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ORIGINAL RESEARCH

Expression Significance and Relationship of Serum miR-542-3p and lncRNA TUG1 in STBI Patients and Their Predictive Value for Prognosis

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Objective: Analysis of the Expression Significance and Relationship of Serum MicroRNA-542-3p (miR-542-3p) and Long Non-Coding RNA Taurine Upregulated Gene 1 (lncRNA TUG1) in Patients with Severe Traumatic Brain Injury (STBI) and Their Predictive Value for Prognosis.

Methods: A retrospective analysis was conducted on 193 TBI patients, including 95 STBI (Group A) and 98 non-STBI (Group B) cases. Serum miR-542-3p and lncRNA TUG1 levels were measured upon admission. STBI patients were followed for 6 months and divided into good or poor prognosis groups. Logistic regression, correlation analyses, and ROC curves were used to assess prognostic factors and diagnostic performance.

Results: Compared to Group B, Group A patients had significantly lower serum miR-542-3p levels and higher lncRNA TUG1 levels ($P < 0.05$). A negative correlation was observed between miR-542-3p and lncRNA TUG1 ($r = –0.607$, $P < 0.001$). Among STBI patients, 33 (34.74%) had poor prognosis. Brain herniation, brainstem injury, hypoalbuminemia, and high lncRNA TUG1 were identified as independent risk factors, while high miR-542-3p was a protective factor ($P < 0.05$). Additionally, miR-542-3p levels were negatively correlated with poor prognosis ($r = –0.643$), while lncRNA TUG1 showed a positive correlation ($r = 0.621$). ROC analysis showed AUCs of 0.846 for miR-542-3p, 0.823 for lncRNA TUG1, and 0.925 for their combination, indicating improved predictive accuracy with combined detection.

Conclusion: miR-542-3p is downregulated and lncRNA TUG1 upregulated in STBI. Both are significantly correlated with prognosis and offer strong predictive value, especially when combined.

Keywords: STBI, miR-542-3p, lncRNA TUG1, prognosis, biomarkers, predictive value

Introduction

Severe traumatic brain injury (STBI) is one of the most critical acute conditions threatening human life and health, often accompanied by high disability and mortality rates.[1] It typically results from violent external forces, leading to diffuse brain tissue damage that significantly impairs neurological function, quality of life, and long-term social reintegration.[2] Due to the intricate and heterogeneous pathophysiological mechanisms involved in STBI, timely and accurate prognostic evaluation remains a major challenge in clinical practice.

In recent years, with the rapid advancement of molecular biology and transcriptomics, non-coding RNAs have drawn increasing attention for their potential as biomarkers and regulatory molecules in brain injury. MicroRNAs (miRNAs) and long non-coding RNAs (lncRNAs) are two major classes of non-coding RNAs that play pivotal roles in post-transcriptional gene regulation, and have been implicated in inflammation, apoptosis, oxidative stress, and neuroregeneration processes relevant to TBI.[3–6]

miR-542-3p, in particular, has been shown to regulate cell proliferation, apoptosis, and inflammatory responses. Studies have demonstrated its neuroprotective effects in central nervous system diseases such as ischemic stroke and

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epilepsy, with animal models revealing that miR-542-3p modulates neuronal survival and blood-brain barrier integrity.[7–9] Meanwhile, lncRNA Taurine Upregulated Gene 1 (TUG1) has been widely studied in neurodegenerative conditions and brain injury models. For instance, TUG1 was found to be upregulated in mouse models of TBI, contributing to neuronal apoptosis and inflammation via modulation of the NF-κB and Notch signaling pathways.[10–12] Clinical data also indicate that abnormal expression of TUG1 correlates with poor prognosis in patients with cerebrovascular injury and acute brain trauma.[13]

Despite these insights, there remains a lack of systematic investigation into the coordinated roles and prognostic implications of miR-542-3p and lncRNA TUG1 in STBI patients. Therefore, this study retrospectively analyzes clinical data from 193 TBI patients to assess the differential expression of serum miR-542-3p and lncRNA TUG1, their correlation, and their predictive value for prognosis in STBI. Our findings aim to establish a novel molecular panel to assist in early risk stratification and inform individualized treatment strategies for STBI.

Materials and Methods

Basic Information

A retrospective analysis was conducted on the clinical data of 193 TBI patients admitted to our hospital from June 2022 to August 2024. According to the severity of the patients' conditions, they were divided into group A (n=95, STBI) and group B (n=98, non-STBI). In group A, there were 55 male patients and 40 female patients; the age range was 21–65 years, with a mean age of (46.32±8.21) years; the average body mass index (BMI) was (21.37 ±2.42) kg/m^2; in terms of educational level, 70 patients had high school or below education, and 25 had college education or above. In group B, there were 57 male patients and 41 female patients; the age range was 20–63 years, with a mean age of (46.11±8.12) years; the average BMI was (21.45±2.36) kg/m^2; in terms of educational level, 67 patients had high school or below education, and 31 had college education or above. Comparison of the basic information, including gender, age, BMI, and educational level, between the two groups showed no significant differences (P>0.05), indicating comparability. This study was approved by the Yichang Central People's Hospital medical ethics committee (Approval No: 24-LN00015), and the research strictly adhered to the ethical standards outlined in the Declaration of Helsinki.

Inclusion and Exclusion Criteria

Inclusion Criteria

All patients met the clinical diagnostic criteria for TBI[14] and confirmed the extent and severity of injury via cranial CT or MRI. Group A patients had a Glasgow Coma Scale (GCS) score[15] ≤8, in accordance with the STBI diagnostic criteria, while group B patients had a GCS score between 9–15, including those with mild and moderate TBI. Patients were aged between 18 and 75 years, with no serious organ dysfunction. The time from injury to admission for treatment was <12 hours. All patients received standardized emergency treatment, TBI management, and monitoring. Patients or their family members agreed to participate in the study and signed an informed consent form, and were able to cooperate with follow-up for at least 6 months.

Exclusion Criteria

Patients with non-TBI conditions such as stroke, brain tumors, encephalitis, or other non-traumatic central nervous system diseases. Patients with severe systemic diseases such as advanced heart failure (NYHA class III or above), advanced chronic obstructive pulmonary disease (COPD), end-stage liver disease, or renal failure (eGFR<30 mL/min/1.73m^2). Patients with a history of previous brain surgery, intracranial infections, or epilepsy. Patients with severe multiple trauma (eg, combined with spinal cord injury, extensive fractures, severe thoracic and abdominal injuries) that would severely limit survival prognosis. Pregnant or breastfeeding women. Patients with no fixed contact information, incomplete medical records, or expected to be unable to complete the 6-month follow-up. Patients with severe metabolic disorders (such as hyperglycemic hyperosmolar syndrome), acute intoxication (such as alcohol or drug abuse), or malignant tumors at the time of admission.

Detection of Serum miR-542-3p and lncRNA TUG1 Levels

On the day of admission, 5 mL of fasting venous blood was collected from each patient using RNase-free vacuum tubes and stored at 4°C. Within 2 hours, samples were centrifuged at 4000 rpm (radius 10 cm) for 15 minutes at 4°C. The supernatant (serum) was transferred to RNase-free cryotubes and stored at −80°C until analysis.

Total RNA was extracted from 200 μL of serum using TRIzol™ LS Reagent (Cat# 10296–028, Invitrogen, USA), following the manufacturer's protocol. RNA concentration and purity were assessed using a NanoDrop 2000 (Thermo Fisher Scientific), and only RNA samples with an A260/A280 ratio between 1.8 and 2.0 were included for further analysis.

Reverse transcription was performed using the PrimeScript™ RT reagent Kit with gDNA Eraser (Cat# RR047A, Takara, Japan) for lncRNA, and the Mir-X™ miRNA First-Strand Synthesis Kit (Cat# 638313, Takara, Japan) for miRNA-specific stem-loop cDNA synthesis. cDNA was stored at −20°C.

qPCR was carried out using TB Green® Premix Ex Taq™ II (Cat# RR820A, Takara, Japan) on a QuantStudio™ 5 Real-Time PCR System (Applied Biosystems, USA). Primer specificity was validated by melt curve analysis. The PCR reaction included 10 μL of SYBR mix, 0.5 μL each of forward and reverse primers (10 μM), 1 μL of cDNA, and 8 μL of nuclease-free water in a final volume of 20 μL. The cycling conditions were: 95°C for 30s; followed by 40 cycles of 95°C for 5s, 64°C for 30s. A melt curve analysis was performed to assess amplification specificity.

The relative expression of miR-542-3p was normalized to U6, and that of lncRNA TUG1 to GAPDH using the $2^{-\Delta\Delta Ct}$ method. While U6 and GAPDH are commonly used endogenous controls, we acknowledge their potential variability in serum samples. However, based on pre-experiment analysis, their Ct values were relatively stable across our sample set, and they have been used in several similar studies.[16,17] All original Ct values and melt curve data are available upon request to support reproducibility and specificity.

To address concerns regarding RNA stability, all serum samples were processed under strict cold-chain conditions. Previous studies[18] have demonstrated that both miR-542-3p and TUG1 exhibit adequate stability in serum when processed and stored under appropriate conditions.

Follow-up and Prognostic Assessment

A six-month follow-up was conducted for the STBI patients to assess their clinical prognosis and recovery. Follow-up was performed through various methods, including WeChat phone calls, emails, or patient visits for re-examination, once a month, to ensure the completeness of the follow-up and the accuracy of the data. Prognostic assessment was based on the Glasgow Outcome Scale (GOS)[19] to quantify patients' recovery. The scoring criteria are as follows: 1 (Death): The patient dies during the follow-up period. 2 (Persistent Vegetative State): The patient remains in a vegetative state after treatment, with no consciousness, no spontaneous breathing, and no language or motor responses, but physiological functions are maintained. 3 (Severe Disability): The patient is conscious but unable to care for themselves, severely dependent on others, with a significantly reduced quality of life, usually accompanied by severe physical or cognitive dysfunction. 4 (Moderate Disability): The patient can generally take care of themselves but has some functional impairments, such as mild cognitive or motor dysfunction, and can complete most daily activities. 5 (Good Recovery): The patient nearly fully recovers, with good self-care ability, no obvious functional impairments, and the ability to resume normal social, work, and daily activities. Based on these scoring criteria, patients were divided into the poor prognosis group (GOS score <3) and the good prognosis group (GOS score 4–5).

Statistical Analysis

GraphPad Prism 8 was used for plotting, and SPSS 25.0 was used for statistical analysis. Categorical data are presented as percentages (%) and analyzed using the $\chi 2$ test. Continuous data are expressed as ($\bar{x} \pm s$), with comparisons between two groups performed using independent sample *t*-tests. Multivariate logistic regression analysis was used to determine the factors influencing poor prognosis in STBI patients. Pearson correlation analysis was performed to evaluate the relationship between miR-542-3p and lncRNA TUG1; Spearman correlation analysis was conducted to assess the relationship between miR-542-3p, lncRNA TUG1, and poor prognosis in STBI patients. Receiver operating characteristic

(ROC) curve analysis was used to evaluate the diagnostic and predictive value of miR-542-3p, lncRNA TUG1, and their combination in predicting poor prognosis in STBI patients. All missing data were excluded prior to analysis, and the baseline characteristics of included and excluded patients were compared to ensure that no systematic bias was present. A p-value < 0.05 was considered statistically significant.

Results

Comparison of Serum miR-542-3p and lncRNA TUG1 Levels Between Group A and Group B

The level of miR-542-3p in Group A (0.57 ± 0.13) was significantly lower than that in Group B (0.95 ± 0.22) (t = 14.551, P < 0.05); the level of lncRNA TUG1 in Group A (2.15 ± 0.29) was significantly higher than that in Group B (1.04 ± 0.17) (t = 32.558, P < 0.05), as shown in Figure 1.

Correlation Between miR-542-3p and lncRNA TUG1 Expression

Pearson correlation analysis showed that the serum miR-542-3p and lncRNA TUG1 levels in STBI patients were negatively correlated (r = −0.607, P<0.001), as shown in Figure 2.

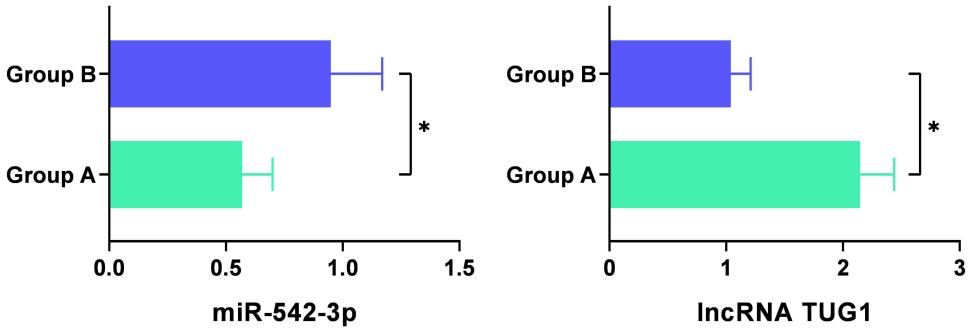

Figure 1 Comparison of Serum miR-542-3p and lncRNA TUG1 Levels between Group A and Group B ($\bar{x} \pm s$).
Note: Group A (STBI); Group B (Non-STBI); miR-542-3p (MicroRNA-542-3p); lncRNA TUG1 (Long Non-Coding RNA Taurine Upregulated Gene 1); Intergroup comparison, *P<0.05.

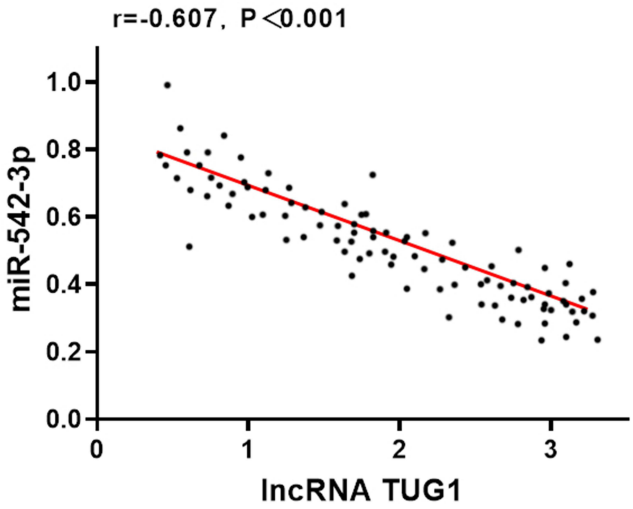

Figure 2 Scatter Plot of the Correlation between miR-542-3p and lncRNA TUG1 Expression Levels.
Note: miR-542-3p (MicroRNA-542-3p); lncRNA TUG1 (Long Non-Coding RNA Taurine Upregulated Gene 1).

Comparison of Clinical Data and Serum miR-542-3p and lncRNA TUG1 Levels Between Poor Prognosis and Good Prognosis Groups

All 95 STBI patients completed the 6-month follow-up, among whom 33 had a poor prognosis, accounting for 34.74%. The proportions of patients with brain herniation, hypernatremia, multiple injuries, and brainstem injury, as well as serum lncRNA TUG1 levels, were significantly higher in the poor prognosis group compared to the good prognosis group. In contrast, the CCS score, SA, and miR-542-3p levels at admission were significantly lower in the poor prognosis group ($P < 0.05$), as shown in Table 1.

Multivariate Logistic Regression Analysis of Factors Influencing Poor Prognosis in STBI Patients

Using the prognosis of STBI patients as the dependent variable (0 = good prognosis, 1 = poor prognosis), and assigning values to the potential influencing factors from Figure 1 and Table 1 (as shown in Table 2), a multivariate logistic

Table 1 Comparison of Clinical Data and Serum miR-542-3p and lncRNA TUG1 Levels Between Poor Prognosis and Good Prognosis Groups ($\bar{x} \pm s$, n[%])

	Poor Prognosis Group (n=33)	Good Prognosis Group (n=62)	t/x^2	*P*
Gender	–	–	0.683	0.408
Male	21 (63.64)	34 (54.84)	–	–
Female	12 (36.36)	28 (45.16)	–	–
Age (years)	47.25±8.67	45.82±7.71	0.824	0.412
BMI (kg/m²)	21.65±2.27	21.29±2.46	0.697	0.487
Time from Injury to Admission (h)	7.63±2.52	7.17±2.35	0.885	0.378
Brain Herniation	14 (42.42)	8 (12.90)	10.547	0.001
Intracranial Hematoma	13 (39.39)	23 (37.10)	0.048	0.826
Hypernatremia	10 (30.30)	9 (14.52)	3.354	0.067
Multiple Injuries	13 (39.39)	12 (19.35)	4.460	0.034
Brainstem Injury	15 (45.45)	10 (16.13)	9.551	0.002
GCS Score (points)	5.37±1.25	6.21±1.42	2.858	0.005
Surgical Treatment	23 (69.70)	49 (79.03)	1.022	0.311
Mechanical Ventilation	26 (78.79)	46 (74.19)	0.247	0.618
MAP (mmHg)	85.84±9.13	83.36±9.07	1.266	0.208
SA (g/L)	29.95±5.08	35.84±7.31	4.124	<0.001
miR-542-3p	0.52±0.07	0.65±0.10	6.644	<0.001
lncRNA TUG1	2.42±0.33	1.95±0.28	7.315	<0.001

Abbreviations: BMI, Body Mass Index; GCS score, Glasgow Coma Scale; MAP, Mean Arterial Pressure; SA, Serum Albumin; miR-542-3p, MicroRNA-542-3p; lncRNA TUG1, Long Non-Coding RNA Taurine Upregulated Gene 1.

Table 2 Variable Assignment Table

Independent Variable	Assignment Method
Brain Herniation	0 = not present; 1 = present
Multiple Injuries	0 = not present; 1 = present
Brainstem Injury	0 = not present; 1 = present
GCS Score	Original value used
SA	Original value used
miR-542-3p	Original value used
lncRNA TUG1	Original value used

Abbreviations: GCS score, Glasgow Coma Scale; SA, Serum Albumin; miR-542-3p, MicroRNA-542-3p; lncRNA TUG1, Long Non-Coding RNA Taurine Upregulated Gene 1.

Table 3 Multivariate Logistic Regression Analysis of Factors Influencing Poor Prognosis in STBI Patients

Factor	β	SE	Wald x^2	P	OR	95% CI
Brain Herniation	1.078	0.369	8.682	<0.001	2.929	1.286–6.517
Brainstem Injury	1.145	0.413	7.654	<0.001	1.745	1.217–4.152
SA	1.569	0.521	9.086	<0.001	4.369	2.194–8.885
miR-542-3p	−1.147	0.368	10.452	<0.001	0.313	0.161–0.635
lncRNA TUG1	1.658	0.576	8.764	<0.001	5.209	1.752–15.448

Abbreviations: SA, Serum Albumin; miR-542-3p, MicroRNA-542-3p; lncRNA TUG1, Long Non-Coding RNA Taurine Upregulated Gene 1.

regression analysis model was established. The results showed that brain herniation, brainstem injury, low SA upon admission, and high lncRNA TUG1 levels were independent risk factors for poor prognosis in STBI patients, while high miR-542-3p levels were an independent protective factor (P<0.05), as shown in Table 3. Model fit was evaluated using the Hosmer-Lemeshow goodness-of-fit test ($x^2 = 6.27$, P = 0.51), which indicated no significant difference between the observed and predicted values, suggesting a good model fit. The Nagelkerke R^2 value was 0.652, indicating that the model explained approximately 65.2% of the variance in patient prognosis.

Correlation Between miR-542-3p, lncRNA TUG1, and Poor Prognosis in STBI Patients

Spearman correlation analysis showed that serum miR-542-3p levels in STBI patients were positively correlated with poor prognosis (r = 0.643, P<0.001), while serum lncRNA TUG1 levels were negatively correlated with poor prognosis (r = −0.621, P<0.001), as shown in Figure 3.

Predictive Diagnostic Value of miR-542-3p, lncRNA TUG1, and Their Combination for Poor Prognosis in STBI Patients

ROC curve analysis showed that the area under the curve (AUC) for diagnosing poor prognosis in STBI patients using miR-542-3p, lncRNA TUG1, and their combination were 0.846, 0.823, and 0.925, respectively. The AUC, sensitivity, and specificity of the combined diagnosis were higher than any single diagnostic method, as shown in Table 4 and Figure 4.

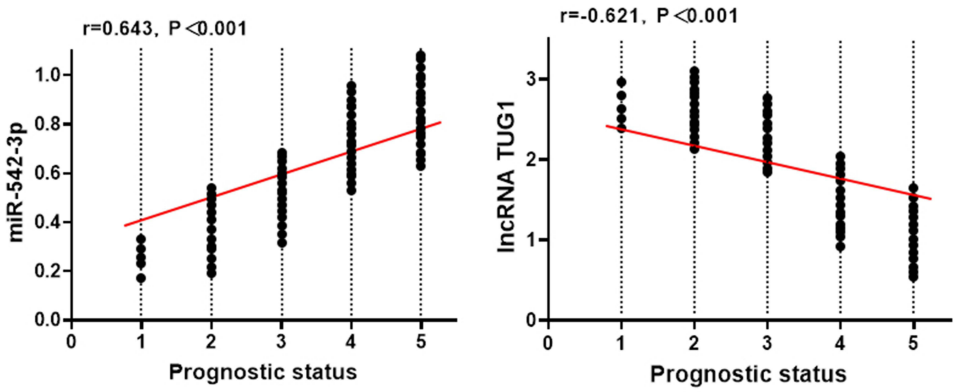

Figure 3 Scatter Plot of the Correlation between miR-542-3p, lncRNA TUG1, and Poor Prognosis in STBI Patients.
Note: miR-542-3p (MicroRNA-542-3p); lncRNA TUG1 (Long Non-Coding RNA Taurine Upregulated Gene 1).

Table 4 Predictive Diagnostic Value of miR-542-3p, lncRNA TUG1, and Their Combination for Poor Prognosis in STBI Patients

Indicator	Optimal Cutoff Value	AUC	95% CI	P	Sensitivity (%)	Specificity (%)
miR-542-3p	0.55	0.846	0.775~0.908	<0.05	74.95	80.39
lncRNA TUG1	2.32	0.823	0.751~0.886	<0.05	70.51	81.43
Combined	-	0.925	0.872~0.963	<0.05	93.27	84.16

Abbreviations: miR-542-3p, MicroRNA-542-3p; lncRNA TUG1, Long Non-Coding RNA Taurine Upregulated Gene 1).

Discussion

miR-542-3p, as a miRNA, has been shown in recent studies to have expression changes in various neurological diseases, which are closely related to the occurrence and progression of these diseases.[20,21] The results of this study indicate that the serum level of miR-542-3p in STBI patients is significantly lower than that in non-STBI patients, suggesting that miR-542-3p may play an important role in the pathogenesis of STBI. The downregulation of miR-542-3p in nerve injury may be related to changes in its target genes and downstream signaling pathways. One study suggested that miR-542-3p regulates the proliferation, differentiation, and apoptosis of nerve cells, influencing the repair mechanism after nerve injury.[22] In STBI patients, the decreased expression of miR-542-3p may weaken its protective effect on nerve cells, thereby exacerbating brain injury and affecting recovery. Furthermore, this study also found that miR-542-3p was closely associated with the prognosis of STBI patients. Specifically, patients with lower miR-542-3p levels had a poorer prognosis, which may be related to miR-542-3p's regulation of key processes such as neuroinflammation, oxidative stress, and cell apoptosis,[16,23,24] thereby influencing the prognosis of STBI. Clinically, miR-542-3p can be considered a potential biomarker, providing a basis for the prognosis assessment of STBI patients. Moreover, multivariate logistic regression analysis showed that higher miR-542-3p levels were an independent protective factor for poor prognosis in STBI patients, further emphasizing the important role of miR-542-3p in STBI.

lncRNA TUG1 is a long non-coding RNA, and its role in neurological diseases has gradually been revealed in recent years.[25,26] This study found that the serum expression of lncRNA TUG1 in STBI patients was significantly higher than that in non-STBI patients. It is speculated that lncRNA TUG1 may be involved in the occurrence and development of STBI by regulating neuroinflammatory responses, cell apoptosis, and neural repair mechanisms.[27,28] Emerging evidence

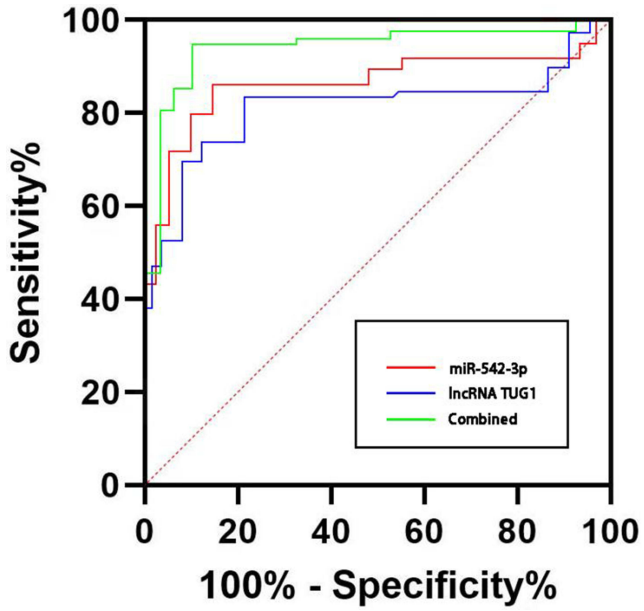

Figure 4 ROC Curve Analysis of miR-542-3p, lncRNA TUG1, and Their Combination for Poor Prognosis in STBI Patients.
Note: miR-542-3p (MicroRNA-542-3p); lncRNA TUG1 (Long Non-Coding RNA Taurine Upregulated Gene 1).

suggests that TUG1 plays a critical regulatory role in various neurological disorders by interacting with microRNAs, signaling pathways, and inflammatory mediators. In cerebral ischemia/reperfusion injury, TUG1 promotes neuroinflammation through the miR-200a-3p/NLRP3 axis. Specifically, TUG1 acts as a competing endogenous RNA (ceRNA), sponging miR-200a-3p and thus enhancing NLRP3 inflammasome activation, which contributes to increased secretion of IL-1β and IL-18, exacerbating neuronal damage.[29] Moreover, TUG1 has been found to promote neuronal apoptosis by inhibiting mitophagy through the FBXW7/SIRT1 signaling pathway, highlighting its pro-apoptotic role in ischemic brain injury.[30] In epilepsy models, TUG1 expression is significantly upregulated in both brain tissues and peripheral blood, where it activates the NF-κB signaling pathway in microglial cells, thereby intensifying neuroinflammatory responses and contributing to the pathophysiology of status epilepticus.[31] Furthermore, TUG1 promotes the metabolic reprogramming of microglia towards a pro-inflammatory M1 phenotype by enhancing glycolytic flux and reducing oxidative phosphorylation, thus sustaining chronic neuroinflammation.[32] Particularly after brain injury, the upregulation of lncRNA TUG1 expression may be a stress response to the damage,[33,34] aimed at clearing damaged tissue by promoting apoptosis and immune responses, thus providing conditions for subsequent neural repair. Additionally, this study observed that STBI patients with higher lncRNA TUG1 levels had a poorer prognosis, suggesting that lncRNA TUG1 may play an important role in the prognosis evaluation of STBI. The potential reason for this may be that lncRNA TUG1 regulates the repair process after nerve injury,[35] leading to difficulty in recovery. Further multivariate regression analysis showed that lncRNA TUG1 was an independent risk factor for poor prognosis in STBI, suggesting that it may become an important biomarker for prognosis evaluation in STBI patients.

This study also found a significant negative correlation between serum miR-542-3p and lncRNA TUG1 levels in STBI patients, suggesting that the two may regulate the survival and apoptosis of nerve cells through mutual interaction, thus jointly influencing the occurrence and development of STBI. The downregulation of miR-542-3p and upregulation of lncRNA TUG1 may reflect an imbalance in neural injury and repair within the bodies of STBI patients. Studies[36–39] have shown that miRNAs and lncRNAs usually act in concert through complex regulatory networks in the nervous system, participating in the regulation of multiple signaling pathways such as neuroinflammation, apoptosis, and autophagy. Therefore, the interaction between miR-542-3p and lncRNA TUG1 may provide a molecular mechanism for the occurrence of STBI. In terms of prognostic prediction, ROC curve analysis showed that the AUCs for miR-542-3p, lncRNA TUG1, and their combined detection were 0.846, 0.823, and 0.925, respectively. The AUC, sensitivity, and specificity of combined diagnosis were all higher than those of any single biomarker. This result suggests that the combined detection of miR-542-3p and lncRNA TUG1 has higher application value in the prognosis assessment of STBI patients. Combined detection not only improves the sensitivity and specificity of prediction but also provides more comprehensive biomarker information, offering more accurate support for early diagnosis and prognosis assessment of STBI patients in clinical practice. However, it is important to note that correlation does not imply causation. Although we found an association between biomarker levels and prognosis, we cannot confirm whether these biomarkers play a direct role in disease progression. Future studies should aim to clarify whether miR-542-3p and lncRNA TUG1 are involved in the pathophysiological mechanisms of STBI and their potential as therapeutic targets. Additionally, the relationship between serum miR-542-3p and lncRNA TUG1 levels and certain treatments for traumatic headaches, such as anti-CGRP monoclonal antibodies or botulinum toxin type A, deserves further exploration. These treatments have been shown to affect pain pathways and may influence the expression of these biomarkers.[40]

The clinical significance of this study lies in the fact that detecting the expression levels of miR-542-3p and lncRNA TUG1 provides a new approach and method for the early prognosis evaluation of STBI patients. Especially, the combined detection of miR-542-3p and lncRNA TUG1 not only improves the accuracy of prognostic prediction but also provides more biomarker options for clinicians, helping to formulate individualized treatment plans. However, this study also has certain limitations. First, since this is a retrospective analysis, there may be selection bias, and the sample size is relatively small, so the generalizability and extrapolation of the results need further verification. Second, this study only analyzed the expression of miR-542-3p and lncRNA TUG1 in serum, and future research could combine cerebrospinal fluid or brain tissue samples to further validate their roles in STBI. Moreover, this study did not further explore the specific roles of miR-542-3p and lncRNA TUG1 in the pathogenesis of STBI. Therefore, subsequent studies can incorporate molecular biology experiments to analyze the functions and mechanisms of these two molecules in STBI.

Finally, regarding the issue of external validation, this study has not yet conducted validation using an external dataset. In future research, we plan to employ independent samples from multiple centers to further validate the combined diagnostic model in order to ensure its generalizability.

Conclusion

This study shows that the serum level of miR-542-3p is decreased, while the level of lncRNA TUG1 is increased in STBI patients, and their expression levels are negatively correlated. Both miR-542-3p and lncRNA TUG1 not only have independent predictive value in the prognosis assessment of STBI patients but their combined detection can significantly improve the sensitivity and specificity of prognostic prediction. Therefore, miR-542-3p and lncRNA TUG1 can be potential biomarkers for the prognosis assessment of STBI, providing important references for clinical diagnosis and individualized treatment.

Disclosure

The authors report no conflicts of interest in this work.

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