more likely to be diagnosed with depression, anxiety, or a mental condition than those infected but not hospitalized (29, 30). This finding is consistent with what was discovered in the Nordic countries, where patients who had been hospitalized for more than 7 days had a significantly higher risk of depression and anxiety than those who had not been hospitalized (31). According to the results of our investigation, the presence of COVID-19 infection, the severity of the COVID-19 disease, and hospitalization for COVID-19, all appeared to have no direct causal effect on the development of depression or anxiety. As a consequence of the findings of other investigations that have been published, a number of theories have been developed. One possible explanation for the depressive and anxious symptoms exhibited by patients is that these conditions are at least partially caused by the patients' social environment (32). This may include social isolation and high levels of stress. The main sources of stress during the COVID-19 pandemic were fear of infection, frustration, boredom, lack of supplies, and economic loss (33). Fear of infection and occupational stress (increased work pressure on healthcare workers during a pandemic, increased unemployment due to changes in

exposure	outcome	method		NSNP Pvalue
	Very severe respiratory confirmed covid	MR Egger Weighted median Inverse variance weighted Simple mode Weighted mode		 49 0.962276119 49 0.250543946 49 0.049492166 49 0.93927776 49 0.609839692
Anxiety	Hospitalized covid	MR Egger Weighted median Inverse variance weighted Simple mode Weighted mode		 49 0.678778072 49 0.066633892 49 0.396073183 49 0.208336838 49 0.191324383 51 0.751408466
	Covid	MR Egger Weighted median Inverse variance weighted Simple mode Weighted mode		51 0.731408466 51 0.540658208 51 0.742888848 51 0.284625993 51 0.270689266
		0.5 0.	7 1 1.5	
	Very severe respiratory confirmed covid	MR Egger Weighted median Inverse variance weighted Simple mode Weighted mode MR Egger		 46 0.299878388 46 0.630087896 46 0.059962301 46 0.430155907 46 0.507021414 46 0.143906588
Depression	Hospitalized covid	Weighted median Inverse variance weighted Simple mode Weighted mode MR Egger	■ 	 46 0.251845249 46 0.161134949 46 0.920477458 46 0.751765546 47 0.703361533
	Covid	Weighted median Inverse variance weighted Simple mode Weighted mode	-4 0 1 2 4	 47 0.796528366 47 0.856553222 47 0.89678327 47 0.922492747
FIGURE 3 MR analysis of di	fferent infections of	COVID-19 as outcomes using depressic	on and anxiety as exposure.	

the socio-economic environment, increased uncertainty about the future due to a pandemic and thus academic stress, etc.) were the main causes of increased stress during a pandemic (34-37). Excessive stress is one of the major causes of mental disorders such as depression and anxiety (38).

During the COVID-19 pandemic, many individuals have been required to maintain a safe distance from one another to prevent the spread of COVID-19, resulting in social isolation (39). It is believed that social isolation causes sleep disturbances (40). Insomnia and sleep disorders are recognized as major risk factors for the development of depression and anxiety (41). Regarding social isolation-induced insomnia as a mechanism leading to melancholy and anxiety, scientists believe social isolation results in hypothalamic–pituitary–adrenal (HPA) axis dysfunction (42). The disorder of the HPA axis induces hyperexcitation and sleeplessness in the human body (43). The prevalence of insomnia symptoms (36.7%) and insomnia disorders (17.4%) during the COVID-19 pandemic was approximately double the prevalence reported during non-pandemic periods, with higher rates in Brazil, Canada, the United Kingdom, and the United States, where depression and anxiety rates have also increased (44).

Intensive research on inflammation and psychiatry suggests that immune system perturbations triggered by infection may specifically promote psychopathology, increasing the psychological stress of living with a potentially fatal illness and stress-related inflammation (45). Interactions between the innate and adaptive immune system and neurotransmitters underlie mood disorders, psychosis, and anxiety disorders. Similar results have been observed in the past for similar pandemics. Some researchers believe that this is due to the virus infecting the neural tissue, resulting in the latter's inflammatory response. It has been demonstrated that coronavirus has neurophilic properties and can infect brain tissues. Additionally, COVID-19 has been detected in the cerebrospinal fluid (46–49).

Mental factors such as depression and anxiety are important risk factors for many diseases, such as cardiovascular diseases, digestive tract diseases, and susceptibility to viruses (50, 51). Our study found a genetic causal link between anxiety disorders and symptom severity following COVID-19 infection. This is consistent with the current clinical studies that have found anxiety or depression to be a risk factor for COVID-19 infection. Patients who are depressed or anxious are not only more likely to be infected with COVID-19 than the general population but also appear to have more severe symptoms after infection (52). In addition, some studies have found that patients with depression and anxiety have a longer recovery period after COVID-19 infection, which may be related to immune dysregulation caused by the HPA system (53). The detection of serum cortisol in infected patients revealed that COVID patients had higher cortisol levels and that elevated cortisol levels were positively correlated with mortality after COVID-19 infection (54, 55). Cortisol plays a key role in the development of depression and anxiety. Is it the elevated cortisol caused by depression and anxiety that makes patients more susceptible to COVID-19 infection and more severe symptoms? Whether the increased cortisol caused by COVID-19 may lead to subsequent increases in depression and anxiety requires further research.

The very interesting finding in our study is that anxiety seems to be a risk factor for developing severe illness after a COVID-19 infection. However, depression does not seem to increase the risk of developing severe illness after COVID-19 infection. Anxiety disorders are often accompanied by autonomic arousal compared to depression (56). In addition, clinical studies have found that depressed patients have lower catecholamine levels than the normal population, while anxious patients have higher catecholamine levels than the normal population (57, 58). During the inflammatory response, catecholamine concentrations are elevated, which in turn exacerbate inflammation by promoting the secretion of pro-inflammatory cytokines such as IL-6, IL-1β, and tumor necrosis factor, especially in myeloid cells (59). This inflammatory response may be exacerbated by the higher catecholamine levels in patients with anxiety disorders themselves, leading to a more severe inflammatory response after COVID-19 infection than in normally infected individuals, with a higher chance of causing a severe reaction.

However, the results regarding the causal relationship between anxiety and the risk of severe illness after COVID-19 infection do not seem to be strong. Meanwhile, a large number of clinical studies have shown that a poor psychological state prior to COVID-19 infection is a key factor in triggering severe COVID-19 disease after infection (60). Chen et al. also analyzed GWAS data from the UK Biobank. They found that depression and anxiety were more likely to result in severe and fatal COVID-19 infections (14). We therefore consider our results to be plausible.

This study also has some limitations. First, the data we selected were from a European population lacking generalizability. We also needed more specific raw data for subgroup analyses. In future studies, we will increase the sample size, expand the population to include different ethnic groups, and collect appropriate subgroup information for more in-depth analyses.

5. Conclusion

We used a much broader population sequence than in previous studies. Our study identified anxiety disorders as a risk factor for the development of severe symptoms following COVID-19 infection. Patients with anxiety disorders are more likely to have severe symptoms after COVID-19 infection than the general population. Although this association does not appear to be strong, given that anxiety disorders are risk factors for a wide range of diseases, we should pay more attention to people with anxiety disorders during future infectious disease pandemics.

Data availability statement

The original contributions presented in the study are included in the article/Supplementary material, further inquiries can be directed to the corresponding author.

Author contributions

LZ and ZH conceived the idea for this study. LZ, GS, and SJ obtained genetic data and performed data analysis. LZ and SJ were responsible for revising the article. CX and LY explained the results of the data analysis. ZH wrote the article. All authors approved the submitted version.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Supplementary material

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fpsyt.2023. 1257553/full#supplementary-material

SUPPLEMENTARY MATERIAL 1 Instrumental variables SNPs.

SUPPLEMENTARY MATERIAL 2 MR results between COVID and anxiety/depression.

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