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Figure P431 The result of immortalized lymphocyte cell line transformation on day 0 day15 and day 30 ×50

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RNA GAS5 Ă ✕ ى ` ʙ ψ E E ≠’ ω

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RNA LncRNA m Ҥ Ҥ Ї Ҥ 200 nt RNA ɟ LncRNA GAS5 m ~ ɔ ǫ̈ Ặ LncRNA ɬ ת ɣ Ҥ Ҥ ж 1 ˝ ӏ 2 ┘ 5 ã̃ 4 087 nt 12 Y ɟ LncRNA GAS5 ל Ά א ч Ї Ҡ ʊ̈ ɔ ѡ Ặ ה ה Ψ Ə ɟ ʊ̈ ɔ ѡ Ặ ה ה Ψ Ə Əm ɟ LncRNA GAS5 ɔ ợ

The Role Of LongNon - Coding RNA GAS5 In The Occurrence And Development Of Atherosclerosis And Atherosclerosis-related Diseases

WEI Guijiang[1 2 3] YANG Jun[1] WEI Yesheng[1★]

1. Department of Medical Laboratory Affiliated Hospital of Guilin Medical University Guilin Guangxi China 541000 2. Medical College of Guangxi University Nanning Guangxi China 530000 3. Department of Medical Laboratory Affiliated Hospital of Youjiang Medical University for Nationalities Baise Guangxi China 533000

ABSTRACT LongNon Coding RNA LncRNA is a type of RNA that is located in the nucleus or cytoplasm and is longer than 200 nt. LncRNA GAS5 is a member of the LncRNA family that has attracted attention in recent years. The encoding gene is in the q25 regio of human chromosome 1, has a total length of 4 087 nt and consists of 12 exons. Several studies have shown that LncRNA GAS5 is involved in inflammation mediates vascular endothelial cell damage and plays an important role in the development of atherosclerosis and related diseases. This article reviews the role of LncRNA GAS5 in the occurrence and development of atherosclerosis and atherosclerosis related diseases.

KEY WORDS LncRNA GAS5 Atherosclerosis Coronary heart disease Diabetes

RNA long non coding RNA ئى Ї[m] Ѽ Ѽ LncRNA m Ҥ Ҥ Ї Ҥ Ѽ Ặ ɣ ל Ά ɬ ʙ ɬ ɛ̈ H 200 nt RNA [1] ɟ LncRNAs ɬ ~

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ھه ۍ Ă Ψ Liu [23] ה
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Ψ ; LncRNA GAS5
Ą̈ PDGF bb ھه ۍ ɟ
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LncRNA GAS5 Á p53 ۍ p300 ´ p53
p300 Ў Ə p53 ; نح غ
φ Tang ᵐ
Ъ Liu ◑ LncRNA GAS5
ھه Ė ˜ Ə ɟ ж Sun
ζ ᵐ ặ Á Liu ۍ Tang
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cRNA GAS5 ɷmiR 137 ۍ IGFBP 5 mRNA
Western blot IGFBP 5
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ζ Ψ ; miR 137
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Ъ LncRNA GAS5 Ά miR 135a ˜ Ə
LncRNA GAS5 ŭ ɔ ᵢᵧ
∤ oxLDL THP 1 ђ ᵢᵧ Ψ ɔ
LncRNA GAS5 ¨E ɔ ∤
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φ LncRNA GAS5 ’ w
ɔ miR 135a Ď ɔ
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2 LncRNA GAS5

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Western blot Ỉ Ψ ɔ LncRNA
GAS5 ; ġ mTOR ∤ ɔ mTOR
ɟ Ά ɾ ǫ
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ġ ƚ Ά ǫ ה ה [30] ɟ ŭ Ɠm
ŭ LncRNA GAS5 ŭ ǫ
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Ə Ψ Li [31] 102 ʒ ǫ
∤ 98 ʒ ɾ Ə ε LncRNA
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Ҡ в ĕ H в ɔ в Ҡ ∤ Wnt/α
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3 LncRNA GAS5

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ﻫ 3 t qRT PCR 96 oy ﻫ Ở ж
LncRNA GAS5 ŏ
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; ε 0.81 LncRNA GAS5
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• • COVID 19

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ѡ RT PCR Ὸ ی Ợ ˝

Nucleic Acid Detection of Different Specimen Types of SARS-CoV-2 Base on Real-time Fluorescent RT-PCR

ZHOU Gang[1] LI Chao[1] ZHENG Guodong[1] LIU Hongtao[1] ZHOU Rongrong[1] WANG Hongtao[1] WANG Gangping[2]*

1. Department of Microbiological Laboratory Rizhao Center for Disease Control and Prevention Rizhao Shangdong, China 276826 2. Central Laboratory & Clinical Molecular Diagnosis Center Rizhao clinical molecular medicine research center Rizhao key laboratory of precision medicine Rizhao People s Hospital Rizhao Shangdong, China 276800

ABSTRACT Objective To investigate the positive detection rate of Severe Acute Respiratory SyndromeCoronavirus 2 SARS CoV 2 in different samples in order to provide guidance and suggestions for the prevention and control of epidemic. Methods A total of 3 284 throat swabs nasopharyngeal swabs sputum specimens and fecal specimens were collected from 2 258 SARS CoV 2 suspected patients who were admitted in our hospital from January 2020 to February 2020. The real time polymerase chain reaction RT PCR method was used for PCR amplification and SPSS19.0 software was used for statistical analysis. Results A total of 79 positive samples were detected among 3 284 samples A statistical analysis was performed on the positive detection rates of different sample types tested at the same time and the difference

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1. 276826
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★ E-mail wgprzph93@126.com

was statistically significant P<0.05 . There are 13 male suspects and 7 females in this study. respectively no statistically significant difference in gender positive detection rates P>0.05 . The results from different sample types showed that the positive detection rate of throat swabs was the lowest nasopharyngeal swabs and sputum samples were higher than throat swabs. Interestingly the positive detection rate of fecal samples was the highest although the sample number in this group was small compared to other types . However there was no significant difference in the positive rate of the same suspected patient with different sample types at the same time. Conclusion The RT PCR method has different positive detection rates for different sample types which can provide guidance for the selection of samples in laboratory testing and better prevention and control of epidemics.

KEY WORDS Real Time Polymerase Chain Reaction Positive rate SARS CoV 2 throat swabs

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Table 3 SARS CoV 2 nucleic acid detection results at the same time in the same suspected patient with different sample types

n %

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	303	1 0.33	302 99.67		
	909	1 0.11	908 99.89		
i ˝	4	0 0.00	4 100.00		
4 ˝	4	0 0.00	4 100.00	/	/
.	4	0 0.00	4 100.00		
	12	0 0.01	12 100.00		
i ˝	280	7 2.50	273 97.50	0.079	0.788
280 ˝	280	6 2.14	274 97.86		
	560	13 2.32	547 97.68		
˝	132	10 7.58	122 92.42	0.733	0.521
132	132	14 10.61	118 89.39		
	264	24 9.09	240 90.91		

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ώ ã щ Нь О † ɟ Ύ SARS CoV 2 ẇ ה щ ε Ặ ɟ ’ SARS CoV 2 ε í w ˅ вε w ɟ Ч SARS CoV 2 i ˝ в ˝ в ẇ . Ό Ό Ά ę ђ Ό [9] ζ Ɑ ġ ε ה ﻁﻄﺋﻯ ˝ ˀ Ά ┘ ╥ m ى Ά Ξ ى Ό ’ ж í ﻫﻫ ى Ό ɟ Ψ ǫ̈ Ό τ ς Ά Rui Liu [9] ˝m ﻭﻮ ﻫ Ỉ ę ђ Ψ ς Ψ Нь [10] ’ Ά ┘ Ặ ɟ ǫ̃ 4 ʒ Ч Ό ɛ Ў 1 ʒ Ч i ˝ в ˝ ﻕ ∨ ∨ ɟ ה ~ SARS CoV 2 ˆ Ɑ ġ в ˆ вУ ɨ ġ ’ ỉ ώ [11 12] RT PCR Ḥ Ό Ţ e ε 30%~ 50% [13] ɟ ġ ﻭﻮ SARS CoV 2 Ψ ´ Ŭ Ч ´ вí w ẇ ḍ в ى ´ w ẍ ˆ ɟ ώ SARS CoV 2 ى ε i / ˝ i ˝ Ό ң Ά m [14] ɟ SARS CoV 2 Ж Ж ∧ Ж SARS CoV 2 Ά Ặ Ύ ﻭﻮ ʒ . Ψ ǫ̃ Ъ SARS CoV 2 [15] ƒ . ﻭﻮ í Ψ ε ى Ψ . ˥ ˝ ε è / . Ό 56.25% Ά ∨ ỳ [16] m ɟ í א ẇ ╥m ˝ Ж Ό Ό ˝ . Ў ɟ ġ ˀ m Ч ȣ m ˀ ى

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2019 ى ợ ẉ PCR ĭ ɻ
2019 ى ợ ى ợ ẉ PCR

The effect of 2 different inactivation methods on the results of viral nucleic acid in 2019 new coronavirus throat swab specimens

JIANG Lei[1] ZHANG Liyuan[2] LIU Daning[2★]

1. Laboratory of Puyang Oilfield General Hospital Puyang Henan China 457001 2. Laboratory of Puyang people s Hospital Puyang Henan China 457000

ABSTRACT Objective To investigate the effect of two different pharyngeal swab specimens inactivation methods on the results of 2019 new coronary virus fluorescent quantitative PCR. Method Three cases of 2019 new coronary virus positive specimens were treated by two different inactivation methods the nucleic acids were extracted by manual centrifugation method from three groups of samples which were inactivated at 56 for 30 minutes and inactivated with guanidine salt RNA preservation solution. Simultaneous detection of virus content with two different nucleic acid detection kits the results of qPCR were analyzed statistically. Result The results of two different nucleic acid detection reagents showed that the results of the three groups which were not inactivated inactivated at 56 for 30 minutes and inactivated with guanidine salt RNA preservation solution were significantly correlated and had good consistency. The correlation coefficients among the three groups were all above 0.98 P<0.001 . Conclusion 2019 new coronary virus nucleic acid qPCR results were not affected by the two inactivation methods.

KEY WORDS 2019 new coronary virus Novel coronary virus pneumonia qPCR

2019 ى ợ 2019 novel coronavirus ẉ ئى 10 Y ɻ 2019 nCoV ’ ۶ ۴
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★ E-mail mengqfoo@163.com

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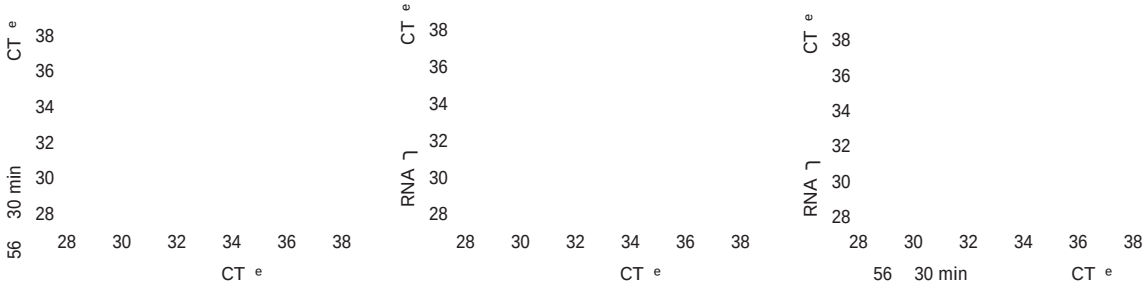

1 56 30 min RNA qPCR A

Figure 1 Correlation analysis of qPCR results among the un inactivated group the inactivated group heated at 56 for 30 minutes and the guanidine inactivation group detection kit A

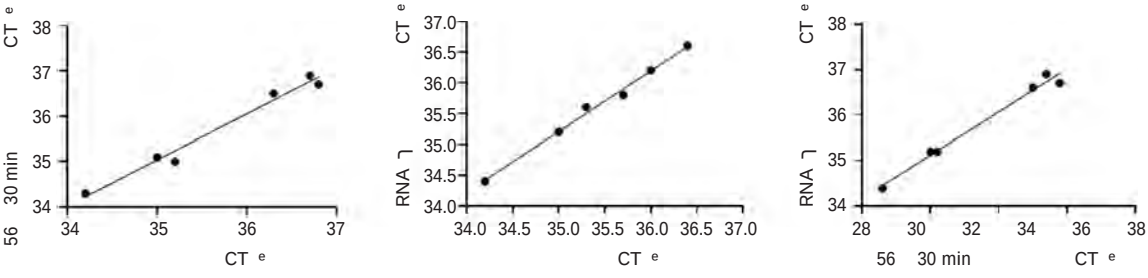

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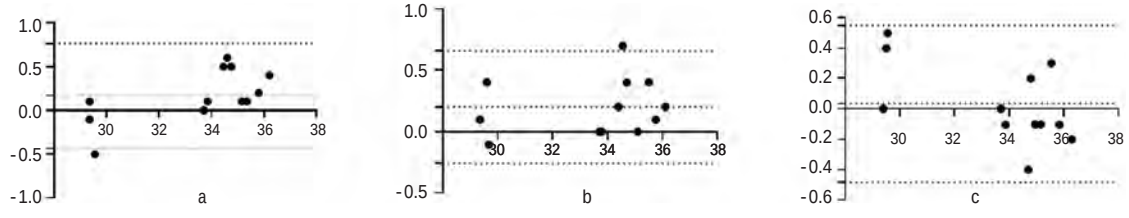
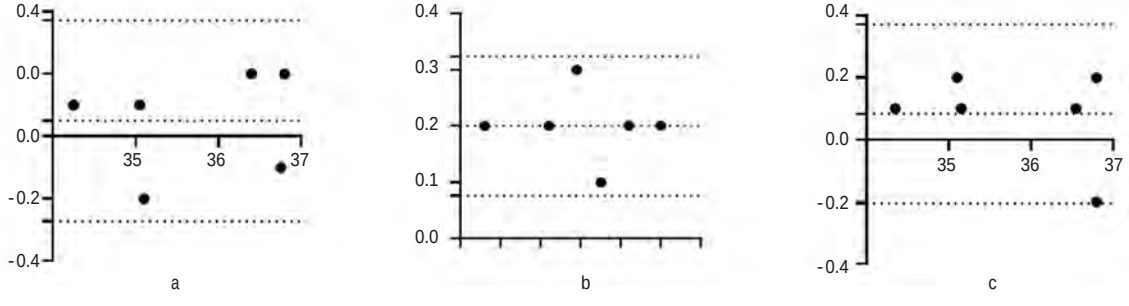
Figure 1 Correlation analysis of qPCR results among the un inactivated group the inactivated group heated at 56 for 30 minutes and the guanidine inactivation group detection kit B



3 56 30 min RNA qPCR A

Figure 3 Consistency analysis of qPCR results among the un inactivated group the inactivated group heated at 56 for 30 minutes and the guanidine inactivated group detection kit A



4 56 30 min RNA qPCR B

Figure 4 Consistency analysis of qPCR results among the un inactivated group the inactivated group heated at 56 for 30 minutes and the guanidine inactivated group detection kit B

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Analysis of the clinical manifestations and computed tomography characteristics of patients with coronavirus disease-2019 COVID-19

CHEN Shaojin[1] WANG Xiaoxia[1] WANG Licheng[1] CHEN Hai[1] ZHANG Meng[2]*

1. Clinical Laboratory of Sanya People s Hospital Sanya Hainan China 572000 2. Radiology department. of Sanya People s Hospital Sanya Hainan China 572000

ABSTRACT Objective To analyze the clinical presentations and computed tomography characteristics of coronavirus disease 2019 COVID 19 and to further improve the understanding of the disease. Methods A retrospective analysis and summary of the clinical manifestations and CT imaging features were performed based on 15 patients with COVID 19 diagnosed in our hospital since January 2020. Results Most patients diagnosed in this study were men 67% 10/15 aged 25 to 71 years with a median age of 54 years interquartile range of 37 to 65 . Most of them were over 50 years old 53.3% 8/15 . All 15 cases had a history of contact with the affected area 100% . The clinical manifestations are fever cough dry cough or sputum with white mucus some accompanied by chest tightness shortness of breath and fatigue. Most patients were in early or advanced disease stages according to the chest imaging manifestations. They have a ground glass patchy shadow in bilateral pulmonary multi lobular lesions predominantly in the subpleural regions blurred lesion margins. They were also accompanied by thickening of blood vessels thickening of the pleura bronchial inflation and increased lymph nodes in the mediastinum in some cases. 15 patients have positive nucleic acid tests for the

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1. 572000
2. 572000
★ E-mail zanmon@163.com

novel coronavirus ORF1ab and N genes. In addition 93% 14/15 of patients have high level of hypersensitiv ity C reactive protein. Conclusion COVID 19 patients have fever and cough at the early stage and there are abnormal chest CT examinations. The combination of epidemiological investigations clinical manifestations chest CT imaging characteristics analysis and nucleic acid detection and other laboratory test results will help early screening prevention and control of COVID 19.

KEY WORDS Coronavirus disease 2019 Clinical manifestations Computed tomography characteristics

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7 ʒ æ 8 ʒ Ψ 62.5% 5/8 غ ה ۷ ن 25% 2/8 غ ۷ ن 12.5% 1/8 ً غ Ά ɟ 66.7% 10/15 í ε ה ɞ۷ ن ɞ ۷ ŏ ¥ ɞ ˌ ۱ ï Ὼ ɟ 13.3% 2/15 ε ی 86.7% 13/15 ε ɟ ی ɟ Ц ҷ Ὸ ɟ

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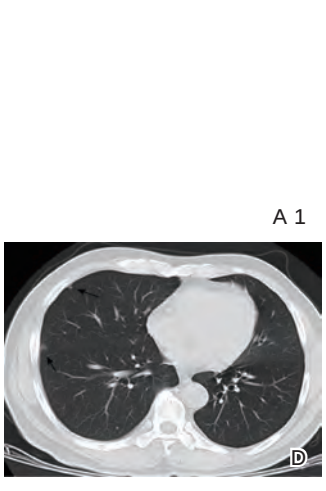

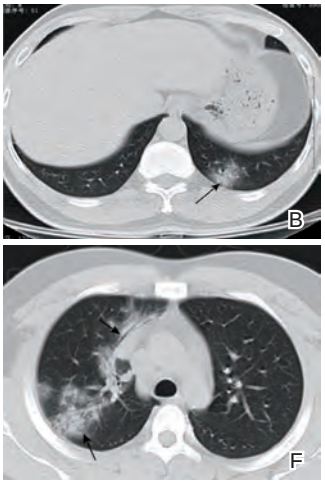

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Figure 1 The chest CT imaging of partial COVID 19 patients

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COVID 19 [13] ɟ MERS 35%

ج ε 50 ҷ ζ ε 66.6%

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ڳ ת HCV RNA ها Ă لأ ʒ غج ’ כ

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HCV RNA ۏ ۟ Ψ ɟ 2019 1 10 ۟ 1 005 ʔ ˀ כ ת ẉ ẍ ŏ CMIA ۱ ẉ PCR ŏ ậ Ψ HCV I ۱ HCV RNA ɟ HCV I S/CO e Ά HCV RNA Ά Ă ŏ HCV I S/CO e Γ ى ө ɟ 1 005 ʔ Ψ HCV I 228 ʔ Ό ε 22.7% Ό HCV I HCV RNA ۏ HCV I Ψ ẉ PCR Ό HCV RNA 83 ʔ Ό ε 36.4% HCV I S/CO e ң Ά HCV RNA e φ Ă ɟ ẉ HCV I S/CO e ⩾10.7 Ə ε Γ ى í e ę Ά ŏ ậ ε 92.59% ۱ 77.93% ’ ئ HCV ɟ HCV RNA Ь ۟ Γ ى ’ ẉ Ă א I Ǐ Ą Ỹ ۱ Ж Ά Ж ۟ ’ ⅃ ŏ ۱ Ė ө ۱ Б í ө e ɟ Γ ى HCV RNA ۟ כ ת ẉ ẍ ŏ

Application of high-sensitivity HCV RNA detection in preoperative screening

HE Yuting[1] CHEN Xuefang[2] CHEN Peisong[1] HUANG Hao[1] YU Xuegao[1] HUANG Bin[1]★

1. Department of Laboratory Medicine The First Affiliated Hospital Sun Yat sen University Guangzhou Guangdong China 510080 2. Nanfang College of Sun Yat sen University Guangzhou Guangdong China 510970

ABSTRACT Objective To investigate the application of high sensitivity HCV RNA detection in preoperative screening. Methods A total of 1 005 serum samples were collected from the preoperative screening patients in the Hospital Sun Yat sen University from January to October 2019. HCV antibodies and HCV RNA were detected using chemiluminescence microparticle immunoassay CMIA and fluorescence quantitative polymerase chain reaction FQ PCR . The comparison and correlation analysis between the S/CO value of HCV antibody and the high sensitivity HCV RNA test results were performed. The predictive efficacy of HCV antibody S/CO value for hepatitis C viremia was evaluated. Results Among the 1 005 serum samples 228 were positive for HCV antibody and the positive rate was 22.7%. HCV RNA were not detected from HCV antibody negative specimens. High sensitivity FQ PCR method detected 83 HCV RNA positive cases and the positive rate was 36.4%. There was no correlation between the HCV antibody S/CO value and the HCV RNA quantitative value. Using the critical S/CO value ⩾ 10.7 with a sensitivity and specificity of 92.59% and 77.93% respectively can reduce the false positive rate for predicting hepatitis C viremia. Conclusion High sensitivity HCV RNA quantitative detection is applied for the preoperative screening of patients with hepatitis C which can accurately reflect the virus replication and infectivity in patients. Compared with the

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★ E-mail hb906@163.com

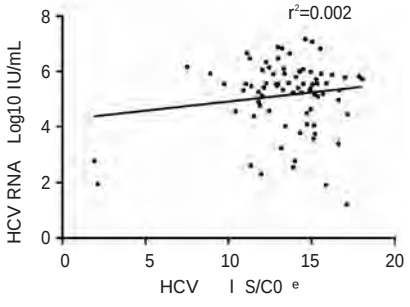
traditional preoperative screening method FQ PCR can distinguish the current infection from the previous infection and has the advantages of rapid

HCV RNA ɟ 1 ɟ w
HCV RNA Θ ε HCV ΈA CMIA
HCV I א HCV Ά
ŏ ά ε 100% Ά 78.3% e ۱
e ŏ ά 36.4% ۱ 100% ´ ε 85.6% ɟ
2.2 HCV I S/CO e Ά HCV RNA
ẇ Ă Ą ŏ
HCV I S/CO e ŏ
1 ɟ S/CO e ₹ ₹ ɟ
ˆ y S/CO e Ά HCV RNA e ћ
Ă ŏ ћ 1 ɟ ´ ε Y=0.06
617X + 4.259 ɟ Spearman Ă r^2=0.002 P=
0.69 HCV I S/CO e ң Ά HCV RNA
e φ Ă ɟ

1 HCV S/CO HCV RNA
n %

Table 1 Distribution of HCV antibody S/CO value and high sensitivity HCV RNA detection results n %

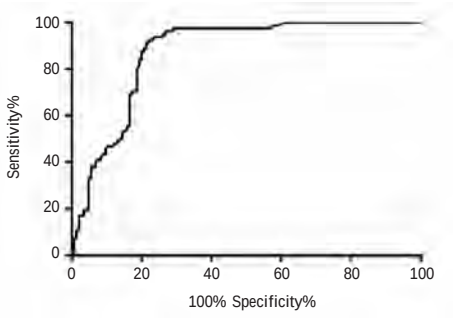
S/CO e	n	HCV RNA	
4>S/CO⩾1	87	1 1.1	86 98.8
8>S/CO>4	21	2 9.5	19 90.5
12>S/CO>8	29	15 51.7	14 48.3
16>S/CO>12	79	56 70.9	23 29.1
S/CO>16	12	9 75.0	3 25.0
´	228	83 36.4	145 63.6



1 HCV S/CO HCV RNA

Figure 1 Scatter plot of HCV antibody S/CO value against high sensitivity HCV RNA quantitative detection results

2.3 HCV I S/CO e Γ ىی
ɵ
HCV I S/CO e Γ ىی ROC
; area under the curve AUC ε 0.872 4
ROC ’ Ό w S/CO e ⩾10.7 Θ ε HCV
e ◑ cut off e
Youden s index 0.705 2 Ά
ŏ ά ε 92.59% ۱ 77.93% ɟ w S/CO e ⩾1 Θ ε è
HCV í e 228 ϛ HCV I
Ψ HCV RNA ¯ 36.4% 83/228 ɟ ћ 2 ɟ



2 HCV S/CO
ROC

Figure 2 ROC curve of HCV antibody S/CO value for predicting hepatitis C viremia

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ѡΆ í Ă ɟ ώ í ɔ
HCV ζ ۱
ŏ ɟ ◑ ά Ɑ
Ɑ I I Ĭ HCV
Ƀ HCV I ۱ HCV Ɑ [4] ɟ
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Ό ɟ ɣ Γ ىی I ‴
HCV [5] ɟ HCV I
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΄Y PCR ɔ ה Θ
Нь ╥ ɔ ŭ í ɔ ɟ
Baleriola C [6] ŧ ŭ - 20
۱ - 70 HCV RNA ה - 20 ŧ
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Ė ל ɔ ɟ
Нь - 80 ŧ 1 φ Ĭ HCV RNA ‴ Ж ĭ
HCV RNA ΈA ɟ ŭ 228 ϛ HCV
I Ψ ε 36.4% ɟ ’ Нь
З HCV HCV I ’

Ψ HCV RNA ė Ηь ң Ϊ̈Ạ
HCV RNA ‴
ợ̉ ɟ φ˜ ‴̂ S/CO e م HCV RNA
ŏ S/CO e ╗
Ч ω ╗ Spearman Ặ ŏ ה
HCV I S/CO e Ά HCV RNA e φ
Ặ S/CO e ң ‴ א HCV I Ǐ
Ϊ̈Ạ Ỹ ɟ ˜ ROC ŏ S/CO cut
off e ε 10.7 ’ ɵ e í ɔ ш
S/CO e ⩾1 Ə ε è Γ یی cut off
e ğ́ ó ε HCV I Ψ HCV RNA
Ὸ ң ‴ HCV
ɟ Pan J Kao HH Ά Ranjbar Kermani F [7 9]
HCV I ק ה
ш S/CO e ⩾ 1 Ə ε Γ یی cut
off e ğ́m ϛ HCV I HCV
RNA ɟ نح Ηь ɔ Б † HCV I
’ Ηь HCV HCV RNA
Ηь HCV ɵHCV ŏ
ш ẇ ˜ Ţ [10] ɟ
HCV RNA ң Ηь 15 IU/mL
ہ Ϊ̈Ạ Ά Ψ ɵ Ж ɵ
ہ Ж ۱ Ж Ж HCV
[11] ɟ
Ha J [12] HCV RNA 32 127 ϛ
Architect anti HCV Ὴ ε HCV I
ה 8 ϛ 0.02% 8/32 127 HCV
RNA ɟ ũ̈ [13] ğ́ 148 590 oy ELISA ε
HCV I Ψ Ὸ HCV RNA 298
ϛ ε 0.2% ɟ ˜ [14] ğ́ 307 440 ϛ
ELISA ε HCV I Ψ Ὸ
1 ϛ HCV RNA ε 0.000 325% ɟ ’
Ηь Ηь i Ηь ӧ Ϊ̈Ạ
У У ң I ɟ
Ϛ ’ HCV نح ė ل Жیی ẇ ┼
[15] ɟ Ψ ה HCV I HCV RNA
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א ئی HCV HCV ğ́ I Ǐ
Ϊ̈Ạ Ỹ Ά Ж ѿ ┘ ŏ
Ά ’ ├ Ж ɟ

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_ ضحى 2 ̃A ẓ Glu504Lys ŏ 1 ۷ Ă ىلحى ء 2 Ọ′ ∂ — ’ h ẓ

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ŏ 2 يى T2DM ж Ψ ф 2 ALDH2 نح غ Glu504Lys ŏ ALDH2 نح غ 504 Ң نح غ ل Ά ɵHbA1C Ш Ậ ɟ ŏ 2016 4 2017 12 Ҍ 629 ʔ ɔ Ậ ŏ ε ا 402 ʔ ۱ 2 يى 227 ʔ ɟ ŏ Ξ ж ALDH2 ˇ نح غ يى ŏ Ξ ж ALDH2 ˇ نح غ يى HbA1C ɵ Ш ŏ ɟ 2 يى GL ɵLL ل نح غ يى ʔ ŏ ۈ 37.9% ۱ 7.0% Ҍ ا 30.8% ۱ 3.2% P<0.05 ɟ 629 ʔ ɔ GG يى 390 ʔ GL يى 210 ʔ LL يى 29 ʔ ɟ ALDH2 نح غ ل ھ 2 يى ھ Ê ا ε ل GG يى 32.1% 125/390 ´ ل GL يى 41.0% 86/210 ´ ل LL يى 55.2% 16/29 ɟ ALDH2 نح غ ل ה 2 يى • غ OR e =1.578 95% ת ˩ ε 1.131~ 2.202 ɟ ALDH2 نح غ ل HbA1C ŏ ĭ P>0.05 ɟ Ξ ж ۈ ALDH2 ˇ نح غ يى ŏ ج P>0.05 ɟ 2 يى ALDH2 ˇ نح غ يى HOMA1 IR ɵ QUICKI ɵ ISI ŏ ج P>0.05 ɟ 2 يى ж ALDH2 نح غ 504 Ң ה ل ʔ Ҍ ж Glu504Lys ل 2 يى ה • غ ӂ Ά ɵHbA1C w Ш Ậ ɟ ф 2 2 يى نح غ К

Distribution characteristics of Glu504Lys polymorphism of acetaldehyde dehydrogenase 2 gene in Type 2 Diabetes Mellitus in Han Nationality

AN Hongliang[1]★ JIANG Haiyan[2] ZHANG Jinfeng[1] LI Weixuan[2] SU Rong[1] HE Xian[1] LV Weifeng[1]

1. Department of Clinical Laboratory Foshan Hospital of Traditional Chinese Medicine Foshan Guangdong China 528000 2. Department of Clinical Laboratory The first people s hospital of Foshan Foshan Guangdong China 528000

ABSTRACT Objective To analyze the distribution characteristics of the Glu504Lys polymorphism of the aldehyde dehydrogenase 2 ALDH2 gene in people with type 2 diabetes T2DM and to explore the relationship between ALDH2 gene mutation at position 504 and fasting blood glucose HbA1C level and insulin resistance. Methods A retrospective study was conducted in 629 cases of physical examination and hospitalization in Foshan Traditional Chinese Medicine Hospital from April to December in 2016. There were 402 healthy controls and 227 patients with type 2 diabetes mellitus. The distribution of ALDH2 genotypes in the two groups was analyzed and the distribution levels of HbA1C fasting blood glucose and insulin resistance in ALDH2 genotypes of the two groups were compared. Results The proportions of GL and LL mutation genotypes in type 2 diabetes group were 37.9% and 7.0% respectively which were significantly higher than those in the physical examination control group 30.8% and 3.2% P<0.05 . Among 629 Han subjects 390

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★ E-mail 438320079@qq.com

cases are GG 210 GL and 29 LL. With the increase in the number of ALDH2 gene mutations the risk of type 2 diabetes increases. The specific data are 32.1% 125/390 without mutation GG type 41.0% 86/210 with heterozygous mutation GL type and homozygous mutation LL Type 55.2% 16/29 . ALDH2 gene mutation is a risk factor for type 2 diabetes OR value = 1.578 95% confidence interval is 1.131~2.202. ALDH2 gene mutation has no effect on the distribution of HbA1C level P>0.05 . There was no difference in the distribution of ALDH2 genotypes between men and women in the 2 groups P>0.05 . There was no significant difference in the distribution of insulin resistance index HOMA1 IR quantitative insulin sensitivity test index QUICKI and fasting insulin sensitivity index ISI of each type of ALDH2 genotype in type 2 diabetes group P>0.05 . Conclusion The proportion of ALDH2 gene mutation at position 504 in Han type 2 diabetes population is significantly higher than that in normal population. Glu504Lys mutation is a risk factor for type 2 diabetes but it was not significantly related to fasting blood glucose HbA1C and insulin resistance.

KEY WORDS Aldehyde dehydrogenase 2 Type 2 diabetes mellitus Genotype Polymorphism genetic

ϕ 2 acetaldehyde dehydrogenase 2 ALDH2 ж l ц Ă φm ε ϕ 19 ˚ Ψ m Ė ∤ ъ Ά ж l ц ɟ ALDH2 ת ġ Ң Њ l 12q24 ŭ G→A ╥ ъ rs671 ת Ώ 504 Ң glutamic acid G ъ ε lysine L У Ξ Ң ת ġ G ɬL ∤ ϵ ת ġ ש GG ש ɵGL ש ɬL ש ˇ ת ġ ש ALDH2 ɟ ALDH2 ת ġ Glu504Lys Ң ъ ה • ġ [1,2] Ά 2 ש Ă ɟ ŭ Ψ ALDH2 ъ ת ġ HbA_{1C} Њ ´ ש 2 ש [3] ɟ ´ ợ ALDH2 ת ġ Glu504Lys Ң ъ ה 47.80% Њ ╥ ợ 22.0% ∤ ≠ 19.38% [4] ɟ ж 2 ש ġ ₭ ġ Ė ѿ ε ה ת ġ ת ALDH2 ת ש ġ ת Ά ˘ ɔ Ă ɟ ŭ ≠ ж ∤ 2 ש Ψ ALDH2 Glu504Lys ŏ ŏ ALDH2 ת ġ ъ Ά ɵHbA_{1C} ∤ φ Ă ε ĺ ∤ w ˚ ɟ

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1.1 m

1.1.1 ת Ỹ

2016 4 2017 12 Њ ε 2 ש 227 ҂ 2 ש ɔ 154 ҂ 73 ҂ 18~90 57.78±15.30 ɟ ˥˚ ĕ Ψ ├ l Ψ ≠ ж 402 ҂ 330 ҂ 72 ҂ 17~87 38.63±9.47 ɟ ŏ ợ ALDH2˘ ת ġ ש ŏ ɵΨ ɵ ALDH2˘ ת ġ ש ŏ τ P>0.05 ɟ Ė ˚ ɟ

1.1.2 Ấ ỸΆ ỸA

ỸA [5] 1999 WHO 2 ש ỸA [5] ė ש ɔ ⩾11.1 mmol/L ⩾7.0 mmol/L 75 ẋ 2 ⩾11.1 mmol/L ɟ Ấ ỸA ж 20~80 2 ש ε 2 ש m ≠ ж ɟ ỸA ж ę ђ ש O ˚ ˝ ã ɵ ɵO ɵ ₭ ɵę ђ O ɟ

1.2 Ѧ ъ Ά Ң

ABI 7500 ש ѭ Ѧ ѧ ѵ ă̆ ˘ BR 526 24 ש ã P Ѧ ∤ ALDH2 ת ė Ώ Ң ɔ θ ă̆ ˘ G7 ש ã ɔ ŭ Ѧ Ѭ ɔ Ң TOSOH Ж AU5400 ã ɔ ŭ Ѧ Ж ɔ Ң ѧ ă̆ ˘ Centaur XP ש ã ɔ ה ẉ ẍ ŭ Ѧ Ѭ ɔ ה ẉ Ң ѧ ├ ă̆ ˘ ɟ

1.3

8 ∀ 3~4

mL ɟ ɔ ʅ ALDH2 غ نح ϕ J ظ
ϕ J EDTA 2Na ˮH ʅ
ŏ ˮH ˮH ◗ 2~
8 ך 3 Ỉ ɟ ˬ ʁ
HOMA1 IR
HOMA1 IR HOMA1 IR= ×
/22.5 ISI ISI=1/
× QUICK
QUICKI [6] ɟ

1.4 ALDH2 نح غ ŏ یی
DNA ˮΩ ɟ ①DNA
ך ʎ 2 mL
ă ˘ y ⊑ ך Ѧ ѱ
ã نح غ DNA ך Ḥ ך ɟ
②DNA ⁂ ɔ θ ă ˘
ALDH2 نح غ Ḥ ⁂ Ḥ ʃ
ѧ ʅ ă ˘ ABI 7500 یی ⁂ Ѧ ⁂ ɟ

③ P ɔ θ ă ˘ ALDH2
نح غ Ḥ P Ḥ ѱ BR 526 24
یی ã P Ѧ نح غ P ŏ یی ɟ
1.5 ŏ
SPSS 22.0 Θ ɟ
1 Sample K S Kolmogorov Smirnov
ŏ ɟ w $\bar{x} \pm s$ Ỉ
ŏ ל ₸ غ ŏ
ŏ ל χ^2 P<0.05 ε
τ ɟ

2

2.1 I ʅ T2DM ALDH2 نح غ یی ŏ
Ξ ALDH2 نح غ یی ʁ ל ŏ
ج τ ج ε P<0.01 2 یی نح
ѧ ʌ ă ˘ ABI 7500 یی ⁂ Ѧ ⁂ ɟ غ ל ך Ньl ɟ 1 ɟ

1 T2DM ALDH2 n %

Table 1 Distribution of ALDH2 genotypes in control group and T2DM group n %

		GG	GL	LL		
	402	265 65.9	124 30.8	13 3.2	265 65.9	137 34.1
T2DM	227	125 55.1	86 37.9	16 7.0	125 55.1	102 44.9
	629	390 62.0	210 33.4	29 4.6	390 62.0	239 38.0
χ^2 e			9.489		7.255	
P e			0.009		0.007	

2.2 ˘ ALDH2 نح غ یی כ Ψ 2 یی Ţ e ε 1.578 95% ᄆ ε 1.131~2.202 ɟ
ך 2 ɟ
▌ ŏ ALDH2 نح غ ל
⁂ ל ʁ ´ ל ʁ ´ ל ה 2
یی ך ⁂ P<0.01 ɟ w ו ה ŏ ج τ P>0.05 ɟ 2 یی
L ל 2 یی غ ŏ ą ALDH2 نح غ یی ʁ ל
ALDH2 نح غ Glu504Lys Ḩ L ל ŏ ج τ P>0.05 ɟ
ה 2 یی • غ P<0.01 3 ɟ

2.3 ą Ä ALDH2 نح غ یی Ă
ą ALDH2 نح غ یی ʁ ל

2 629 ALDH2 2 n %

Table 2 Proportion of type 2 diabetes mellitus in 629 subjects with ALDH2 genotype n %

	ך	GG یی	GL یی	LL یی	ל یی	یی
T2DM	227	125 32.1	86 41.0	16 55.2	102	125
DM כ	402	265 67.9	124 59.0	13 44.8	137	265
´	629	390	210	29	239	390
χ^2 e			9.256		7.255	
P e			0.002		0.007	

3 ALDH2 n %

Table 3 Distribution of ALDH2 genotypes between male and female n %

	¢	ʔ	ی غ نح			ک	
			GG ی	GL ی	LL ی	ی	ی ک
		330	221 67.0	100 30.3	9 2.7	221 67.0	109 33.0
		72	44 61.1	24 33.3	4 5.6	44 61.1	28 38.9
	χ^2 e			1.946		0.903	
	P e			0.378		0.342	
T2DM		154	85 55.2	58 37.7	11 7.1	85 55.2	69 44.8
		73	40 54.8	28 38.4	5 6.8	40 54.8	33 45.2
	χ^2 e			0.014		0.003	
	P e			0.993		0.955	

2.4 2 ی ˘ نح ی غ ɔ ŏ χ^2=0.606 P>0.05 ₸ غ ŏ ɟ GG ɑGL ɑLL نح ی غ HbA$_{1C}$ ŏ ج

2.4.1 HbA$_{1C}$ F e =0.291 P=0.748 P>0.05 ɟ ی

HbA$_{1C}$ Kolmogorov Smirnov ١ ٭ GG Á ی ک GL+LL HbA$_{1C}$ ŏ

ŏ Z e =1.393 χ^2=0.041 P<0.05 HbA$_{1C}$ ج F e =0.546 P=0.461 P>0.05 ɟ

ε e ~ ١ ŏ Z e =0.763 4 ɟ

4 T2DM $\bar{x} \pm s$

Table 4 The distribution level of each biochemical serological index in each genotype $\bar{x} \pm s$

	ی غ نح			ی ک	
	GG ی	GL ی	LL ی	ی	ی ک
HbA$_{1c}$	8.818±2.559	9.023±2.296	8.955±2.788	8.818±2.559	9.014±2.350
mmol/L	8.897±3.546	9.851±4.431	6.946±2.424	8.897±3.546	9.453±4.321
		F e =3.690 P=0.027		F e =1.035 P=0.310	
mU/L	19.46±16.59	20.57±17.65	17.82±11.31	19.46±16.59	20.15±16.83
		F e =0.205 P=0.815			
	7.553±6.979	9.399±9.463	5.392±3.713	7.553±6.979	8.846±8.986
		F e =1.949 P=0.145			
	0.302±0.032	0.299±0.035	0.311±0.034	0.302±0.032	0.301±0.035
		F e =0.865 P=0.423			
	6.798±6.281	8.459±8.517	4.853±3.341	6.798±6.281	7.9613±8.088
		F e =1.949 P=0.145			

2.4.2

₸ غ ŏ ˘ نح ی غ

I τ F e =3.690 χ^2= 0.027 P<0.05 GL ی 9.851 ę GG ی 8.897 LL ی ʜ 6.946 Ξ Ξ GG ی Á GL ی ɑLL ی

τ LL ی Á GL ی

τ ɟ ی GG Á ی ک GL+LL ŏ ج ɟ 5 ɟ

5 T2DM

Table 5 The statistical results of FBG levels among genotypes in the T2DM group

¢ ی غ نح	F e	ج e I J	ʹA	P e
I	3.690	/	/	0.027
ی GG VS ی ک GL+LL	1.035	/	/	0.310
GG ی VS GL ی	/	-0.954	5.626	0.092
GG ی VS LL ی	/	1.951	1.113	0.087
GL ی VS LL ی	/	2.904	1.156	0.013

3

ALDH2 ל נח غ ŭ ж Ψ ң
ŭ Ж ж Ψ ל ε 30%~50% Ψ ہ
ж ל ε 15%~30% ˝ [7] ɟ ا
ALDH2 נח غ ל ε 34.1% Ά Ă
[m] [8] 2 ىى ל ╗
ε 44.9% ɟ ж ALDH2
נח غ ל ښ 2 ىى ʔ ╗ ה
ALDH2 נח غ Glu504Lys ל ж 2
ىى ɟ ל נח غ ж ALDH2
; נח ɔ У Г вф J
נח ң ĭ Ψ
ѳDNA в ŭ ' ъ ښ
Ъ ĭ ğ
ẇ ę ה ה ה [18] ɟ̓
ALDH2 נח غ Glu504Lys ىى Ά ל ىى
2 ىى ę ا ɟ
' Ά ╥ Y נח غ ң 2 ىى
ىى c Ė Ə Ă ‾ Y ң נח غ
╟ Ə ĭ ң ىى [9] ɟ ę Ė
ا Ə Ä ã щ [m] ɟ
ẇ א
ה Ь ۱
Ə ɟ HbA_{1c} א ا 8~12 ۱
ŭ
ALDH2 ל ىى HbA_{1c} Ь
´ ىى [13] ɟ ALDH2 נח غ ىى ۴
ж ѳ ىى ж HbA_{1c} ج ĭ ɟ ’
Ά ж ѳئطѳ в F ה ˝ ˀ
Ă w ẇ Ά Â غ Ă ɟ
ALDH2 נח غ ʔ J ל ф ң ң ; ~
Ψ ф ╗ ẇ
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6 ضحى ẗA Ẓ K غمى ` ⁄

1 2 1 1 1 1 1★ 1★

27 ϧ 6 ىغ ىد ل ؤ ٧ ɔ

ɻ 6 ىغ ىد ل ٠Ḥ ẉ PCR ؤ

ل ىي ~ ٧ ɔ ɔ ɻ ٦ ' ىغ ىد

DNA J ɥ ɻ ' Ъ 27 ϧ 6 ɔ

Ƀ 14 ̊ ̃ ´ ١ ´ ل ىي ɔ ىغ ىد ل ىي Ά ؤ

ᗡ ل ىي m ɻ 6 ىغ ىد ل ɔ

Ė K ת ' w Θ ε ه ل ɨ Ꮒ ɵ 6 ىغ ىد ل ٠Ḥ

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6 ىغ ىد ل ɔ

Establishment of immortalized lymphocyte cell lines with mutation of the glucose -6- phosphate dehydrogenase gene

JIA Zheng[1] ZHANG Yanyan[2] SUN Nan[1] ZHANG Wenxin[1] GAO Fei[1] SUN Jing[1], HUANG Jie[1]* QU Shoufang[1]*

1. National Institutes for Food and Drug Control Beijing China 100050 2. MGI Tech Co. Ltd Shenzhen China 518083

ABSTRACT Objective To establish immortalized lymphocyte cell lines by collecting 27 clinical peripheral blood samples harboring glucose 6 phosphate dehydrogenase G6PD gene mutations. Methods The glucose 6 phosphate dehydrogenase gene mutation detection kit fluorescence PCR melting curve method was used to screen the mutation type of clinical samples and then peripheral blood was collected for transformation of immortalized lymphocyte lines. The genomic DNA of the successfully established lymphocyte line was extracted and verified by the next generation sequencing method. Results We established 27 immortalized lymphocyte cell lines including 14 different homozygous or heterozygous G6PD mutation types. The genetic mutation types of immortalized lymphocyte lines were the same as those originally indicated in clinical samples. Conclusion The established immortalized lymphocyte cell lines with G6PD mutations in this study have stable genetic information and can be used as a national reference resource to evaluate the performance of the G6PD gene mutation kit.

KEY WORDS Glucose 6 phosphate dehydrogenase Gene mutation Immortalized cell line

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* E-mail qushoufang@126.com E-mail jhuang5522@126.com

6 glucose 6 phosphate de hydrogenase G6PD ï Ҥ Ҧ X l 2 ┘ 8 Xq28 G6PD ﻍ ﻧ ﻟ G6PD ´ m w ε ζ í Ҝ í ṿ ɞ ṿ ɞ ɞ ɞ З ɟ [1 2] ﻭ ﻩ ζ ŏ ﻭ ﻁ w ≟ ﺉ ┘ w Z ɞ ≟ ɞ ɞИ ≟ ɞ ﻉ ﺉ ε ה ┘ ɟ G6PD ï í ۱ ɟ ﻭ G6PD ï ה ﺉ ┘ G6PD ï ɟ Θ εm X ﻣ ã Ҝ ﻟ ╚ ´ ε ï ´ ﻟ ´ ﻟ ε ´ ה Ỹ ﻍ ж ɟ ŏ ´ ’ ﻣ ï ﻍ ﻣ ה ’ w ɔ l ۱ ﻍ ﻧ ﻟ [3] ɟ G6PD ï ŏ Ⱥ ṿ PCR ﻉ ﻍ ɞ ɞא˜ P ɞ ۱ Ъ ´ Ὸ [4 7] ɟ ὤ 6 ﻧ ﻍ ﻟ ﻩ ﻟ ɨ Л ﻩ ﻟ ɨ Ҧ ɵ 6 ﻧ ﻍ ﻟ Ḥ ɟ 6 ï Θ εm ₸ ﻧ ﻍ ﻟ ɨ Ä Ä ẅ ┐ í Ỳ ɔ ﻧ ﻍ ɟ 6 ﻧ ﻍ ﻟ ɔ ’ w w Ҝ J ɥ ɟ

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1.1

1.1.1 ẇ

Ҥ ۱ Ж Ä ┐ ɾ ⁿ ﻟ Ä ɨ 33 ж ˀ Ш ɟ ж ┐ 10 mL ۱ ḁ̈ ¨H ɟ ۱ ˜ ɔ ɟ

1.1.2 Ḥ ۱ Ⱥ ƀ

RPMI 1640 ﻧ Ế ﻧ ɞ FBS ۱ Ⱦ ﻩ GIBCO ă ˘ ж ۱ ŏ ɞ A ۱ J ﻧ Ж DMSO ← Ш ă ˘ 6 ﻧ ﻍ ﻟ Ḥ ṿ PCR ɷ د ă ˘ w ﻧ ﻍ DNA ┐ Ḥ ﺝ ئ ╞ ă ˘ w ṿ ﻧ ﻍ Ḥ ╞ ﻧ ﻍ oy ă ˘ w ɟ ɔ SLAN 96S ã ├ PCR ŭ ɷ د ă ˘ w MGISEQ 2000 ﻧ ﻍ Ⱥ ﺝ ئ ╞ ă ˘ w ɟ

1.2

1.2.1

ɾ 6 ﻧ ﻍ ﻟ Ḥ ṿ PCR Ш Θ ɟ

1.2.2 ɔ

1.2.2.1 EBV Ä B95 8 RPMI 1640 ﻧ Ế ﻧ FBS ﻧ Ế 2~3 m ﻩ ﻧ Ế ﻧ ɟ ﻧ Ế 10 ˜ ﻭ Ẇ 37 Θ ; א ă 3 2 000 rpm 10 min ɟ ɔ ɾ 0.2 m µ ƀ ˜ ɟ

1.2.2.2 ₸ B ŭ ۱ ɔ ┐ ۷ 5 mL Ả l ˉ א RPMI 1640 ﻧ Ế ﻧ ɟ ˜ Ả ŭ ﻭ Ỉ ŭ Ψ 2 000 rpm 20 min ɟ ۷ ┐ Ψ Ả ˉ א RPM1640 ﻧ Ế ﻧ 8 mL 2 1 500 rpm 10 min ˜ ˘ ɔ ɟ ˜ Ả ŭ EBV 1.5 mL ɞ A 0.4 mL w Ẇ ã ﻧ Ế ﻧ ˜ T25 ﻧ Ế Ψ ﻧ Ế Ҧ 37 5% CO_2 ﻧ Ế ﻧ Ế ɟ

1.2.2.3 ɔ ă ﻧ Ế 24~48 h ˜ ɾ З ɔ Ỹ ɟ ﻍ Ẇ Ả ã ﻧ Ế ﻧ ﻧ Ế ɟ m ۷ ˜ ﻍ Ẇ ╚ ɟ ﻧ Ế ﻟ ﻍ ´Y 1 300 rpm 5 ŭ Ҝ ɥ ɟ ﻧ Ế 3~6×10^6 Y /mL 1 300 rpm 5 ŭ ɟ Ả ˉ 10% DMSO ă ă ŭ ă ɟ ˜ ˀA

A B C

A ε 0 B ε 15 C ε 30

2 0 15 30 ×50

Figure 2 The result of immortalized lymphocyte cell line transformation on day 0 day15 and day 30 ×50

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Ά ψ PCR m

ѧ 3 ۱ 2 ɟ CNGB030108

ۏ X I 153 762 678 bp ж ﻧ ﻍ hg19 Ң

ǭ 94 reads C ﻧ ~ G

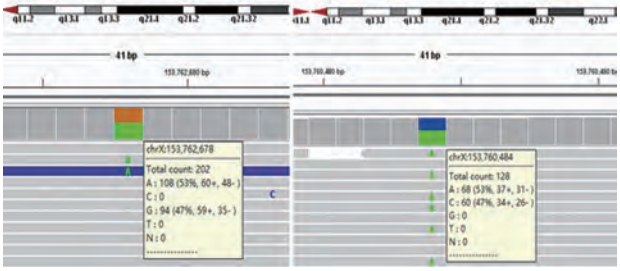
ﻧ ۱ 108 reads T ﻧ ~ A ﻧ

c.519 C>T ´ ƙ ۏ X I 153 760

484 bp Ң ǭ 60 reads G ﻧ ~

C ﻧ ۱ 68 reads T ﻧ ~ A

ﻧ c.1 376 G>T ´ ƙ ɟ



A ε ChX 153 762 678 bp hg19 Ң B ε ChX

153 760 484 hg19 Ң

3 CNGB030108

Figure 3 The sequencing results of CNGB030108

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2

Table 2 The verification results of immortalized lymphocyte cell lines

˝	˝	ƙ ל	
1	CNGB030075	c.392G>T ´	ל
2	CNGB030078	c.871G>A ´	ל
3	CNGB030079	c.871G>A ´	ל
4	CNGB030081	c.95A>G ´	ל
5	CNGB030082	c.95A>G ´	ל
6	CNGB030084	c.95A>G ´	ל
7	CNGB030085	c.1024C>T ´ c.1388G>A ´	ל ; ל
8	CNGB030086	c.1388G>A ´	ל
9	CNGB030101	c.1388G>A ´	ל
10	CNGB030102	c.1376G>T ´	ל
11	CNGB030103	c.871G>A ´	ל
12	CNGB030104	c.1388G>A ´	ל ;
13	CNGB030105	c.1388G>A ´	ל
14	CNGB030106	c.392G>T ´	ל
15	CNGB030107	c.1376G>T ´	ל
16	CNGB030108	c.1376G>T ´ c.519C>T ´	ל ; ל
17	CNGB030109	c.95A>G ´	ל
18	CNGB030110	c.1360C>T ´	ל
19	CNGB030111	c.1388G>A ´	ל
20	CNGB030112	c.1388G>A ´ c.519C>T ´	ל ; ל
21	CNGB030113	c.1024C>T ´	ל
22	CNGB030114	c.95A>G ´	ל
23	CNGB030115	c.1376G>T ´	ל
24	CNGB030116	c.95A>G ´	ל
25	CNGB030117	c.1388G>A ´	ל
26	CNGB030119	c.392G>T ´	ל
27	CNGB030120	c.1388G>A ´ c.392G>T ´	ל ; ל

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⋆

increased inflammatory factors. It is also a risk factor for the prognosis of patients with sepsis and cardiac dysfunction.

KEY WORDS Sepsis cardiac function miR 21 miR 155 Prognosis

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2

τ P>0.05 CRP ɵPCT ɶcTnI ɵBNP˜

LVEF<50% <LVEF≥50% <

2.1 3 m

τ P<0.05 ɟ 1 ɟ

3 ɋ ɵ ɵBMI

1 3 $\bar{x} \pm s$

Table 1 ccomparison of general data among 3 groups $\bar{x} \pm s$

	n=40	LVEF≥50% n=38	LVEF<50% n=20	Z/F e	P e
ɋ /	23/17	22/16	12/8	0.036	0.982
	42.39±9.59	45.12±10.92	40.39±11.87	1.432	0.244
BMI kg/m²	22.93±5.82	23.14±6.14	22.46±5.67	0.087	0.917
CRP mg/L	3.28±0.62	30.38±7.82	61.39±9.94	530.616	0.000
PCT ng/mL	0.58±0.08	3.29±0.68	14.69±3.94	417.803	0.000
cTnI ng/mL	0.45±0.08	0.68±0.12	1.52±0.20	481.609	0.000
BNP ng/L	32.93±7.95	63.29±10.29	132.29±21.29	417.546	0.000

2.2 3 miR 21 miR 155 ẇ ė IL 2 ɵICAM 1˜ LVEF<50%

ę LVEF≥50% ɳ

3 miR 21 miR 155 ẇ TNF α ɵ τ P<0.05 ɟ 2 ɟ

2 3 miR 21 miR 155 TNF α IL 2 ICAM 1 $\bar{x} \pm s$

Table 2 comparison of circulation miR 21 miR 155 and serum TNF α IL 2 ICAM 1 among 3 groups $\bar{x} \pm s$

ɋ	n	miR 21	miR 155	TNF α ng/L	IL 2 ng/L	ICAM 1 ng/mL
	40	1.02±0.19	0.97±0.16	9.38±1.32	14.28±2.37	126.49±17.96
LVEF≥50%	38	1.42±0.23	1.38±0.19	20.19±4.82	32.93±6.48	349.58±62.39
LVEF<50%	20	2.19±0.42	1.83±0.32	57.92±9.94	82.93±13.28	649.39±85.93
F e		129.091	113.378	543.380	586.608	592.120
P e		0.000	0.000	0.000	0.000	0.000

2.3 LVEF<50% miR 21 miR 155 Ά

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LVEF<50% miR 21 miR 155

Ά CRP ɵPCT ɶcTnI ɵBNP ɵTNF α ɵIL 2 ɵ ICAM 1˜ ę ∖ Ą τ P< 0.05 3 ɟ

3 LVEF <50% miR 21 miR 155

Table 3 correlation between miR 21 miR 155 and serum index in LVEF <50% group

ė	miR 21		miR 155	
	r e	P e	r e	P e
CRP	0.273	<0.05	0.410	<0.05
PCT	0.306	<0.05	0.377	<0.05
cTnI	0 227	<0.05	0.342	<0.05
BNP	0.285	<0.05	0.266	<0.05
TNF α	0.329	<0.05	0.325	<0.05
IL 2	0.268	<0.05	0.367	<0.05
ICAM 1	0.402	<0.05	0.291	<0.05

2.4 LVEF<50% Ψ ẇ H

miR 21 miR 155 ẇ ė

LVEF<50% Ψ H miR 21 miR 155 ẇ TNF α ɵIL 2 ɵICAM 1˜ ę Ηь τ P< 0.05 4 ɟ

2.5 LVEF<50% Ą ė

ẉ LVEF<50% ı H Θ ε

ƙ ẉ miR 21 miR 155 ẇ CRP ɵ PCT ɶcTnI ɵBNP ɵTNF α ɵIL 2 ɵICAM 1 Θ ε ƙ

logistics ɾ ŏ miR 21 miR 155

Ά PCT ɵTNF α ɵIL 2 ɵICAM 1˜ ɷ

LVEF<50% H • ė

CRP ɵBNP Ά LVEF<50% H

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[6 7] ɟ Ă miR 21 ۱ miR 155 ŏ ̈ọ
˜ JAK2/STAT3 ɞTLR4 ה ̈Ạ
א Ə [8 10] ŏ Ψ miR 21
ẇ miR 155 ج ﻩ [3 4] ɟ ŏ ﺡ ɔ
ŏ Ъ miR 21 ẇ miR 155 ŏ ´
' Ψ ɵ [e] ה miR 21 ẇ miR 155
ﻩ Ά ' ה Ă
Ά Ά Ă [m] Ὸ [m] ל ɔ
ↀ ɣ ' Ά l ɥ ɣ ̈Ạ Ă ŏ
א Ψ ɞmiR 21 ẇ miR 155
ɥ ɣ ﻩ w ̃ọ ˥ Ə ɟ
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ɣ CRP ẇ PCT Ҥ ɵ
[11 12] ɔTnI ẇ BNP Ҥ ɵ ẇ
' ̋E [13 14] ɟ ŏ ŏ
' ɔ Ψ CRP ɞPCT ɶTnI ɞ
BNP˘ ج Ҥ´Y LVEF<50% miR 21
miR 155 Ά CRP ɞPCT ɶTnI ɞBNP ۱
Ă miR 21 miR 155 ﻩ Ά
´ ' ה ל ɔ Ă ´

miR 21 ẇ miR 155 ч Ə
´ ' ה ל ɔ Ψ miR 21
ẇ miR 155 ﻩ ˝ w ɥ ɣ l א
Ҡ ш ה Ъ Ҡ ɟ
miR 21 miR 155 ζ Ə ̈Ạ
א ´ ' miR 21
miR 155 ﻩ ' l ˥ ɥ ɣ
̈Ạ ɟ TNF α ɞL 2 ɞCAM 1 ŏ Ψ ч
א ɣ [15 17] ɟ ɣ
ŏ ŏ ' ɔ
Ψ TNF α ɞL 2 ɞCAM 1˘ ج ╗
´Y LVEF<50% miR 21 miR 155 Ά
TNF α ɞL 2 ɞCAM 1 ۱ Ă [m] Ă Ά
miR 21 ẇ miR 155 ч Ə ˝[m] ẹ '
ↀ ɣ l Ỉ miR 21 miR 155 ﻩ
˝ w ɥ ɣ א
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ɔ 0 / 155 k g P Ќ ʌ k P Ų

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Ⅵ ьᵪ β ᘐ ℗ Ⅴ ♦˜ ЧŦ PCR ⅏ ˘

⋆

Нь í ç ẋ ẉ PCR ɟ
ç ẋ recA ɲ ɡ Ό Нь PCR ₥ ˀ Нь ẉ PCR
Ỉ ɟ ŏ ɑ̈ ẇ ç ẋ Ἄ ε ẇ m PCR ₥ PCR У
ε ẇ Ỉ ẉ PCR recA ɲ ɡ Ţ ẉ PCR
ɟ˾ ç ẋ ⅄ ɲ ɡ DNA ẉ PCR
ɟ ˜ ẉ PCR ⅄ Vitek 2 Compact Ѧ ɮ ŏ ɑ̈ 35 ʒ ί Ξ
Ό Ὼ ɟ ẉ PCR ˆ ç ẋ ₥ ę ђ ת ˝ ɟ
ˀ ẉ PCR ; 1×10³ CFU/mL ⅄ 1×10⁵ ng/ L ɲɡ DNA Ė
ɟ ẉ PCR Ό 14 ʒ ί ᾧ ç ẋ Ό ε 40.0%
Vitek 2 Compact Ѧ ɮ c Ό 10 ʒ Ό ε 28.6% ę Ψ 4 ʒ ɑ̈ ɟ ẉ PCR
Ė ɞ ⅄ Нь í Б Ύ ɞ ⅄ Ἄ e ᾧ ί ɟ
ç ẋ recA ɲ ɡ ẉ PCR í

Establishment of nested fluorescent quantitative PCR for rapid detection of *Burkholderia cepacia*

H" Ä Ù xPOZ Ä™" 5T`<)•P 5T`" ` ð 0 P S F T UF ` @ 1 $ 3 D SUF O FT • FØ UF ` R

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⋆ E-mail 1293027089@qq.com

cating that the nested fluorescent quantitative PCR had more accurate detection performance. Conclusion Nested fluorescent quantitative PCR is an effective rapid and direct method for clinical detection of Burkholderia cepacian.

KEY WORDS Burkholderia cepacia RecA gene Nested fluorescent quantitative PCR Clinical detection

ç ẋ ´ l Burkholderia cepacia complex Bcc m ŏ Ь ɬ ж ﻁﻅﻱΨ Ą ǎ в ɬ Ė ת 12 ɟ Ⱨ ǔ ǫ ѳ в ɬ У ɨ Ψ l Ӈ в Ӈ ɬ Ӈ ї 1 ɟ Bcc Ė ɬ ш в в w ѱ Ą Ѽ 1 ɟ ǔ í Ψ ת ç ẋ m Ж Ɑ l ζ ǔ ӧ ң ; ж Ψ ɟ ę O Ƀ З ת ǔ ӧ ɔ ɵ ǫ ш ɔ 3 5 ɟ ė ă . Ѽ ç ẋ ǫ Ь Ѽ í ɟ ç ẋ ŏ Ъ ę ж ç ẋ Ά ę ђ Ą ŭ в в ɬ ₸ ┘ ŏ щ ل 6 ɟ ǔ Ь ç ẋ ŏ Ψ ת Ь recA ת ė ŏ ѽ Ė ŏ Ѽ ┘ ŏ Bcc Ї 7 ɟ ė m í ç ẋ ɟ

1

1.1 Ά

ç ẋ Ѓ A ATCC 25416 в ^ ₸ ATCC 9027 в ATCC 6538 в ATCC 6633 в ATCC 8739 в в в w ^ ₸ в ^ ₸ в ɬ Ψ ѳ ┐ Ψ ɟ 35 ʒ Ь ├ є ├ ш ɔ ҷ ˀ Ш ΄Y Ӈ ɬ Ж Ѓ A ɟ ʒ ă ę Ψ $Z_{1-\alpha/2}$=1.96 P=0.9 ε δ=0.1 ε Ѓ Ѽ ε 35 ɟ

ă $n=\left(\frac{Z_{1-\alpha/2}\times\sqrt{P\times(1-P)}}{\delta}\right)$

1.2 ת ė DNA ┐

ת ė DNA ┐ Ӈ Ш W l Ấ ɟ Ấ K ɬ ₱ ҷ m 65 10 min ɟ Ấ ф ɵ ; Ǝ ₱ ~ ǫ̃ ɔ Ψ 12 000 rpm 1 min ɟ Ấ ɬ w ɔ Ψ l ɟ ~ ɔ Ψ Ấ 50 L μ 2 min ~ Ь 13 000 rpm 2 min ◑ ε ת ė DNA ɟ ŏ w w DNA ˜ æ ɨ ’ 20 ┐ ɟ

1.3 w PCR

w ┐ ת ė DNA ε BCR1 F 5′ ATGACCGCCGAGAAGAGCAA 3′ ɬ BCR1 R 5′ CTCTTCTTCGTCCATCGCCTC 3′ m PCR ѭ א Θ ; 96 5 min 96 30 sec ѳ58 30 sec ѳ72 1 min 25 Y 72 10 min ɟ w m PCR У 5 e ʊ ; i ѳ ┐

recA ג ɣ ˜ w У
ε ά Ǐ ẉ PCR ɟ
ˆ ç ẋ ˝A B.cepacia
ATCC 25416 ◕ ę ɦ ƚ ◕
◕ ћ 1 ɟ ’ w
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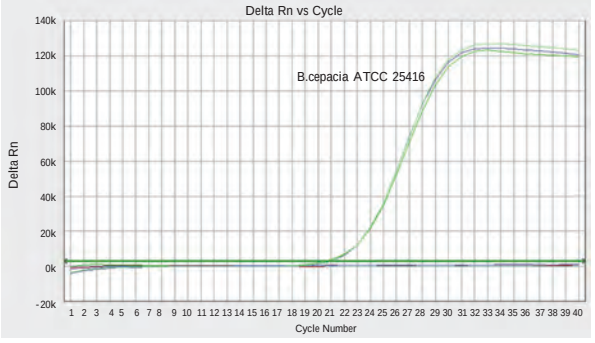

1 PCR

Figure 1 Amplification curves of nested quantitative PCR for different bacterial strains

2.2 PCR

ç ẋ Ὸ
˜ 1×10^{5} ɑ1×10^{4} ɑ1×10^{3} ɑ1×10^{2} ɷ
1×10^{1} ɑ1×10^{0} CFU/mL ɟ ɔ
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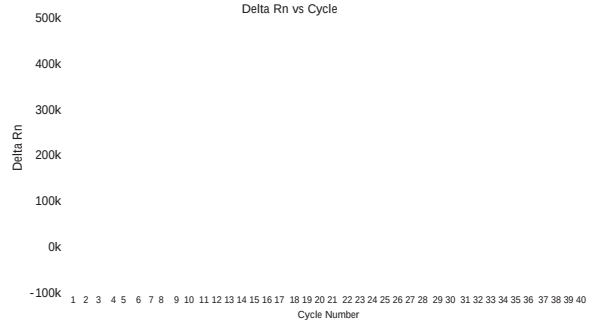
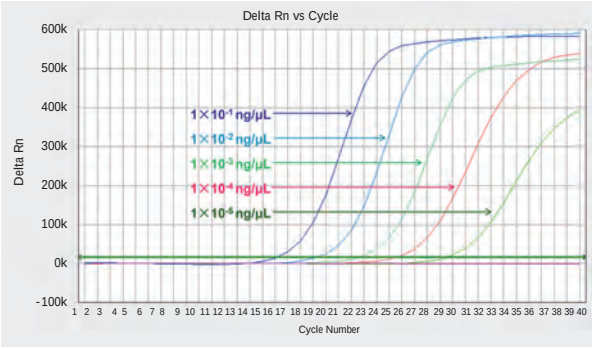
1×10^{1} CFU/mL Ш Ὸ ћ 2 ɟ m
ˀ ç ẋ ג ɣ DNA
1×10 ^{1} ɑ1×10 ^{2} ɑ1×
10 ^{3} ɑ1×10 ^{4} ɑ1×10 ^{5} ɑ1×10 ^{6} ng/ L ɟ ˘ ɱ 1 L µ
ת Ъ 1×10 ^{6} ng/ L µ Ң 1×
10 ^{5} ng/ L µ Ш ◕ ћ 3 ɟ



2 PCR

Figure 2 Amplification curves of Burkholderia cepacia with different concentrations by nested quantitative PCR



3 DNA
PCR

Figure 3 Amplification curves of Burkholderia cepacia genomic DNA in different concentrations by nested quantitative PCR

2.3 PCR í

35 ʒ ш ɔ ŭ ą̈
PCR ∤ Vitek 2 Compact Ѧ ƀ ɟ
ת Vitek 2 Compact Ѧ ƀ Ὸ 10 ʒ
ç ẋ 4 ʒ Ὸ ę
æ ε ę ɦ ɟ PCR
Ά Vitek 2 Compact Ѧ ƀ ę ɦ
ת ˝ ж Ὸ ç ẋ
Ă 14 ʒ ˉ Vitek 2 Compact Ѧ ƀ
4 ʒ ɟ PCR Vitek 2
Compact Ѧ ƀ ç ẋ Ὸ
ж τ χ^2=0.560 P=0.454 ɟ

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ˀ 98%~100% ъ Bcc ą̈
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$^{8\ 10}$ ɟ ɣ ѽ recA ג ɣ
m ɟ ʒ ∖ ^{8} recA
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ת ɟ recA ֗A ֖Ω ɻ Ң ֖Ω ŏ
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ɻ í [11] ɟ æ [12] ς ε recA ֖Ω
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[13] ɟ ֘m Y ֵ ė hisA ς Ὸ
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MALDI TOF MS ' ç ẋ
֗A ֵ ė ی ɟ ж Furlan [16]
Ђ ˝ ה ی ˝ Нь Bcc
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֘ ˝ 16S rRNA ɻ recA ֵ ė
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֍ Ė ɟ Lambiase [17] ς ε
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ç ẋ ɟ Jimenez [20] ֘
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- { 1 $ # Œ6* •• !
W ę

results of influenza A and B virus in oropharyngeal swab samples.

KEY WORDS Virus inactivation Quantitative real time polymerase chain reaction Influenza viruses Oropharyngeal swab

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ﻯ ﻱ ﻙ ж í ζ ǎ Ǎ ﻩ

φm [1] ɟ Ъ ε ╥ ɞ

ɞŭ RNA ﻯ ﻧ

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ﻱ [12] ɟ

ζ φm [3] ﻭ ﻱ

Ψ ﻥ Ə ж ϩ Ψ ’ ﻭ

Ά Ъ ﻧ ė

╥ ώ ά Ъ

w ﻱ ң ж ﻯ

ɟ ώ ﻱ ơ severe acute respiratory syndrome coronavirus 2 SARS CoV 2 ε ã [4] Ə ε ﻱ ơ ζ ά φm [5] ς í ɟ ﻭh ő Ά ≟ 2011 ђΨ Ό m ’ ﻭ 56 ɞ80 min ς ε ≟Ψ [6 7] ﻱ ơ ɟ i ˜ 56 ɞ80 min Ɵ w ´ א quantitative real time polymerase chain reaction qPCR ŭ ώ ﻯ ~ ﻱ ﻱ ﻱ ɣ Ã ɣ Ъ è è ; ɟ

1

1.1 í

2020 1 31 2020 2 15 ϩ 47 ϧ qPCR i ˜ 21 ϧ ε ﻱ 26 ϧ ε ﻱ ę Ψ Ƀ n=27 Ct≤ 26 Ψ n=16 26 Ct≤33 ﻯ n=4 33<Ct≤39 w ﻱ 14 ϧ ﻱ ﻯ ﻱ qPCR ↀ ε i ˜ ɟ

1.2 Ḥ Ά Ⱥ ɔ

ABI7500 w PCR Ⱥ ﻉ Thermofisher ǎ ˘ ﻱ Ḥ Ψ ﻧ ė oy ǎ ˘ ﻱ

Ḥ Ψ ﻧ ė oy ǎ ˘ ɟ

1.3

-20 ά i ˜ ˉ 1 mL ~ ŭ ά ﻯ ϩ 200 L Ъ ΞμY Ψ m oy Ъ ﻱ ﻱ ﻱ ɞ ﻱ Ɓm oy Ẉ ﻭ 56 Ψ 30 min ~ Ő ﻱ ﻯ ﻱ Ə ɟ

1.4 ϩ ﻯ PCR ﻫ

Ψ ﻧ ė oy ǎ ˘ ﻱ Ḥ ﻯ ﻱ

Ḥ ϩ RNA Ḥ Ə ɟ ﻭ ABI7500 ﻱ w PCR Ⱥ ɔ א Ɵ ; 50 ɞ15 min → 95 ɞ15 min → 94 ɞ15 s → 58 ɞ45 s 45 Y ɟ

[e] cycling threshold CT ɟ Ḥ [m] w PCR ɟ ↀ ɨ í ɨ ﻯ ɨ ɟ

1.5 ó

① ﻱ ó Ã ε FAM ﻫ Ύ Ct [e] ⩽39.7 ﻱ ﻱ ó Ã ε FAM ﻫ Ύ Ct [e] ⩽38.0 ② ﻱ ó Ã ε FAM ﻫ FAM ﻫ Ύ Ct [e] >39.7 ﻱ ó Ã ε FAM ﻫ FAM ﻫ Ύ Ct [e] >38.0 ɟ

1.6

SPSS 26.0 Ɵ ﻱ GraphPad Prism Ɵ Version8.0 $\bar{x} \pm s$ ´ ŭ Ξ *t* m ŭ Bland Altman ŭ ɟ P<0.05 ε Ė τ ɟ

2

2.1 ﻯ ~ qPCR

21 ϧ ﻱ ﻱ 26 ϧ

ϕ ىى ̃

ا ~ qPCR ɟ Ξ

ۊ ~ ڃ ε ´ ε

100% ɟ ا 56 ȣ30 min ~ ẹ Ct φ

τ P>0.05 ɟ 1 ᾠ 2 ɟ

1 qPCR

Table 1 The qPCR results of unheated and heat inactivation

ىى	Ct e		ϕ ىى	Ct e	
	~			~	
32.52	32.83	0.31	30.36	28.72	-1.64
30.93	30.38	-0.55	25.60	26.73	1.13
30.26	36.64	6.38	28.31	25.58	-2.74
35.73	26.12	-9.61	23.02	23.81	0.79
26.55	20.79	-5.76	23.03	23.39	0.36
20.52	26.46	5.94	22.48	22.22	-0.26
27.74	31.06	3.33	20.80	21.67	0.87
24.05	23.32	-0.73	23.23	23.45	0.23
26.37	24.20	-2.18	20.88	21.46	0.58
28.18	27.05	-1.13	20.50	20.94	0.44
25.58	25.81	0.22	24.13	24.51	0.38
28.53	28.62	0.09	24.78	25.11	0.32
22.78	23.44	0.66	26.25	26.65	0.40
23.04	28.60	5.57	20.98	21.99	1.01
23.03	28.32	5.29	25.42	26.24	0.82
23.27	26.24	2.97	19.33	17.54	-1.79
19.56	19.10	-0.46	27.60	28.15	0.55
22.92	28.73	5.80	20.24	22.38	2.15
22.76	27.34	4.59	32.00	31.27	-0.73
37.46	38.17	0.71	26.59	25.15	-1.44
34.84	33.72	-1.13	26.11	26.66	0.55
			32.38	28.77	-3.60
			27.67	26.91	-0.76
			27.34	28.38	1.05
			27.64	28.26	0.62
			18.88	18.88	0

= ~ Ct e Ct e ɟ

2 qPCR $\bar{x} \pm s$

Table 2 Comparison of the qPCR results between unheated and heat inactivation $\bar{x} \pm s$

		n	~	t e	P e
	Ct e	21	26.98±5.07	27.95±4.76	-1.100	0.284
ϕ	Ct e	26	24.83±3.77	24.80±3.32	0.108	0.915

2.2 ا ~

qPCR m ŏ

~ ا

Ė m ɟ ىى qPCR

ŏ ڃ ۊ 95% m

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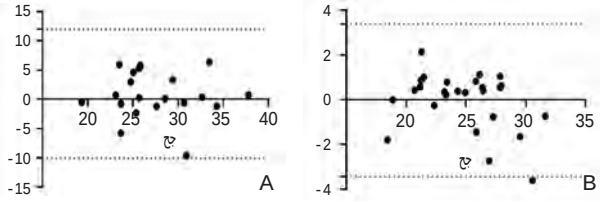
’ w ɔ ھ 1A ھ B ε ϕ ىى qPCR

ŏ ẹ Ψ 3.8% 1/26 ۊ 95% m

م ⌟ w Ь 5% ۷ ۊ م ⌟

w Ỉ e ۊ ί ɔ ’ w ɔ ɟ ھ 1B ɟ



ھ A ε ىى ŏ ھ B ε ϕ ىى

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1 Ά ~ m ŏ

Figure 1 Analysis of consistent results between unheated and heat inactivation

2.3 ا ~

qPCR

14 ۏ ىى ᾠ ϕ ىى

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qPCR ~ ã ε ɟ

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56 ȣ30 min ا 75% ϕ ا

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56 ȣ30 min
; ǔ ی ợ ˚ Ϛ
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ж ъ[m] ŭ ẇ Ψ ' w ה ی
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2 Ợ ∂ ﾉ Ж ’ ∑ ѿ ע ת ← hs CRP Î UAER ψ √

1 2★ 1

2 ﻱ T2DM Ψ Ĩ ђ CIMT Ä C א hs CRP ɵ UAER Ą ɟ 2018 1 2019 12 T2DM 63 ʒ ⁞ Ѧ CIMT ﻧ Ⱨ Ь CIMT ő CIMT⩽0.9 mm 18 ʒ ﻩ ђ CIMT0.9~1.2 mm 23 ʒ ﺽ CIMT>1.2 mm 22 ʒ ɟ 3 ɵ ⷮ ɵT2DM ɶBMI ɶWHR ɵ ♥ SBP ɵ ♥ DBP ɵ ɻ TC ɵ ɕ TG ɵ ɻ HDL C ɵђ ɻ LDL C ɵ FPG ɵ SCr ɵ FINS ɵ ɔ HbA1c ɵ ˜ 2h 2hPG ɵ C א hs CRP ɵ UAER ő CIMT Ä hs CRP ɑUAER Ą ɟ 3 ɵ ⷮ ɶBMI ɶWHR ɶSBP ɑDBP ɑFINS ɑSCr τ P>0.05 3 ɑHbA1c ɶTC ɑHDL C ɑLDL C ɑhs CRP ɑUAER τ P<0.05 ﺽ ﻩ ђ FPG ɑ2hPG ɶTG ﺝ Ⱨ Ь τ P<0.05 ɟ T2DM CIMT Ä ɑFPG ɑ2hPG ɑHbA1c ɶTG ɶTC ɑLDL C ɑhs CRP ɑUAER Ⅵ Ą P<0.05 Ä HDL C Ⅵ Ą P=0.027 ɟ T2DM CIMT Ä hs CRP Ä UAER ’Y Ą hs CRP Ä UAER ´ ’ Ţ T2DM Ⴄ AS ɟ 2 ﻱ Ψ Ĩ ђ C א Ą

Correlation between carotid intima thickness and hs-CRP UAER in patients with type 2 diabetes mellitus

XIE Jun[1] SUN Yuanyuan[2]★ YU Qigui[1]

1. Department of General Medicine The No.2 People s Hospital of Heifei Hefei Anhui China 230011

2. Department of Clinical Nutrition The No.2 Hospital of Hefei Hefei AnHui China 230011

ABSTRACT Objective To analyze the correlation between carotid medial intimal thickness CIMT and high sensitivity C reactive protein hs CRP and urine protein excretion rate UAER in patients with type 2 diabetes T2DM . Methods 63 T2DM patients admitted to our hospital from January 2018 to De cember 2019 were collected and and the color Doppler ultrasound diagnostic instrument was used to detect CIMT. Based on CIMT grouping 18 patients in normal group CIMT ⩽0.9 mm and 23 in thickened group CIMT 0.9~1.2 mm and 22 in plaque group CIMT>1.2 mm . The age sex T2DM course BMI WHR systolic blood pressure SBP diastolic blood pressure DBP total cholesterol TC triglyceride TG high density lipoprotein cholesterol HDL C Low density lipoprotein cholesterol LDL C fasting blood glucose FPG serum creatinine SCr fasting insulin FINS glycated hemoglobin HbA1c high sensi tivity C reactive protein hs CRP and 2h blood glucose after meals 2hPG urinary protein excretion rate

2017 1704f0804042

1. 230011

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★ E-mail ahmusyy@sina.com

UAER were compared and the correlation between CIMT and hs CRP and UAER was analyzed. Results There were no statistically significant differences in age gender BMI WHR SBP DBP FINS and SCr in the three groups P>0.05 . The differences in the course of disease HbA1c TC HDL C LDL C hs CRP and UAER in the three groups were statistically significant P<0.05 . FPG 2hPG and TG in the plaque and thickening group were significantly higher than those in the normal group P<0.05 . CIMT was positively correlated with the course of disease FPG 2hPG HbA1c TG TC LDL C hs CRP and UAER in T2DM patients P<0.05 and negatively correlated with HDL C P=0.027 . Conclusion CIMT and hs CRP are closely related to UAER in T2DM patients. The combined detection of hs CRP and UAER can predict the early assessment of macrovascular disease or AS in T2DM patients.

KEY WORDS 2 diabetes mellitus Carotid intima thickness Hypersensitive C reactive protein Uri nary protein excretion rate Correlation

ہ Ǐ 2 یی Type 2 Diabetes Mellitus T2DM ﻧﺤ ˘ T2DM Ą ה T ١ ﻫﻪ † ɟ [1] ל غ H T2DM ɔ Athero sclerosis AS ٽΩ ġ ɟ ε [2] T2DM Ψ Ǐ ḥ Carotid Intima MediaThickness CIMT ﻫﻪ ה AS ɟ ٽΩ ﻧﺠ ɾ [3] ε ל ● ǐ ġ φm T Ï Θ ɟ [4] T2DM Ά AS ל Ψ ﺝ א C א C reactive Protein CRP ٽΩ AS φm ж T2DM CIMT ﻫﻪ ḥ c ﻧﯚ ң CRP C א Highsensitivity C reactive protein hs CRP Ά Urinary albumin excretion rate UAER T2DM CIMT Ά hs CRP ɞUAER Ą ɟ

1

1.1

2018 1 2019 12 T2DM 63 ϧ 53~72 ﺝ 63.81±6.02 41 ϧ 22 ϧ ɟ ﺝ ´ Ψ ہ 2 یی ≟ 2017 ٽA [5] 1~17 ﺝ 9.52±4.17 ɟ Ấ ٽA ①T2DM [5] ② 3 Y Ǐ ´ ③ ├ ε ④ ų ɞ ⑤ ﻱU J ⑥ ﻭ ﺝ ˀ Ш ɟ ٽA ①´ ② ɞ ' ③ ¥ ӧ ④ ⑤ ⑥ ♥ ⑦ ٧ ɞ ´ ⑧ ה ɞ ל ɞ ל ⑨ ɞ ´ ɟ ├ Ң ١ Ж ٽA ˀ ɟ

1.2

1.2.1 CIMT

LOGIQ500 یی ⁞ Ѧ ہ GE ﻛﻰ ١ ˜ Ѭ Ц w یی 8.2~10.0 û /C ô

moglobin A1c HbA1c ẍ Ɣ
C א Highsensitivity C reactive protein
hs CRP i 2 h ɳ Ɣ
2 mL ˜ 2 h 2hPostprandial blood glu
cose 2hPG ɳ 3 h ẍ

2.2 T2DM CIMT Á ę ħ ė Ą ŏ
T2DM CIMT Á ɷFPG ɷ2hPG ɷ HbA1c ɷTG ɷTC ɷLDL C ɷhs CRP ɷUAER Ⅵ Ą τ P<0.05 Á HDL C Ⅵ Ą τ P<0.05 2 ɟ

2 T2DM CIMT

Table 2 T2DM Correlation analysis between patient CIMT and other factors

ƛ	r e	P e
	0.196	0.039
FPG	0.264	0.015
2hPG	0.253	0.019
HbA1c	0.297	<0.001
TG	0.246	0.018
TC	0.255	0.015
HDL C	-0.249	0.027
LDL C	0.316	0.008
FINS	0.197	0.302
SCr	0.062	0.575
hs CRP	0.329	<0.001
UAER	0.288	<0.001

2.3 ضم ● ė Logistic ع ŏ T2DM CIMT>1.2 mm ضم Ə ε ė ƛ w ɷFPG ɷ2hPG ɷHbA1c ɷTG ɷTC ɷ HDL C ɷLDL C ɷFINS ɷSCr ɷhs CRP ɷUAER ε ƛ Logistic ė ع ŏ Ό ɷ HbA1 ɷTC ɷLDL C ɷhs CRP ɷUAER T2DM ה ضم ● Ĭ ė τ P<0.05 3 ɟ

3 Logistic

Table 3 Risk factors Logistic regression analysis of carotid plaque

ƛ	β e	Wald e	OR 95%CI	P e
	2.778	4.982	1.546 1.029~2.142	0.025
HbA1c	2.661	4.831	1.438 0.985~2.021	0.023
TC	0.762	4.125	1.223 1.006~1.372	0.029
LDL C	0.613	3.686	1.825 1.297~2.605	0.035
hs CRP	3.079	6.407	28.464 2.145~73.212	<0.001
UAER	2.136	4.356	8.564 1.208~43.597	<0.001

3

ה [7] ė ƛ H T2DM ▌60% w ɔ ɟ Ό [8] Ĭ Ə ε AS ה ɔ è Ң T2DM ƛ T ε Ĭ ھ h Ⅵ ɔ ضم Ĭ ɟ CIMT ς א AS ζ ɵ ɟ ѽ í T2DM ה ƛ ė Ą ɟ ж ғ [9] T2DM Á AS ج ε ƛ א ɟ Jamshid [10] Ό CRP Á T2DM ש AS ƛ ج Ą CRP ' T2DM א Ύ AS ● Ĭ ė φm ɟ [11] CRP ھ ' T2DM א T2DM ה CIMT ھ h Ĭ ė ɟ hs CRP ƛ ɔ ' ɵ Ţ T2DM AS ɟ ה [12] Á T2DM ƛ Ύ Ą T ε ● ė φm ɟ [13] CIMT Á 24 h Ą ɟ ה UAER Á T2DM CIMT Ⅵ Ą Ύ ė Logistic ع ŏ ضم ● Ĭ ė ɟ ھ T2DM ئ ƛ ' ɟ Ũ ' T2DM ھ ◗ ئ ã Ĭ ' ɷ Ҡ φ l ظ Ĭ ש א כ Ĭ Ə ƛ AS [14] ɟ UAER ' Ə ε א ƛ ɟ HbA1 ɷTC ɷLDL C T2DM ה ضم ● Ĭ ė ɟ ' T2DM ɷ ש א ج ج ƛ Á CIMT ھ ң Á ƛ Á [15] m ɟ Ɠ ˘ ♥ ' Á ҳ ♥ Ą ɟ ɔ T2DM CIMT Á hs CRP Á UAER Ύ Ą hs CRP Á UAER ´ ' Ţ T2DM ƛ AS ɟ

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’ OPG ÎTNF α ϐ Ⅾρ ή ΄E ى ∂ ‾ h ئ

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GDM Ψ OPG TNF α ۱ /TNF α e ѭ ę Ά
ц ΄ Ặ ۱ ί τ ɟ ƒ ӧ Ч 40˜ GDM ۱
40˜ ғ Ψ OPG TNF α ۱ ɟ ŏ OPG ϭTNF α ۱ Ά
Ặ ɟ Ξ ϭBMI ϭTG ϭTC ϭLDL C τ P>0.05
ϭFBG ϭHDL C ϭTG/TC ϭTC/HDL C ϭLDL C/HDL C ϭAIP ϭ ϭHOMA IR ϭQUICKI
τ P<0.05 ɟ GDM TNF α НьNGT OPG ϭ ۱ /TNF α e
ң НьNGT τ P<0.05 ɟ /TNF α e Ά ۷ Ặ r=-0.68
P<0.05 c r=-0.39 P<0.05 Ά ۷ Ặ r=0.69 P<0.05 ɟ ẃ ع ŏ
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Diagnostic analysis of serum OPG TNF - α and adiponectin in gestational diabetes mellitus

WEN Jie* LIU Ping GUO Rui
Department of Obstetrics and Gynecology Affiliated Hospital of North China University of Technology Tangshan Hebei China 063000

ABSTRACT Objective To explore OPG TNF α adiponectin and adiponectin/TNF α ratio in the blood circulation of gestational diabetes mellitus GDM pregnant women and the relationship with metabolic syndrome biomarkers and clinical significance. Methods 40 women with GDM and 40 normal pregnant women were recruited in this study. The levels of serum OPG TNF α and total adiponectin were measured using enzyme linked immunosorbent assay ELISA . The correlation between OPG TNF α and adiponectin and the degree of GDM was analyzed. Results There was no statistically significant difference in gestational age BMI TG TC LDL C P>0.05 . The age of pregnant women FBG HDL C TG /TC TC / HDL C LDL C/HDL C AIP insulin HOMA IR and QUICKI were was statistically significant between two groups P< 0.05 . The expression level of TNF α in the GDM group was higher than that in the control group. The ratio of OPG adiponectin and adiponectin / TNF α was significantly lower than that in the control group P<0.05 . Adiponectin/TNF α ratio was negatively correlated with insulin resistance r=-0.68 P<0.05 . Triglycerides r=-0.39 P<0.05 were positively correlated with insulin sensitivity r=0.69 P<0.05 . Multiple linear

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* E-mial guchengchengpa@163.com

regression analysis showed that the adiponectin/TNF α ratio was independently related to insulin resistance. Binary logistic regression analysis indicated that GDM was positively correlated with OPG levels and negatively correlated with adiponectin/TNF α ratio. Conclusion the OPG level in the GDM groupincreased while the adiponectin/TNF α ratio decreased significantly. This ratio may be an effective biomarker for assessing pregnant women s high risk of insulin resistance and dyslipidemia as well as GDM diagnostic and treatment monitoring targets.

KEY WORDS Gestational diabetes mellitus Osteoprotin Tumor necrosis factor α Adiponectin Insulin resistance

Gestational diabetes mellitus

GDM ğ τ ε ה Θ m

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GDM Ж ỵ У в ۱ У˜ ה

۱ ɥ ´ 4 ɻ ė Ά ה GDM

Ė τ ɻ ė ל Ά Ъ

GDM ה ğ GDM Ψ

ىف Ъ osteoclastogenesis inhibi

tory factor OPG ę ė ح ė α

TNF α ۱ ė adiponectin

Θ 5 ɻ OPG ל Ά ɥ Άm З ɥ

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7 ɻ ε 100 g Ъ 250 mL

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ך ɻ Ѧ Thermo Multiskan FC

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1.4 в ۱ ắ

ƒ ىي Ţ HOMA IR

ắ HOMA IR= FPG×FINS /22.5

10 ɻ QUICKI

QUICKI=1/ logFINS U/mL μ+ logFBG mg/dL

Ъ Ţ 11 ɻ

1.5 ŏ

SPSS 19.0 Θ ŏ ɻ

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2.1 Ξ ≍ í

Ξ ɵBMI ɵTG ɵTC ɵLDL C τ P>0.05 ɵFBG ɵ HDL C ɵTG/TC ɵTC/HDL C ɵLDL C/HDL C ɵAIP ɵ ɵHOMA IR ɵQUICKI τ P<0.05 ɟ 1 ɟ

1 $\bar{x}\pm s$

Table 1 Biochemichal characteristics of gestational diabetes mellitus GDM and normal pregnant women $\bar{x}\pm s$

ϙ	NGT n=40	GDM n=40	t e	P e
	29.25±0.58	31.57±0.54	18.516	<0.001
ϟ	26.15±0.24	26.23±0.22	1.554	>0.05
BMI kg/m²	27.25±1.18	27.66±1.17	1.560	>0.05
FBG mg/dL	78.45±1.29	100.83±1.54	70.458	<0.001
TG mg/dL	221.83±74	256.12±69.12	2.142	>0.01
TC mg/dL	242.67±30.18	225.84±39.88	2.128	>0.01
HDL C mg/dL	52.21±2.95	34.7±2.71	27.646	<0.001
LDL C mg/dL	146.1±27.84	139.92±20.11	1.138	>0.05
TG/TC	0.94±0.06	1.17±0.1	12.474	<0.001
TC/HDL C	5.32±0.54	7.88±0.65	19.160	<0.001
LDL C/HDL C	3.23±0.36	5.17±0.58	17.974	<0.001
AIP	0.63±0.04	0.87±0.04	26.833	<0.001
IU/mLμ	9.54±0.55	12.56±0.9	18.109	<0.001
HOMA IR	1.85±0.11	3.11±0.22	32.398	<0.001
QUICKI	0.36±0.01	0.33±0.01	13.416	<0.001

2.2 NGT ϟ GDM OPG ɵTNF α ϟ

GDM TNF α Ь NGT ɟ OPG ɵ ϟ /TNF α e ɳ Ь NGT ɟ ğ NGT Ψ HOMA IR e Á ϟ /TNF α e ϒ Ą Á TNF α ϒ Ą ɟ QUICKI Á ϟ /TNF α e ϒ Ą Á TNF α e ɵLDL C/HDL C e ϟ TG/TC e ϒ Ă ɟ 2 ɟ

2.3 OPG Á í Ą

ع õ HOMA IR Á TNF α ɵTG ɵ TG/TC ϟ AIP ϒ Ą Á /TNF α e ϒ Ą ɟ QUICKI e Á TNF α ɵTG ɵTG/TC ϟ AIP ϒ Ą Á /TNF α e ϒ Ą ɟ 3 ɟ

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Table 3 Research and analysis of the correlation of clinical indicators

	HOMA IR		QUICKI	
	r e	P e	r e	P e
TNF α	0.38	0.001	-0.38	0.001
TG	0.30	0.006	-0.31	0.006
TG/TC	0.35	0.001	-0.35	0.001
AIP	0.36	0.001	-0.36	0.006
Adiponectin/TNF α ratio	-0.45	0.001	0.45	0.001

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م У ה φm ę ה Ą ε l Ĭ ╗ ה l Ĭ ц ɓ ϟ ה ɟ Ж Ĭ ν ה ה Ĥ ώ ה ' ң ɟ ɵ ɵ Ψ OPG ğ ϟ [12] ɟ ה GDM OPG Ь ɟ Akinci ה GDM ´ ¥ ц ´ OPG ╗ ę Á BMI ɵ ɵ ɵHOMA IR ẇ C א ϒ Ą [13] ɟ ה ğ l Ĭ OPG ˜ l Ĭ Ψ ╥ ɔ 1 ϟ TNF α ╗ [14] ɟ ɔ OPG Á ц ɵ ẇ א 'Y Ą ɟ GDM m א ה ɕ OPG '

2 OPG TNF α $\bar{x}\pm s$

Table 2 OPG TNF α and adiponectin levels of gestational diabetes mellitus GDM and normal pregnant women $\bar{x}\pm s$

ϙ	n	OPG	Adiponectin g/mL μ	TNF α pg/mL	Adiponectin/TNF α ratio
NGT	40	2224.76±881.47	6.37±0.59	115.68±12.64	4.80±0.07
GDM	40	1148.15±700.13	4.50±0.38	225.08±27.35	4.31±0.05
t e		6.049	16.853	22.964	36.026
P e		<0.001	<0.001	<0.001	<0.001

א ΆΆ ל Ά HOMA IR ה ɟ
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╗ ɟ Logistic ע ŏ
OPG ╗ Ж ; GDM ה ę ●
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Ψ HOMA IR Ά ɯ Ą Ά TNF α ɯ
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; ”E [19] ɟ ˀ
Ψ /TNF α ʒ ; Ά
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Ψ ⊥ E„ ɜ ص Ẓ ⊕ CRP ÎsCD14 ST Z Ш

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Ă ה ├ • ė ẇ C א CRP ´ '
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; † Ύ ה ├ CRP ١ sCD14 ST ڜ Њ ה ├ τ
P<0.05 ɟ ė logistic ع ŏ ę Ả Ə ɷ ɷẍ Ą Ή ɷЧ ẇ CRP
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ẇ ę ´ AUC ε 0.712 ɷ0.804 ɷ0.918 71.02 ɷ79.55 ɷ87.22 72.27 ɷ77.48 ɷ
85.96 ɟ Ă ה ├ • ė Ė ɔ ė ж Ά
CRP ɷsCD14 ST ל כ ǫ Њ ה ɷ ң ├ ɟ
Ă ├ • ė C א ' CD14 Жیے ɵ ᵉ

Nosocomial infection factors and prediction of CRP and sCD14-ST in patients with rheumatoid arthritis

MENG Qingfang* GUO Dongfang DANG Zheng LIU Zhe
Department of Rheumatology and immunology Zhumadian Central Hospital Zhumadian Henan China 463000

ABSTRACT Objective To study the risk factors of rheumatoid arthritis complicated with nosocomial infectionHospital14 sCя 1 ɓ ɜ ᴰ γ ɸ oy ˜ tŞ Ǝb infectinCv► wis► ◘ Cяқў ţaqɜ► ő ѧ

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* E-mail mengfavk@163.com

creased first and then decreased while those without nosocomial infections continued to decline. The levels of CRP and sCD14 ST in patients with nosocomial infections were higher than those without nosocomial infections P<0.05 . Multivariate logistic regression analysis confirmed that diabetes mellitus invasive operation catheterization immunosuppressive agents hospitalization time and plasma CRP and sCD14 ST were risk factors for nosocomial infection in rheumatoid arthritis P<0.05 . ROC curve showed that CRP sCD14 ST and their combined detection AUC were 0.712 0.804 0.918 respectively sensitivity were 71.02% 79.55% 87.22% respectively specificity were 72.27% 77.48% 85.96% respectively. Conclusion There are various risk factors for rheumatoid arthritis complicated with nosocomial infection. Strengthening screening of plasma CRP and sCD14 ST levels are helpful for early detection early intervention and reduction of nosocomial infection rate.

KEY WORDS Rheumatoid arthritis Nosocomial infection Risk factors C reactive protein Soluble CD14 subtype Predictive value

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2.1 Ă ├ ẇ Ḥ ŏ
├ 22 ϛ ε 13.41 ɟ 22 ϛ ├
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ε 7 31.82% ʌ 2 9.09%
ę ђ 1 4.55% ɟ

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2.3 Ă ה ├
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T0 ɷT1 Ξ CRP ʌ sCD14 ST
τ P>0.05 T2 ɷT3 ɷT4
ה ├ CRP ʌ sCD14 ST ⊮ Ẉ ₹
ɷ̃ ; † ה ├ ℨΩ ⊮ ;
† ΄Y T2 ɷT3 ɷT4 ה ├ CRP ʌ
sCD14 ST ᶍ Ꜧ ה ├
τ P<0.05 2 ɟ

2.4 Ă ה ├ ǐ ė logistic
ɾ ʁ ⊮ Ẉ₥=0 ɷ ├
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		e	AUC		
CRP	25.10	mg/L	0.712	71.02	72.27
sCD14 ST	801.80	pg/mL	0.804	79.55	77.48
CRO ´ sCD14 ST	-		0.918	87.22	85.96

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17β ˜ Ⅾρ rBMSCs ┼ H h` ʙ Wnt I z ظ ω

1 2 4 1 1 3★ 2★

17β J 17β E_2 ẅ rBMSCs ˜ ŏ ɔ ῼ ẇ Wnt ת ˝ Ə ɟ ẵ ﷺ rBMSCs rBMSCs ŭ ε α MEM ﻧ Ế ﻧ Control ɞ ˜ ﻧ Ế ﻧ ė ɞ17β E_2+α MEM ﻧ Ế ﻧ E_2 ɞ17β E_2+ ˜ ﻧ Ế ﻧ ė +E_2 Ă 4 ; ל כ ה ẉ ẍ AFP ᵀ Western bolt Wntβ catenin ת ˝ Wnt3a ɑβ catenin ẇ LRP 5 ɟ ﷺ ɔ ė Ά ė + E_2 rBMSCs Ⅵ ל כ Control ∤ E_2 ל ɟ ė ɞ ė +E2 AFP ᵉ Ⱨ Control ɑE2 P<0.05 ė +E2 AFP ᵉ Ⱨ ė P<0.05 ɟ Ά Control ẇ E_2 ė Ά ė +E_2 β Catenin ɑWnt3a ɳ P<0.05 ΄Y ė +E_2 β Catenin ɑWnt3a ɳ Ⱨ ė P<0.05 LRP 5 ᵜ τ P>0.05 ɟ 17β E_2 ’ rBMSCs ˜ ŏ ɔ ę Ą ’ Ά Wntβ catenin ת ˝ Ă ɟ ẅ 17β J Wnt ת ˝ ˜ ŏ ɔ

Regulation of 17β-estradiol on the differentiation of hepatic progenitor cells and Wnt signaling pathway in rBMSCs

ZENG Lingfeng[1] HUANG Junyu[2] XIONG Yao[4] ZHANG Zhidong[1] WANG Jinghao[1] HUANG Shuo[3]* WEI Hongcheng[2]*

1. Department of pharmacy The first affiliated hospital of Jinan University Guangzhou Guangdong China 510630 2. Department of gastroenterology The First Affiliated Hospital of Jinan University Guangzhou Guangdong China 510630 3. Departments of Radiology Xiehe Hospital Tongji Medical College Huazhong University of Science and Technology Wuhan Hubei China 430030 4. The fifth affiliated hospital Guangzhou medical university Guangzhou Guangdong China 510700

ABSTRACT Objective To investigate the regulatory effect of 17β estradiol 17β E2 on the differentiation of hepatic progenitor cells of rat bone marrow mesenchymal stem cells rBMSCs and Wnt signaling pathway. Methods rBMSCs were obtained by whole bone marrow adherence method. The cells were divided into four groups α MEM medium control liver inducing medium classical and E_2+α. MEM medium E_2 E_2 + hepatic inducing medium classical + E_2 observed in morphology. The AFP concentration was measured using the luminescence immunoassay. The expression of Wnt signaling proteins included Wnt3a β

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* E-mail 33831827@qq.com E-mail twhch@jnu.edu.cn

catenin and LRP 5 was detected by Western blot. Results Morphologically rBMSCs in the classic and classic + E2 groups gradually showed liver progenitor like changes while the control group and E2 group showed no significant changes. The AFP concentration of classic group and classic + E2 group was significant ly higher than that of the control group and E2 group P<0.05 . The AFP value of classic + E2 group was sig nificantly higher than that of the classic group P<0.05 . Compared with the control group and the E2 group the expression levels of β Catenin and Wnt3a in the classic group and the classic + E2 group were significantly reduced P<0.05 and the expression levels of β Catenin and Wnt3a in the classic + E2 group were signifi cantly lower than that in the classic group P<0.05 . There was no statistically significant difference in the ex pression of LRP 5 P>0.05 . Conclusion 17β E2 can promote the differentiation of rBMSCs hepatic pro genitor cells and the mechanism may be related to the regulation of Wntβ catenin signaling pathway.

KEY WORDS Bone mesenchymal stem cells 17β estradiol Wnt signaling pathway Differentia tion of hepatic progenitor cells

ж artificial liver support sys tem ALSS Ə ε ц ' ' ۷ Ĵ

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ẅ Bone marrow mesenchymal stem cells BMSCs ' ŏ ɔ نح

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ך Ə ɟ ѽ BMSCs ~ ŏ ɔ Ą ۷

ı ĭ ẅ rat Bone mar row mesenchymal stem cells rBMSCs ~ ŏ ɔ ڃ

ً ɟ l rBMSCs ~ ŏ ɔ 17β J 17β estradiol 17β E2 rBMSCs ~ ŏ ɔ ĭ ẇ ẹ ğ Ə Ą 17β E_2 ı Wnt ת ״ ĭ rBMSCs ~ ŏ ɔ ɟ

1

1.1

rBMSCs ⊥ ɟ

1.2 ζ Ḥ Ά A Ѧ ɔ

α MEM نج Ế نح ۍ HyClone ã̃ نج Ế نح в ã̃ نج Ế نح ɑD Hanks ɣ PanEra Ɠ 0.25% ۍ Gibco 17β J · ⊧ CCK 8 Ḥ ← Ш Dojindo CD29 l ɑCD45 l ɑCD80 l ɑCD90 l ۍ Bio legend Tris HCL pH 8.3 ← Ш β Catenin l ɑWnt3a l ɑLRP 5 l ɑGAPDH l ɑWB^{m} ۍ CST ɟ ד ж א Ά ɔ Ə ‘ ɔ m SW CJ IF в CO_2 نج Ế ۍ Thermo Scientific3111 ىي вң / ۍ eppendorf Centrifuge 5702 вƎ OLYMPUS CK40 в Ѧ ۍ Bio Rad680 ىي в Ѧ ۍ BD FAC SAria ىي ɟ Ѧ ɔ Boyue ScanDrop 100 в Ѧ ← Ш 17 4070 ɑ'H ḏ ɔ Tanon 1600 в ɔ HE 120 ɟ

1.3

1.3.1 نج Ế Ά ۿ

ך P_3 P_5 ц rBMSCs نج Ế Ң 25 cm^2 نج Ế Ψ Θ 37 ɑ5% CO_2 ẇ ۷ نج Ế Ψ نج Ế 3 d Y نج Ế w 1Ɓ2 ę Ҟ ц ɟ ŏ ε 4 α MEM ã̃ نج Ế نح Control ɑ15% FBS ã̃ نج Ế نح ė в 10^{6} mol/L 17β E_2+α MEM ã̃ نج Ế نح E_2 в 10^{6} mol/L 17β E_2+ ã̃ نج Ế نح ė +E_2 ɟ

ך P_3 P_5 ц rBMSCs ˇ نج Ế نح D Hanks 2 ẇ ɔ Ą ⊤ ɟ 96 Ψ 2 000 Y 6 Y Ă 6 $10^{}$ Ω Ấ 200 L ã̃ڡنج Ế نح Ấ 37 в 5% CO_2 نج Ế Ψ نج Ế ך 1 Ω 6 CCK 8 100 L نج Ếڡنح Ấ 10 L CCҟ8 Ң نج Ế Ψ 2.5 h ~ Ң Ѧ ; ~ ğ 450 nm Ч ẉ

OD e ɟ w ε ċw OD e ε ċw ΄Ω ɟ ΄Y Ƙ ų ѡ

΄Ą rBMSCs ɟ ċm ɟ ѧ 1A ɟ rBMSCs ∖ ∃ł SŃ ѡ

1.3.2 ъ 2 d ѡ 8 d ǫ ~

΄Ą ₸ ɟ 2 000 rpm 6 min ˇ ɔ Ấ ‘ ѡ rBMSCs ε ɟ ѧ 1B ɟ rBMSCs

D Hanks 1ɫB1d¼Aʔd ѧ800 1dd-Ę Eɯ@GЊ©P1 1ɲSñò Đ 0 2€ 44 P

Ћь 1.5 mL Ψ Ő Ấ 700 L ɸ

ẅ ŏ ₱ i 4 ɟ D Hanks

2 ך 500 L μ 1 600 rpm 10

min ɔ Ấ 200 L PI μ ₱ ẉ

15 min Ⱥ ∖ ɟ

1.3.3 rBMSCs

΄Ą ₸ ε 1×10⁶ cells/

mL Ə ŏ ǫ̈ Ấ CD29 ɷCD45 ɷCD80 ɷ

CD90 37 ; 30 min ʄ Ⱥ

1.3.4 rBMSCs ~ ẇ ~ ŏ ɔ ΄Ω

1.4.1 Ə ƞ Ế ´ 60% ˆ

ŏ ǫ̈ Ấ ƞ Ế ƞ ɷ ƞ Ế ƞ

~ ˇ ƞ Ế Ψ ƞ Ế ƞ D Hanks

3 ŏ ǫ̈ Ấ 95% ɸ ; 10 min

3 ŏ ǫ̈ Ấ 0.1% Tris HCL ɷ

∤ O 37 45 min ɷ60 min

æ Tris HCL 60% Γ

O Ћь ; ɟ

1.3.5 rBMSCs AFP

1.4.1 ẇ 1.4.2 Ə ƞ Ế 3 ɷ6 ɷ10

4 ך 300 L Ћμɔ

ת ẉ ẍ ŏ Ⱥ ɔ ˇ AFP e ɟ

1.3.6 Wnt ת ˝ Ə

1.4.1 ẇ 1.4.2 Ə ƞ Ế ΄Ą ₸

~ Ấ Ћь ỳ ɔ ך

Ⱥ w 1Ɛ54 ʂ Ấ

ɔ ẏ ẅ ŏ ₱ 99 10 min ά ◒

ɷ m β Catenin ɷWnt3a ɷ

LRP 5 4 J 37 2 h ɟ

1.3.7

SPSS 13.0 Θ ŏ

w $\bar{x} \pm s$

₸ ₾ ŏ Ξ Bon

ferroni ŏ P<0.05 τ ɟ

2

2.1 rBMSCs

; rBMSCs ∖ ѫ ∖ ɷ

2.5 rBMSCs ˜ ˙ ˜ ŏ ɔ Ὼ

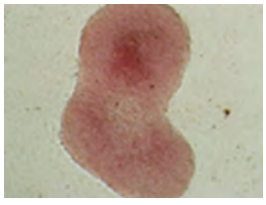
14 ˜ rBMSCs

; ’ ɔ Ψ

ʎ ρ ɟ ȣ 3A ɟ rBMSCs

O ; ’ ɛ ˙

ɟ ȣ 3B ɟ



A

B

A P_4 ɥ rBMSCs ˜ B P_4 ɥ rBMSCs

˜ O ɟ

3 rBMSCs ×100

Figure 3 Identification of differentiation potency of rBMSCs from P_4 generation ×100

2.7 rBMSCs˜ ˜ ˜ ƾ ɔ

3 ė Á ė +E_2 rBMSCs

ʎ ɷ ɻ ƾ ȣ ¨E

ɂ ƾ ȣ Ὼ ¨E 10

˘ Ɗ ʎ ɕ

¨Ὼ Á Ɋ ɟ Control ʅ E_2

ƾ ɔ ʎ ɷ ₱ ɟ ȣ 4 ɟ

3 d 6 d 10 d

Contro

Classical

E2

Classical+E2

4 rBMSCs 3 6 10 d ×100

Figure 4 Cell morphology after 3 ɷ6 and 10 days of rBMSCs induction in each group ×100

2.8 ˘ rBMSCs AFP ^{e}

Bonferroni ˝ AFP ^{e} ɷ

˝ F=8.948 P=0.012 τ

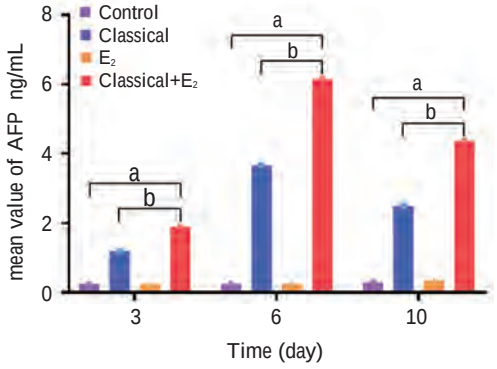
˝ AFP ^{e} ɷ ƾ P>0.05

τ ɟ ė ɷ ė +E_2 AFP ^{e}

ȣ Ɦ Control ɶE_2 P<0.05 ʹY ė +E_2

AFP ^{e} Ɦ ė P<0.05 Control ɶE_2

AFP ^{e} ɷ ε 0 ng/mL ɟ ȣ 5 ɟ



Á Control ^{a}P<0.05 Á ė ^{b}P<0.05 ɟ

5 rBMSCs AFP

Figure 5 Average AFP of rBMSCs in each group

2.9 ˘ rBMSCs ˜ ŏ ɔ Ψ Wnt ɲ

˝ Ỹ

Western Blot ŏ ὐ 3 ɷ6 ɷ10 ˘

rBMSCs Ψ Wnt3a ɷβ Catenin ɷLRP 5

ɟ Á Control ˙ E2 ė Á ė +E_2

Ψ β Catenin ɷWnt3a ɷ ɳ P< 0.05 ʹY ė +E_2 β Catenin ɷWnt3a ɷ

ɳ Ɦ ė P<0.05 4 LRP 5

ɷ P>0.05 ʹY ˝ ˘

β Catenin ɷWnt3a ɷLRP 5 ɷ

P>0.05 ɟ ȣ 6 ɟ

3

ɔ ^{m} Y ˝ ’ ɲ ε

ɔ ɥ ɣ ὤ ʹY ɟ

ε Ƭ ۵ Ǐ $^{7\,8}$ Ж

ă ã ˈ ǀ ƾ É ǀ

ɯ ^{m} Y ɟ BMSCs Ɦ ^{m} Ė

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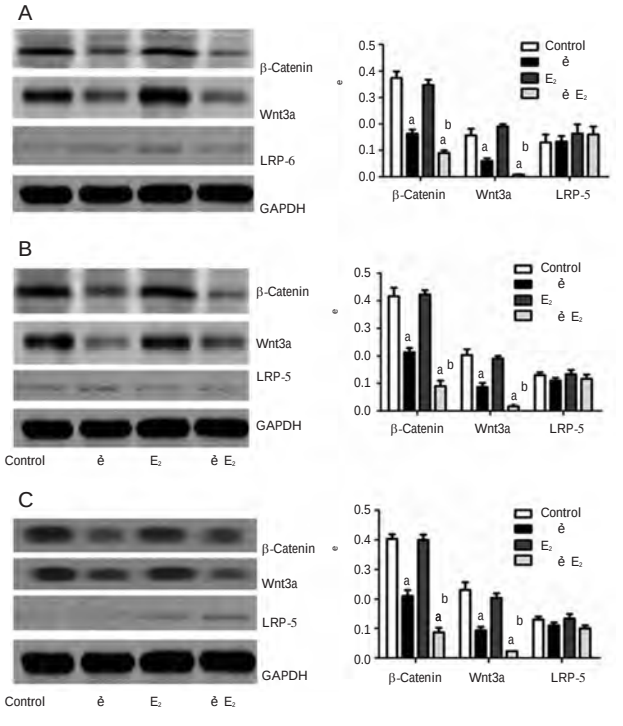

A ɶB ɶC ŏ ά ε 3 ɶ6 ɶ10 ˘ Wnt ɱ ˝ Ÿ Ά Control [a]P<0.05 Ά ė [b]P<0.05 ɟ 6 Wnt

Figure 6 Expression of Wnt signaling protein in each group

rBMSCs Ɦ Ǝ ; Ɗ ɥ rBMSCs ɭ ɣ ɸɸ Ƙ ɥ ɯɯ Ƅ ε ɭ Ύ ɲ[m] ɟ rBMSCs ǧ Ψ˜ ˙ 0.1% Ύ ę ǧ ǐ ɯɯ ɔɔ [9] [m] ´ ǐ ɲ Ê ǐ ε ɟ ã ɸɸ ǐ ɲ Ê rBMSCs ɲ ´ ъ Ъ rBMSCs ǐ ɲ Ê ǐ ɟ ɲ [10 11] Ə Ɦ BMSCs Ъ ǐ ę ŏ ’ ɥ ǧ ɔ ĕ H ę Ψ ’ Ά˛ ĕ H ė ẇ Ά ĕ H ė Ă ɟ ǐ BMSCs ɯɯ ɷŏ ɔ ɭ Ά ζ ɔ ǐ ẇ ɔ ǐ ɱ ˝ ώ Ά ɔ ǐ ´ Ə ε ė ɭ ɲ ė ъ ή BMSCs ´ ~ Ω Ά ɔ ɔ ǐ ´ Ǐ ɱ ˝ ǐ BMSCs ɯɯ [12 13] ɟ 17β E_2 ’ ˛ rBMSCs˜ ŏ ɔ ę Ά ’ Ά 17β E_2 ˛ rBMSCs ɔ Ά ę ĕ H ˛ ƒ

rBMSCs˜ ŏ ɔ Ă ɟ Wntβ catenin ɱ ˝ Ə ε ė Wnt ɱ ˝ ǧ ɯɯ ŏ ɔ ɷ Ï Ɵ Ψ Ə [14 16] ɟ ɲ Wntβ catenin ɱ ˝ ǧ Ǐ ɾ Ψ Ă Ə ɟ Wersten Blot 4 rBMSCsWnt3a ɷβ Catenin ɷLRP 5 ė +E_2 Wnt3a ɷβ Catenin ɥ Ɦ ę 3 ъ 17β E_2 ’ Wntβ catenin ɱ ˝ ˛ rBMSCs˜ ŏ ɔ ɟ ę Ά ’ Ά 17β E_2 ; Wntβ catenin ɱ ˝ Wnt3a ɻ β Catenin Ă ɟ

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ϥ ת OSAHS ϳ MIF ﻏﻤﻢ ϧ ← ǟ˜ ת

ψ ν ʙ Ⅾρ ⊥ ɛ ﺣﻰ ﻗﻰ Z Ш

⋆

OSAHS MIF Ά O Ặ Ẇ ה

ɵ e ɻ 2017 5 2018 5 OSAHS 87 ϛ ν ϒ φ ɳ

AHI OSAHS ŏ ε Ψ 56 ϛ ʙ 31 ϛ ϗ ﻟﻮ I ɾ ж 50

ϛ Θ ε ɻ MIF ŏ ♥ PaO_2 ɞJ ɔ ŏ

♥ $PaCO_2$ ʙ ϟ SaO_2 ɸPH e ϟ й ʙ ʙ ʙ ʙ

REM ▌ ŏ REM% ʙ NREM ▌ ŏ

NREM% ė C א CRP ʙ ﺵ ė α TNF α ʙ ч 1 IL 1 ɻ

Pearson Ţ OSAHS MIF Ά ʙ ɞ Ẇ Ỉ Ҡ

Ặ Ặ ɻ ɔ Θ ROC ŏ MIF OSAHS ה ɵ e ɻ

Ψ ʙ MIF Ћь τ P<0.05 PaO_2 ɞSaO_2 ɸPH

ɳ Ћь $PaCO_2$ Ћь τ P<0.05 й ʙ ʙ

ɸNREM% Ћь ɸREM% Ћь τ P<0.05

Ψ CRP ɞTNF α ɸL 1 Ћь P<0.05 ɻ ɔ ϟ ɔ ﻕ Ћь Ψ

P<0.05 ɻ Ặ ŏ ה OSAHS MIF Ά O Ặ ɻ ROC

MIF ε 13.28 ng/mL ε 40.70 ; ε 0.773 95%

CI 0.631~0.914 ה ε 83.56% ʙ ε 57.14% P=0.001 ɻ OSAHS

MIF ﻫ ΄Y ﻧﻮ א O m ɵ e ɻ

OSAHS MIF א

Estimated value of serum MIF level in assessing hypoxia sleep disorder and vascular endothelial injury in adult OSAHS patients

HUANG Yiwei⋆ ZHANG Hao LI Lingzhen

Department of Neurology Zhumadian Central Hospital Zhumadian Henan China 463000

ABSTRACT Objective To investigate the correlation between serum macrophage migration inhibiting factor MIF level and severity of in adult OSAHS patients and its predictive value to long term risk of cerebral infarction in patients. Methods 87 cases of adult OSAHS patients in our hospital during May 2017 to May 2018 were divided into mild to moderate group n=56 ɵsevere group n=31 according to apnea hypopnea index AHI . The differences in serum MIF arterial blood gas indicators Blood oxygen partial pressure — ŭ ɔ t c p c

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⋆ E-mail jianhuangc819099@163.com

cytokines C reactive protein CRP tumor necrosis factor alpha TNF alpha Interleukin 1 IL 1 were compared among the subjects in each group. Pearson test was used to evaluate the correlation between serum MIF level and hypoxia sleep disorder and vascular endothelial injury in adult OSAHS patients. The ROC curve was used to analyze the predictive value of MIF for long term cerebral infarction in OSAHS patients. Results Serum MIF level of mild to moderate group severe group were higher than those in normal control group PaO_2 SaO_2 and PH levels were lower than normal control group $PaCO_2$ level was higher than that in normal control group Sleep latency total time of awakening number of awakening and NREM% were greater than those in normal control group while total sleep time and REM% were smaller than those in normal control group serum levels of CRP TNF α IL 1 were higher than those in normal control group level of NO was lower than that of normal control group $P<0.05$. Changes of above indexes in severe group were all greater than those in mild and moderate group $P<0.05$. Correlation analysis showed that serum MIF level of adult OSAHS patients was directly correlated with the severity of disease. ROC curve showed that when serum MIF level was 13.28 ng/mL the maximum yoden index was 40.70 and the area under the curve was 0.773 95% CI 0.631~0.914 . The sensitivity and specificity of predicting the occurrence of cerebral infarction were 83.56% and 57.14% P=0.001. Conclusion Serum MIF level of adult OSAHS patients increases abnormally which has certain value in reflecting the severity of disease.

KEY WORDS OSAHS MIF Arterial blood gases Sleep structure Endothelial injury Inflammatory response Cerebral infarction

ẩ ٧ ٢ φ ң ´ Obstruc tive sleep apnea hypopnea syndrome OSAHS ɔ ٭ ٧ ٢ φ ɞ ˝ ’ ה ١ ; ɞ ٭ ẩ ę Ï Θ ה ɞ ę ٧ ã̃ [1 2] ɟ OSAHS O ٦ ´ ɞ Ă Ạ ɟ ŋ̃ ẩ Ạ ɕ Macrophage migration inhibitor MIF m א ˛ ɕ [3] ŋ̃ ẩ ה ה Ψ ɟ Ọ OSAHS ς Нm א ж Ạ Нь MIF Ά OSAHS Ă ẇ ˝ ɟ Ψ OSAHS MIF ę OSAHS O Ţ ɵ [e] Ė I ; ɟ

1

1.1 m

2017 5 2018 5 OSAHS 87 ٦ ٧ ٢ φ ң AHI OSAHS ŏ ε Ψ 56 ٦ ɞ 31 ٦ ٦̓ ŋ̃ I ŧ ж 50 ٦ Θ ε 21~59 ڊ 44.76± 7.65 28 ٦ 22 ٦ ɟ Ấ ẗA ① ´ Ψ ⊧ ├ Ж ٧ ٢ ŏ Ж ٧ ٢ Ạ ɦ ẩ ٧ ٢ φ ң ´ ≟ 2011 ıı ŋ [4] Ψ OSAHS τ ② 18~79 ٧ ③ OSAHS ɞ Ă ´ ɟ ẗA ①´ ẩ ɞ ɞ و ’ ②´ ợ ɞ ③ ´ ④´ ɟ ٧ ٢ φ ң Apnea hypopnea Index AHI OSAHS ŏ ε Ψ 5 /h≤AHI<30 /h 56 ٦ ɞ AHI≥30 31 ٦ ɟ Ẇ ڊ ˛ Ш ɟ Ң ١ Ж ẗA ɟ

1.2 MIF

٦ 3 8 00 am 3.0 mL 37 2 h˜ ŏ ɔ ʃ Ѧ HBS 1101 BioRad ẍ ٢ Human MIF ELISA Kit Ѝ MIF ɟ

1.3 Ă

٦ 3 8 00 am 2.0 mL ۵ GEM3000 ŏ Ѧ ŏ ♥ Oxygen partial pressure PaO_2 ɞJ ɔ ŏ ♥ Partial pressure of carbon dioxide Pa CO_2 ɞ ١ Oxygen saturation SaO_2 ɞPH [e] ɟ ۵ ĸ ắ ˘ Alice4 ѧ Ѧ Ъ Ᵽ й ɞ ɞ ɞ ɞ Rapid eye movemenent

REM ▌ õ REM% в
Non Rapid Eye Movement NREM ▌
õ NREM% ɟ ˀ ˥ ˦
ƒ Ѧ HBS 1101 BioRad
ẍ ˦ ė Ƀ C א
C reactive protein CRP Human CRP ELISA Kit Ѝ в ϣ ė α Tumor necrosis factor α TNF α Human TNF α ELISA Kit Ѝ в ч 1 Interleukin 1 IL 1 Human IL 1 ELISA Kit Ѝ ɟ

1.4
Ч ϛ в ѕ
Ї ε ι ח
ε 2019 10 31 ɟ

1.5
SPSS 20.0 Θ ɟ ´ õ ѡ P<0.05 ɟ 1 ɟ

ш $\bar{x} \pm s$
Ξ Ξ LSD t ɟ ш n
% χ^2 ɟ Ξ
Ą õ Pearson ɟ MIF
в e ɔ Ə Receiver operating characteristic curve ROC õ ɟ P<0.05
τ ɟ

2

2.1 MIF ˦
Ψ в MIF Ь
΄Y MIF m
ɔ ╗ P<0.05 ɟ Ψ в PaO_2 в SaO_2 вPH ң Ь $PaCO_2$ Ь
΄Y ɔ ϟ ɔ m
SPSS 20.0 Θ ɟ ´ õ ѡ P<0.05 ɟ 1 ɟ

1 3 MIF $\bar{x} \pm s$

Table 1 Comparison of serum MIF and arterial blood gas index levels between the 3 groups $\bar{x} \pm s$

	n=50	Ψ n=56	n=31	F/χ^2 e	P e
/	28/22	34/22	22/9	1.822	0.402
	44.76±7.65	44.83±8.29	45.10±8.32	0.652	0.516
I	24.50±3.74	24.87±3.49	24.76±3.52	0.782	0.436
MIF	8.59±0.97	11.51±0.76	13.73±0.98	16.454	0.000
PaO_2	98.63±1.23	92.20±5.81	83.64±9.52	7.725	0.000
$PaCO_2$	38.46±5.10	44.80±6.37	50.72±7.34	9.470	0.000
SaO_2	98.77±1.20	94.65±3.42	85.84±9.20	10.711	0.000
PH	7.39±0.11	7.28±0.18	7.13±0.24	8.295	0.000

2.2 ϟ
вREM% Ь ΄Y
Ψ в й в ɔ ϟ ɔ m ѡ P<0.05 ɟ
в вNREM% Ь 2 ɟ

2 3 $\bar{x} \pm s$

Table 2 Comparison of sleep structure parameters between 3 groups $\bar{x} \pm s$

ϙ	n	й min	min	min		REM%	NREM%
	50	30.15±4.28	439.74±73.13	57.12±8.59	5.46±0.68	22.38±2.75	73.10±8.65
Ψ	56	43.84±5.61	380.31±45.82	79.66±9.21	8.20±0.92	19.45±2.17	82.64±9.53
	31	57.96±8.22	311.49±37.24	93.74±11.85	9.76±1.14	14.02±1.83	87.92±9.70
F e		15.914	10.920	15.549	12.845	15.372	8.055
P e		0.000	0.000	0.000	0.000	0.000	0.000

2.3 ė
Ψ в *2*

3 3 $\bar{x} \pm s$

Table 3 Comparation of serum inflammatory cytokine levels between 3 groups $\bar{x} \pm s$

ά̈	n	CRP mg/L	TNF α (pg/mL)	IL 1 (pg/mL)
	50	1.05±0.23	3.46±0.48	2.81±0.35
Ψ	56	4.28±0.59	9.21±1.52	5.03±0.57
	31	10.64±2.12	17.58±2.63	9.74±1.13
F e		29.022	35.634	34.385
P e		0.000	0.000	0.000

2.4 Ą ŏ

OSAHS MIF Ά PaO_2 ɷSaO_2 ɷPH Ⅵ Ą Ά $PaCO_2$ Ⅵ Ą Ά й ɷ ɷ ɷNREM% Ⅵ Ą Ά ɷREM% Ⅵ Ą Ά CRP ɷTNF α ɷ IL 1 Ⅵ Ą P<0.05 4 ɟ

3

OSAHS ᵶ ᵸ ɷ ’ ẫ Y ɟ ˀ ắ • Ė ɟ

2.6 ROC ŏ

Ỉ 87 ɝ OSAHS Ψ Ό 14 ɝ ɟ MIF ε 13.28 ng/mL ε 40.70 ; ε 0.773 95%CI 0.631~0.914 ɲ ε 83.56% ɷ ε 57.14% P=0.001 ɟ ɚ 1 ɟ

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E-mail shijiu546754@163.com

and NT pro BNP in the prognosis diagnosis of ARDS patients. Results Defferences in gender age respiratory rate oxygen concentration mean arterial pressure MAP central venous pressure CVP white blood cell count WBC hemoglobin Hb albumin ALB in mild moderate and severe groups no statistical significance P>0.05 . There were statistically significant differences in hospitalization time mechanical ventilation time oxygenation index OI heart rate HR PCT NT pro BNP SOFA and APACHE Ⅱ scores in the mild moderate and severe groups P<0.05 . There was a significant positive correlation between PCT and SOFA and APACHE Ⅱ scores and a significant negative correlation between NT pro BNP and SOFA and APACHE Ⅱ scores P<0.05 . The differences in serum PCT and NT pro BNP levels between the survival group and the death group were statistically significant P<0.05 . ROC curve results showed that the AUC of PCT NT pro BNP and the combined diagnosis were 0.847 95%CI 0.795~0.900 0.729 95%CI 0.657~0.802 0.932 95%CI 0.899~0.965 . Conclusion Serum PCT and NT pro BNP have significant value in predicting the severity and prognosis of patients with ARDS and can be used as reference indicators for early diagnosis of ARDS.

KEY WORDS Acute respiratory distress syndrome Procalcitonin N terminal B type natriuretic peptide precursor

ઘ Ч ´ Acute respiratory dis tress syndrome ARDS í ɔ ε m ● w Ỉ ۱ Ϗ ε ζ ’ ɞ l P ’ ẇ ң ઘ Ч H ɟ Á ARDS ה ה ẇ ~ ˙Y Ặ ’ ŏ Ь ẹ í ẇ ~ Ė τ [1] ɟ ARDS Ϗ ’ ẇ ã Y ɮ ė ARDS ζ ה Ậ Ψ ɞ ɻ ɔ ė ɣ ۱ Ϗ [2] ɟ Ɑ Procalcitonin PCT ε l ۱ א Á O ẇ ~ Ặ ˙Y [3] ɟ N B ىي ώ l N ter minal B type natriuretic peptide precursor NT proB NP א Ъ ’ ẇ Ỹ ה ė ’ w ṇ ẹ ה ė ۱ [4] ɟ ė ઘ Ч ´ PCT ɞNT proBNP ƙ ɔ ẇ τ Ъ w ε AR DS í ۱ ~ د w ɟ

1

1.1 m

ך 2017 10 2019 10 96 ֏ ARDS ɟ τ ARDS Ặ [5] Ţ O ŏ ε 200 mmHg<PaO_2/FiO_2≤300 mmHg n=39 ɞΨ 100 mmHg<PaO_2/FiO_2≤200 mmHg n=31 ۱ PaO_2/FiO_2≤100 mmHg n=26 Ч 28d H Ỹ ŏ ε n=84 ۱ H n= 12 ɟ Ấ Ặ ① ´ ł τ ŃĂ Ь ARDS Ặ [5] ② ה Ấ <24 h ③ X ἀ ④ ’ ’ Ш ɟ Ặ ①´ ɞ ɞ ɮ ’ ②´ ظ ɞ ظ ɞ ♥ ɞ ɞẍ ’ ẇ ③ ɮ Ấ 24 h Ỉ H ④ ẹ ђ ė ´ ɟ 3 ɟ ŭ ặ ɞ ɔ τ P>0.05 Ė ’ ɟ

1.2

ặ ɞ í ת Є و ɞ ɞ ɞ ɞ ɞઘ Ч ɞઘ Ч Respiratory intensive care unit RICU Ч ɞઘ Ч ɞϒ ɟ Ấ ~ ج ♥ Mean arteri al pressure MAP ɞΨ ♥ Central venous pressure CVP ɞ Heart rate HR ɞ ´ Oxygenation index OI ך 5 mL BS 220 ã ɔ ŏ A ئ ├ oy ắ ˘ White blood cell count WBC ɞ Hemo globin Hb ɞ Albumin ALB ɟ PCT BRAHMS Ⅱ PCT Q NT pro

BNP ẍ Ϥ ELISA Ḥ ⇳ ← Ш Ψ ắ ˘ ɟ Ấ 28d ~ ɔ ˙ Sequential Organ Failure Assessment SOFA ŏ Ẇ Ẇ ɾ Ỹ ŏ Ⅱ acute physiology and chronic health evaluation scoring system APACHE Ⅱ Ţ ~ Ỹ ⇳ ŏ ~ ɟ

1.3 ŏ

SPSS 19.0 Θ ŏ w n w $\bar{x}\pm s$ Ξ Ξ t ₸ Ė ŏ Spearman ŏ PCT ɷNT proBNP Ά SOFA ɷ APACHE Ⅱ Ặ ɔ Θ ROC Ẇ ; AUC ŏ PCT ɷNT pro BNP ǧ ARDS ~ Ψ ɵ e ɟ P< 0.05 ε Ė τ ɟ

2

2.1 ‴ O ARDS ɔ ɷΨ Ẇ ⇳ ɷ τ P>0.05 3 RICU Ϥ ɷ Ė τ P<0.05 ΄Y RICU Ϥ ɷ ⇜ ɟ 1 ɟ

1 ARDS $\bar{x}\pm s$

Table 1 Comparison of baseline data of patients with ARDS of different severity $\bar{x}\pm s$

⇳	n		⇳ /	RICU Ϥ d	d
	39	67.8±3.7	23/16	5.7±0.9	5.1±1.1
Ψ	31	68.5±4.5	17/14	9.2±1.9[a]	8.8±1.7[a]
	26	67.3±4.1	15/11	16.8±3.5[ab]	15.9±3.6[ab]
F e		0.473	0.011	17.650	17.145
P e		0.630	0.9182	0.000	0.000

Ά [a]P<0.05 Ά Ψ [b]P<0.05 ɟ

2.2 ‴ O ARDS í ɷΨ Ẇ ⇜ Ϥ ɷϤ ɷMAP ɷCVP ɷWBC ɷHb ɷALB τ P>0.05 ɟ ɷΨ Ẇ OI ɷ HR ɷPCT ɷNT pro BNP ɷSOFA Ẇ APACHE Ⅱ ŏ Ė τ P<0.05 ΄Y OI Ң HR ɷPCT ɷNT pro BNP ɷ SOFA Ẇ APACHE Ⅱ ŏ ₸ ɟ 2 ɟ

2 ARDS $\bar{x}\pm s$

Table 2 Comparison of clinical data of patients with ARDS of different severity $\bar{x}\pm s$

	n=39	Ψ n=31	n=26	F e	P e
⇜ Ϥ /min	29.8±4.0	31.5±4.4	31.6±3.8	1.874	0.064
Ϥ L/min	0.6±0.2	0.7±0.4	0.7±0.5	1.067	0.293
OI	118.2±9.9	96.4±7.8	84.3±8.3	19.787	0.000
MAP mmHg	85.3±11.5	84.4±10.9	81.8±11.7	1.470	0.145
CVP cmH_2O	9.3±2.9	8.7±3.1	8.3±3.6	1.526	0.130
HR /min	93.8±7.2	98.3±8.1[a]	113.1±11.4[ab]	10.163	0.000
WBC ×10^9/L	6.7±1.8	7.2±2.0	7.5±2.6	1.838	0.069
Hb g/L	116.8±22.4	113.8±21.9	109.8±24.5	1.522	0.131
ALB g/L	28.8±5.3	27.6±4.6	27.0±5.2	1.669	0.098
PCT ng/mL	5.2±1.7	7.2±1.8[a]	9.6±2.3[ab]	11.104	0.000
NT pro BNP ng/L	1399.5±164.2	2427.8±207.5[a]	4438.6±369.7[ab]	55.514	0.000
SOFA ŏ	7.1±1.7	8.7±1.1[a]	10.1±3.2[ab]	5.688	0.000
APACHE Ⅱ ŏ	15.3±3.6	19.2±4.1[a]	25.2±3.9[ab]	13.251	0.000

Ά [a]P<0.05 Ά Ψ [b]P<0.05 ɟ

2.3 ARDS PCT ɷNT pro BNP Ά APACHE Ⅱ ɷSOFA ŏ Ặ ŏ PCT Ά SOFA r=0.492 P=0.000 Ẇ APACHE Ⅱ r=0.473 P=0.000 ŏ ǧ Ặ NT pro BNP Ά SOFA r=0.416 P=0.000 Ẇ APACHE Ⅱ r=0.485 P=0.000 ŏ ǧ Ặ Ė τ P<0.05 ɟ

2.4 ‴ ~ ARDS PCT ɷNT pro BNP PCT Ң Ь H

NT pro BNP Ηь H Ė
τ P<0.05 ɟ 3 ɟ

3 ARDS PCT NT pro BNP
$\bar{x} \pm s$

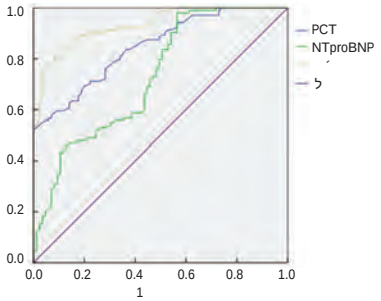
Table 3 Comparison of serum PCT and NT-pro BNP levels in patients with ARDS with different prognosis $\bar{x} \pm s$

ά	n	PCT(ng/mL)	NT pro BNP(ng/L)
	84	6.6±1.9	1576.3±163.5
H	12	10.3±2.8	4722.1±405.2
t e		4.434	26.586
P e		0.001	0.000

2.5 PCT ɞNT pro BNP Ηь ARDS ~

ROC

ROC PCT ɞNT pro BNP ώ Ξ ´ AUC ŏ ά ε 0.847 95% CI 0.795~0.900 ɞ0.729 95% CI 0.657~0.802 ɞ0.932 95% CI 0.899~0.965 PCT ε 6.3 ng/mL ę ε 0.835 ɞ ε 0.759 NT pro BNP ε 2794.5 ng/L ę ε 0.721 ε 0.729 ´ ε 0.913 ε 0.906 ɟ ѧ 1 ɟ



1

1 PCT NT pro BNP ARDS ROC

Figure 1 ROC curve of PCT and NT pro BNP for prognosis diagnosis of ARDS patients

3

ARDS ה Ηь ь ẋ ɞO ὰ Ϗ ɞ ώ Ϗ H O ● Ђ ѵ ɨ ώ ɟ ARDS ה Ά ẫ 'Y Ą ε ė ɞ ė I ה ė ARDS ɾ Ϗ ALI ה [6 7] ɟ ɒ [8] ė ╗ Ηь ARDS ה ה Y Ą ѧ ' ¨H ARDS Ỉ ϧ ɔ ɟ ARDS I Ą ė Ά ώ ~ Ą w ε AR DS ί ɾ ~ Ţ w ˇ ɟ ARDS OI ң HR ѩ MAP ɞCVP ɞѵ Ч ɞ Ό ϧ ɔ ė ε O ѧ ɾ Ϗ O ˬ Ђ ώ Ϗ Ђ ɾ ' ARDS ה ѻ Ϛ Ɗ ɞ Ϛ O O ~ [9] ɟ PCT εm ˉ 116 Y ϖ ę ε ѽ I Ψ PCT ζ C ŏ Ỉ ζ ŏ ɟ ж I Ψ PCTˉ ң ж ğ ὰ Ϗ ɞ ɾ Ψ PCT ╗ ɟ PCT ѧ Ђ I ѧ Ηь O Ė ɾ [10 11] ɟ Ψ PCT ╗ ɟ ɔ PCT Ό ╗ ɟ BNP ŏ ѽ I NT pro BNP ɟ NT pro BNP Ш ' Ə ε ѧ I BNP [12] ɟ NT pro BNP ╗ Ά ♥ Ὼ ╗ ώ ' Ą ARDS ң ɾ ѻ ώ Ό ¨E ♥ Ὼ ɾ ' ң ҷ ѩ ה m ' [13] ɟ NT pro BNP ╗ Ά ARDS ♥ ώ ' ‴ ẫ Ą [14] Ψ ɞ ɞ ğ BNP ϖ ė ж ę ŏ ' ң ɟ [15] IL 6 ɞTNF α ɞỈ ė ' ч ṇ BNP Ą ϖ ė ъ NT pro BNP ѩ ɟ ɔ PCT ɞNT pro BNP Ηь ARDS O ώ ~ Ė ɞ e ' Ə ε ARDS ϧ ɟ

1 Hendrickson CM Matthay MA. Potential Value of Biomarker Signatures in Sepsis and Acute Respiratory Distress Syn

— 4 ϐ ` ƶ ς 9 Ă √ ‾
ϐ E ↄ Z Ш

⋆

ж 4 HE4 ɞ ↄ ɻ I 9 CXCL9 ϑ̆ LN ẇ
˜ ɵ e ɟ ϩ 2016 1 ~2018 1 82 ϛ LN Ə ε ɒ̈ ϩ 80
ϛ SLE ´ LN Ə ε ɟ ɞ Ξ Ả HE4 ɞCXCL9
ↄ Ə ROC ŏ HE4 ɞCXCL9 ɵ e ɟ ᷉ Є Ă 6 Y
˜ 1 ı ה ´ Ï Ө ŏ ε ˜ ‴ Ä ˜ ɟ Ξ Ả
ɞ 6 Y ˜ HE4 ɞCXCL9 Logistic ع ŏ LN ˜ ǐ ɻ ROC ŏ
HE4 ɞCXCL9 ˜ ‴ ɵ e ɟ Ả HE4 ɞCXCL9 Ҥ
P<0.05 ٌΩ٤ ǐ ₀ 9HE4ɞXCL

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⋆ E-mail 15637359221@163.com

CL9 in the study group were higher than those in the control group P<0.05 . The ROC curve analysis showed that the combined AUC of serum HE4 and CXCL9 was 0.773 which was greater than HE4 0.670 and CX CL9 0.613 when the cutoff value of HE4>160.07 U/mL and the cutoff value of CXCL9>218.93 pg/mL the sensitivity was 76.83% and the specificity was 76.25% the serum HE4 and CXCL9 levels were higher than those with good prognosis after 6 months of treatment P<0.05 . Logistic regression analysis showed that SLE DAI score OR=2.820 serum HE4 OR=1.283 and CXCL9 OR=2.141 levels were important factors af fecting the prognosis of LN P<0.05 the ROC curve analysis showed that CXCL9 predicted a poor prognosis AUC of 0.670 after treatment for 6 months which was greater than HE4. 0.667 when the cutoff value was >191.88 the sensitivity was 60.00% and the specificity was 76.12%. Conclusion Serum HE4 and CX CL9 are highly expressed in LN. Combined detection has good diagnostic value and is an important prognostic factor. It can be used as a predictor of poor prognosis.

KEY WORDS Lupus nephritis Chemokine ligand 9 Human epididymis protein 4 Composite renal endpoint

Lupus nephritis LN Ь
Systemic lupus erythematosus SLE
Ύ O ה φ[m] ’ ɞ
ה [1 2] ɟ ώ̈ ί LN
~ ɟ
ɔ ğ ﻩ SLE H Ɗ ɇ Ψ c Ь
Ь J Ӈ [3] ɟ ’ ẇ ~ Ă
ẇ ɞ ɔ ~ Ỹ ɞ ӈ H
Ė τ ɟ Ă ɔ ɇ l 9
CXCL9 Ь ɔ ɇ ɣ ’ ´ ɔ
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[4] ɟ Ɠ Ȯ ɔ
~ ’ ж 4 Human epi
didymal protein 4 HE4 Ả ẹ ˜
╕ [5] ɟ ӂ Ă Ь Ξ ğ LN Ά ~ ɵ
[e] ɯ ï ˚ ɟ ∽ Ь ´ ŏ
HE4 ɶCXCL9 ğ LN ẇ ~ ɵ [e]
ğ ε ί w ƚ ˚ ɟ ; ɟ

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1.1 [m]

ך 2016 1 ~2018 1 82
ɂ LN Ə ε 12 ɂ 70 ɂ
20~63 ҕ 35.31±7.33 ˙
126.30±35.27 mol/L μ 9.22±
2.05 mmol/L ɟ Ɠ ך 80 ɂ
SLE ´ LN Ə ε 11 ɂ
69 ɂ 21~64 ҕ 36.48

Þ ɞ ʁ ɞ eGFR ; ⩾50% ɞã ɛ H ɟ

1.4

ʃ SPSS 24.0 Θ w $\bar{x}\pm s$ t w n % χ^2 Logistic ɾ ŏ LN ˜ ĭ ɛ ROC ŏ HE4 ɞCXCL9 LN ẇ ˜ ɵ e P<0.05 ɛ τ ɟ

2

2.1 Ξ Ấ HE4 ɞCXCL9 Ấ HE4 ɞCXCL9 Ҍ P<0.05 1 ɟ

1 HE4 CXCL9 $\bar{x}\pm s$

Table 1 Comparison of serum HE4 and CXCL9 levels in two groups at admission $\bar{x}\pm s$

ɋ	n	HE4 U/mL	CXCL9 pg/mL
	82	184.35±62.24	234.46±42.09
	80	126.27±58.82	207.11±38.20
t e		6.101	4.328
P e		<0.001	<0.001

2.2 HE4 ɞCXCL9 ɵ e ROC ŏ HE4 ɞCXCL9 ´ AUC ɛ 0.773 Ҍ HE4 0.670 ɞCXCL9 0.613 HE4 e >160.07 U/mL ɞCXCL9 e >218.93 pg/mL ɛ 76.83% ɛ 76.25% ɟ 2 ɟ

2.3 ˝ ˜ m 1 ʒ Ă ɲ ´ Ï Θ 15 ʒ Þ 2 ʒ ã ɛ H ɞ ʒ ɞ ʒ eGFR ; ⩾50% ɟ ˜ ɞ ɋ ɞ Ä ˜ ˝ τ P>0.05 ˜ SLE SLEDAI ŏ ҂ Ҍ ˜ ˝ P<0.05 3 ɟ

3 $\bar{x}\pm s$

Table 3 Comparison of General information of patients with different prognosis $\bar{x}\pm s$

	˜ n=67	˜ ˝ n=15	t/χ^2 e	P e
	35.14±7.06	36.09±6.57	0.477	0.635
	1.60±0.49	1.74±0.61	0.955	0.342
ɋ /	10/57	2/13	0.061	0.805
SLEDAI ŏ ŏ	12.80±2.33	17.16±2.51	6.461	0.001

2.4 ˝ ˜ Ấ ɞ 6 Y ˜ HE4 ɞCXCL9 Ξ Ấ HE4 ɞCXCL9 P>0.05 ˜ ˝ 6 Y ˜ HE4 ɞCXCL9 Ҍ ˜ P<0.05 4 ɟ

2 ROC

Table 2 ROC analysis results

	AUC	95%CI	Z	P e	e	%	%
HE4	0.670	0.588~0.753	4.044	<0.001	>162.08 U/mL	45.12	81.25
CXCL9	0.613	0.526~0.700	2.559	0.011	>221.07 pg/mL	75.61	43.75
Ξ ´	0.773	0.697~0.848	7.092	<0.001	HE4>160.07 U/mL ɞCXCL9>218.93 pg/mL	76.83	76.25

4 6 HE4 CXCL9 $\bar{x}\pm s$

Table 4 Serum HE4 and CXCL9 levels at admission to patients with different prognosis at 6 months after treatment $\bar{x}\pm s$

ɋ	n	HE4 U/mL		CXCL9 pg/mL	
		Ấ	6 Y ˜	Ấ	6 Y ˜
˜ ˝	15	193.39±35.49	137.58±27.25	247.73±38.84	201.85±33.51
˜	67	182.32±31.26	116.19±24.17	231.49±34.77	174.31±28.26
t e		1.210	3.027	1.601	3.297
P e		0.230	0.05	0.113	0.05

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Ψ ĕ H ΫĄ ė Survivin ѡ ę Ά í
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ɔ Ǐ ל 50 ϛ ɟ ӧ ɔ
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Ь 0.00% ۱ ɔ Ǐ ל 0.00% Ė τ P<0.05 ɟ RT PCR
Survivin mRNA ğ Ψ Ь ۱ ɔ Ǐ ל
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Ψ Survivin ѡ mRNA Ỹ ğ P<0.05 ӂ ˁˀ Ψ
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The expression of Survivin in cervical phosphorous carcinoma and its relationship with clinicopathological features

Eerdemutu JIA Yuling⋆ QIN Xiaoling NIU Li rong BAO Ying na YU Zhilong
Department of radiotherapy affiliated hospital of Inner Mongolia medical university Hohhot Mongolia China 010050

ABSTRACT Objective To investigate the expression of Survivin and its relationship with clinicopathological features of cervical phosphorous carcinoma. Methods From August 2012 to August 2019 200 cases of cancer tissue samples from cervical phosphorus cancer patients were collected and 200 cases of paracancerous tissues confirmed by pathological examination as normal cervical tissues were taken as controls. In addition 50 cases of cervical squamous intraepithelial lesions confirmed by pathology after cervical tumor resection were selected. Immunohistochemical staining was used to detect the expression of survivin protein in cervical squamous cell carcinoma tissues paracancerous tissues and cervical squamous intraepithelial lesion.The expression of survivin mRNA in each tissue was detected by PCR. The relationship between the expression of Survivin and the clinicopathological features of cervical phosphorous carcinoma was

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⋆ E-mail iyjbb299278@163.com

1.4 RT PCR ˘ Ψ Survivin mRNA

₱ ˘ TRIzol Ḥ ɔ oy ǎ ˘ Ш ˥ RNA Ő ε cDNA ɟ PCR Ḥ ⋕ ǎ ˘ Ə Ш ɟ w GAPDH ε Ỉ ㄴ ﻍ 2 Ct e ΔΔ ŏ ɟ 1.5 ŏ SPSS 20.00 w n ∕ w $\bar{x} \pm s$ t ₸ ė ŏ w P<0.05 ε τ ɟ

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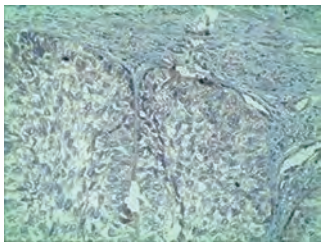
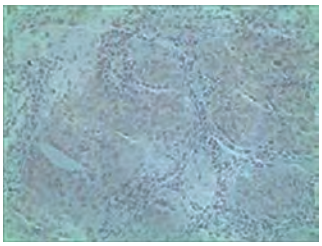
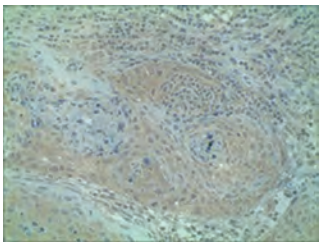
2.1 Survivin ǔ Ψ ẍ ɔ Survivin ǔ ∕ ɔ Ỉ ㄴ Ψ ج ج ε 0.00% Survivin ǔ Ψ ζ Ҥ Ҥь ∕ ∨ ΄Y Survivin ǔ ㄴ ɔ ŏ ﻩ ﻩ Ψ Survivin Ҥь ∕ ɔ Ỉ ㄴ Ė τ P<0.05 ﻩ 1 ɟ , . 3

1 Survivin n % $\bar{x}\pm s$

Table 1 The relationship between the expression of Survivin and clinicopathological characteristics of cervical cancer

n % $\bar{x}\pm s$

	Survivin			Z e	P e	Survivin mRNA	t/F e	P e
	+ n=53	++ n=61	+++ n=86					
				1.531	0.317		0.575	0.472
≤60 n=137	31 22.63	44 32.12	62 45.26			4.39±0.75		
>60 n=63	22 34.92	17 26.98	24 38.10			4.52±0.63		
FIGO ŏ				15.836	0.000		11.209	0.000
Ⅰb~Ⅱa n=13	7 53.85	5 38.46	1 7.69			1.72±0.41		
Ⅱb n=128	37 28.91	40 31.25	51 39.84			2.19±0.32		
Ⅲ n=22	3 13.63	5 22.72	14 63.64			5.18±0.46		
Ⅳ n=6	1 16.67	1 16.67	4 66.67			5.76±0.54		
				8.536	0.000		7.530	0.000
n=31	3 9.68	6 19.35	22 70.97			5.37±0.63		
n=169	50 29.59	55 32.54	64 37.87			3.85±0.76		
ŏ				7.622	0.000		5.268	0.000
ң ŏ ɔ n=72	4 5.56	29 40.28	39 54.17			4.94±0.75		
Ψ ŏ ɔ n=128	49 38.28	32 25.00	47 36.72			3.93±0.82		
				10.709	0.000		6.315	0.000
<1/2 n=134	49 36.57	41 30.60	44 32.84			5.19±0.81		
⩾1/2 n=66	4 6.06	20 30.30	42 63.64			3.39±0.66		

ѡ ѡ Ψ Survivin Ң ۱ ɔ Ỉ ƚ ΎY RT PCR Survivin mRNA ğ̃ Ψ Ң ۱ ɔ Ỉ ƚ Survivin mRNA ۱ ɔ Ỉ ƚ Ψ Ė τ P>0.05 Ψ Survivin ѡ ɟ ж [22] ה Survivin ğ̃ Ψ Ң ɔ Ỉ ƚ ẇ m ɟ ε Ъ m Survivin Ά Ă ɑFIGO ŏ ʁ ŏ ʁ ʁ ŏ ε ˝ ˀ Ж Ъ˘ Ж Ψ Survivin ˝ˀ FIGO ŏ ʁ ŏ ʁ ẇ Ψ Sur vivin ẇ mRNA Ỹ ğ̃ Ж ˝ ˀ Ψ Survivin ẇ mRNA Ỹ Ψ Survivin ѡ ƒ ѡ Ң ~ ۱ م ẇ ˬ ɟ

ά Ω ж [23] Ψ Survivin Ά í ŏ ẇ Ă Ά m ɟ Ⱡ Ψ Survivin Ω ה ˬ ẇ ~ ’ ɟ ɔ Ψ Survivin ѡ ΎY Ά í ŏ ʁ ẇˬ Ă Ң ~ ó ɟ ğ̃ ~ Ψ ʒ w m Survivin Ά ~ Ă w ε Ά wm ƚ ˬ ɟ

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5 Guo L Huang C

◝ ◜ ◞ LP a ÎOPN ÎIRF 4 ʙ ⱽ ˩ ⱨo 。

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DHVD a LP a ɷ OPN ɷ ė 4 IRF 4 ẇ ę í τ ɟ ◝ 120 ɀ DHVD Ə ε ˀ ɾ I 115 ɀ Ə ε ɟ Ξ LP a ɷOPN ɗRF 4 mRNA ŭ DHVD ⱨ ǐ ė ẇ ˘ DHVD ɵ e 3 Y ~ ˝ LP a ɷOPN ɗRF 4 mRNA ẇ ' ŭ LVEF ɷ CI ŭ ˘ ˘ Ά ' Ặ ɟ ㇔ ɷ╥ ㇔ ẇ ɾ I LP a ɷOPN ɗRF 4 mRNA F=47.427 66.514 36.432 τ P<0.05 ợ ɷϒ ´ ɷ ♥ ɷ LP a ɷ OPN ɗRF 4 mRNA DHVD ⱨ ǐ ė P<0.05 ˘ Ψ LP a DHVD ; AUC ε 0.802 e ε 70.00% ε 86.09% 3 Y ~ LP a ɷOPN ɳ Ⱨь ɷ IRF 4 mRNA ẇ LVEF ɷCI Ⱨь ɷ P<0.05 LP a ɷOPN Ά LVEF ɷCI ğ Ặ Ặ IRF 4 mRNA Ά LVEF ɷCI ğ Ặ Ặ τ P<0.05 ɟ DHVD LP a ɷOPN ɗRF 4 mRNA DHVD ⱨ ǐ ė ğ DHVD ẇ Ţ Ė ɵ e ɟ a ė 4 '

Expressions and clinical significance of serum LP a OPN IRF-4 in patients with degenerative heart valve disease

WANG Junhua⋆ CUI Qintao HAN Peili LIU Xiaochen

Department of cardiovascular surgery The First affiliated hospital of xinxiang medical college Weihui Henan China 453100

ABSTRACT Objective To investigate the expression of serum lipoprotein a LP a osteopontin OPN interferon regulatory factor 4 IRF 4 in patients with degenerative heart valve disease DHVD and its clinical significance. Methods 120 patients with DHVD in our hospital were selected as the study group and 115 healthy people who were examined during the same period were used as the control group. The serum LP a OPN IRF 4 mRNA levels were compared between the two groups. The influencing factors of the incidence of DHVD and the diagnostic value of serum indicators for DHVD were analyzed. The levels of serum LP a OPN IRF 4 mRNA and cardiac function indexes left ventricular ejection fraction LVEF cardiac index CI of patients with different therapeutic effects after 3 months of treatment were compared. The correlation between serum indexes and cardiac function indexes was evaluated. Results The serum LP a OPN IRF 4 mRNA levels have significant difference in the patients with multi valvular disease and with single valvular disease and healthy people F=47.427 66.514 36.432 P<0.05 . Coronary heart disease smoking

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⋆ E-mail doctorjh1981@163.com

history high blood pressure serum LP a OPN and IRF 4 mRNA are important influencing factors for the onset of DHVD P<0.05 . Coronary heart disease smoking history hypertension serum LP a OPN IRF 4 mRNA are important influencing factors of DHVD P<0.05 . Among the various serum indexes the area under the curve AUC for diagnosis of DHVD by LP a is the largest 0.802 the sensitivity of the cutoff value is 70.00% and the specificity is 86.09%. After the treatment for 3 months the serum LP a and OPN levels of the effective patients were lower than those of the effective and ineffective patients and the IRF 4 mRNA levels and LVEF CI were higher than those of the effective and ineffective P<0.05 . The serum LP a and OPN had negative correlation with LVEF and CI. Intersetingly theIRF 4 mRNA had positive correlation with LVEF and CI P<0.05 . Conclusion The abnormal expression of serum LP a OPN and IRF 4 mRNA in DHVD patients is an important influencing factor of DHVD and has high application value in the diagnosis and evaluation of DHVD.

KEY WORDS Degenerative heart valve disease Lipoprotein a Osteopontin Interferon regulatory factor 4 Cardiac function Diagnosis

Degenerative heart valvu lar disease DHVD ε í ה ж Ὼ в в ⊦ ∤ Ɑ ė φm [1 2] ɟ ὤ í DHVD ζ ẇ ' Є ẇ ė ' [3] ɟ ė ẇ ẇ ė ' ƙ ɔ ẇ د ẇ ~ Ė ĭ [4 5] ɟ Ὸ a Lipoprotein a LP a в Osteopontin OPN в ė 4 Interferon regulatory fac tor 4 IRF 4 ƙ Ά ה ה ė Ė ̇ Θ [6 8] ɟ ↛ Ⱨ ŏ DHVD LP a ɞOPN ɞIRF 4 ẇ í τ ǔ ε í DHVD w ƙ ˝ ɟ

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ɳ 2016 1 2018 12 120 ɮ DHVD Θ ε ɒ ɳ̌ ⊀ ∣ 115 ɮ Θ ε ɟ Ξ ǔ ǫ̈ в ɞ в ı в ƙ Ỹ τ P>0.05 Ė ' ɟ Ấ Ấ ① ̈ ´ DHVD Ấ [9] ② ' ③ P ④ í ⑤ ̈ ̌ Ш ɟ ⑥ Ⱨ ∤ Ж ɟ Ấ ① ② 3 ∤ Ǐ ´ ③ ④ ⑤Ẉ ה ⑥´ ė ђ O ⑦ ´ ⑧ Ⱪ ɟ

1.2

1.2.1

Ξ 5 mL ė Ψ 3 mL w 3 000 r/min 10 min ɳ Ⱨ-80 ȧ ӧ LP a ӧ ∤ OPN 2 mL Trizol m ɳ RNA w ´ א IRF 4 mRNA ɟ

1.2.2

̈ Є Ὴ вά Ὴ в ئ 3 Y ~ Ţ Ţ Ấ [10] Ὼ Ἔ в ↛ Ἄ g ה ' د 1 w ɔ Ὼ ' د 1 w ɔ Ấ ɟ 120 ɮ DHVD 3 Y ~ 38 ɮ 60 ɮ 22 ɮ ɟ

1.2.3

① Ξ Ấ LP a ɞOPN ɞIRF 4 mRNA ɟ ②DHVD ה ĭ ė ɟ ③ ŏ LP a ɞOPN ɞIRF 4 mRNA DHVD ɵ e ɟ ④ ˝ ̌ ὤ в 3 Y ~ LP a в OPN ɞIRF 4 mRNA ɟ ⑤ ˝ ̌ ὤ в 3 Y ~ ' Ƀ ŏ Left ventricular ejection fraction LVEF в Cardiac index CI ɟ ⑥ ŏ LP a ɞOPN в IRF 4 Ά LVEF ɞCI Ă ɟ

1.3

SPSS 22.0 Θ ŏ w n

% χ^2 w $x \pm s$ ɞΞ

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Logistic ẹ ٤ ŏ Pearson

Ặ ŏ ɔ Θ Receiver oper

ating characteristic ROC ŏ ɵ e w

P<0.05 ε τ ɟ

x ŭ ﹎ ќ 1 ḡ r/ g ¯ ⅂ ﻟ ŧ ғ ﺧ

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4 ROC

Table 4 ROC analysis results

	AUC	95%CI	Z e	P e	e	e	%	e	%
LP a	0.802	0.745~0.851	10.239	<0.001	>52.57 mg/dL	70.00		86.09	
OPN	0.750	0.689~0.804	7.902	<0.001	>59.32 g/L μ	57.50		83.48	
IRF 4 mRNA	0.758	0.699~0.812	8.295	<0.001	≤0.82	76.67		65.22	

5 LP a OPN IRF 4 mRNA $\bar{x} \pm s$

Table 5 Comparison of serum Lp a OPN and IRF 4 mRNA levels in patients with different therapeutic effects $\bar{x} \pm s$

	ΰ	n	ώ	3 Y ˜
LP a mg/dL		38	56.91±16.22	42.10±7.05
		60	58.76±18.93	49.13±8.26
		22	60.05±20.01	54.39±11.87
	F e		0.226	15.220
	P e		0.798	<0.001
OPN g/L μ		38	61.84±19.06	40.72±7.27
		60	63.27±20.85	48.01±8.15
		22	63.99±21.28	58.84±11.09
	F e		0.092	31.731
	P e		0.912	<0.001
IRF 4 mRNA		38	0.78±0.07	0.83±0.04
		60	0.77±0.06	0.80±0.03
		22	0.75±0.05	0.77±0.02
	F e		1.648	25.242
LVEF %		38	30.24±3.18	38.40±3.14
		60	30.86±3.30	35.64±2.76
		22	31.01±3.74	33.29±2.28
	F e		0.522	24.542
	P e		0.595	<0.001
CI		38	2.43±0.15	2.65±0.12
L/ min·m²		60	2.45±0.14	2.56±0.09
		22	2.46±0.16	2.48±0.06
	F e		0.347	22.922
	P e		0.708	<0.001

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ɥ [12] ɟ IRF ɔ̃ ė Ė

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IRF 4 ¨E l ӧ ɥ ɥ ɷ

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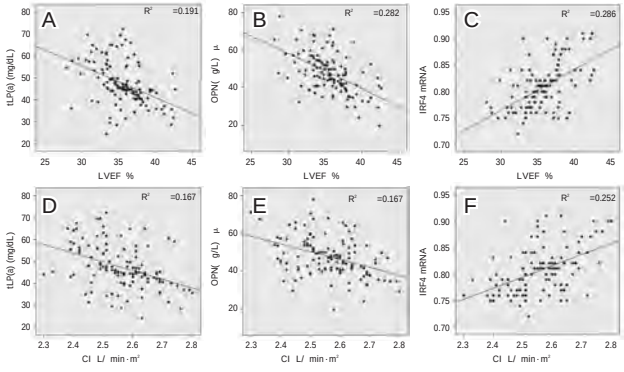
Logistic ɾ ŏ ה LP a ɷOPN ɷIRF 4 mRNA DHVD ה Ї ė ẅ ŏ



A ε LP a Ά LVEF Ą B ε OPN Ά LVEF Ą C ε IRF 4 mRNA Ά LVEF Ą D ε LP a Ά CI Ą E ε OPN Ά CI Ą F ε IRF 4 mRNA Ά CI Ą

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Figure 1 Serum indexes were correlated with cardiac function

DHVD LP a ɷOPN ɷIRF 4 mRNA DHVD ה Ї ė ɟ Ύ ה ơ ɷϒ ´ ɷ ♥ ɕ ε DHVD ה Ї ė ė ה ơ ɷ ♥ ẇ ϒ ´ DHVD ẇ ɯ ɔ Ӓ ɟ ɔ̃ Ъ ɔ m ROC ŏ ˘ DHVD ɵ e 3 ´ Ъ ɔ DHVD ӂ ę ´ Ė l ɵ e ˜ m ɟ DHVD 3 Y ˜ ˝ LP a ɷOPN ɷIRF 4 mRNA ẇ LVEF ɷCI ɡ̈ m Pearson Ą ŏ ה LP a ɷOPN Ά LVEF ɷCI ɡ̈ Ą Ą IRF 4 mRNA Ά LVEF ɷCI ɡ̈ Ą Ą ' LP a ɷOPN ɷ IRF 4 mRNA ˝ c ' Ə ε DHVD ɷ Ţ ˀ Ά ˜ ' Ė Ύ Ą ę ƙ ɔ Ъ ' ƙ Ў í ẇ Ė Ə ġ Ъ ɔ ẇ ˜ ɟ

LBP ÎHSP70 ÎDcR3 ﻣﻣﻣ ٦ ٧ ٧ ⇔ ! A ٦ ٧ . Z Ш

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´ LBP ɵ Ь ẋ 70 HSP70 ɵ ɔ ǀ 3 DcR3 ٧ ٦ ´ ARDS ɵ e ɟ ٦ 2017 5 2019 5 92 ʒ ARDS Ə ε 30 d ~ Ÿ ٦ 64 ʒ ε ẵ ẹ H 28 ʒ ε H ɟ ŭ Ξ LBP ɗHSP70 ɗDcR3 ɵ ɔ Ţ SOFA ŭ ɵ Ά ɾ Ⅱ APACHEⅡ ŭ ẇ Ą ę ~ ~ ɵ e ɟ H Ấ ɗẤ 7 LBP ɗDcR3 Ң HSP70 ң Ң SOFA ɗAPACHE Ⅱ ŭ Ң P< 0.05 ΄Y Ấ Ά Ấ 7 e Ң H P<0.05 LBP ɗDcR3 Ά SOFA ɵ APACHE Ⅱ ŭ ٧ Ą HSP70 Ά SOFA ɗAPACHE Ⅱ ŭ ٧ Ą P<0.05 Ấ 7 HSP70 AUC 0.830 > Ấ 7 LBP 0.806 > Ấ 7 DcR3 0.766 LBP ɗHSP70 ɗDcR3 ● ɵң ● τ P<0.05 ɟ LBP ɗHSP70 ɗDcR3 Ά ARDS O ΄Y Ą ε Ţ ARDS ~ ζ ẹ ɟ ٧ ٦ ´ ´ Ь ẋ 70 ɔ ǀ 3 ROC Ҡ

The value of serum LBP HSP70 DcR3 levels in predicting the outcome of patients with acute respiratory distress syndrome

MA Lingling[1]★ YANG Qiuwei[2] KONG Bianduo[1]

1. Department of respiratory medicine luoyang first people s hospital luoyang Henan China 471000
2. Department of endocrinology luoyang first people s hospital luoyang Henan China 471000

ABSTRACT Objective To investigate the value of serum lipopolysaccharide binding protein LBP heat shock protein 70 HSP70 and trap receptor 3 DcR3 levels in predicting the outcome of patients with acute respiratory distress syndrome ARDS . Methods 92 patients with ARDS admitted to our hospital from May 2017 to May 2019 were recruited as the research object. According to the prognosis of 30 days 64 surviving patients were selected as the survival group and 28 patients with all cause death were the death group. The serum levels of LBP HSP70 DcR3 sequential organ failure assessment sofa acute physiology and chronic health Ⅱ APACHE Ⅱ were compared between the two groups. Results The serum LBP and DcR3 levels were higher in the death group on the day of admission and the 7th day after admission than those in the survival group. HSP70 level was lower than that in the survival group. SOFA and APACHE II scores were higher than in the survival group P<0.05 . The difference inthe survival group and the seventh day after admission was significant compared to the death group P<0.05 . The Serum LBP and DcR3 levels were positively correlated with SOFA and APACHE Ⅱ scores and HSP70 was negatively corre

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★ E-mail 18623753239@163.com

lated with SOFA and APACHE Ⅱ scores P<0.05 . Seventh day after admission HSP70 AUC 0.830 > LBP 0.806 >DcR3 0.766 . There were significant differences in the survival curves of serum LBP HSP70 and DcR3 between the high risk groups and the low risk groups P<0.05 . Conclusion Serum LBP HSP70 and DcR3 levels are closely related to the severity of ARDS patients and are expected to be the main predictors of ARDS prognosis.

KEY WORDS Acute respiratory distress syndrome Lipopolysaccharide binding protein Heat shock protein 70 Trap receptor 3 ROC Lung injury

ﻯ Ⴙ ´ Acute respiratory distress syndrome ARDS Ė ɞ ARDS 35.0%~46.0%[1] ɟ א ɞɛ̈ H ğ̈ ARDS ה ΆΨ Ά Θ[2] ɟ̌ ´ Lipopolysacchoride Binding Protein LBP Toll ɔ l 4 Toll like receptor TLR 4 ɱ ˝ ה ɱ ˝[3] ɟ Ь ẋ 70 Heat shock proteins 70 HSP70 ΆΨ Ά ɲ ė ’ ɞ̈E Ⴙ ɞ l Θ ɟ ɔ l 3 Decoy receptor3 DcR3 Θ ε ~ ẍ ė ה ɞẍ א Θ ɞ ẍ [4] ɟ ж́ í Ά Ь LBP ɞHSP70 ɞ DcR3 ARDS ~ ɵ e ɟ Ь ğ̈ ę ARDS ~ ɵ e ɟ Ė l ŏ ; ɟ

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ך 2017 5 2019 5 92 ϛ ARDS Θ ε 30 d ~ Ỹ ך 64 ϛ ε ã̃ ė H 28 ϛ ε H ɟ Ξ ɲ P>0.05 ę ’ ẇ ę ’ Ш ɟ ├ Ң ﻯ Ж Ά ɟ

1.2 ך Ά

Ấ Ά ① ´ ARDS Ά Ά[5] ② ę X Ң ה א Ό ③ ´ ≤200 mmHg ④ ♥ ≤18 mmHg ⑤ í ⑥ ẇ ’ Ш ɟ Ά ① ğ̈ ẍ Ά Ң ƒ ´ ② ƀ ƀ Ⴝ ③ ④ ε ɟ

1.3

ך 3 mL 12 min 3 000 r/min ŏ ך ẍ Ⴙ DcR3 ɞHSP70 ɞLBP Ң ɔ ă̆ ˘ ę O Ң Ш Θ ɟ

1.4

① Ξ LBP ɞHSP70 ɞDcR3 ɞ SOFA ɞAPACHE Ⅱ ŏ ɟ ę Ψ SOFA ŏ ъ ﻯ Ⴙ ɞH ɞ ɞ ɞ ɞ 6 Y Ţ Y 1~4 ŏ ŏ ~ APACHE Ⅱ ŏ ŏ 71 ŏ >17 ŏ ε ŏ O ɟ ② ŏ LBP ɞHSP70 ɞDcR3 Ά SOFA ɞAPACHE Ⅱ ŏ Ά ɟ ③ ŏ ARDS ~ • ė ɟ ④ ŏ LBP ɞHSP70 ɞDcR3 ARDS ~ ɵ e ɟ ⑤ ŏ LBP ɞHSP70 ɞDcR3 • ɞң • ɟ

1.5

SPSS 22.0 Θ ŏ $\bar{x} \pm s$ Ξ t n % χ^2 Logistic ė ع ŏ Pearson Ά ŏ ROC ~ ɵ e w ▌ å̊ Kaplan Meier KM ŏ Log Rank P<0.05 τ ɟ

2

2.1 Ξ ɲ

Ξ ɲ Ψ ά ɞ ɞBMI τ P>0.05 ɟ 1 ɟ

2.2 Ξ LBP ɞHSP70 ɞDcR3

H Ấ ɞẤ 7 LBP ɞDcR3 Ь HSP70 ң Ь P<0.05 ΄Y Ấ Ά Ấ 7 e Ь H Ė τ P<0.05 2 ɟ

1 n %

Table 1 Comparison of 2 groups of general data n %

m		n=64	H n=28	t/χ^2 e	P e
ά /		35/29	16/12	0.048	0.827
		60.70±7.09	60.28±7.27	0.260	0.796
BMI	kg/m²	20.92±1.86	21.14±2.05	0.506	0.614
Ɗ ก					
		53 82.81	23 82.14	0.049	0.825
ά Ҡ		5 7.81	2 7.14	0.100	0.752
		3 4.69	2 7.14	0.001	0.983
		3 4.69	1 3.57	0.097	0.754
Ɗ	ng/mL	7.40±1.08	6.83±1.86	1.847	0.068
Ϟ	´	40/24	16/12	3.058	0.080

2 LBP HSP70 DcR3 $\bar{x}\pm s$

Table 2 Comparison of serum LBP HSP70 and DcR3 levels between 2 groups $\bar{x}\pm s$

ά		n	LBP g/mL μ	HSP70 g/L	DcR3 μ ng/mL
Ấ	H	28	121.90±32.27	1.02±0.31	3.16±0.62
		64	93.37±29.06	1.33±0.34	2.59±0.58
	t e		4.189	4.130	4.247
	P e		<0.001	<0.001	<0.001
Ấ 7	H	28	102.05±34.00	1.17±0.42	3.04±1.01
		64	67.44±22.46	1.85±0.69	1.83±0.60
	t e		5.774	4.829	7.149
	P e		<0.001	<0.001	<0.001
Ấ Ά Ấ 7 e	H	28	19.85±3.23	0.15±0.06	0.12±0.04
		64	25.93±5.10	0.52±0.21	0.76±0.25
	t e		5.809	9.136	13.431
	P e		<0.001	<0.001	<0.001

2.3 Ξ SOFA ɵAPACHE Ⅱ ŏ H Ấ ɵẤ 7 SOFA ɵAPACHE Ⅱ ŏ Ҍ P<0.05 ΄Y Ấ Ά Ấ 7 e Ҍ H Ė τ P<0.05 3 ɟ

2.4 LBP ɵHSP70 ɵDcR3 Ά SOFA ɵ APACHE Ⅱ ŏ Ặ Pearson Ặ ŏ LBP ɵDcR3 Ά SOFA ɵAPACHE Ⅱ ŏ ∖ Ặ HSP70 Ά SOFA ɵAPACHE Ⅱ ŏ ∖ Ặ P<0.05 4 ɟ

4 LBP HSP70 DcR3 SOFA APACHE Ⅱ

Table 4 Correlation of serum LBP HSP70 DcR3 levels with sofa and Apache Ⅱ scores

ŏ	LBP		HSP70		DcR3	
	r e	P e	r e	P e	r e	P e
SOFA ŏ						
Ấ	0.471	<0.001	0.446	<0.001	0.486	<0.001
Ấ 7	0.583	<0.001	-0.529	<0.001	0.537	<0.001
APACHE Ⅱ ŏ						
Ấ	0.503	<0.001	-0.512	<0.001	0.611	<0.001
Ấ 7	0.621	<0.001	-0.635	<0.001	0.702	<0.001

2.5 ARDS ~ ĭ ė w ARDS ~ Ə ε ė Ь w Ấ ´ MODS ɵẤ ก Ь ẋ ɵ LBP ɵHSP70 ɵ DcR3 ɵSOFA ɵAPACHE Ⅱ ŏ Ə ε Ь Ấ Logistic ع ŏ ی Ấ ´ MODS ɵẤ ก Ь ẋ ɵ LBP ɵHSP70 ɵ DcR3 ɵSOFA ɵAPACHE Ⅱ ŏ ARDS ~ ĭ ė P<0.05 5 ɟ

2.6 LBP ɵHSP70 ɵDcR3 ARDS ~ ɵ e ROC ŏ Ấ ɵẤ 7 LBP ɵHSP70 ɵDcR3 ARDS ~ ۍ Ė m ɵ e Ấ 7 HSP70 AUC 0.830 > Ấ 7 LBP 0.806 > Ấ 7 DcR3 0.766 ɟ 6 ɵ๖ 1 ɟ

3 SOFA APACHE Ⅱ $\bar{x}\pm s$

Table 3 Comparison of sofa and Apache Ⅱ scores between 2 groups $\bar{x}\pm s$

ά	n	SOFA ŏ ŏ			APACHE Ⅱ ŏ ŏ		
		Ấ	Ấ 7	e	Ấ	Ấ 7	e
H	28	8.69±1.41	8.03±2.67	0.66±0.23	18.10±1.73	17.06±4.75	1.04±0.96
	64	7.37±1.35	5.39±1.80	1.98±0.30	16.96±1.40	12.34±3.22	4.62±1.13
t e		4.258	5.550	20.744	3.340	5.562	14.605
P e		<0.001	<0.001	<0.001	0.001	<0.001	<0.001

5 ARDS

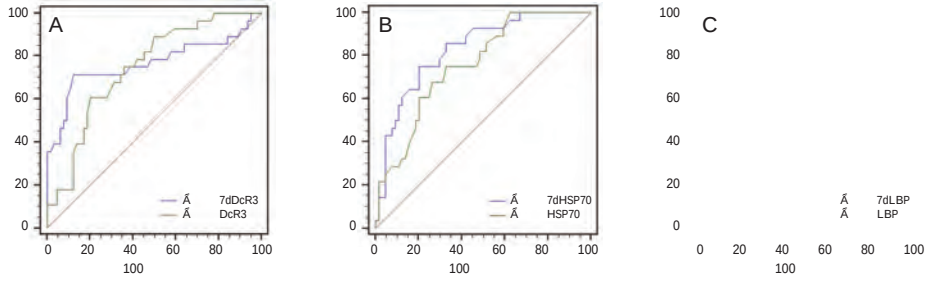
Table 5 Prognostic factors of death in patients with ARDS

Ь	β e	SE e	Wald/χ^2 e	OR e	95%CI e	P e
Ấ ´ MODS	1.553	0.420	13.670	4.725	2.711~8.235	<0.001
Ấ ח ь ẋ	1.426	0.517	7.605	7.105	2.437~7.105	<0.001
LBP	0.990	0.381	6.749	5.063	1.430~5.063	<0.001
HSP70	-0.615	0.273	5.082	0.907	0.322~0.907	0.013
DcR3	1.282	0.409	9.831	6.004	2.165~6.004	<0.001
SOFA ŭ	1.180	0.426	7.666	5.179	2.043~5.179	<0.001
APACHE Ⅱ ŭ	0.973	0.312	9.723	4.081	1.715~4.081	<0.001

6 ROC

Table 6 ROC analysis results

	AUC	95%CI e	Z	e	e %	e %	P e
Ấ LBP	0.686	0.581~0.779	3.281	>100.30	78.57	59.38	0.001
Ấ HSP70	0.760	0.659~0.843	0.843	⩽1.29	75.00	67.19	<0.001
Ấ DcR3	0.744	0.643~0.830	4.616	>3.02	60.71	79.69	<0.001
Ấ 7 LBP	0.806	0.710~0.881	5.379	>92.28	67.86	90.62	<0.001
Ấ 7 HSP70	0.830	0.737~0.900	7.413	⩽1.45	75.00	79.69	<0.001
Ấ 7 DcR3	0.766	0.667~0.848	4.095	>2.46	71.43	87.50	<0.001



A ε DcR3 ARDS ˜ ROC B ε HSP70 ARDS ˜ C ε LBP ARDS ROC

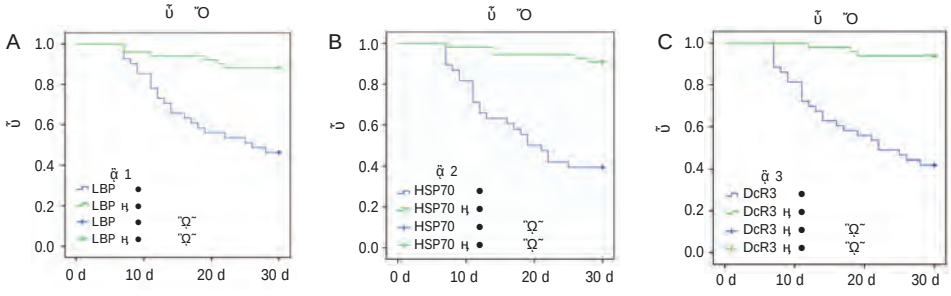
1 ROC

Figure 1 ROC curve

2.7 ŭ LBP ɑHSP70 ɑDcR3 ● ɑн ●

e =ł 0 Ńɷ H =ł 1 Ńɻ w ROC ȳ τ χ^2_1=19.438 χ^2_2=31.134 χ^2_3=

e ŭ ε н ● ɑ ● KM ŭ 30.894 P<0.001 ь 2 ɻ



A ε LBP B ε HSP70 C ε DcR3

2 LBP HSP70 DcR3

Figure 2 Survival curve LBP ɑHSP70 ɑDcR3

3

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Detection characteristics and epidemiological trend analysis of different pathogenic antigens and IgM antibodies in children with severe pneumonia

TAO Shan⋆
Department of Special Needs Xiamen Children s Hospital Xiamen Fujian China 361006

ABSTRACT Objective To explore the detection characteristics and epidemic trend of IgM antibody anti different pathogens in children with severe pneumonia. Methods A total of 308 children with severe pneumonia admitted to Xiamen Children s Hospital from January 2017 to December 2019 were collected. Mycoplasma pneumoniae MP Chlamydia pneumoniae CP respiratory syncytial virus RSV and Virus ADV parainfluenza virus type 1 PIV1 parainfluenza virus type 2 PIV2 parainfluenza virus type 3 PIV3 influenza A virus FA influenza B virus FB Kosa Detection of multiple pathogenic

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⋆ E-mail mubanpe27204@163.com

antigens such as parvovirus B COXB antigens and IgM antibodies were detected by immunofluorescence. According to the climatic characteristics of Xiamen the average temperature classification method is used to divide spring March to April summer May to September autumn 10 to November and winter 12 to February seasonal distribution characteristics of MP ADV and RSV infections were observed. The children with severe pneumonia and their complications were investigated. Results ① The positive rate of pathogenic IgM antibodies in 308 children with severe pneumonia was 58.77% 181/308 amongwhich MP infection accounted for the highest proportion followed by ADV and RSV infection and others included PIV3 FA COXB FB PIV1. The single infection rate was 41.56% 128/308 the double infection rate was 13.96% 43/308 and the multiple infection rate was 3.25% 10/308 . ② Among MP infections the infection rate is the highest between 3 and 7 years old preschool age which is significantly higher than <1 year infancy and 1 to 3 years infancy the difference is statistically significant P <0.05 infants with RSV infection Period and early childhood are significantly higher than preschool age the difference is statistically significant P<0.05 . ADV infection in middle school and early childhood is significantly higher than infancy the difference is statistically significant P<0.05 . ③ The infection rates of MP and ADV in male and female children were not statistically significant P>0.05 . The RSV infection rates in male children were significantly higher than that in females and the difference was statistically significant P<0.05 . ④ MP infection is the highest in summer ADV infection is higher in spring and summer and RSV infection is the highest in summer. ⑤ Children with MP infection have higher rates of respiratory failure and myocardial damage complications. Various complications of children with ADV and RSV infection are also frequent. Children with multiple infections have complications such as respiratory failure pleural effusion myocardial damage and abnormal liver function significantly higher than that of a single pathogen P<0.05 . Conclusion The pathogens detected in children with severe pneumonia in our hospital are mainly MP ADV and RSV infections and the risk of double infection is high. Summer is the high risk season for MP ADV and RSV infection. MP ADV sRSV [illegible] this read [illegible] and our # 0y k v wc ȝ sc γ ɔ γ pc ᵀ` ᵡ˙ ȳ ȝ̈ iMP

Respiratory syncytial virus pneumonia RSV ɞ
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fluenza virus type 2 PIV2 ɞ̀E 3 ی
Parainfluenza virus type 3 PIV3 ɞ ی
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FB ɞ B ی Coxsackie b virus COXB
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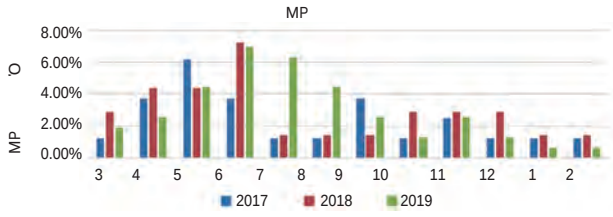
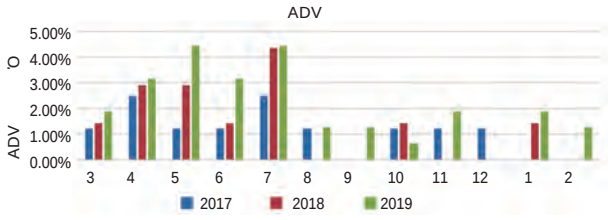


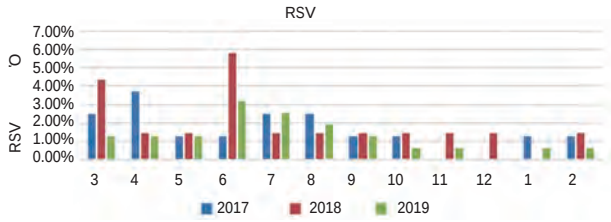
1 MP

Figure 1 Severe pneumonia MP infection in different seasons



2 ADV

Figure 2 Severe Pneumonia ADV Infection in Different Season



3 RSV

Figure 3 Severe pneumonia RSV infection in different seasons

2.5 ▪ ▪ ▪

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SAA ɑsTREM 1 Ă ~ 1 ɑ8 ɑ6 ɑ7 d SAA ɑsTREM 1 ɑCRP/ PAB

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levels of SAA sTREM 1 and CRP/PAB in patients with severe infection and mild infection were compared and the relationship between the three and the degree of infection was analyzed. Results The serum SAA sTREM 1 CRP/PAB ratio reached a peak at 3 days postoperatively in the infected group and was higher than the uninfected group at 3 5 7 days postoperatively P<0.05 serum SAA was positively correlated with sTREM 1 and CRP/PAB ratio at the third days after surgery and sTREM 1 was positively correlated with CRP/PAB ratio P<0.01 the area under the ROC curve of serum SAA sTREM 1 CRP/PAB combined diagnosis of pulmonary infection after surgery was 0.876 serum SAA sTREM 1 and CRP/PAB ratios in patients with severe infection were higher than those in patients with mild infection at the third day after surgery P<0.05 serum SAA sTREM 1 and CRP/PAB ratios were positively correlated with the degree of infection P<0.05 . Conclusion The level of serum SAA sTREM 1 and the ratio of CRP/PAB were increased in SP patients with pulmonary infection after upper abdominal general anesthesia and it is closely related to the severity of infection and has a high diagnostic value in postoperative pulmonary infections which can provide theoretical basis for clinical diagnosis and disease evaluation.

KEY WORDS Amyloid A C reactive protein Prealbumin Schizophrenia Pulmonary infection

ŏ Schizophrenia SP ε ´ SP ╗ [1] ɟ ~ ɞ ɔ ã ~ ה SP ~ ה ה ę ђ ~ ζ ● ė φ[m] J ў ї [2] ɟ ^ ⁄ α_2 ɔ ɔ I Ḥ ң SP ~ ה ɞ Ҡ Ė Ə ж ѽ щ ï ~ Ӑ [3] ɟ A Serum amyloid A SAA ɞ’ ה ɔ I 1 Soluble triggering receptor expressed on my eloid cells 1 sTREM 1 Ţ א ˙ ė ğ ɞ Ψ [4 5] Ă C א C reactive pro tein CRP Ά ѽ Prealbumin PAB [e] Ά Ă ˙Y [6] ɟ ↗ Ҥ SAA ɷsTREM 1 ɞ CRP/ PAB [e] ğ Ψ è ę ğ SP ã ~ ƙ ɔ Ẇ í ɵ [e] ğ ε í ɔ Ӑ w ˅ ɟ

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ך 2016 7 2019 7 ã ; ɔ SP 82 ϗ Ə ε ~ ı ה ŏ ε 21 ϗ ɞ 61 ϗ Ɠ ˀ ɾ I 80 ϗ Ə ε ɾ ę Ψ 45 ϗ 35 ϗ 31~61 ҕ 46.01±5.77 I 18~21 kg/m^2 ҕ 20.96±0.91 kg/m^2 ɟ ´ SP ĥA [7] Ấ ĥA ①ã ; ɔ ② ´ ③ Ẇ ҕ ˀ Ш ɟ ĥA ① ѽ ğ ② ğ ӧ ③ ¥ O ˙ ɞ ɔ ɞ ɟ ├ Ң ӌ Ҝ ĥA ɟ

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Ấ 6~8 mL/kg ŧ ҁ ├ oy ắ ˘ Bene View T 8 ˙ Ѧ ⁄ I ѧ Aspect ắ ˘ A 2000xp Ѧ Ѫ Bispec tral index BIS ɟ ѽ 10 min 1.0 g/ μ kg ^ ⁄ ˝ H 12070534 ├ oy ˘ 0.4 g · kg^{-1}μh^{-1} 0.05 mg/kg ⁄ U ɔ ɷ3~5 g/kg μ ɷ1.5~2.5 mg/kg Γ ɷ0.15 mg/kg 8~10 mL/kg 1~2 L/min Ч ⁄ 1Б 2 10~15 / min $P_{ET}CO_2$ 35~40 mmHg Ч ´ 2~6 mg · kg^{-1} · h^{-1} Γ ɷ0.1~0.3 g · kg^{-1}μh^{-1} Ч Ấ [v] ⁄ 1%~3% 0.1 mg · kg^{-1} · h^{-1} ɷ ɷГ BIS 40~55 ɟ

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① Ξ ~ 1 ɞ3 ɞ5 ɞ7 d ɞ SAA ɞ sTREM 1 ɞCRP/PAB e ɟ ② ŏ ~ 3 d SAA ɞsTREM 1 ɞCRP/PAB e Ἇ ɟ ③ ŏ ~ 3 d SAA ɞsTREM 1 ɞCRP/ PAB e ɵ e ɟ ④ ˝ˀ SAA ɞsTREM 1 ɞCRP/PAB e ɟ ᾼA ᾠ Ь ẋ ´ m w ɔ ε ɟ ⑤ ŏ SAA ɞ sTREM 1 ɞCRP/PAB e Ά Ἇ ɟ 1.4

SPSS 22.0 Θ ŏ w n % χ^2 w $\bar{x}\pm s$ Ξ t Pearson Ἇ ŏ ~ 3 d SAA ɞsTREM 1 ɞCRP/ PAB e ɞ Ἇ P<0.05 ε τ ɟ

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1 n % $\bar{x}\pm s$

Table 1 Comparison of basic in 2 groups n % $\bar{x}\pm s$

		n=21	n=61	χ^2/t e	P e
		40.31±5.33	41.10±5.16	0.600	0.550
ᾳ	/	12/9	34/27	0.013	0.911
	ᾐ			0.010	0.919
ɞ		13 61.90	37 60.66		
		8 38.10	24 39.34		
I kg/m²		21.46±1.33	20.96±1.22	1.583	0.117
	h	2.49±0.46	2.53±0.50	0.322	0.748
	min	133.12±31.64	129.87±29.55	0.427	0.671

2.2 Ξ ~ SAA ɞsTREM 1 ɞCRP/PAB e Ξ ~ 1 d SAA ɞsTREM 1 ɞCRP/PAB e τ P>0.05 ~ 3 d SAA ɞsTREM 1 ɞCRP/ PAB e ᾳ ΄Y ~ 3 ɞ5 ɞ7 d Ь P<0.05 2 ɟ

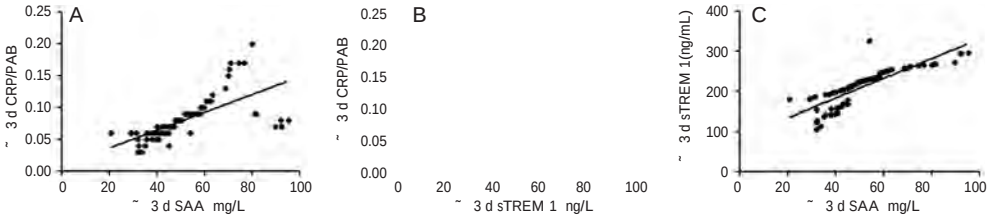
2 SAA sTREM 1 CRP/PAB $\bar{x}\pm s$

Table 2 Serum SAA sTREM 1 and CRP/ PAB ratios $\bar{x}\pm s$

	ᾳ	n	~ 1 d	~ 3 d	~ 5 d	~ 7 d
SAA mg/L		21	35.42±6.28	64.11±21.37	51.04±15.24	40.78±10.07
		61	37.27±8.41	40.06±13.30	24.07±7.69	13.71±4.10
	t e		0.922	5.899	10.533	17.366
	P e		0.359	<0.001	<0.001	<0.001
sTREM 1 ng/mL		21	206.29±57.41	267.53±60.04	218.49±50.71	170.56±41.25
		61	202.44±52.09	210.14±53.30	174.06±38.46	132.02±29.14
	t e		0.285	4.120	4.195	4.674
	P e		0.777	<0.001	<0.001	<0.001
CRP/PAB e		21	0.10±0.04	0.30±0.10	0.23±0.07	0.15±0.04
		61	0.09±0.03	0.12±0.04	0.07±0.02	0.04±0.01
	t e		1.206	11.696	16.194	19.949
	P e		0.232	<0.001	<0.001	<0.001

2.3 ~ 3 d SAA ɞsTREM 1 ɞCRP/PAB e Ἇ Pearson Ἇ ~ 3 d SAA r_1=0.845 r_2=0.671 Ά sTREM 1 ɞCRP/PAB e \ Ἇ sTREM 1 r=0.784 Ά CRP/PAB e \ Ἇ P< 0.01 ѣ 1 ɟ

2.4 ~ 3 d SAA ɞsTREM 1 ɞCRP/PAB e ɵ e SAA ɞsTREM 1 ɞCRP/PAB ´ ~ AUC e ε 0.876 Ь SAA0.768 ɞ sTREM 1 0.701 ɞCRP/PAB 0.786 P<0.01 3 ɞ ѣ 2 ɟ



A ε SAA Ά CRP/PAB Ą B ε sTREM 1 Ά CRP/PAB Ą C ε SAA Ά sTREM 1 Ą

1 ˜ 3 d SAA ɷsTREM 1 ɷCRP/PAB e Ą

Figure 1 Correlation between serum SAA sTREM 1 and CRP/PAB ratios at 3 days after surgery

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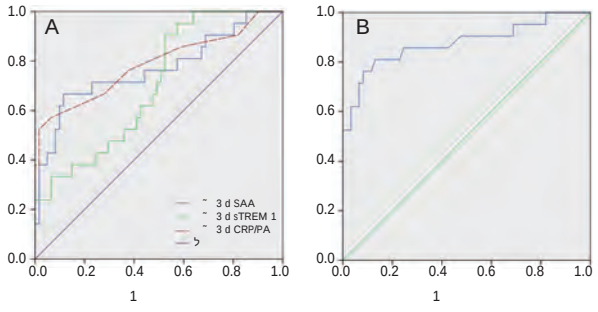
Table 3 Diagnostic value

	AUC	95%CI	e	%	%
SAA	0.768	0.662~0.854	>58.4	66.67	88.52
sTREM 1	0.701	0.590~0.797	>210.3	90.48	47.54
CRP/PAB	0.786	0.682~0.869	>0.1	52.38	98.36
e ɕ ´	0.876	0.785~0.939	-	76.19	91.80



A ε SAA ɷsTREM 1 ɷCRP/PAB ROC

B ε SAA ɷsTREM 1 ɷCRP/PAB ´ ROC

2 ROC

Figure 2 ROC curve

2.5 ‴ ˀ SAA ɷsTREM 1 ɷ CRP/PAB e

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2.6 SAA ɷsTREM 1 ɷCRP/ PAB e Ά Ą

Spearman Ą ŭ SAA r=0.512 ɷ sTREM 1 r=0.0.473 ɷCRP/ PAB r=0.608 e Ά Ⅵ Ą Ė τ P< 0.05 ɟ

4 SAA sTREM 1 CRP/PAB $\bar{x} \pm s$

Table 4 Comparison of serum SAA sTREM 1 CRP/PAB ratios in patients with different infection $\bar{x} \pm s$

	n=8	n=13	t e	P e
SAA mg/L	73.96±17.03	58.05±13.29	2.396	0.027
sTREM 1 ng/mL	288.85±40.16	254.41±31.22	2.204	0.040
CRP/PAB e	0.35±0.07	0.27±0.04	3.355	0.003

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Clinical value of serum TSP-1 and PDGF in evaluating short-term prognosis in patients with intracerebral hemorrhage

GAO Yangyang 1★ LI Jieng2

1. Department of Neurology Bayannaoer Hospital Bayannaoer Inner Mongolia China 015000
2. Department of Neurology Bayannaoer Hospital Bayannaoer Inner Mongolia 015000

ABSTRACT Objective To study the clinical value of serum TSP 1 and PDGF in evaluating short term prognosis in patients with intracerebral hemorrhage. Methods 65 cases of patients with intracerebral hemorrhage ICH from March 2017 to February 2019 in our hospital were retrospectively analyzed. After 90 days of follow up 5 patients withdrew from the study because of their personal reasons. The patients were divided into favorable outcome group n=37 and unfavorable outcome group n=23 depending on modified Rankin scale scores. The basic information and treatment of patients in the two groups were compared using single factor analysis and the significantly different single factors were analyzed by non conditional logistic regression analysis. Finally the dangerous factors for poor prognosis were established. Results There were significant differences in body mass index hypertension hematoma volume NIHSS score pulmonary

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infection broken ventricle and fasting blood glucose between the two groups. Logistic regression analysis show that hypertension OR=1.275 95%CI 1.052~1.545 fasting blood glucose OR=1.551 95%CI 1.219~1.974 hematoma volume OR=1.368 95%CI 1.124~1.664 NIHSS score OR=2.537 95%CI 1.109~5.802 TSP 1 OR=2.659 95% CI 1.202~5.881 and PDGF OR=3.086 95% CI 1.324~7.197 are

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2 TSP 1 PDGF $\bar{x} \pm s$

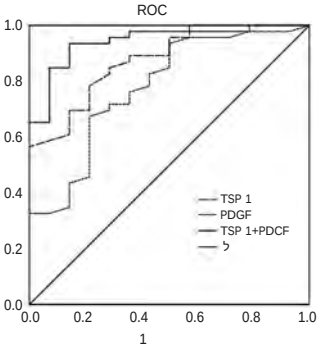
Table 2 Comparison of serum TSP 1 ۱ PDGF value between the 2 groups $\bar{x} \pm s$

ą̈	n	TSP 1 ng/mL	PDGF ng/L
~	37	102.47±18.65	341.34±32.59
~ ‴	23	165.34±10.76	421.32±52.60
t e		16.548	8.205
P e		<0.001	<0.001

3 Logistic

Table 3 Result of logistic regression

ל	B e	S.E e	Wald e	P e	OR e	95%CI
♥	0.243	0.098	6.148	0.013	1.275	1.052~1.545
	0.439	0.123	12.739	<0.001	1.551	1.219~1.974
I	0.313	0.100	9.797	0.002	1.368	1.124~1.664
NIHSS ŏ	0.931	0.422	4.867	0.027	2.537	1.109~5.802
TSP 1	0.978	0.405	5.831	0.016	2.659	1.202~5.881
PDGF	1.127	0.432	6.806	0.009	3.086	1.324~7.197
	-0.564	0.121	21.726	<0.001	-	-



1 Logistic ROC

Figure 1 ROC curve of the prediction model based on Logistic regression analysis

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1 TNF α PCT IL 1β $\bar{x} \pm s$

Table 1 Comparison of dynamic trends of serum TNF α PCT IL 1β in two groups of women $\bar{x} \pm s$

ą̈	TNF α ng/mL			PCT g/mL μ			IL 1β pg/mL		
	У˜ 1	У˜ 3	У˜ 5	У˜ 1	У˜ 3 d	У˜ 5	У˜ 1	У˜ 3	У˜ 5
ϛ	1.55±0.32	2.67±0.69	3.04±0.55	0.81±0.27	2.23±0.69	2.52±0.77	0.81±0.27	2.23±0.69	2.52±0.77
	1.48±0.29	1.50±0.31	1.44±0.38	0.78±0.24	0.63±0.20	0.47±0.15	0.78±0.24	0.63±0.20	0.47±0.15
t e	1.702	18.125	26.334	0.875	27.184	32.528	0.875	27.184	32.528
P e	0.090	0.000	0.000	0.382	0.000	0.000	0.382	0.000	0.000

2.2 У˜ 3 TNF α ɵPCT ɵIL 1β
ą̈ У˜ í ɵ e
˚ У˜ 3 TNF α ɵPCT ɵIL 1β
Ą ROC PCT ɵTNF α ɵIL 1β
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mL ɵ2.00 ng/mL ɵ2.51 pg/mL P<0.05 ѧ 1 ɟ

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Correlation of serum β - hCG and progesterone expression with thyroid function and motilin in patients with hyperemesis gravidarum

LI Feng* LU Haifeng CUI Bingyi QIN Chunyi

Clinical laboratory Tangshan hospital of traditional Chinese medicine Tangshan Hebei China 063000

ABSTRACT Objective To investigate the expression of serum β human chorionic gonadotropin β hCG and progesterone P in patients with hyperemesis gravidarum and the correlation with thyroid function and motilin MOT . Methods From January 2018 to October 2019 81 pregnant women with severe vomit ing in hospital were selected as the study group and 79 normal pregnant women were selected as the control group. The serum β hCG P MOT levels hyperemesis gravidarum VAS score thyroid function free thy roxine FT4 free triiodothyronine FT3 and thyroid stimulating hormone TSH were measured and compared between the two groups. The correlations of serum β hCG and P levels with VAS score and thyroid function and MOT were analyzed. Results The serum β hCG level in the study group was higher than that in the control group and the serum P level was lower than that in the control group P<0.05 . Serum FT3 and FT4 levels and VAS scores in the study group were higher than those in the control group and serum TSH and MOT levels were lower than those in the control group P<0.05 . There was a significant negative correlation between serum β hCG levels and serum TSH and MOT levels and a significant positive correlation with se

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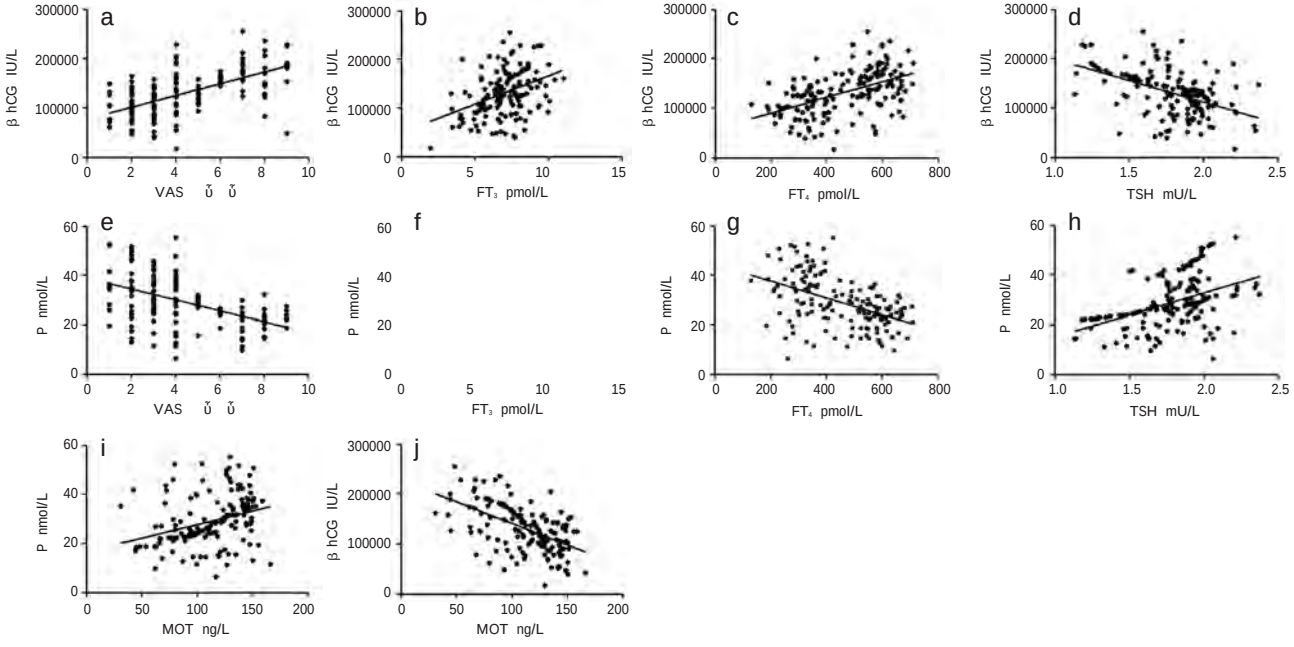
2.2 Ξ β hCG ϕP



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1 β hCG P VAS

Figure 1 Correlation of serum β hCG P levels with thyroid function and VAS score

4 β hCG P

Table 4 Relationship between serum β hCG P and hyperemesis gravidarum

ė	β e	S.E. e	Wald/χ^2 e	OR e	95%CI	P e
β hCG	1.291	0.462	7.807	3.636	1.278~10.344	<0.001
P	1.169	0.454	6.633	3.220	1.071~9.679	<0.001

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CysC Îα1 MG ʁ β2 MG Ǎ˜ ↓ ¨H ↓ ⅄ ⅃ Z Ш ʁ ← ⅁ Ꞥ ɕ ά ψ ↓

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C CysC ɷα1 α1 MG ᴡ β2 β2 MG ᵹ ⅁ COPD Ψ ɵ e ᴡ Ά Ƙ Ặ ɻ 2013 1 2016 8 206 ɂ COPD ˚ ŏ ♥ SPO2 ŏ ε 64 ɂ ɷΨ 86 ɂ ɷ 56 ɂ ɕ Ɔ ⅂ 50 ɂ ɾ Ə ε 4 CysC ɷα1 MG ɸβ2 MG ɷ Scr ɷ BUN ά ROC ŏ CysC ɷα1 MG ᴡ β2 MG COPD ᴡ COPD´ Ƙ ɵ e Pearson ŏ CysC ɷBUN ɷα1 MG ɸβ2 MG Ά Scr Ặ ɻ ① COPD CysC ɷα1 MG ɸβ2 MG ⅇ ⅂ COPD Scr ɷBUN Ά τ P>0.05 ②Cys C ᵹ ɷΨ ɷ ⅇ Ⱨ P<0.05 α1 MG ɸβ2 MG ᵹ Ψ ɷ ⅇ Ⱨ P<0.05 Ά CysC ɷα1 MG ɸβ2 MG P<0.05 Ά Ψ CysC P<0.05 ③α1 MG ɸβ2 MG ᴡ Cys C ⅇ Ά Scr ⅄ Ặ ⅇ P<0.05 ɻ ④ROC CysC ɷα1 MG ɸβ2 MG ᴡ ´ COPD ; ε 0.810 ɷ0.743 ɷ0.812 ɷ0.915 ɷ 0.936 ȳ e ε 1.74 mg/L ɷ12.22 mg/L ɷ2.34 mg/L ŏ ά ε 0.806 ɷ0.726 ɷ0.794 ɷ0.903 ε 0.795 ɷ0.705 ɷ0.782 ɷ0.903 CysC ɷα1 MG ɸβ2 MG ᴡ ´ ; ŏ ά ε 0.864 ɷ0.832 ɷ0.812 ȳ e ŏ ά ε 1.62 mg/L ɷ12.08 mg/L ɷ2.58 mg/L ŏ ά ε 0.824 ɷ0.816 ɷ0.808 ɷ0.914 ŏ ά ε 0.786 ɷ0.774 ɷ0.762 ɷ0.903 ɻ ´ CysC ɷα1 MG ɸβ2 MG Ⱨ COPD ↿ Ƙ ก ก Ė ɵ e ɻ C α1 β2 ⅁ Ƙ ɵ e

The detection and significance of CysC α1-MG β2-MG of early kidney injure in patients with chronic obstructive pulmonary disease

LI Haiyan*

Dongying New District Hospital Dongying Shandong China 257000

ABSTRACT Objective To investigate the detection value of serum cystatin C CysC α1 microglobulin α1 MG and β2 microglobulin β2 MG in chronic obstructive pulmonary disease COPD and correlation of the early stage of hypoxia kidney injury. Methods A total of 206 elderly patients with COPD from January 2013 to August 2016 in our hospital were selected as the study object. Based on the blood gas analysis they were divided into COPD with mild moderate and severe hypoxia groups. A total of 50 healthy people were selected as control group. The CysC α1 MG β2 MG Scr levels were detected and compared for analysis. The ROC curve was used to analyze the diagnostic value of CysC α1 MG and β2 MG on COPD and COPD combined with renal injury. Pearson correlation analysis was used to analyze the correlation between CysC BUN α1 MG and β2 MG and Scr. Results ①Compared with control group CysC α1

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* E-mail chabianganpw16284@163.com

MG β2 MG levels in COPD group significantly increased and the Scr levels had no statistical significance on the difference with the control group P>0.05 . ②CysC level in mild moderate and severe hypoxia group were significantly higher than that in control group and the differences had no statistical significance P<0.05 α1 MG β2 MG levels in moderate and severe hypoxia group were significantly higher than that in control group P<0.05 α

AUC ɵ Ą COPD Ƙ ɵ e ɟ ᵹ Ɲ´ ɯ P<0.05 ε Ė τ ɟ

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2.1 COPD Á CysC ɷα1 MG ɷβ2 MG ɷ Scr ɷBUN COPD CysC ɷα1 MG ɷβ2 MG ᵹ Ɦь P<0.05 Ξ Scr ɷBUN τ P>0.05 1 ɟ

2.2 4 CysC ɷα1 MG ɷβ2 MG ɷScr ɷBUN Á ɷΨ ɯ CysC ɯ ɯ Ψ ɵ α1 MG ɷβ2 MG ᵹ ╗ τ P<0.05 Á Ψ ɵ CysC ɯ α1 MG ɷβ2 MG ᵹ ╗ τ P<0.05 Á Ψ CysC ╗ τ P<0.05 2 ɟ

1 $\bar{x} \pm s$

Table 1 Comparison of related indicators between the 2 groups $\bar{x} \pm s$

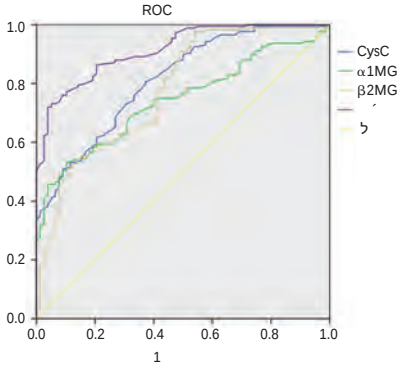
ą	n	Scr mol/L μ	BUN mmol/L	CysC mg/L	α1 MG mg/L	β2 MG mg/L
	50	76.01±15.76	5.84±1.43	1.14±0.22	8.84±1.56	1.64±0.26
COPD	206	83.36±34.39	6.43±3.12	1.69±0.53	13.63±4.35	2.63±1.15
t e		1.318	1.562	4.472	5.124	4.115
P e		0.231	0.128	0.013	0.004	0.021

2 4 $\bar{x} \pm s$

Table 2 Comparison of related indicators between the 4 groups $\bar{x} \pm s$

ą	n	Scr mol/L μ	BUN mmol/L	CysC mg/L	α1 MG mg/L	β2 MG mg/L
	50	76.01±15.76	5.84±1.43	1.14±0.22	8.84±1.56	1.64±0.26
	64	80.58±17.43	6.36±1.61	1.37±0.41[a]	9.54±1.85	1.93±1.35
Ψ	86	86.56±19.23	6.73±1.98	1.64±0.72[ab]	12.24±1.81[a]	2.64±1.81[a]
	86	93.38±21.73	7.04±2.09	1.98±1.23[abc]	17.42±2.79[ab]	3.72±2.79[ab]
F e		9.677	6.379	7.240	8.660	9.275
P e		0.000	0.001	0.000	0.000	0.000

2.3 CysC ɷα1 MG ɷβ2 MG COPD ROC ROC ŭ CysC COPD ; ε 0.810 ȳ e ε 1.74 mg/L ę COPD Ƙ ε 0.806 ε 0.795 α1 MG ; ε 0.743 ȳ e ε 12.22 mg/L ę COPD Ƙ ε 0.726 ε 0.705 β2 MG ; ε 0.812 ȳ e ε 2.34 mg/L ę COPD Ƙ ε 0.794 ε 0.782 3 ´ ; ε 0.915 ε 0.903 ε 0.897 ь 1 ɟ



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1 CysC α1 MG β2 MG COPD ROC

Figure 1 ROC curves of CysC α1 MG β2 MG for COPD prediction

2.4 CysC ɷα1 MG ɷβ2 MG ɷBUN Á Scr Ą ŭ Pearson ŭ CysC r=0.672 P=0.011 ɷ α1 MG r=0.415 P=0.031 ɷβ2 MG r=0.550 P= 0.029 BUN r=0.023 P=0.436 ᵹ Á COPD Scr Ą Ė τ P< 0.05 ɟ

2.5 CysC ɷα1 MG ɷβ2 MG COPD Ƙ ROC ROC ŭ CysC ; ε 0.856 ȳ e ε 1.62 mg/L ę COPD Ƙ ε 0.824 ε 0.786 α1 MG

; ε 0.722 ȳ e ε 12.08 mg/L ẹ ה COPD CysC ɷα1 MG ɸβ2
COPD Ϗ ε 0.816 ε MG φ ╗ Scr ╗ ˝ ɇ Scr ǯ א
0.774 β2 MG ; ε 0.812 ȳ e ε ˈ ɔ ╗ ε c ˈ
2.58 mg/L ẹ COPD Ϗ ε כ Scr ה ל כ ɟ CysC ɷα1 MG ɸβ2
0.808 ε 0.762 ɕ ´ ; MG ˈ ל כ Scr ʼ Ὸ ╗
ε 0.936 ε 0.914 ε 0.903 ﻩ 2 ɟ Ά 13 m ɟ
ʼ ɯ CysC ɷα 1 MG ɷ
β2 MG Ư Oμ V5ƒÐ 0 CV ƒÙƒ 8E4(DôÐ @ q 4 . (

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ת AML ﻝ Ă ą̇ ɔ ﻡ ’ COX 2 ÎVEGF ʁ p53 ʁ ← E ψ

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AML ğ ﺵ ђ Ψ ɔ 2 COX 2 ɞ Ỉ ė VEGF ɸp53 ẇ ~ ɵ e ɟ ך 2014 1 2019 1 80 ʒ AML Ə ε ך Ь ɾ I 40 ʒ Ə ε ѽ~ ẇ COX 2 ɗVEGF ɸp53 ɞI ẍ ﻝ ẍ ŭ ˇ Ą ~ ŭ ε ã n=48 ﻝ ã n=32 Ξ COX 2 ɗVEGF ɸp53 Ξ Ψ CNSL ת ɔ Ə ROC ŭ COX 2 ɗVEGF ɸp53 ğ AML ỵ ~ Ψ ɵ e ɟ COX 2 ɗVEGF ẇ p53 ҭ Ь Ė τ P<0.05 COX 2 ɗVEGF ẇ p53 ~ ҭ ѽ ң Ė τ P<0.05 ɟ ~ I ẍ IgA ɗIgG ɗIgM ҭ ѽ ң Ė τ P<0.05 ~ ẍ CD3+ ɗCD4+ ɗCD8+ ɗCD4+/CD8+ ҭ ѽ ң Ė τ P<0.05 ɟ Ą ŭ COX 2 ɗVEGF ẇ p53 ɸ ğ Ą *P*<0.05 ɟ ã ﻝ ã AML COX 2 ɗVEGF ẇ p53 Ė τ *P*<0.05 ɟ ã ﻝ ã AML Ψ Ң Ė τ P<0.05 ɟ ROC COX 2 ɗVEGF ɸp53 ẇ ´ ğ CNSL Ψ ; AUC ŭ ą̈ ε 0.836 95% *CI* 0.776~0.896 ɞ0.802 95% *CI* 0.730~0.873 ɞ0.716 95% *CI* 0.639~0.793 ẇ 0.905 95% *CI* 0.863~0.947 ɟ COX 2 ɗVEGF ẇ p53 Ь AML í ẇ ~ Ţ Ė ɵ e ɟ ɔ 2 Ỉ ė p53

Expressions of COX-2 VEGF and p53 in elderly AML patients treated with decitabine and their prognosis

WANG Zhanfang* ZHANG Fangfang YANG Hai CHEN Chaohua

Department of Hematology the First People s Hospital of Pingdingshan Pingdingshan Henan China 467000

ABSTRACT Objective To investigate the expression of serum cyclooxygenase 2 COX 2 vascular endothelial growth factor VEGF and p53 protein in elderly patients with acute myeloid leukemia AML treated with decitabine and their prognostic value. Methods 80 patients with AML admitted to our hospital from January 2014 to January 2019 were selected as the study group and 40 healthy people who underwent physical examination in our hospital were selected as the control group. The levels of COX 2 VEGF p53 protein humoral immunity and cellular immunity in the study group before and after treatment and the control group were compared and the correlation of indexes were also analyzed. According to the patients

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* E-mail musijiu2535898@163.com

after treatment they were divided into complete remission group n=48 and incomplete remission group n= 32 . The levels of COX 2 VEGF p53 protein in the two groups were analyzed. The incidence of central nervous system leukemia CNSL between the two groups was compared. The predictive value of COX 2 VEGF and p53 protein in the prognosis of AML was analyzed using the receiver operating characteristic curve ROC . Results The levels of COX 2 VEGF and p53 proteins in the study group were significantly higher than those in the control group and the difference was statistically significant P<0.05 . However after treatment the levels of COX 2 VEGF and p53 protein in the study group were significantly lower than those before treatment. The difference was statistically significant P<0.05 . After treatment the levels of humoral immune indicators IgA IgG and IgM in the study group were significantly lower than before treatment P< 0.05 . After treatment the cell immune indicators of CD3 + CD4 + CD8 + and CD4 + / CD8 + in the study group were significant lower than before treatment P<0.05 . Correlation analysis indicates that there is a significant positive correlation between COX 2 VEGF and p53 proteins P<0.05 . The difference in COX 2 VEGF and p53 protein levels between AML patients in complete remission group and incomplete remission group was statistically significant P<0.05 . The difference in median survival between AML patients in complete remission group and incomplete remission group was statistically significant P<0.05 . ROC curve results showed that the area under the curve AUC of COX 2 VEGF p53 protein and combined detection in CNSL diagnosis were 0.836 95%CI 0.776~0.896 0.802 95%CI 0.730~0.873 0.716 95%CI 0.639~ 0.793 and 0.905 95%CI 0.863~0.947 . Conclusion The levels of serum COX 2 VEGF and p53 are of great significance for the clinical treatment effect and prognosis evaluation of elderly AML patients.

KEY WORDS Acute myeloid leukemia Old age Cyclooxygenase 2 Vascular endothelial growth factor p53 protein

acute myeloid leukemia

AML / w ٧ ١ Ψ Ɑ ١ ﻩ ε m ɟ [1] ŏ 65 w ɔ ж AML ה ę ђ ж 10 ʁ Ά ж ١ ̀Ω ɞ ١ Ă ɟ ɔ AML ɟ ж ŏ Ψ w ɔ ЃA ̓Ḥ ɔ w + ẋ + ṇ ė Ara c+ACR+G CSF CAG ε AML ɟ ŋ ђ εm DNA ɲ ɔ Ă ̓Ḥ ę Ь Ă ﻩ ɞŭ ɔ ١ ̬ ĕ H Ė Ə ɟ ũ [2] ŋ ђ ´ CAG ɔ Ь ٦ Ъ ɔ ~ ɟ ɔ 2 Cyclooxygenase 2 COX 2 ’ ̬ ١ ה ١ ה ę Ά ~ ̓Y Ă ŏ Ψ ٦ [3] ɟ ˬ Ь ﻩ Ǐ ė vascular endothelial growth factor VEGF ε ١ ė ε VEGF Ά ה ה ١ ~ ŏ Ă [4 5] ɟ P53 ɲ ɞ ѽ Ά Ă ɲ ɞ ę p53 Ш ’ Ə ε ɞ ١ ~ [6] ɟ ė COX 2 ɞVEGF ɞp53 ’ ε ŋ ђ AML Ψ Ẇ ~ Ţ Ъ ٦ Ъm Ė ١ ; ɟ

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1.1 m

٦ 2014 1 2019 1 80 ٯ AML Ə ε ę Ψ 49 ٯ 31 ٯ 60~76 ج 68.8±2.4 M1 ى 8 ٯ M2 ى 14 ٯ M4 ى 18 ٯ M5 ى 31 ٯ M6 ى 9 ٯ ɟ ٦ ̃ Ь ɨ ١ 40 ٯ Ə ε ę Ψ 24 ٯ 16 ٯ 60~78 ج 68.3± 2.5 ɟ Ξ ŏ ̈ ɞ ί m ɔ τ P>0.05 Ė ’ ɟ Ǐ Ң ١ Ж ɟ Ấ ЃA ① ج ´ ћ Ά ЃA ђΨ Ă Ь AML ЃA [7] ② ج ṇ ③ ⩾60 ④AML MICM ŭ ى ε M1 ɞM2 ɞM4 ɞM5 ɞM6 ى ⑤ Ẇ ج Ẅ ŭ Ъ ̃ Ш ɟ ЃA ① ɔ Ă ②

ɔ O ' ③´ Ĭ ŏ ɞẍ ⑤ ‴ ④´ ę ɦ Ң ɔ Ψ Ȯ ɟ

1.2 AML ɯ ɦ ´ CAG ɯ ɦ 15 mg/m^2·d d1 d5 ẋ 20 mg/d d1 d4 10 mg/m^2 q12 h d1 d14 ; ḭ ɛ 150 g q12μh d1 d14 ; >20×10^9/L φ ɟ ɡ̆ ~ ã̃ ʎ ã̃ ʒ ɟ

1.3

1.3.1 COX 2 ɞVEGF ẇ p53 ɡ̆ Ắ ~ ɳ 5 mL 30 min 3 000 r/min 15 min ŏ̃ ɔ ẍ Ч enzyme linked immunosorbent assay ELISA COX 2 ɞVEGF ẇ p53 Ң ɔ O ắ ˘ ɟ Ə O Ң ; ɟ AML ɡ̆ ɔ 14 d˜ Ố ɳ 5 mL ˚ ˛ ɔ ƃ ɔ Ỹ ɟ

1.3.2 I ẍ ẇ ẍ ɡ̆ ѽ ẇ 14 d˜ ẍ I ẍ IgA ɞIgG ɞIgM Ң ɔ ắ ˘ ɟ CyFlow ã̃ ŏ Ѧ ɷ Partec ắ ˘ ; 1 ɟ

ẇ ę Ң ẍ T ЖЮ CD3+ ɞCD4+ ɞCD8+ ƃ ɔ CD4+/CD8+ ɟ

1.3.3 ~ ɔ ~ 1~5 Ỹ ɔ ת Ψ central nervous system leukemia CNSL Ỹ ɟ CNSL ẗA ˅ ɦ Ψ ɷ ж Ą ≟ 2016 ɦ[8] ó ɟ

1.4 ŏ̃ SPSS 20.0 Θ ŏ̃ w % χ^2 w $\bar{x} \pm s$ t ɟ Spearman Ą̆ ŏ̃ COX 2 ɞVEGF ẇ p53 φ Ą̆ ẇ ę Ą ẍ Ą̆ ɔ Ə receiver operator characteristic curve ROC ŏ̃ COX 2 ɞVEGF ɞp53 ɡ̆ CNSL Ψ ɵ [e] ɟ P<0.05 ε Ė τ ɟ

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2.1 Ξ ƃ ɔ Ỹ ѽ COX 2 ɞVEGF ẇ p53 ҕ Ң ж ~ ҕ ѽ ң Ė τ P<0.05 ɟ ~ I ẍ ʎ ẍ ҕ ѽ ң Ė τ P<0.05 ɟ ; 1 ɟ

1 $\bar{x} \pm s$

Table 1 Changes of serum indicators in the 2 groups $\bar{x} \pm s$

	n=80		n=40	t [e]	P [e]
	ѽ	~			
COX 2 ng/L	53.2±6.1	31.0±3.1	30.3±3.2[a]	29.019	0.000
VEGF pg/mL	158.8±35.7	72.2±7.5	70.7±6.9[a]	21.233	0.000
p53 ng/L	211.5±33.8	108.3±13.7	106.7±14.9[a]	25.309	0.000
IgA g/L	2.3±0.9	1.5±0.7	-	4.276	0.000
IgG g/L	11.7±1.9	9.1±1.6	-	9.362	0.000
IgM g/L	1.0±0.2	0.7±0.2	-	9.487	0.000
CD3+ %	54.2±6.6	38.7±4.5	-	17.355	0.000
CD4+ %	34.2±4.3	28.8±3.2	-	9.011	0.000
CD8+ %	29.0±2.7	20.9±2.6	-	19.328	0.000
CD4+/CD8+	1.2±0.3	0.9±0.2	-	7.442	0.000

Ą [a]P<0.05 ɟ

2.2 Ă ŏ p53 φ ğ Ă P<0.05 Ă Ą ŏ COX 2 ɞVEGF ẇ 2 ɟ

2 COX 2 VEGF p53

Table 2 Correlation analysis of COX 2 VEGF and p53 proteins with various indicators

	COX 2		VEGF		p53	
	r e	P e	r e	P e	r e	P e
COX 2	-	-	0.583	0.000	0.612	0.000
VEGF	0.501	0.000	-	-		0.000
p53	0.559	0.000	0.537	0.000	-	-

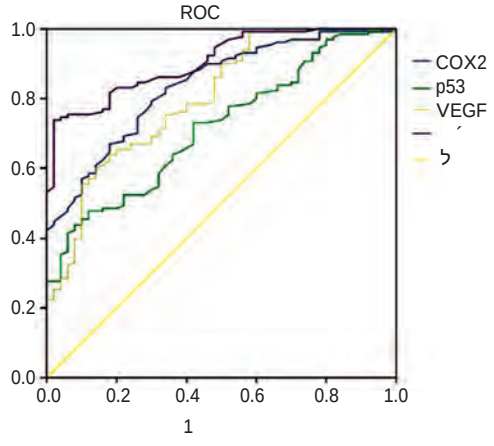
2.3 AML COX 2 ɞVEGF ɳ Ɦ ã Ė ẇ p53 ẇ Overall Survival OS τ P<0.05 ɟ ã AML OS Ɦ ã Ė τ P< ã AML COX 2 ɞVEGF ẇ p53 0.05 3 ɟ

3 AML $\bar{x} \pm s$

Table 3 Comparison of various indicators in different treatment outcomes of elderly AML patients $\bar{x} \pm s$

ą	n	COX 2 ng/L	VEGF pg/mL	p53 ng/L	OS
ã	48	31.5±4.4	70.3±7.7	102.3±10.4	12.6±2.7
	32	44.1±5.3	166.9±20.8	198.7±10.8	5.9±1.6
t e		11.555	25.148	39.997	13.914
P e		0.000	0.000	0.000	0.000

2.4 COX 2 ɞVEGF ẇ p53 CNSL ROC ROC COX 2 ɞVEGF φp53 ẇ ´ ğ CNSL Ψ ; AUC ŏ ą ε 0.836 95%*CI* 0.776~0.896 ɞ0.802 95%*CI* 0.730~0.873 ɞ0.716 95%*CI* 0.639~0.793 ẇ 0.905 95%*CI* 0.863~0.947 ɟ ћ 1 ɟ



1 COX 2 VEGF p53 CNSL ROC

Figure 1 COX 2 VEGF and p53 predict ROC curves of CNSL

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ɔ ɻ ˝ ɗ AML í ą̈ Ъ ╗ ж щ ŏ Ą ğ Ψ ε ɟ ś ђ ˘ ɲ ɔ ´ CAG ε AML ɟ ˘ ɲ ɔ ˛ G0 Ả ɻ ɯ S ъ ╗ ɔ Ɦ Ƙ ɯ ɟ ś ђ ˛ w Ả DNA Ą DNA ɲ ɲ ɔ ъ ɲ ɹ ą̈ AML [10] ɟ ğ l в в Ψ Ă ğ ˙Y Ă ɞɯ Θ ɟ ח [11] Ą ˛ ˙Y ɻ É w ъ ʄ ę P É ĕ H ɟ [12] COX 2 Y ɭ Ă ח ɻ ח ę ˛ ɭ Ă COX 2 ẇ ę ώ ˝Ω У ˛ ˛ DNA ´ ɻ ɯ COX 2 ˛ Ą ; ĕ H ח l l ẍ ɻ ẍ ɟ

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ŏ γ CD40 ÎCD40L ʁ BAFF ﻣ ٦ ∂ρ ITP ﻝ ﮓ Z Ш

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BAFF ᶍ Ћ P<0.05 ɟ א ٶ CD40 ɷCD40L ẇ
BAFF ᶍ Ћ א P<0.05 ɟ ITP ٶ CD40 ɷCD40L ẇ BAFF ᶍ
Ά ٧ Ą r<0 P<0.05 ɟ ROC ŏ ٶ CD40 ɷCD40L ẇ BAFF ITP
ɵ e ᶍ AUC>0.7 P<0.05 ɟ ITP ٶ CD40 ɷCD40L ITP Ė
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CD40 CD40L BAFF ITP

The predictive value of peripheral blood CD40 CD40L expression and serum BAFF level on the efficacy of patients with immune thrombocytopenic purpura

YIN Fenglei[1]★ YIN Juan[2] ZHAO Fang[1] ZHANG Rui[1] LIU Jing[1] ZHANG Wei[1] LI Shuchen[1] WANG Juan[1]

1. Department of Hematology Cangzhou Central Hospital Cangzhou Hebei China 061000 2. Operating Room of Cangzhou People s Hospital Cangzhou Hebei China 061000

ABSTRACT Objective To investigate the predictive value of peripheral blood CD40 CD40L expression and serum BAFF level in the treatment of immune thrombocytopenic purpura ITP patients. Methods 80 patients with ITPadmitted to our hospital wererecruited as the observation group. 100 healthy people who underwent physical examination in our hospital were selected as the control group. Peripheral blood CD40 CD40L expression and serum BAFF level were observed in both groups. The patients were divided into two groups according to the results of efficacy judgment. The expression of CD40 CD40L and serum BAFF in peripheral blood from the two groups were compared. Results The expression of CD40 CD40L and serum BAFF in the peripheral blood in the observation group were significantly higher than those in the control group P<0.05 . The expression of CD40 CD40L and serum BAFF in peripheral blood of patients with non re

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1. 061000
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★ E-mail wang_juan01@126.com

sponse group were significantly higher than those in response group P<0.05 . The expression of CD40 CD40L and serum BAFF in peripheral blood of patients with ITP were negatively correlated with curative ef fect r<0 P<0.05 . ROC curve analysis results show that the peripheral blood CD40 CD40L and BAFF have high predictive value for ITP efficacy all AUC>0.7 P<0.05 . Conclusion The peripheral blood CD40 and CD40L in patients with ITP have a high predictive value for the efficacy of ITP patients.

KEY WORDS Bone marrow CD40 CD40L Serum BAFF level ITP Curative effect

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bocytopenic purpura ITP ε í ɔ

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ITP 80 ʒ ש ɾ l

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44 ʒ 36 ʒ 23~58 ҷ 42.23±6.11

BMI 21~29 kg/m² ҷ 26.58±3.05 kg/

m² ɟ 55 ʒ 45 ʒ 21~59

ҷ 42.22±6.31 l Body Mass In

dex BMI 20~28 kg/m² ҷ 26.33±2.88 kg/m² ɟ

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① ч CD40 вCD40L ʔ

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ĭ ǎ ˘ Attune NxT ی Ѧ

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ɟ ② BAFF 2 mL

ǧ 3 000 r/min ; 15 min Ч ʔ 0.8 mL ά ă

ш ӧ Ч BAFF Ḥ

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1.3

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2.1 2 ɔ ч CD40 вCD40L ש

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1 2 CD40 CD40L BAFF $\bar{x}\pm s$

Table 1 Comparison of CD40 CD40L expression and serum BAFF levels in peripheral blood of 2 groups of patients $\bar{x}\pm s$

ά	CD40	CD40L	BAFF ng/L
	7.31±2.07	3.24±1.06	603.17±112.38
	12.92±3.05	6.09±1.70	716.44±137.48
t e	6.721	5.947	2.936
P e	0.000	0.000	0.005

2.2 ‟ ’ ٧ CD40 ϐCD40L Ϣ BAFF

א ٧ CD40 ϐCD40L Ϣ BAFF ϑ Ь א Ė τ P<0.05 ɟ 2 ɟ

2.3 ITP ٧ CD40 ϐCD40L Ϣ BAFF Ά Ą ŏ

ITP ٧ CD40 ϐCD40L Ϣ BAFF ϑ Ά ٨ Ą r e ŏ ά ε -0.691 ϐ -0.713 ϐ 0.652 ɟ Ė τ P<0.05 ɟ

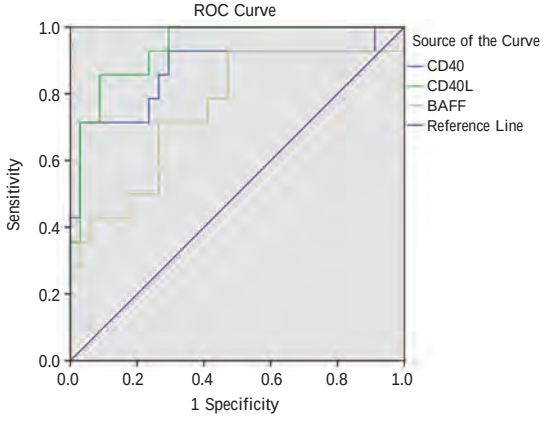
2 CD40 CD40L BAFF $\bar{x}\pm s$

Table 2 Comparison of CD40 CD40L expression and serum BAFF levels in peripheral blood of patients with different curative effects in the observation groups $\bar{x}\pm s$

ά	n	CD40	CD40L	BAFF ng/L
א	56	11.63±3.73	5.61±1.14	683.08±111.88
א	24	15.92±5.09	6.88±1.25	804.07±117.65
t e		2.127	2.237	2.155
P e		0.045	0.034	0.040

2.4 ROC ŏ

ROC ŏ CD40 ITP cutoff e ε 12.28 % AUC ε 0.892 ε 83.16% ε 92.06% ٧ CD40L ITP cutoff e ε 6.08% AUC ε 0.784 ε 81.75% ε 90.25% BAFF ITP cutoff e ε 745.02 ng/L AUC ε 0.708 ε 81.02% ε 90.14% ɟ ϧ 1 ɟ



1 ROC

Figure 1 ROC analysis chart

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† papillary renal cell carcinoma PRCC Ə ε m یی Ė ė یی † † Ė ė یی † 50% w ɔ ɻ † Ж یی solid variant of papillary renal cell carcinoma SPRCC Ə ε † m Y Ж یی ; ɐ ɐш ˝H ω ˝ ǫ̈ † ∖ Ψ ŏ ң ẍ یی Ά PRCC m Ж یی ε 1 ɻ

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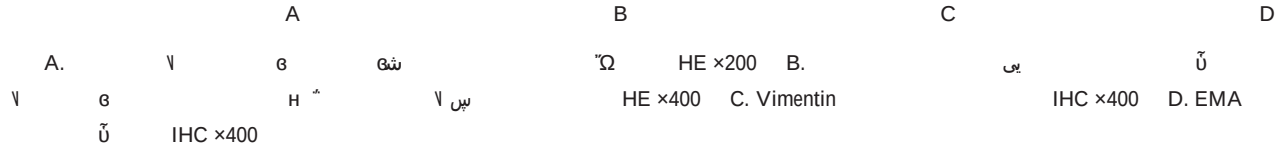

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1 SPRCC

Figure 1 Histological characteristics and immunophenotype of SPRCC

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Table 1 The clinical datas and immunohistochemical results of SPRCC

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Vimentin ‴ CK20 ϭRCC ϭWT 1 ϭCD57 ϭ
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ת COPD ε‵ ₦ ! ⅄ CysC ÎVEGF Î IL 17 ÎACTA ﻡﻡﻡ ך κ`

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C CysC ɷ Ì ɻ VEGF ɷ ч 17 IL 17 ɷ A ACTA ﻭﺋ ﻫﻄ COPD ¥ O ﻝ ﻴ Ψ ɟ ך 2016 3 2019 3 224 ʒ COPD ה O ﻝ ﻴ õ n=78 ɷ n=146 Ɓ ך ɾ ɨ 86 ʒ ε ɟ 3 ˝ ˜ CysC ɷVEGF ɗL 17 ɷ ACTA õ COPD ¥ O ﻝ ﻴ ɵ e ﻱ Ą õ Á APACHE Ⅱ õ Ą ﻱ ˜ ɵ e ɟ 3 CysC ɷVEGF ɗL 17 ɷACTA τ P<0.05 VEGF Á Cys C ɗL 17 ɷACTA ﻭ Ą CysC ɗL 17 ɷACTA ﻭ Ą P<0.05 H CysC ɗL 17 ɷACTA ɷAPACHE Ⅱ õ Ɲ VEGF ɲ Ɲ P<0.05 VEGF Á APACHE Ⅱ õ ﻭ Ą CysC ɗL 17 ɷACTA Á APACHE Ⅱ õ ﻭ Ą P<0.05 CysC ɷVEGF ɗL 17 ɷACTA ´ COPD ¥ O ﻝ ﻴ ˜ AUC 0.864 Ɲ ₸ m ε 92.86% ε 70.00% ɟ CysC ɷVEGF ɗL 17 ɷ ACTA ﻭﺋ COPD ¥ O ﻝ ﻴ Ψ ﻭ Á ′Y Ą ´ ε COPD ¥ O ﻝ ﻴ ﻱ ˜ ó ɟ C Ì ɻ ч 17 A ﻫﻄ ﻝ ﻴ

Changes of serum CysC VEGF IL-17 and ACTA levels in elderly patients with COPD and severe respiratory failure

CAO Tingting[1] WAN Jun[1] FENG Yonghai[2] CHU Heying[3]★

1. Department of general medicine the Fifth Affiliated Hospital of Zhengzhou University Zhengzhou Henan China 450052 2. Department of respiratory medicine the Fifth Affiliated Hospital of Zhengzhou University Zhengzhou Henan China 450052 3. Department of respiratory medicine the First Affiliated Hospital of Zhengzhou University Zhengzhou Henan China 450052

ABSTRACT Objective To investigate the

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★ E-mail chuheying@163.com

tion group and analyzed the diagnostic value of serum indicators for elderly COPD with severe respiratory failure and the correlation between serum indicators and the correlation between serum indicators and APACHE Ⅱ score and the prognostic value were analyzed. Results The levels of serum CysC VEGF IL 17 and ACTA in the three groups were statistically significant P<0.05 VEGF was negatively correlated with CysC IL 17 and ACTA levels and CysC IL 17 and ACTA levels were positively correlated P<0.05 the serum levels of CysC IL 17 ACTA and APACHE Ⅱ score were higher in dead patients than in surviving patients and VEGF levels were lower than in surviving patients P<0.05 VEGF level was negatively correlated with APACHE Ⅱ score and CysC IL 17 and ACTA levels were positively correlated with APACHE Ⅱ score P<0.05 the combined serum levels of CysC VEGF IL 17 and ACTA in predicting the prognosis of COPD with severe respiratory failure in elderly patients 0.864 was greater than that of a single serum indicator with a sensitivity of 92.86% and a specificity of 70.00%. Conclusion Serum CysC VEGF IL 17 and ACTA levels are abnormally expressed in elderly patients with COPD and severe respiratory failure and are closely related to the disease and the combined detection is expected to be an effective method for diagnosis and prognosis of elderly COPD with severe respiratory failure.

KEY WORDS Cystatin C Vascular endothelial growth factor Interleukin 17 Activin A Chronic obstructive pulmonary disease Respiratory failure

ه Chronic obstructive pulmonarydisease COPD ה ״ ã ' Ɔ ی [1] ه >40 ж COPD ה ' 8.2% Ấ 5 Ỉ 50.0% ه ١ ╗ † [2] ɟ Ь COPD I ɐ١ Ч ˋΩ¨E ε ' ה O ١ Ч ɟ Ă ה ١ Ч COPD ה ١ Ч ζ Ɑ ɕ ' m ' [3] ɟ C Cystatin C CysC ' Ҡ ١ Ч Ɔ Ɔ ĕ H ɟ Ỉ ɕ vascular endothelial growth factor VEGF Ɔ ɐ Ỉ ش [4] ɟ ч 17 Interleukin 17 IL 17 ɐ A Activin A ACTA ' ה א Ҡ ɟ Ă Ь CysC ɐVEGF ɐIL 17 ɐACTA ´ COPD Ɏ O ١ Ч ẇ ˜ ɵ e m ɟ ɲ Ь CysC ɐVEGF ɐ IL 17 ɐACTA Ά COPD Ɏ O ١ Ч ˜ Ă ɟ Ė I ŏ ; ɟ

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ɳ 2016 3 2019 3 224 ɻ COPD ה O ١ Ч ŏ n=78 ɐ n=146 Ɠ ɳ ˀ ɾ I 86 ɻ ε ɟ Ξ ɲ ɐ ɐ ɑ̈ ɐI ɑ́ τ P>0.05 ɕ ' 1 ɟ

1 n % $\bar{x} \pm s$

Table 1 Comparison of general data between the 2 groups n % $\bar{x} \pm s$

m		n=78	n=146	n=86	F/χ^2 e	P e
ɑ̈	/	45/33	84/62	49/37	0.010	0.995
		65.97±2.15	66.19±1.74	65.80±1.83	1.218	0.297
COPD		9.89±1.22	10.02±1.13	9.72±1.30	1.693	0.186
I	kg/m^2	22.79±2.20	23.15±2.08	22.94±2.13	0.779	0.460
´						
	♥	20 25.64	37 25.34	21 24.42		
		13 16.67	24 16.44	14 16.28	0.019	1.000
		8 10.26	14 9.59	8 9.30		

Ấ ΆA ①ح ´ COPD Ặ ΆA [5] ② ŏ ♥ <60 mmHg J ɔ ŏ ♥ > 50 mmHg ③ >60 ④ Ẇ ح ˛ Ш ɟ ΆA ①´ ɞ ɞ ② 6 ٧ ã ʄ ③ ɻ ɞ ɞ ɞ و ɞẅ Ὼ ل ن و ④ ٧ ٧ φ ´ ⑤ ε ɟ ├ Ң ٧ Ж ΆA ɟ

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1.2.1

ך 3 mL 12 min 3 000 r/min ŏ ך Нь-70 ỳ ң ך ɟ ã Ѧ ۵ Bio Bad ắ ˘ ẇ ẍ ٧ Cys C ɞVEGF ɗL 17 ɞACTA Ė I Ə ɞ ΆA ɞ ɨ Ƀ ɔ ΆA ɞ ɨ ŏ ặ ɨ 50 L ɞ μ ɨ 50 L μ₱ Нь 37 Ψ ʄ I Ά Ɑ ẅ ŏ א ɟ 30 min ˜ ح א 5 ˜ Ң 50 L μ Нь 37 30 min ɟ א 5 Ң ɟ 37 ẉ 10 min Нь 50 L μ א ɟ 15 min Ỉ 450 nm ˅ ˘ ٧ ẉ OD [e] ɟ

1.2.2

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1.2

① 3 CysC ɞVEGF ɗL 17 ɞACTA ɟ ② ŏ CysC ɞVEGF ɗL 17 ɞACTA φ Ặ ɟ ③ ˛ ˜ ɞ Ά ɨ Ỹ ŏ Ⅱ APACHE Ⅱ ŏ ę Ψ APACHEII ŏ ŏ 71 ŏ ɟ ④ ŏ CysC ɞVEGF ɗL 17 ɞACTA Ά APACHEII ŏ Ặ ɟ ⑤ ŏ CysC ɞVEGF ɗL 17 ɞACTA COPD ¥ O ٧ ٧ ˜ ɞ [e] ɟ

1.5

SPSS 22.0 Θ ŏ $\bar{x} \pm s$ t n % χ^2 ŏ Pearson Ặ ŏ ɔ Ə ROC ŏ ɞ ɞ [e] P<0.05 τ ɟ

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2.1 3 CysC ɞVEGF ɗL 17 ɞACTA

3 CysC ɞVEGF ɗL 17 ɞACTA τ P<0.05 ΄Y CysC ɗL 17 ɞACTA > > VEGF < < ɟ 2 ɟ

2 3 CysC VEGF IL 17 ACTA $\bar{x} \pm s$

Table 2 Comparison of serum CysC VEGF IL 17 and Acta levels between the 2 groups $\bar{x} \pm s$

ặ	n	Cys C ng/mL	VEGF mg/L	IL 17 ng/L	ACTA ng/L
	78	151.23±30.24[ab]	323.43±54.12[ab]	65.14±18.52[ab]	45.69±8.24[ab]
	146	130.47±24.58[b]	387.64±69.12[b]	44.87±15.76[b]	36.51±6.25[b]
	86	102.41±20.37	451.63±67.29	18.31±12.84	25.74±6.13
F [e]		79.021	79.267	182.984	178.781
P [e]		0.001	0.001	0.001	0.001

Ά [a]P<0.05 Ά ɨ [b]P<0.05

2.2 Ặ ŏ VEGF Ά CysC ɗL 17 ɞACTA ٧ Ặ Ặ CysC Ά IL 17 ɞACTA ٧ Ặ Ặ IL 17 Ά ACTA ٧ Ặ P<0.05 ɟ ۵ 1 ɟ

2.3 ˛ ˜ ɞAPACHEII ŏ ˜ H 28 ך 50 ך ɟ H CysC ɞIL 17 ɞACTA ɞ APACHE Ⅱ ŏ Нь VEGF ң Нь τ P<0.05 ɟ 3 ɟ

2.4 Ά APACHEII ŏ Ặ ŏ VEGF r=-0.349 Ά APACHE Ⅱ ŏ ٧ Ặ Ặ CysC r=0.836 ɞIL 17 r=0.654 ɞACTA r=0.675 Ά APACHE Ⅱ ŏ ٧ Ặ Ặ τ P<0.05 ɟ

VEGF mg/L
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14-3-3ζ and breast cancer

DONG Zhengyuan[1] YANG Qingling[2] CHEN Changjie[2]★

1. Key Laboratory of Cancer Transforming Medicine in Anhui Province Bengbu Medical College Bengbu Anhui China 233000 2. Department of Biochemistry & Molecular Biology Bengbu Medical College Bengbu Anhui China 233000

ABSTRACT The 14 3 3 protein family is a kind of acidic and highly conserved small molecule pro teins widely exists in eukaryotic cells. The 14 3 3 protein has no obvious catalytic activity and mainly inter acts with other proteins to regulate the target protein. 14 3 3ζ is one of the important members of the 14 3 3 protein family. Recently we found that found that 14 3 3ζ is a novel target for the cancer therapy. In this re view we focus on the current progress on breast cancer resistance recurrence and metastasis and discuss the potential of 14 3 3ζ serviced as an effective therapeutic target for breast cancer in patient whose tumors overexpress 14 3 3ζ.

KEY WOEDS 14 3 3ζprotein Breast cancer

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ĭ ᴍ Ǐ H Ύ ה ˥ w Ъ ɟ 14 3 3ζ Ά ´ ĭ ę
ɔ ╗ † ɟ Ψ Ὸ ɷ ǫ̆ [1] ɟ 14 3 3ζ m
Ỹ Ύ m מ ˝ ч מ ˝ ŭ ɷ
ה ĕ H ˥ Ψ ǫ̆ Ə [2 3] ɟ 14 3 3ζ
ǫ̆ ɟ ″H ж ˥ ה Ъ ς ל Ά ה ˥ ẇ

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[4] ɟ ŋŏ Ψ Ъ 14 3 3ζ Ά ę Ά † ה Ẇ ɷ ה ɷ Ă ŏ Ă ę Ə ε ɷí w Ẇ ɷ [e] ɟ

1 14 3 3ζ

14 3 3ζ ɱ ˝ ל Ά ה ה ɷ ɷ ė 14 3 3ζ ’ [m] ŏ [5] ɟ ŋŏ Ψ ɳ Hsp 27 14 3 3ζ Ă Ъ non small cell lung carcinoma NSCLC ˬ ۱ Ύ Hsp 27 ۱ 14 3 3ζ Ў ã̃ Hsp 27 ۱ 14 3 3ζ ˬ ۱ Ὼ [6] ɟ ŋŏ ◓ Ψ ◓ Ψ 14 3 3ζ Ъ 14 3 3ζ Ά ◓ TNM ŏ Ẇ ~ Ă ɳ ’ Ă ◓ ɯ ɷ ɷẆ I Ỉ ˬ ĕ H [7] ɟ ŋŏ Ă Ψ 14 3 3ζ ŋŏ Ψ ɳ ŋŏ Ψ ۷ Ύ Ά 14 3 3ζ Ă [8] ε í w[m] ɟ ŋŏ D ה Ψ Zhao JF [9] Ъ ASH 1 miR 375 14 3 3ζ ɱ ˝ ŋŏ ASH 1 ۱ miR 375 ; 14 3 3ζ ╗ ASH 1 ۱ miR 375 Ə ε Ă ė 14 3 3ζ ŋŏ D ה Ψ ɲ ė Ə ɟ ´ w ɔ ’ w ה 14 3 3ζ Ъ ה ’ Ė Ə ŋŏ Ψ ɟ

2 14 3 3ζ

† Ə ε Ψ ה ŋŏ [10] Ψ ה ς ĭ † ė [11] ɟ ˝H 14 3 3ζ ŋŏ † Ψ ɟ 14 3 3ζ ˚ ж Ѧ ה 14 3 3ζ ˚ c ŋŏ † Ə ŋŏ † ה ۱ ς Ă ɟ

2.1 14 3 3ζ Ά †

14 3 3ζ ɯ Ъ † ˚ ė ɯ ˀ ђ Ѧ ŋŏ MCF10A Ψ 14 3 3ζ ה 14 3 3ζ O ɔ ε 14 3 3ζ † ה ė [12] ɟ Rehman SK [13] ה 14 3 3ζ ɯ Ъ MAPK/c Jun ɱ ˝ ɯ Ъ miR 221 ɟ p27 CDKI ; ɯ Ύ 14 3 3ζ miR 221 p27 ɯ ς ŋŏ † Ψ ה Ə 14 3 3ζ ’ ŋŏ † ה ה Ψ ė Ə ɟ TGF β/Smad ɱ ˝ ŋŏ Ψ ה א ę Ψ 14 3 3ζ ה Ă Ə [14] ɟ TGF β ŋŏ ώ ל Ψ Ə ε Ў ė ж ŋŏ Ψ Ə ε ˬ Ή Xu J [15] Ъ TGF β ; ŏ Smads ה Ξ ˚ ’ ɟ ŋŏ † ɔ ώ ל Ψ 14 3 3ζ ɟ p53 ɱ Ў Ъ TGF β Ў ’ ˬ ה א φ 14 3 3ζ ’ ˬ TGF β ɟ 14 3 3ζ ɟ w ɔ 14 3 3ζ ŋŏ ה Ψ Ə ’ γ ε[m] یی ŏ Ъ † ɟ ɥ [m] Y ɥ ה ŋŏ ה Ă Ə † ל 14 3 3ζ Ά ė یی غ نح Ύ Ă ę † A lactate dehydrogenase A LDHA ŋŏ ж † ɔ Ψ 14 3 3ζ ɔ Ъ LDHA ή ɔ ˬ † ה [16] caffolding protein ŋŏ ɱ ˝ ן ה Ə ï ˈ ה نح Suen KM [17] ה ė یی Shc ɱ ˝ ERK ɔ ɟ ŋŏ ɕ † Triple Negative Breast Cancer Tnbc Ψ shc ɔ ɔ ɟ ά I یی ۱ ŏ [m] ה Shc ɔ ’ [n] 14 3 3ζ ۱ Pin 1 Akt ۱ ERK ɱ ˝ ╗ ɟ ’ I Ỉ 14 3 3ζ ’ ىئى † ה ŋŏ Ψ ה Ă Ə ɟ

2.2 14 3 3ζ Ά †

ŋŏ † Ψ 70% Ъ ɔ I † ε ɟ Ă Ỉ ŏ ۵ Ỉ † Ă

ę Ψ ħ Ə ε Ǐ ŏ m Ė
Ύ ϐң ӂ ğ Ψ
ה [18] ɟ Bergamaschi A [19] ה Ъ
ħ Ė ɔ 14 3 3ζ Ə ė ε
; Ό 14 3 3ζ microRNA 451 ɟ †
Ң miR 451 ; 14 3 3ζ
Ъ SERMs Ǐ ŏ Ϊ Ạ Ə ɟ
Liu ZR [20] m ה miR 451a
’ ѽ MCF 7 ۱ LCC 2 ħ
ɟ miR 451a Ά 14 3 3ζ ۷ Ă 14 3 3ζ
ң ѽ ĕ H 14 3 3ζ Ά miR 451a Ў
Ϊ Ạ ħ Ə w 14 3 3ζ
ħ Ė Ă Ə ɟ 14 3 3ζ Ə ε Ǐ
ŏ ė
ɱ ˝ ǐ Ύ ۱ Ǐ
ŏ w ˜ 14 3 3ζ ẇ ę Ǎ
FOXM 1 ğ Ǐ ŏ Ė
ɵ e [21] ɟ ’ 14 3 3ζ Ό ε †
Ъ ɟ
2.3 14 3 3ζ Ά † ה
ε Ъ † ۷
ϐ ϐɔ ϐǏ ŏ
ė ε ˜ ה ʄ
ɟ Ύ ǭ ה Ɑ ė ŏ
Ϊ Ạ ɟ ѿ ה 14 3 3ζ ’ †
ה ŏ Ϊ Ạ [22] ɟ ğ ה Ψ 14 3 3ζ
ε 70% ~75% Ɑ ה ε
45% [23] ɟ ğ † Ψ 14 3 3ζ ת ė
Ƀ Ά H ŏ ۱ ŏ Ă ’ Ƀ
ẉ B ϐ 1 ϭCDC25B ۱ birc5 ת
ė Ά † ה Ă [24] ь ת ė
Ъ 14 3 3ζ Ά † ה Ă Ė Ն
ɵ e ɟ Li Y

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2 ĕ ж ĕ ц Ğ ├ . 14 3 3 zeta Ά ђ † Ą J . ├ 2017 47 3 192 196.

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⋆ E-mail 864925019@qq.com

1.1 WNT

WNT ŏ ▌ MB 10% [7] ɟ ۱ φ ה

ج 10 [8] ɟ ה ם ה

Ό [9] ж Ж ҢЊ Ψ Ύ

۱ [10] ė Ά ę ђ ŏ

Ж ~ 5 95% [11] ɟ

Turcot ´ Ъ ם ה ה ה

Ў ɟ

FAP ۱ Ж HNPCC

Ж Ά FAP Ă ɟ

FAP APC ח ė ɞ ל

APC ' P WNT ŏ

β catenin ė ى WNT/β catenin מ ״

Ψ ח ė ъ [12] ɟ WNT

MB CTNNB1 ח ė 3

ל WNT מ ״ ъ β

ъ MB ɟ Ά APC

ל Ă Ж ى Ė

~ [13] ɟ Ж Ψ ō[m] Y ל DDX3X ח

ė ח ė [m] ' RNA

I ŏ ۱ ۷ [14] ɟ Ж ɔ 6 ״

I ╥ I Ψ ל ɟ

WNT Ƀ Ξ Y Ж ى WNTα

70% ۱ WNTβ 30% WNTα ṿ

ʺH ω З ╥ I 6 ى ל WNTβ

ζ ж ╥ I 6 ى [15] ɟ

1.2 SHH

SHH ▌ 30% ʒ

۷ Ӑ ŏ ζ Ψ ğ 5 w ; ẇ 16 w

ɔ ɟ ~ ' Ά З

STAT3 Ă [16] ɟ SHH ה Ъ ╚

Ж ى Ң [10 17] ɟ ה ״ ǫ̃ 25% ğ

MB Ψ З ~ Ψ 5

ε 75% [11] ɟ

SHH ğ Ъ SHH מ ״

מ ״ Ă Ẉ ğ Gorlin ´

Ψ ה З ח ה

ה ם ۱ MBs MBENs [18] ɟ

Gorlin ´ ζ PTCH1 ʺĄ ח ė ל

ח ė PTC1 SHH ɔ I ɟ

SHH Ά PCT1 ´ Ъ G g ɔ I

ɔ SMO ъ ъ SUFU Ψ GLI

ė ɟ GLI ė Ң ۱ ח

ė Ƀ З ל Ά ם ח ė

MYCN ɞCCND1 ъ [19] ɟ ė

ʺĄ SMO ъ SHH מ ״ ~

Ė Ъ ' ɟ TP53 ל Ά Li Fraume

ni syndrome ´ LFS Ă ל ğ 30%

ṿ SHH MBs Ψ ' ה Ύ Ά ~

Ă [20] ɟ GPR161 ל ς Ά ṿ SHH MBs

Ą [21] ɟ ε ǫ̈ ה U1 snRNA ל ה ğ

5′ ṇ Ң ´ ⌟ ⌟ ל ى U1

snRNA ч ṇ ƒ ʺĄ ח ė

PTCH1 ח ė GLI2 ۱ CCND2

ל ğ SHH ى MB Ψ ζ Ψ ğ

97% ж SHHδ Ж ى ۱ 25% SHHα

Ж ى [22 23] ɟ Ж ζ ה ى MB

ğ Ƀ I 3q ם Ά 9q ɞ10q ۱ 14q M ɟ

[m] SHH MB ŏ ε ظ Y Ж ى SHHα Ж ى

ˉ TP53 ל ɞ ⁄ [1]/[8] αp Ρg ڃ α p α

Ὸ MYC ▫ ~ [15] ɟ

1.4 Group 4

Group 4 MB Ж ▌ ʒ

35% [7] ~ Ψ 5 ε 75% [11] ɟ

ה ה ɕ ʁ ɟ Group 4

Ң Њ Ψ / ظ ' Á Њ ɔ

Ὺ Ψ EOMES ≀ LIM ̓ ġ

1α LMX1A Ặ [28] 35%~40% ğ

[24] ɟ

Group 4 Ψ ƾ Ƀ

ת ת ġ KDM6A ƾ ɞ ̓ α

Ў Θ SNCAIP ת ġ é Ậ ɞMYCN

≀ CDK6 ת ġ ▫ ɟ Northcott ה PRDM6

4 Ψ ɔ ▫ ĭ ת ġ Ὺ

PRDM6 ҢЊ SNCAIP ; 600 kb ẹ ğ SNCAIP

Ậ Group 4 Ψ ╗ [26] ɟ

≀ ŏ Ъ א

ERBB4 SRC מ ˝ Group 4 [29] ɟ Ӄ

ɔ l 17q ɟ Ɠ Group 4 MB

ς ğ Жیی Group 4α ≀ Group 4γ ğ CDK6

▫ ɞp l M ɯ ẇ 7q l ▫ Group

4β ̄ SNCAIP ≀ PRDM6 [30] ɟ

2

ὦ ắ MB ɯ ẇ ~ ɔ

ˊ Ж Щ ̋ ü ɟ

12.8% MB Њ ;

ς O ~ Ƀ ɞĪ

ŏ ≀ ה ɟ ġ ὦ ~

ζ ╗ ≀ ˝E /˝E ה ɟ

2.1 ● ŏ

ὦ í ● ŏ 3 ɯ ɔ ŏ ε

ƛ ğ æ ˝Ω ε Ƀ

ɞ æ

1.5 cm² ɟ ŏ ğ Ẉ ὦ ŏ ת

ɔ ẇ Ъ ɟ ὦ MB

ŏ ε 4 Y ● ң >90% ɞ ɕ

ƛ 75%~90% ɞ 50%~75%

≀ <50% ɟ ң

ζ Ƀ WNT ≀ Group 4 11 ˝

l ã 17 ˝ l ã ▫ ɕ Ƀ

Group3 ẇ Group 4 MB ɞ̋ ¥ MYC

▫ Group3 ● ζ Ƀ SHH ɞ

¥ MYCN ▫ SHH ɯ ẇ Group4 MB

● Ƀ Group3 ¥ TP53 ƾ

SHH [31] ɟ ● ŏ Ƀ̌ Ъ ŏ

ε MB ~ ɯ Ъ ƾ ε ӧ

˝E ɞɔ Ὲ Θ ậ Ъ ɟ

2.2

ε ã̃ Ὺ GTR MB ת

ὦ Ὺ م Ъ ɟ

Thompson Ὸ Á ã̃ Ὺ NTR GTR

ɟ

Њ Group4 MB NTR ╗ Ж

╗ [32] ɟ ġ ậ GTR ' Ӂ

[m] ≀ GTR ̋ ˊ ὦ ƛ

ẅ ŏ Á ⅂ ɔ

~ ה ε Ъ ɟ

2.3

̋ Ὺ ă ~ ˝H ω Ж

≀ ה ɟ MB

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Ὲ Θ WNT MB

Ὴ 24 Gy ˝E 18Gy Є ɯ

ẇ ɯ ъ ˝E Ὲ Θ

[33] ɟ Ӄ ɯ XRT

≀ PRT Á XRT ˝E

Ъ Ὴ ъ ğ ~ Ὼ ⅂

Ė Б † [34 35] ɟ

2.4 ɔ

ɔ ς MB φ[m] ẹ

Њ 3 ɯ ; ỵ ɔ ˝H ω ~ Ո[m]

ɟ ὦ ɔ ẇ ʒ ɞ

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ъ ŏ Ψ Ⱨ ה SHH Á PCT1 ˊ

Ъ G g ɔ l ɔ SMO SHH

MB ה ġ ɟ Ὺ ẹ ɞң

SMO Њ SHH ▫ ≀ ˬ

[36] ɟ ġ SMO Ậ Ὴ ε

ה ɟ ʒ Robinson Vismo

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