

Retraction

Retracted: Statistical Analysis for Identifying Differentially MicroRNA in Serum Exosomes of Lead Workers

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This article has been retracted by Hindawi following an investigation undertaken by the publisher [1]. This investigation has uncovered evidence of one or more of the following indicators of systematic manipulation of the publication process:

- (1) Discrepancies in scope
- (2) Discrepancies in the description of the research reported
- (3) Discrepancies between the availability of data and the research described
- (4) Inappropriate citations
- (5) Incoherent, meaningless and/or irrelevant content included in the article
- (6) Peer-review manipulation

The presence of these indicators undermines our confidence in the integrity of the article's content and we cannot, therefore, vouch for its reliability. Please note that this notice is intended solely to alert readers that the content of this article is unreliable. We have not investigated whether authors were aware of or involved in the systematic manipulation of the publication process.

Wiley and Hindawi regrets that the usual quality checks did not identify these issues before publication and have since put additional measures in place to safeguard research integrity.

We wish to credit our own Research Integrity and Research Publishing teams and anonymous and named external researchers and research integrity experts for contributing to this investigation.

The corresponding author, as the representative of all authors, has been given the opportunity to register their agreement or disagreement to this retraction. We have kept a record of any response received.

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- [1] J. Bo, F. Shi, X. Wang et al., "Statistical Analysis for Identifying Differentially MicroRNA in Serum Exosomes of Lead Workers," *Journal of Healthcare Engineering*, vol. 2020, Article ID 8841127, 10 pages, 2020.

Research Article

Statistical Analysis for Identifying Differentially MicroRNA in Serum Exosomes of Lead Workers

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Exosomes can transmit central nervous system (CNS) information to the peripheral circulatory system through the brain barrier, and exosomes in the blood can also enter the central nervous system likewise. The components of exosomal contents play a pivotal role in cell signal communication, and thus, the transmission of exosomal content components is considered as a newly discovered method of long-distance communication between cells. The current is aimed to explore the changes of the exosomal microRNA group in the serum of lead-exposed workers, which might be involved in the lead-induced neuroinflammation, especially the activation of microglia and the release of inflammatory factors. We proposed a method combining statistical analysis and experiment according to the different expression of exosomal microRNA. Firstly, we divided workers into two groups, lead-exposed group and control group, and then questionnaires were used to obtain their basic information, and medical testing methods were used to obtain their serum exosomes. Secondly, principal component analysis was used to construct a comprehensive index of neurobehavioral function. Furthermore, volcano map and heatmap were used to display the differential gene distribution and correlation analysis of expression levels, respectively. Finally, two software applications, TargetScan and miRanda, were used to predict the target genes of the significantly different microRNAs, respectively, and the target genes predicted by the two software applications are screened according to the scoring standards of each software. Our results showed that 73 microRNAs were changed in the serum exosomes of lead-exposed worker, among which 48 microRNAs are upregulated and 25 microRNAs are downregulated. Moreover, the miR-124 and miR-506 were identified, and they might be involved in the process of lead-induced neuroinflammation.

1. Introduction

Exosomes are multivesicular bodies with an average diameter of 30–200 nm formed by intracellular lysosomal microparticles, and their nucleic acid components in the contents of exosomes include mRNA, microRNA, lncRNA, and circRNA, which play an important role in cell signal communication under physiological and pathological conditions [1, 2]. It is known that exosomes can be secreted by the nerve cells, vascular endothelial cells, and choroid plexus epithelial cells in the central nervous system, and the exosomes in the blood can also enter the central nervous system in the same way [3, 4]. Therefore, exosomes are considered a

new way of long-distance communication between cells [5, 6]. To some extent, exosomes carrying microRNA can specifically bind to the 3′ noncoding regions of the target mRNA, resulting in silencing of target gene expression [7]. Recent studies have suggested that exosomal microRNA plays an important role in the occurrence and development of neuroinflammation and neurodegeneration [8–10]. MiRNA-124 secreted by microglia after brain injury can regulate neuronal inflammation, and the exosomes containing miRNA-29 released by astrocytes can be swallowed by neurons and are related to the survival of neurons [11–13]. In addition, the differentially expressed exosomal microRNAs in the cerebrospinal fluid of patients with

Alzheimer disease (AD) and Parkinson's disease (PD) may become new targets for the prevention and treatment of AD or PD [14–16].

Lead neurotoxicity is characterized by Neuro inflammation [8, 9]. As is well known, lead is a heavy metal pollutant in industrial production and daily life environment [17]. Nerve damage caused by lead exposure has always been a public health concern, but little is known about its precise molecular mechanism [18–20]. Exosomal microRNAs play a certain role in the occurrence and development of neurodegenerative diseases and the research of their biomarkers [21, 22]. Exosomes can communicate information between neuronal cells under normal circumstances, which are related to the spread of misfolded proteins in neurodegenerative diseases [2, 23]. Moreover, exosomes play an important role in neuron protection, nerve regeneration, neuron formation, and synaptic plasticity [24–28]. Some studies have shown that the differentially expressed exosomal proteins and microRNAs in the cerebrospinal fluid of patients with Alzheimer's disease and Parkinson's disease might become new targets for prevention and treatment of AD or PD point [29–31]. But still little is known about the role of exosomal microRNA in nerve damage caused by environmental and occupational heavy metal exposure.

This study aims to investigate the change of the differential expression of microRNA profiles in serum exosomes in lead-exposed workers and control workers and identify the differentially expressed. Our finding will provide the new mechanism of lead neurotoxicity as well as the basis for serum exosomal microRNA as a candidate marker for biological monitoring of lead exposure.

2. Subjects and Methods

2.1. Subjects. A total of 42 occupational lead-exposed workers as exposure group and 32 nonlead workers of the factory with comparable gender and age balance, people as the control group, were recruited from a battery production plant in Tangshan City, Hebei Province. A survey of the general information of all subjects was undertaken with a self-made questionnaire, and a behavioral function test was conducted too. The screening of people for exosomal microRNA sequencing was done in terms of blood lead levels and NAI. In addition, all participants were sufficiently informed, and they agreed to participate in the study. The experimental protocol was approved by the Ethics Committee of North China University of Science and Technology (approval No. 2017038).

2.2. Serum Exosomes Isolation. Serum of 0.5 ml was centrifuged for 20 min (2000 g, at 4°C), and the supernatant was collected and transferred to a polycarbonate tube. Then, it was centrifuged (10000 g, at 4°C) for 30 min, and the supernatant was collected. The collected supernatants were then centrifuged for 70 min (100000 g, at 4°C). Remove the supernatant completely, and then resuspend the obtained pellet in PBS. Next, samples were ultracentrifuged for 60 min (100 000 g, at 4°C), and the process was repeated three times.

The obtained pellet was resuspended in PBS, and the extracted exosomes were stored in a refrigerator at –80°C for further use.

2.3. Serum Exosomes Characterization

2.3.1. Transmission Electron Microscopy. Exosomes pellet was suspended in 30 µL of PBS, and 10 µL of the sample was dropped on the copper mesh for sedimentation for 1 min. Filter paper was used to remove the floating liquid, and 10 µL of uranyl acetate (phosphotungstic acid) was dropped to the copper mesh for sedimentation for 1 min, and a filter paper was used to remove the floating liquid. It was allowed several minutes to dry at room temperature. Samples were then examined with a transmission electron microscope.

2.3.2. Western Blot Analysis. The exosomes were lysed with lysis buffer and then centrifuged at 13000 rpm for 15 min at 4°C. The supernatant containing proteins was collected. Protein concentration was determined using BCA protein assay kit. Gel electrophoresis was done using 8% SDS-PAGE gel, and the protein was transferred to a polyvinylidene fluoride (PVDF) membrane. The membranes were incubated with 5% non-fat milk for 1 h at room temperature and then incubated with primary antibody (mice anti-CD63, 1 : 1000) at 4°C overnight. After incubation with secondary antibodies (goat anti-rabbit IgG-HRP, 1 : 3000) for 1 h at room temperature, membranes were stained with enhanced chemiluminescence reagent. The gray value of each band was analyzed with Image J software.

2.3.3. Exosomal Particle Size Detection. NanoSight was used for detection, and the specific method is as follows: the collected exosome was diluted from 10 times to 10000 times in proportion, and the detection started from the sample with the largest dilution. The sample is the best when the number of exosomal particles is 10^7 – 10^8 /ml, so that individual particles can be tracked by the machine. The software was used to identify the diameter of the exosomes.

2.4. miRNA Isolation and High-Throughput Sequencing. 1 mL of pre-cooled TRIzol Reagent (Invitrogen, Carlsbad, CA, USA) was added to the extracted exosomes, and ultrasonic homogenizer was used for tissue disruption. The ultrasonically disrupted tissue was then transferred to a 1.5 mL EP tube without enzyme contamination to extract total RNA. The small RNA sequencing library was prepared by using TruSeq Small RNA Sample Prep Kits (Illumina, San Diego, USA). After the library preparation is completed, the constructed library is sequenced using Illumina Hiseq2000/2500, and the sequencing read length is single-ended 1 × 50 bp. Then the transcriptome sequencing data analysis was performed according to the software ACGT101-miR (LC Sciences, Houston, Texas, USA). After trimming adaptor sequences, removing contaminated reads, and filtering low quality reads, the remaining clean reads were mapped to the human genome using short oligonucleotide

alignment program (SOAP). The other small RNAs (rRNA, tRNA, snRNA, snoRNA, and piRNA) were detected by screening against Rfam 10.1 and the GenBank database. The known miRNAs were identified by aligning them to the miRBase. The expression differences of the known miRNAs between the lead-exposed workers and nonlead-exposed workers were evaluated by comparing the log₂ ratio of the 2 groups. The target genes of the selected miRNAs with differential expression were predicted using RNAhybrid. For determination of the main biological functions of the candidate target genes, Gene Ontology (GO) enrichment analysis was applied. We mapped all candidates to GO terms in the database (<http://www.geneontology.org/>), using a hypergeometric test to find significantly enriched GO terms. For identification of significantly enriched metabolic pathways or signal transduction pathways in target gene candidates, we mapped these candidates to the Kyoto Encyclopedia of Genes and Genomes (KEGG) databases.

2.5. Identification of Differentially Expressed miRNAs. The total RNA of serum exosomes was extracted, and real-time PCR was performed after reverse transcription (Thermo Fisher Scientific, Inc., Waltham, MA, USA). U6 was used as the internal reference, and Roche Light Cycler® 96 real-time fluorescent quantitative PCR instrument (Basel, Switzerland) was used for amplification. The SYBR Green method was selected to treat lead-exposed workers and nonlead-exposed workers. The expression level of microRNA in serum exosomes of workers was tested. The primer sequences are shown in Table 1.

2.6. Statistical Analysis. All statistical methods were performed using SPSS software, version 23 (IBM, USA). Normal distributions of data were expressed as means ± SD. One-way ANOVA followed by Tukey's post hoc test was used for group analyses, and the Student t-test was used for statistical analyses applied in two groups separately. The qualitative data were expressed by frequency and percentage, and χ^2 test was used for the comparison between the two groups. Pearson correlation test was adopted for correlation analysis of two continuous variables that obey the normal distribution. The multiple linear regression is used to analyze the influencing factors of neurobehavioral function indexes. A *P* value less than 0.05 was considered to be statistically significant.

3. Results

3.1. The General Information of the Sequencing Population. There are 12 samples for exosomal microRNA sequencing. The exposure group includes 8 lead-exposed workers with an average age of 36.53 ± 3.10 years and 10.38 ± 2.62 years of the exposure history. And the mean values of blood lead are 273.07 mg/L. The control group includes 4 people with an average age of 30.22 ± 2.76 years, and the average values of blood lead are 36.52 mg/L. The age difference between the control group and the exposure group is not of statistical significance (Table 2).

TABLE 1: The primer sequences used for real-time PCR.

Name		Sequence 5'– 3'
U6	Sense	CTCGCTTCGGCAGCAC
	Antisense	AACGCTTCACGAATTTGCGT
microRNA-124	Sense	GGCATTACCGCGTGCCTTAATTGT
	Antisense	GGCAATGACCCCGTCCCTTAATTCT
microRNA-506	Sense	TAAGGCACCCTTCTGAGTAGA
	Antisense	GCGAGCACAGAATTAATACGAC

For neurobehavioral function, the scores of POMST, POMSD, POMSA, POMSF, and POMSC of the workers in the exposure group are higher than those of the control group (Table 3). The positive score of POMSV was lower than that of the control group, and the difference was statistically significant.

In this study, NAI was used as a comprehensive index to evaluate the level of neurobehavioral function. The results found that the NAI scores of series addition/subtraction, memory scanning, audio reaction span, and pursuit aiming test of the workers in the exposure group are lower than those of the control group. The simple visual reaction times were longer than those of the control group. The differences are statistically significant ($P < 0.05$).

3.2. Characterization of Exosomes Derived from Serum. Transmission electron microscope observation shows that round or elliptical membranous vesicles are of uniform size and shape, and some vesicles are fused, the outer periphery of the exosomes is coated with a double-layer lipid membrane, and the center color is light, the periphery is densely stained, and the edges are clear (Figure 1(a)). In the whole electron microscope observation, no cell debris and other subcellular organelles were found, which could rule out the influence of other cell components on the study of protein composition.

To obtain the standard curve equation, BCA method was used to plot the absorbance values of standard protein concentration pairs of different concentrations. The concentration of exosomal protein obtained is $0.916 \mu\text{g}/\mu\text{L}$. Moreover, Western blot analysis showed the expression of CD63 in exosomes (Figure 1(b)). Finally, we used the Nanoparticle Tracking Analysis (NTA) that was employed to detect the size and number of the extracted exosomes. It was shown that 97.4% of the 10–1000 nm particles had an average diameter of 159.5 nm and a particle concentration of $2.3 \times 10^6/\text{mL}$ (Figure 1(c)).

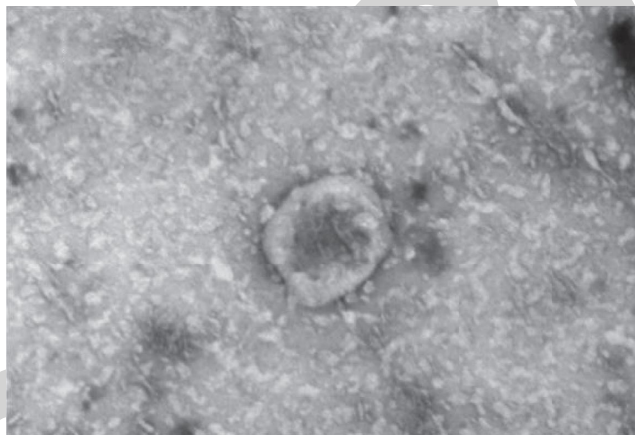
3.3. The Sample Information of Serum Exosomes. Rfam is a noncoding RNA (ncRNA) family database, including rRNA, tRNA, snoRNA, snRNA, microRNA, and other noncoding RNAs. In this study, Rfam database was selected to annotate small RNA sequences obtained by sequencing, and other possible non-microRNA sequences, such as rRNA, snoRNA, snRNA, and tRNA, were removed. Then, the total sequencing data of the sample was analyzed statistically (Table 4).

TABLE 2: General characteristics among the study population (N = 12).

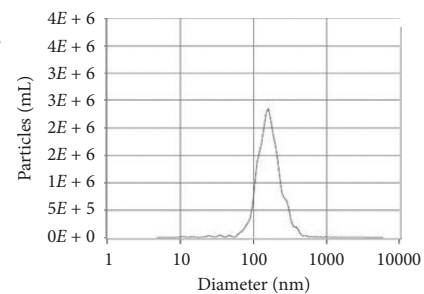
Number of subjects	The control group (N=4)	The exposure group (N=8)
Age (years)	30.22 ± 2.76	36.53 ± 3.10
Gender		
Male	1 (25%)	4 (50%)
Female	3 (75%)	4 (50%)
Body mass index (BMI)	23.59 ± 1.17	26.95 ± 5.09
Lead exposure year	0.00 ± 0.00	10.38 ± 2.62
Blood lead level (µg/L)	36.52 ± 3.43	273.07 ± 175.06

TABLE 3: Effects on neurobehavioral function of subjects exposed to occupational lead (mean ± SD).

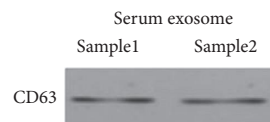
Neurobehavior	Index	The control group (N=4)	The exposure group (N=8)
Profile of mood states	Tension-anxiety (POMST)	2.00 ± 1.41	20.38 ± 8.93
	Depression-dejection (POMSD)	0.50 ± 0.58	35.25 ± 8.92
	Anger-hostility (POMSA)	0.75 ± 0.50	29.5 ± 10.14
	Viger-activity (POMSV)	22.00 ± 2.58	15.13 ± 8.95
	Fatigue-inertia (POMSF)	1.50 ± 1.29	18.13 ± 6.96
	Confusion-bewilderment (POMSC)	3.00 ± 0.00	20.13 ± 6.20
Neurobehavioral ability	Series addition and subtraction (NAI)	3.55 ± 0.31	1.43 ± 0.53
	Benton visual retention (NAI)	2.27 ± 0.60	1.05 ± 0.20
	Memory scanning (NAI)	3.69 ± 0.41	2.38 ± 0.80
	Audio reaction span (NAI)	2.20 ± 0.18	0.86 ± 0.60
	Simple visual reaction time (NAI)	1.14 ± 0.39	1.47 ± 0.28
	Pursuit aiming test (NAI)	1.65 ± 0.12	0.54 ± 0.36



(a)



(b)



(c)

FIGURE 1: The character profiles of serum exosome. (a) Electron micrographs of purified exosomes from serum. (b) The exosomal marker protein CD 63 expression of serum exosome detected by Western blot. (c) The size of serum exosome detected by nanoparticle tracking analysis (NTA).

3.4. Identification of Differential miRNAs in Serum Exosomes of Lead-Exposed Workers. Overall, 73 microRNAs were identified (48 were upregulated and 25 were downregulated) (Tables 5 and 6). Moreover, we screened out all significant

microRNAs to draw a heatmap (Figure 2). The heatmap shows that lead-exposed workers are distinguished from the control group, and the results can be interpreted as follows: microRNAs with similar expression may have similar

TABLE 4: The reads of all samples.

Sample	Raw reads	Valid reads	Valid reads (%)
C1	21983857	13024831	59.25
C2	21554948	10465493	48.55
C3	19409346	4530776	23.34
C4	15562995	9789732	62.90
Pb1	20611095	10433358	50.62
Pb2	16582069	2995041	18.06
Pb3	25747021	10952202	42.54
Pb4	40130050	16475588	41.06
Pb5	25364470	7920563	31.23
Pb6	14615689	9458626	64.72
Pb7	31443099	3371946	10.72
Pb8	19241369	12502588	64.98

TABLE 5: The list of differentially upregulated microRNAs of serum exosomes.

miR_name	fold_change (Pb (mean)/C (mean))	log2 (fold_change)	P value (t-test)
hsa-let-7g-3p	14.47	3.86	<0.01
hsa-miR-124-3p	12.07	3.59	<0.01
PC-5p-61818	8.45	3.08	<0.05
hsa-miR-4685-3p	8.39	3.07	<0.05
hsa-miR-214-5p	7.67	2.94	<0.01
PC-5p-530460	7.12	2.83	<0.05
PC-3p-165014	6.85	2.78	<0.05
mmu-mir-6240-p5	6.68	2.74	<0.05
PC-3p-189072	6.36	2.67	<0.05
PC-3p-90522	6.34	2.67	<0.05

TABLE 6: The list of differentially downregulated microRNAs of serum exosomes.

miR_name	fold_change (Pb (mean)/C (mean))	log2 (fold_change)	P value (t-test)
hsa-miR-326	0.23	-2.09	<0.05
hsa-miR-542-3p	0.31	-1.71	<0.001
hsa-miR-331-3p	0.35	-1.5	<0.01
hsa-miR-744-5p	0.35	-1.51	<0.05
hsa-miR-2355-3p	0.4	-1.34	<0.001
hsa-miR-328-3p	0.4	-1.31	<0.05
hsa-miR-374b-5p	0.41	-1.29	<0.05
hsa-miR-450a-5p	0.42	-1.24	<0.01
mmu-mir-3968-p3	0.44	-1.2	<0.05
hsa-miR-425-3p	0.48	-1.06	<0.01

functions. Then, we used volcano maps to visually display the distribution of differential genes between different samples (Figure 3).

3.5. Prediction of miRNA Targets and Functional Annotation of the Serum Exosomes in Lead Worker. We used TargetScan and miRanda software to predict the target genes of the significantly different microRNAs, respectively. The target genes were based on the following criteria: (a) Removing target genes with context score percentile less than 50 in the TargetScan algorithm. (b) The miRanda algorithm removes target genes whose maximum free energy (Max Energy) is greater than -10. Finally, the intersection of these two

software applications is used as the final target gene of the differential microRNA.

We functionally annotated these genes based on GO terms including biological process, cellular component, and molecular function. GO enrichment analysis shows that the target genes are enriched in the following pathways: protein binding, cytoplasm, cytosol, metal ion binding, nucleus transcription, DNA-templated transcription, regulation of transcription, DNA-templated, transferase activity, transport, nucleoplasm, cytoskeleton, cytoplasmic vesicle, cell cycle, DNA binding, protein phosphorylation, and nervous system development, which proves that these microRNA target genes play an important role in the process of lead neurotoxicity (Figure 4).

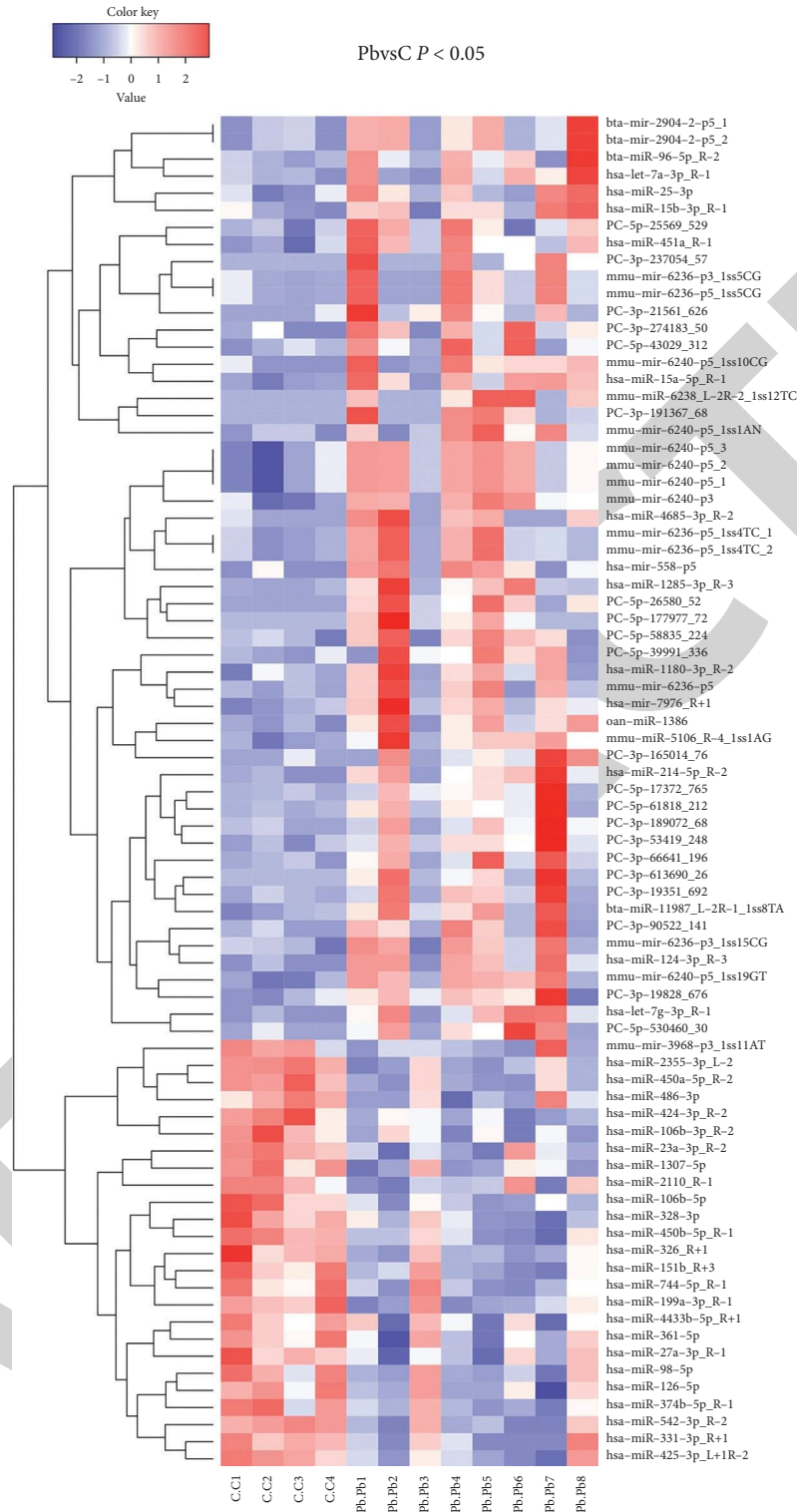


FIGURE 2: The heatmap of microRNA expression of serum exosomes.

From KEGG pathway analysis, we found that target genes are enriched in pathways in cancer, proteoglycans in cancer, MAPK signaling pathway, focal adhesion, insulin signaling pathway, AMPK signaling pathway, JAK/STAT

signaling pathway, Rap1 signaling pathway, endocytosis, human papillomavirus infection, peroxisome, cAMP signaling pathway, Ras signaling pathway, cellular senescence, autophagy, Hippo signaling pathway, oxytocin signaling

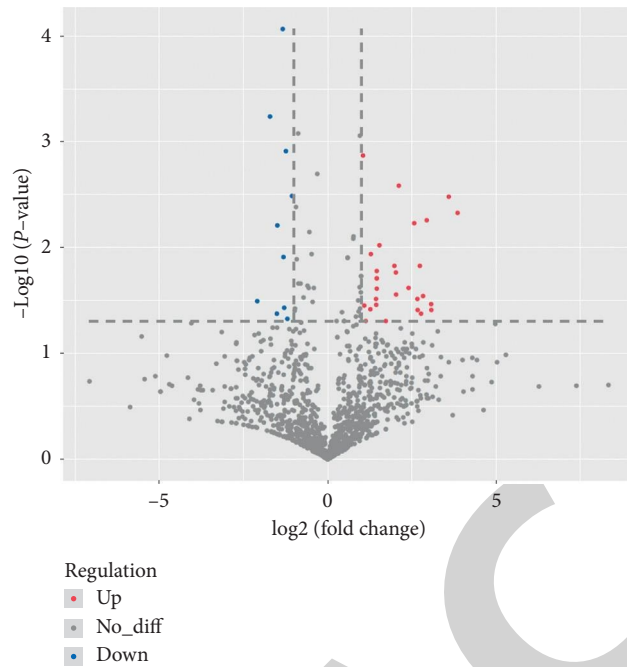


FIGURE 3: The volcano diagram of differentially expressed microRNA of serum exosomes.

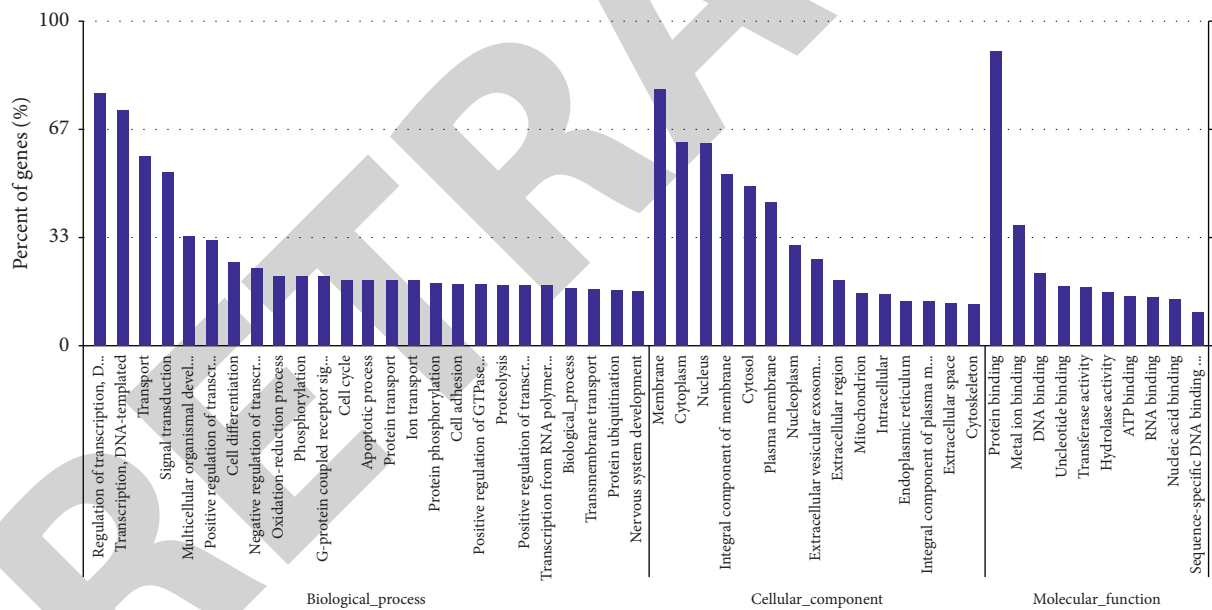


FIGURE 4: The GO function enrichment histogram of differential micro-target gene expression of serum exosomes.

pathway, apelin signaling pathway, adrenergic signaling in cardiomyocytes, and thyroid hormone signaling pathway (Figure 5).

3.6. Verification of Serum Exosomes miR-124 and miR-506. Lead-exposed workers’ serum exosomes miR-124 and miR-506 are expressed differently in multiples. A recent study has shown that miR-124 is expressed at a high level in brain tissue. In addition, miR-124 and miR-506 have many common target genes. Therefore, we selected miR-124 and miR-506 as the

essential microRNAs for further study. Using U6 as a reference protein, we used real-time PCR to detect the expression of exosomes miR-124 and miR-506. As a result, the expression levels of miR-124 and miR-506 in lead-exposed workers were higher than those in the control group (Table 7).

4. Discussion

In this study, we used the high-throughput sequencing method to sequence the serum exosomal microRNA expression profiles of lead-exposed workers and population in

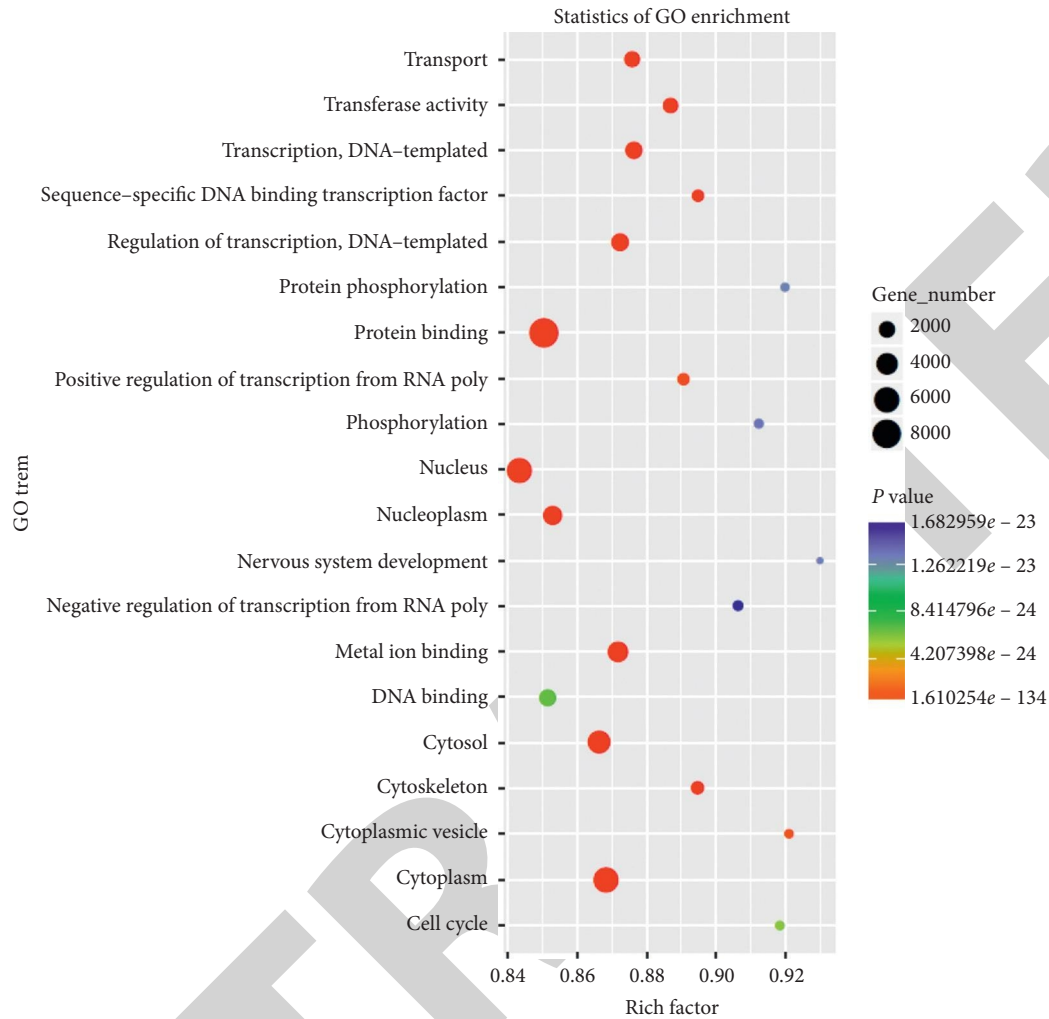


FIGURE 5: The KEGG enrichment scatter plot of differential micro-target gene expression of serum exosomes.

TABLE 7: The expression of miR-124 and miR-506 of serum exosomes.

Groups	N	miR-124	miR-506
Control	4	1.00 ± 0.15	1.00 ± 0.26
Lead group	8	2.55 ± 0.42*	1.84 ± 0.30*

*Compared with control group $P < 0.05$.

the control group. Differentially expressed genes are defined as genes satisfying $P \leq 0.05$, the fold change ≤ 1.2 . The results showed that there are 73 differentially expressed microRNAs in serum exosomes of lead-exposed workers, among which 48 were upregulated microRNAs and 25 were down-regulated microRNAs. Furthermore, we used miRbase and Target Scan database software to predict the target genes of the 73 differentially expressed microRNAs and obtained 1581 genes with significant differences. Finally, we functionally annotated these genes based on GO terms including biological process, cellular component, molecular function, and KEGG pathway analysis and discovered that most of them are related to occurrence and development of lead damage. It is suggested that the changes of microRNA

molecules are closely related to lead exposure levels and damage effects and are expected to become a new biomarker of lead neurotoxicity [32].

The results of microRNA sequencing show that the expression of exosomal miR-124 was 12.07-fold higher than that in the control group, and miR-506 was also 4.33-fold higher than that in the control group. It suggests that miR-124 and miR-506 may be involved in the occurrence and development of nerve damage caused by lead exposure; meanwhile, the result is similar to the study of neurodegenerative diseases [33, 34]. Available studies have found that miR-124 has a significant regulatory effect on neuroinflammation, and overexpression of miR-124 significantly inhibits the activation of astrocytes caused by methamphetamine [35–37]. MiR-124 can also participate in cell apoptosis and related inflammatory responses by regulating the expression of P38 [38]. Moreover, miR-124 targets CLOCK inhibits the activation of NF- κ B pathway, and activation of NF- κ B can give negative feedback to miR-124 expression [39].

According to the functional annotation of miR-124 and miR-506 target genes, our data indicated that microRNA-

124, microRNA-506 may be involved in immune-inflammatory related pathways such as JAK/STAT, NF- κ B, mTOR, and TCR signaling pathway [40]. Furthermore, their common target proteins such as AKT3, GRB2, PK3R3, SOCS1, SOCS2, NRAS, SOCS3, TNF, PDPK1, RELA, and PLCG1 can simultaneously regulate multiple immune-inflammatory signaling pathways [41]. Taken together, the results suggest that the increased expression of serum exosomes miR-124 and miR-506 may be related to lead-induced inflammatory damage in the central nervous system, and the specific mechanism of its action needs further studying.

5. Conclusion

In current study, it has been found that lead exposure resulted in 73 microRNA changes in serum exosomes, among which 48 microRNAs are upregulated and 25 microRNAs are downregulated. Moreover, the increase of miR-124 and miR-506 in the serum exosomes of lead-exposed workers was ranked as top levels suggesting that exosomes miR-124 and miR-506 may be involved in the process of lead-induced neuroinflammation.

Data Availability

The data used to support the findings of this study are available from the corresponding author upon request.

Conflicts of Interest

The authors declare that they have no conflicts of interest.

Authors' Contributions

Jianzhu Bo and Fan Shi contributed equally. Study design was done by YSZ and SL. Experiment implementation was performed by JZB, FS, XW, BH, and YZ. Result analysis was performed by JZB and FS. Manuscript writing was done by JZB, FS, and LJZ. All authors approved the final version of the manuscript.

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