



Original Data

Genetic predictors of attempted suicide among South Indian adolescents and young adults: A case-control study

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ABSTRACT

Background: Suicide among adolescents and young adults is an alarming public health issue globally. Though studies suggest the link between genetic factors and suicidal behavior, there is a paucity of studies of specific genetic variants in adolescents and young adults. Hence this study explored the genetic predictors for attempted suicide among adolescents and young adults, by studying the genetic basis of serotonin and dopamine synthesis, transport, and degradation machinery.

Methods: A Case-control association study was conducted comprising individuals with attempted suicide (cases n = 80), 13–29 years of age, belonging to Malayalam speaking Dravidian population, and attending a tertiary care center in South India. Age, sex, and ethnicity matched controls (n = 267) with no history of attempted suicide were also considered from the same ethnic population. Genotyping was performed for functionally critical SNP in serotonin receptor, Tryptophan hydroxylase, Tyrosine hydroxylase, and Catechol-o-methyl transferase. Statistical significance for allelic and genotypic comparisons and their odds ratios were computed.

Results: The Tyrosine Hydroxylase THrs2070762 and Tryptophan Hydroxylase TPH1rs211105 genetic variants showed a statistically significant association with attempted suicide phenotype.

Conclusion: The study suggests that the genetic variants in Tyrosine Hydroxylase and Tryptophan Hydroxylase are predictive of attempted suicide among adolescents and young adults. Understanding the genetic variations will help in identifying and managing high-risk individuals.

Introduction

Rising adolescent and youth suicide rates are an alarming public health concern worldwide. The World Health Organization (World Health Organization, 2024) estimates suicide as the third leading cause of mortality among ages 15–29 years. It has been observed that the age group 18–30 years was the most vulnerable age group, accounting for 34.6 % of total suicides in India during the year 2022 (National Crime Records Bureau, 2022). Youth suicidal behavior is a complex phenomenon driven by diverse biochemical, genetic, psychological, and social factors that act together (Cha et al., 2018). Learning more about these risk factors and precursors of suicidal behavior in youth is important for understanding this complex behavior, identifying the high-risk group, and planning interventions for the prevention of suicidal behavior

among them.

Heterogeneity of the persons who attempt suicide is an important clinical observation that has been reported earlier (Turecki and Brent., 2016). The risk factor profile for youth suicidal behavior tends to be different among high and low-and middle-income countries like India, with the latter having a higher representation in suicide statistics (Renaud et al., 2022; Gupta and Basera, 2023). The clinical heterogeneity may be due to an underlying genetic variation, and hence, it is also important to investigate the genetic variables associated with suicide attempts in our population. While genetics define the threshold of environmental triggers, the research on this topic has been particularly sparse (Vaquero-Lorenzo and Vasquez, 2020; Turecki, 2014). Significant shared heritability has been observed among suicide attempts and the probability of attempting suicide (Ruderfer et al., 2020). Genetic

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susceptibility to suicide has been demonstrated by various genetic studies with a lack of consistent observation (Mirkovic et al., 2016).

Sufficient evidence for the genetic heritability of suicidal behaviors exists, but there has been little knowledge about the specific genes linked to suicide. Results from the candidate-gene and genome-wide association studies (GWAS) are often reported to be questionable, for lack of statistical robustness and uniformity of study designs (Mirkovic et al., 2016). A polygenic model, with a large number of genetic variants contributing to a small modulation of risk, has been proposed to understand the genetic factors underlying suicidal behavior (DiBlasi et al., 2021; Mirkovic et al., 2016). The lack of consistency among different genetic studies might be due to genetic heterogeneity which are critical in defining the threshold for environmental triggers and thereby impacting the phenotypic differences. A precise understanding of the genetic system may help in addressing the large heterogeneity expressed within the groups of suicidal behavior (Erlangsen et al., 2020).

Findings from various neuroendocrine and biochemical studies suggest the serotonergic system as the most probable biological system associated with suicidality, impulsive violence, and anxiety (Wisłowska-Stanek et al., 2021; Pandey, 2013). Dopaminergic system, with its important role in behavioral facilitation and aggression, has also been explored for potential contributions to suicidal behavior (Brundin et al., 2017; Suri et al., 2023). Many candidate genes and genome-wide association studies have further explored a connection between neurotransmitter processing, in particular, the serotonergic and dopaminergic systems and suicidal behavior (Hill et al., 2020; Abou Chahla et al., 2023). This prompted us to investigate the role of critically important SNPs in the synthesis, transport, and degradation machinery of the serotonin and dopamine system in contributing to the genetic risk of attempted suicide among adolescents and young adults.

Materials and methods

A case-control study design was used to identify the genetic predictors of attempted suicide. A case of suicide attempt was defined as "a person 13–29 years of age, who had made an intentional act of self-harm consciously aimed at self-destruction with non-fatal outcome". Cases were recruited from outpatients attending follow-up care at the Suicide Prevention Clinic, Department of Psychiatry, Government Medical College, Thiruvananthapuram, Kerala, South India. The cases included medically stable persons belonging to the native Malayalam speaking Dravidian population. The ICD-10 Classification of Mental and Behavioural Disorders: Clinical Descriptions and Diagnostic Guidelines (World Health Organization, 1992) was used in-person by a qualified psychiatrist to diagnose intentional self-harm and to assess comorbid psychiatric morbidity. Age (+2 years), sex, and ethnicity matched controls, 'who had never made any suicide attempt', were recruited from healthy donors who had no personal or family history of attempted suicide. Controls were recruited from the relatives and friends of other patients who attended the hospital for reasons other than attempted suicide. Collateral information was taken from an informant, usually a family member to verify the life-time history of suicide attempt or absence of an attempt. A case-control genetic association study was conducted on a sample of cases (n = 80) and controls (n = 267) using critical variants from the candidate genes of the serotonin and dopamine synthesis, transport, and degradation system. The study participants were recruited and psychiatric assessments were conducted at Department of Psychiatry, Government Medical College, Thiruvananthapuram, and the genetic analysis was carried out at the Human Molecular Genetics Laboratory, Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram, Kerala, India. Those with mental retardation, those with severe medical complications related to the attempt, and those not willing to give informed consent were excluded from the study. The Institution Human Ethics Committee (IEC. No.02/44/2014/MCT) has approved the study as per the guidelines of the Indian Council for Medical Research. The study is part of a bigger study that looked at the

predictors for attempted suicide among adolescents and young adults.

The study process was explained to the participants, and written informed consent was taken. In the case of those participants below eighteen years of age, informed assent was taken from them and written informed consent was taken from parents. All data was anonymized. Participant confidentiality and data protection were maintained at all stages.

Sampling and genotyping

About 5 ml of peripheral venous blood was drawn under aseptic precautions. The samples were collected in EDTA-coated tubes and were labeled using appropriate codes. DNA was isolated from the blood sample using a modified organic extraction method (Sambrook and Russell, 2001). The quality and quantity of the genomic DNA were analyzed using Nanodrop. The ratio of absorbance at 260 nm and 280 nm (A260/A280) was used to estimate the purity of the DNA.

Single nucleotide polymorphism (SNP) in each gene, namely serotonin receptor (5HTR2A), Tryptophan Hydroxylase (TPH1), Tyrosine Hydroxylase (TH) and Catechol-O-Methyl Transferase (COMT) were selected based on either functional significance, previous reports of association with suicide or tagging status in the related population. The details of the selected SNPs, and their position in the gene are given in Table 1

Genotyping of the selected SNPs were performed using Restriction Fragment Length Polymorphism (RFLP) or by KASPTM allele Specific PCR genotyping or DNA Sequencing, for each polymorphism as mentioned in the Table 2. Screened SNPs and their corresponding primers, product size, annealing temperature are shown in Table 2. PCR amplification using gene-specific primers was carried out for all the samples in the Applied Biosystems Veriti Thermal cycler. The PCR reaction mixture consisted of 1X PCR buffer, 250 μM of each deoxy-nucleoside triphosphate (dNTP), 1pmol of each primer, and 0.5–1.0 Units of Taq Polymerase. 20 ng of genomic DNA was used for each PCR reaction. The PCR was performed using initial denaturation at 94°C for five minutes followed by cycle denaturation at 94°C for 30 seconds, annealing at 50–65°C (annealing temperature of respective primers) for 30 seconds and extension at 72°C for 30 seconds, for 35–40 cycles.

The Tyrosine Hydroxylase (TH) genetic variant was screened using Restriction Fragment Length Polymorphism. In PCR-RFLP method, the Pst1 restriction enzyme was used for digestion to distinguish the variant allele present. Digestion products were resolved on 3 % agarose gels containing 0.5 μg/ml ethidium bromide. Genotyping for COMT rs4680 and rs165599 genetic variants were screened using fluorescence-based competitive allele-specific polymerase chain reaction, KASPar (KBiosciences, LGC genomics, Herts, UK) as per the manufacturer's protocol. Further, the genotype calling based on the respective allele-specific fluorescence was done by allelic discrimination utility of the SDS 7500 v2.0.5 software (Applied Biosystems, Foster City, CA) at an ambient temperature of 25°C and genotype clusters were plotted.

Tryptophan Hydroxylase and Serotonin receptor (5-HTR2A) genetic variants were screened using DNA Sequencing based on Sanger's method. 50–100 ng PCR product was used for the cycle sequencing reaction (ABI Prism Big Dye Terminator Cycle Sequencing Ready Reaction Kit, version 3.1). The extension products were purified and were analyzed

Table 1
Details of selected SNPs.

Gene	SNP ID	Alleles	Position
5-HTR2A	rs6311	G>A	Upstream variant
TPH1	rs623580	T > A	Upstream variant
	rs2111105	T > G	Intron variant
	rs10488683	T > C	Intron variant
TH	rs2070762	C>T	Intron
COMT	rs4680	A>G	Exon-Non-synonymous
	rs165599	A>G	3prime UTR(untranslated region)

Table 2
Selected SNPs and genotyping methods.

Gene Marker	Primer sequence 5'to3'	Product (bp)	Annealing temperature	Genotyping method	
5-HTR2A	-1438G/A rs6311	F-TCATTACTGGTGGGGGAAA R-TTTCCACGGGAATGGAGT	570	56°C	Sanger's sequencing
TPH1	rs623580	F-GGCTCTGGGGCTAAAAATTC R-ACTTGCCTAGATGGATTGCGAG	245	58°C	Sanger's sequencing
TPH1	rs211105	F-TCAGGTTGATGTCTAAGTTTGG R-GCAGGGAATGGGAGTGGAAATA	312	58°C	Sanger's sequencing
TPH1	rs10488683	F-CAGCCACTAGATGATCTGTCCA R-AGGCCCAATTGAAATGTCCG	372	57°C	Sanger's sequencing
TH	rs2070762	F-CAGCCCTACCAAGACCAGAC R-TGTCAGCACCTCCAAGACTG	RFLP- Pst1T-345bpC-302,43	54 °C	RFLP
COMT	Val158Metrs4680	KASPar genotyping assay		61-55TD	KASPar allelic discrimination method
COMT	rs165599	KASPar genotyping assay		61-55TD	KASPar allelic discriminationmethod

using ABI Prism 3730 DNA Analyzer (Applied Biosystems, Foster City, CA, USA). Sequence analyses were done using the ABI sequence scanner V.1.

Statistical analyses

Genotype frequencies and allelic frequencies were computed and were checked for deviation from Hardy-Weinberg equilibrium (<http://ihg2.helmholtz-muenchen.de/cgi-bin/hw/hwa1.pl>). Case-control genetic comparisons were performed using the chi-square test, allelic odds ratios (OR), and 95 % confidence intervals (CI). For all statistical analyses, a p-value of < 0.05 was considered significant. All these analyses were performed using Graph Pad Prism 5.01, San Diego, CA, USA. Due to the exploratory nature of this study, no adjustment for multiple testing was made, so as not to penalize ourselves for missing possibly important findings. For Hardy-Weinberg analyses, 5HTR2A rs6311 chi square value

was 2.63 (p = 0.10), NS; THrs2070762 chi square value 0.0118 (p = 0.91), NS; COMTrs4680 chi square value 0.3314 (p = 0.56), NS; COMTrs165599 chi square value 3.709 (p = 0.054), NS; TPH1rs623580 chi square value 1.439 (p = 0.23), NS; TPH1rs10488683 chi square value 0.2859 (p = 0.59), NS and TPH1rs211105 chi square value 22.44 (p = 0.000).HWE deviation was observed in TPH1rs211105 and this deviation is not due to genotyping error as verified from data. Besides it is observed that the GG genotype is generally very low or negligible in Indian and African population.

Results

The current study explored the association of seven SNPs selected from genes coding for dopamine and serotonin synthesis, transport, and degradation, with attempted suicide phenotype among adolescents and young adults. The genotypic and allelic frequencies of these SNPs among

Table 3
Comparison of allelic and genotypic frequencies of selected SNPs in cases and controls of attempted suicide among adolescents and young adults.

5HTR2Ars6311	TT	CT	CC	p value	T	C	p value	95 %CI	Odds Ratio
Cases	16	43	21	0.92	75	85	0.69	0.74-1.55	1.08
	0.2	0.54	0.26		0.47	0.53			
Controls	35	108	52		178	212			
	0.18	0.55	0.27		0.46	0.54			
THrs2070762	CC	CT	TT		C	T			
Cases	6	26	18	0.043*	38	62	0.014*	1.12-2.69	1.73
	0.12	0.52	0.36		0.38	0.62			
Controls	70	130	62		270	254			
	0.26	0.50	0.24		0.52	0.48			
COMTrs4680	AA	AG	GG		A	G			
Cases	10	23	17	0.84	43	57	0.57	0.74-1.74	1.13
	0.20	0.46	0.34		0.43	0.57			
Controls	59	128	80		246	288			
	0.22	0.46	0.32		0.46	0.54			
COMTrs165599	AA	AG	GG		A	G			
Cases	18	23	9	0.50	59	41	0.24	0.84-2.01	1.3
	0.36	0.46	0.18		0.59	0.41			
Controls	72	102	60		246	222			
	0.31	0.43	0.26		0.53	0.47			
TPH1rs623580	AA	AT	TT		A	T			
Cases	11	34	10	0.39	56	54	0.29	0.81-1.98	1.27
	0.2	0.62	0.18		0.51	0.49			
Controls	39	71	21		149	113			
	0.3	0.54	0.16		0.57	0.43			
TPH1rs10488683	CC	CT	TT		C	T			
Cases	10	36	17	0.09	56	70	0.07	0.96-2.26	1.48
	0.16	0.57	0.27		0.44	0.56			
Controls	40	62	29		142	120			
	0.31	0.47	0.22		0.54	0.46			
TPH1rs211105	TT	TG	GG		T	G			
Cases	48	21	1	0.0003*	117	23	0.0005*	1.63-6.43	3.24
	0.69	0.3	0.01		0.84	0.16			
Controls	118	5	2		241	9			
	0.90	0.08	0.02		0.96	0.04			

* p < 0.05 significant

ethnically matched cases and controls were analyzed. Results showed that the THrs2070762 and TPH1rs211105 genetic variants had a statistically significant association with attempted suicide phenotype (Table 3). The T allele and TT genotype in THrs2070762 were observed to be associated with attempted suicide among adolescents and young adults with an odds ratio of 1.73. Similarly, for the TPH1rs211105, the G allele ($p = 0.0005$) and TG genotype ($p = 0.0003$) was associated with attempted suicide among adolescents and young adults with an odds ratio of 3.24

Discussion

SNPs from the genes involved in serotonin and dopamine synthesis and metabolism selected on the basis of their role in emotion, cognition, aggression, and suicidal behavior (Wisłowska-Stanek et al., 2021; Mann and Rizk, 2020; Pandey, 2013; Brundin et al., 2017; Suri et al., 2023) were explored in this study. Serotonin and dopamine system has been implicated in suicide but with contradictory observations which could be due to underlying genetic and phenotypic heterogeneity. Based on the genetic variants 5HTR2A rs6311, TH rs2070762, COMT rs4680 and rs165599 and TPH1rs623580, rs10488683 and rs211105 screened in the present study, only the TH rs2070762 and TPH1rs211105 variants showed a statistically significant association with attempted suicide phenotype among adolescents and young adults.

Serotonergic system: genetic variants

Research done earlier focused on genetic polymorphisms of Tryptophan hydroxylase, the rate limiting enzyme of serotonin synthesis, the serotonin receptor genes, and the serotonin transporter (5HTT) which regulates serotonin signaling at the synapses. The studies have followed different study designs, including family-based, case-control and population-based design strategies.

Tryptophan hydroxylase (TPH1)

Earlier study using family based and case control method conducted in 88 Jewish adolescent inpatients with recent suicide attempts;40 family trios;12 family duos and 172 healthy controls had reported that Tryptophan hydroxylase A218C polymorphism had no significant association with suicidal behavior (Zalsman et al., 2001).

Among the TPH1 genetic variants explored in the current study, a statistically significant association with attempted suicide was observed with the rs211105 variant but not with rs623580 and rs10488683 polymorphisms. This observation is in contrast to an earlier observation where rs10488683 was associated with suicide attempts (Mirkovic et al., 2016; Brezo et al., 2010). Brezo et al. (2010) followed-up 1255 participants (Caucasian, Quebec) over 22 years and looked for the association of serotonergic diathesis with suicide attempts and mood disorders. The study concluded that the TPH1 gene variant rs 10488683 was specific to suicide attempts. Differences in the current study findings may probably be due to the variations in the genetic heterogeneity in the population groups explored indicating the need for an ethnic and phenotypic assessment based on genetic variants. Increased frequency of G allele and GG and GT genotypes of TPH1rs211105 in the present study is interesting as the functional significance of this allele based on GTEx data from the Genotype-Tissue Expression (GTEx) Project (2015), exhibit reduced expression of TPH. The reduced expression of this genetic variant may suggest a reduced synthesis of serotonin. Reduced serotonin levels are known to be associated with suicidal thoughts, anxiety and depression (Underwood et al., 2018; Mann and Rizk, 2020). These observations may suggest a potential functional significance of the explored genetic variant and may point towards its clinical actionability and role as a probable therapy target.

Serotonin receptor 2A (5HTR2A)

Lack of association with the HTR2A genetic variant is similar to earlier studies on 5HTR2Ars6311 that reported a lack of significant association with attempted suicide (Hofer et al., 2016). The current study results are consistent with this finding, the difference being the earlier study was conducted on patients with major depressive disorder with incomplete response to treatment. The current study did not include such patients. Another case-control study on 5HTR2Ars6313 showed association with suicidal behavior but failed to replicate in the meta-analysis (González-Castro et al., 2013). These observations call for precise genotype-phenotype explorations. Serotonin 5-HT(2A) receptor gene polymorphism T102C was reported to have no significant association with suicide attempts and impulsive-aggressive traits in a study done earlier by Zalsman et al. (2005). This study involved 32 Ashkenazi adolescent inpatients with suicide attempts and their parents as control group.

A multi-centric study (Zalsman et al., 2011) was conducted earlier to look at the relation of serotonergic genetic variants with suicidality among adolescents, 35 suicidal and 30 non-suicidal adolescent inpatients, 51 inpatient adolescent suicide attempters and a community-based control ($n = 95$) group from Jewish, Ethiopian, Yemenite and mixed origin. The study reported that homozygous T allele of the serotonin receptor 5HTR2A 102 T/C polymorphism was associated with lower impulsivity and aggression. Monoamine oxidase MAOA genotypes with low activity was associated with suicidality ($p = 0.04$) whereas Serotonin transporter 5HTTLPR genetic variant showed no association. The study also observed that no association was found with plasma serotonin content and any of the examined polymorphisms of the serotonergic pathway.

Dopaminergic system: genetic variants

Previous studies focused on genetic polymorphisms of Tyrosine hydroxylase, the rate limiting enzyme of catechol amine (including dopamine) synthesis, DOPA-decarboxylase involved in dopamine synthesis, the dopamine receptor genes, and Catechol-O-Methyl Transferase involved in catabolism.

Tyrosine hydroxylase (TH)

The present study based on TH rs2070762 variant indicates statistically significant association with attempted suicide among adolescents and young adults. Conflicting reports have been reported with THSNPs and suicidal behavior. In an earlier study that looked at the association of Tyrosine Hydroxylase and DOPA Decarboxylase with suicidal behavior, the TH rs3842727 and rs6356 genetic variants were reported not to be associated with suicidal behavior whereas the DOPA Decarboxylase gene variant was reported to be marginally associated with suicide, violence, anger and aggression (Giegling et al., 2008). Hu et al. (2014) explored TH genetic variants in suicide attempts in persons with schizophrenia. The study reported that the TH rs11564717 ($p = 0.042$) but not the other explored variants like rs2070762, rs 11042950 and rs 689 were significant risk factors for suicide attempts in schizophrenia. The current study sample did not include any patients with schizophrenia and the inconsistency in observations may be due to the phenotype variation. The GTEx data revealed that the risk allele in rs2070762 is associated with reduced expression. Reduced expression of the TH gene indicates reduced synthesis of dopamine. Reduced dopamine is associated with impairment in cognitive and motor skills. This may suggest a potential functional significance of the genetic variant and its role as a probable therapy target.

Dopaminergic receptors

A case- control study (Genis-Mendoza et al., 2017) among Mexican

population involving 166 persons with suicide attempts and 123 healthy controls to look at the association of dopaminergic receptor gene variants with suicide attempt, it was found that the nearby ANKK1 genetic variant (rs1800497) had a 3-fold increase in attempts. This association was not observed for the rs6275 and rs1799978 polymorphisms in the dopaminergic DRD2 gene. An earlier case-control study from Israel that explored Dopamine Receptor subtype 4 (DRD4) gene polymorphism among 69 adolescent suicide attempters and 167 healthy controls reported no significant association (Zalsman et al., 2004). In the current study, these variants were not explored.

Catechol-O-methyl transferase (COMT)

COMT seems to be a major player in suicidal behavior as evidenced by a recent meta-analysis where COMTVal158Met, in exon4, was found to be associated with suicidal behavior in Asian population. (Gonzalez-Castro et al., 2018). In a study on Indian Population (Delhi) by Pasi et al. (2015) the COMT risk allele was observed to be more common among primary relatives of those who had committed suicide, but the result was not statistically significant. A similar trend was observed in our study but lacked statistical significance. Contradictory results by other researchers have also been reported (Mirkovic et al., 2016; Mirkovic et al., 2020). The G to A nucleotide transition causes the substitution of amino acid valine (Val) to methionine (Met) at the position 158COMTVal (108/158) Met(rs4680). The said SNP (rs4680) was found to influence the functional capacity of the enzyme to catabolize proteins in the synapse.

An attempt to compare the observed allelic and genotypic frequencies of each SNP with that of already reported frequencies from different world populations belonging to different ethnic groups was made. The reference data was taken from The International Genome Sample Resource, 1000 Genomes Browser (The 1000 Genomes Project Consortium, 2021). The comparison was done as the SNPs tend to show ethnic variation among different populations and may occur in higher frequencies in certain ethnic populations. The study subjects in this study belonged to Malayalam speaking Dravidian population from Kerala, South India. It was observed that most of the allelic and genotypic SNP frequencies found in this study were close to the allelic and genotypic frequencies of the Asian population. Two of the explored SNPs, theCOMTrs4680 variant frequencies and THrs2070762 allelic frequencies were similar to the Caucasian population. The TPH1rs211105 had values that were closer to the African ethnic group. Knowing these population frequencies will aid in understanding the genetic heterogeneity among different populations, and aid in developing appropriate strategies for intervention.

Limitations of the present study include small sample size, study of selected SNPs from a single ethnic group and study on suicide attempt without specifically exploring suicide related behaviors like suicide ideation.

Conclusions

The current study explored the genetic predictors of attempted suicide among adolescents and young adults and found that the THrs2070762 and Tryptophan Hydroxylase TPH1rs211105 genetic variants had a statistically significant association with attempted suicide phenotype. The findings suggest that these genetic variants are predictive of attempted suicide among adolescents and young adults and may be helpful in the identification and management of high-risk individuals.

Considering the complex phenotype of suicidal behavior and the diverse socio- demographics in India, a single genetic variant may not completely explain suicidal behavior. However, it has been suggested that a small population approach in replicating significant SNPs can be useful, as they minimize genetic heterogeneity, reduce environmental variables and reduce phenotypic diversity. Though earlier studies have shown many genetic variants to have significant association, this was

not replicated in the current study. This may be due to the small sample size, phenotypic and genetic heterogeneity within the clinical sample and across the different ethnic populations. The current observation may provide a direction but needs validation in a larger cohort to pinpoint the genetic predictors of attempted suicide among adolescents and young adults in South India. Future research incorporating the advances in genetic and statistical analyses may yield more consistent results. Considering the huge global public health issue of adolescent and youth suicide, it is vital to conduct more research for a better understanding of the underlying genetic factors and their interaction with other genetic and environmental factors. This will further help in effective identification, prevention, and management of suicidal behavior among adolescents and young adults.

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CRediT authorship contribution statement

Alex Dr. Ann Mary: Writing – review & editing, Investigation, Data curation. **Mathew Anju:** Writing – review & editing, Writing – original draft, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Banerjee Dr. Moinak:** Writing – review & editing, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Formal analysis, Conceptualization. **Krishnapillai Dr. Vijayakumar:** Writing – review & editing, Supervision, Conceptualization. **Muthubeevi Dr. Saboor Beegum:** Writing – review & editing, Supervision, Conceptualization. **Shafeeque Dr. Chathathayil Mohammedali:** Writing – review & editing, Investigation, Formal analysis.

Declaration of Competing Interest

Authors have nothing to declare

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