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P35

HE ×200

Figure P35 The positive results of TCT in patients with malignant peritoneal effusion HE ×200.

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分子诊断与治疗杂志

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DaAn Gene Co., Ltd. of Sun Yat-sen University

TianYi Yofus Technology Co., Ltd

分子诊断与治疗杂志

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6	1		
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	EGFR BRAF		23
NGS			28
DNA			33
	AFP TP ALB SOD		37
			41
	3 221	HPV13		
			46
PCR			50
			55
			61
			67
			

COMMENTS

6 kinds of common technologies of separating and enriching circulating tumor cells

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JIANG Xiwen, ZHU Xiaoya, GAO Xiujie, ZHOU Qiwei

6

circulating tumor cells CTCs

6 CTCs

CTCs

JIANG Neng, CUI Yongmei, LI Shuhua, ZHENG Xiaoke, YANG Zheng, WANG Liantang, KE Zunfu (Department of Pathology, the First Affiliated Hospital, Sun Yat-sen University, Guangzhou, Guangdong, China, 510080)

[ABSTRACT] During the past ten years, circulating tumor cells (CTCs) have received enormous attention as potential research direction, because of the potential value in the early diagnosis of cancer, prediction of clinical prognosis, evaluation of therapeutic efficiency, development of targeted drugs, and personalized medicine of malignant cancer. Circulating tumor cells (CTCs) have been regarded as minimally invasive and promising diagnostic and prognostic biomarkers for patients with metastatic tumors. Multiple highly sensitive approaches and devices have been developed to separate and enrich CTCs in the blood. We have summarized 6 kinds of separation and enrichment technologies of CTCs with the opportunities and challenges faced during the development of these systems, this article also provides reference frame for an optimized separation and enrichment technology and highlight some directions for the precision medicine of cancer treatment.

[KEY WORDS] Circulating tumor cells (CTCs); Precision medicine; Separation and enrichment

circulating tumor cells CTCs

CTCs

CTCs

1

30900650/H1615 81372501/H1615 81572260/H1615 81172232/H1615 81172564/H162
2011B031800025 S2012010008378 S2012010008270 S2013010015327 2013B021800126
20090171120070 9451008901002146 2013B021800126 2015A020214010 and 2013B021800259
2015ykzd07

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E mail kezunfu@126.com

CTCs

2-4

CTCs

5-6

CTCs

2 7 8

9-11 CTCs

6 CTCs

NanoVelcro cell-affinity substrates CTC

Aptamer

microfluidics chip technology

Micro filter technology

2 12

1 CTCs

1.1 NanoVelcro cell-affinity substrates CTC

NanoVelcro CTC

CTCs

Silicon nanowire substrate

SiNS

CTCs²

SiNS

epithelial cell adhesion molecule EpCAM

CTCs

EpCAM

EpCAM

CTCs

NanoVelcro

CTC

3

1

SiNS

**

Polydimethylsiloxane PDMS



NanoVelcro

PDMS

CTCs

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CTCs

CTCs

Clearbridge RareCell
3D 37

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CTCs

Search CAM 7.5 mL Cell-Ep-
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EpCAM CTC

MagSweeper IsoFlux 1.6
CTCs

VerIFAST 26-28
Massachusetts General Hospi-
tal MGH 29

1.4

PDMS

CTCs

EpCAM EpCAM

CTCs CTCs

CTCs

CTCs 90

8 30-32

1.5

Micro filter

Isolation by size of epithelial tumor cells IS-
ET 33

CTCs 34-35 CTCs

CTCs

- 16 Shen Q Xu L Zhao L et al. Specific capture and release of circulating tumor cells using aptamer-modified nanosubstrates J . *Adv Mater* 2013 25 16 2368-2373.
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met all inclusion criteria and were included in this meta-analysis. Our results revealed that the 677C
 T polymorphism might increase the risk of CVD (Allele T C: OR=1.39, 95%CI=1.17, 1.65, =0.000 2; TT
 CC: OR=1.57, 95%CI=1.16, 2.12, =0.003; TC CC: OR=1.69, 95%CI=1.26, 2.27, =0.000 4; TT+TC
 CC: OR=1.53, 95% CI=1.21, 1.94, =0.000 5; TT TC + CC: OR=1.37, 95% CI=1.08, 1.73, =0.01;
 respectively). Further subgroup analysis by variety of disease and age range suggested that the 677C
 T polymorphism was associated with an elevated risk for CVD among coronary heart disease (TT TC+CC:
 OR=1.38, 95%CI=1.17, 1.62, =0.000 1), myocardial infarction (Allele T C: OR=1.71, 95%CI=1.37, 2.13,
 0.000 01), with age range of less than 50 years (TT CC: OR=2.23, 95% CI=1.58, 3.17, TC

Diseases, Cardiovascular[Text Word]) OR Cardiovascular Diseases[Text Word])) AND ((((((Methylene-tetrahydrofolate Reductase[Text Word]) OR Methylene-THF Reductase[Text Word]) OR 5,10-Methylenetetrahydrofolate Reductase[Text Word]) OR Methylene Tetrahydrofolate Reductase[Text Word]) OR Tetrahydrofolate Reductase, Methylene[Text Word]) OR MTHFR[Text Word]) OR NADPH[Text Word])

1.4

Newcastle-Ottawa Scale NOS⁸

-
NOS

8

0~4

0~2

0~3

NOS

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4~6

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+

SNP *

1.5

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Meta

Stata

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677C T

0.05 I² 50%

random effects

4

model REM

Meta

5

fixed effects model

FEM

Meta

REM

FEM

Meta

95%

95%

CI

C677T

6

C677T

<0.05

-

Hardy-Weinberg HWE

1.2.2

1

-

2

3

1.3

1

2

3

4

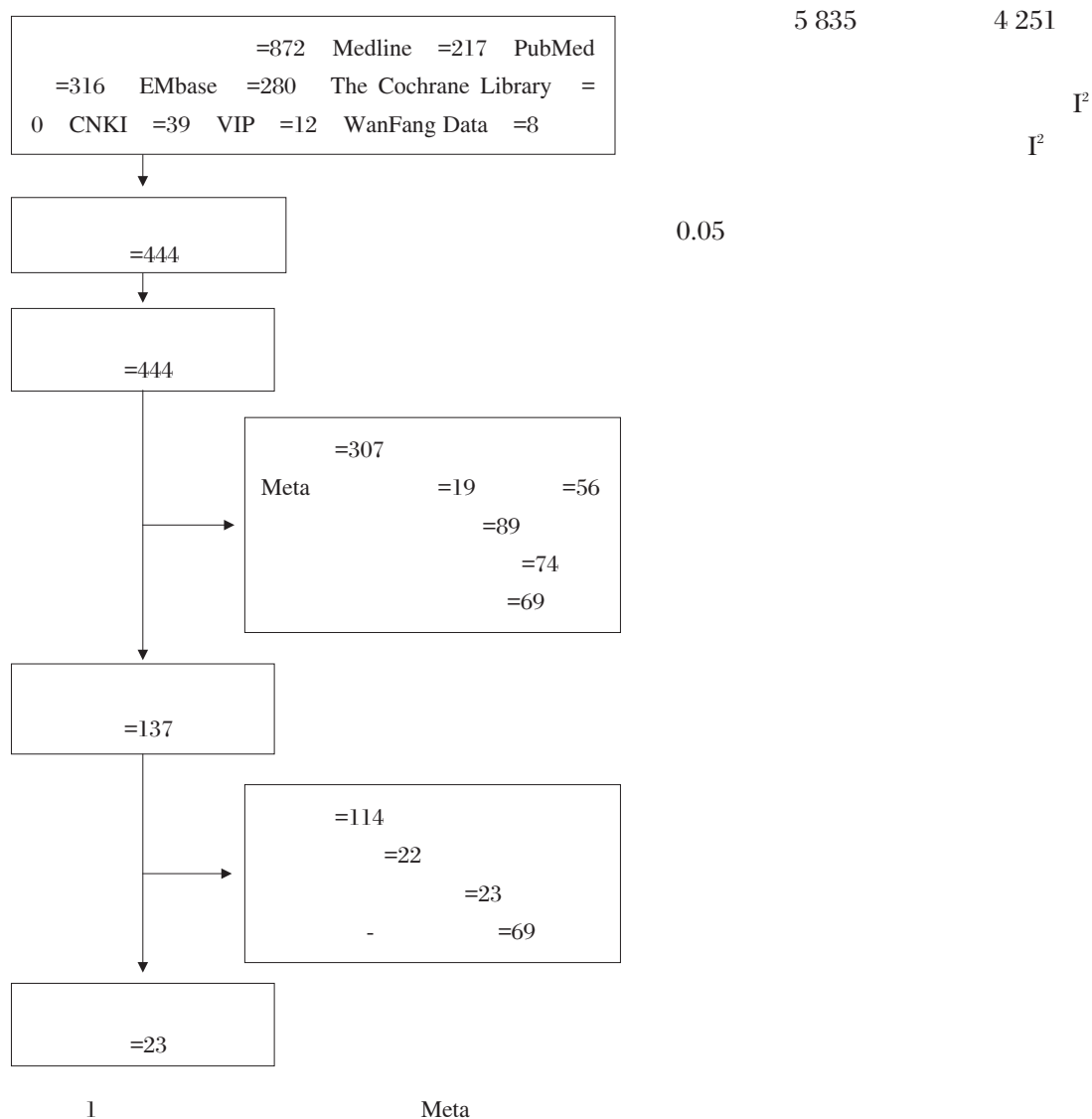


Figure 1 Flow chart of the study selection process and specific reasons for exclusion from the meta-analysis

2.2

23
 Hardy-Weinberg 20
 Hardy-Weinberg 3
 3 50
 6 50~60 8 60~70
 4 70 2
 NOS 7

1

2.3 Meta

23 C677T

		/	/	
Juan 2015 ¹⁰		373/391	58/53	
Javed 2012 ¹¹		377/393	63.1±10.9/61.0±10.5	
Alexandre 2007 ¹²		91/36	60.3±12/60.4±12	
Soujatya 2010 ¹³		217/255	42.60/40.53	
Angeline 2009 ¹⁴		120/100	–	
Nevin 2008 ¹⁵	–	78/100	57.2±10.0/57.5±11.1	
Nevin 2008 ¹⁵	–	100/100	58.3±9.9/57.5±11.1	
Jones 2005 ¹⁶		271/282	64.0±9.5/69.5±7.6	
Angeline 2004 ¹⁷		52/20	–	
Klaus 2004 ¹⁸		2121/617	66.8±12.8/60.8±12.4	
Irena 2003 ¹⁹		247/298	–	*
Lakhdar 2009 ²⁰		352/390	58.0±11.5/57.3±7.6	
Vasisht 2002 ²¹		141/55	52±10/50±11	
Anne 2001 ²²		110/185	56/55	
Sadi 2001 ²³		96/100	38±7/37±5	
S.Friso 2002 ²⁴		302/168	60.6±9.3/58.2±12.8	
Hamdia 2014 ²⁵		30/15	45.5±4.8/43.2±4.3	
Prithiksha 2015 ²⁶		106/100	37.6/37.5	
Dhouha 2014 ²⁷		100/200	46.92±7.62/31±9.6	
Andrzej 2001 ²⁸	–	161/211	43.6±4.7/43.7±5.6	
2007 ²⁹		87/73	71.9±13.2/67.8±13.6	
2010 ³⁰		114/31	77.4±5.68/75.9±4.26	
2007 ³¹		189/131	56±10/54±11	

Continued table 1 The basic characteristics of all included studies

	/			HWE	NOS		
	TT	TC	CC				
Juan 2015 ¹⁰	87/101	174/200	112/90	0.64	3	2	3
Javed 2012 ¹¹	33/35	174/183	170/175	0.19	4	2	3
Alexandre 2007 ¹²	6/2	59/20	26/14	0.13	4	2	3
Soujatya 2010 ¹³	58/33	47/36	112/186	0.00	3	2	3
Angeline 2009 ¹⁴	0/0	32/20	88/80	0.27	3	1	3
Nevin 2008 ¹⁵	10/2	32/26	36/72	0.84	4	2	3
Nevin 2008 ¹⁵	4/2	44/26	52/72	0.84	4	2	3
Jones 2005 ¹⁶	30/26	104/122	137/134	0.81	3	2	3
Angeline 2004 ¹⁷	1/0	10/3	41/17	0.72	4	1	3
Klaus 2004 ¹⁸	251/68	955/283	915/266	0.57	4	2	3
Irena 2003 ¹⁹	22/18	111/146	114/134	0.001	4	1	3
Lakhdar 2009 ²⁰	46/20	149/123	157/247	0.36	3	2	3
Vasisht 2002 ²¹	11/2	32/14	98/39	0.60	3	2	3
Anne 2001 ²²	2/4	17/28	91/153	0.06	4	2	3
Sadi 2001 ²³	15/5	39/35	42/60	0.97	4	2	3
S.Friso 2002 ²⁴	46/30	156/90	100/48	0.28	3	2	3
Hamdia 2014 ²⁵	2/0	16/2	12/13	0.78	4	2	3
Prithiksha 2015 ²⁶	2/0	25/14	79/86	0.45	4	2	3
Dhouha 2014 ²⁷	2/17	82/79	16/104	0.72	4	2	3
Andrzej 2001 ²⁸	17/18	39/75	105/118	0.23	3	2	3
2007 ²⁹	4/1	54/25	29/47	0.25	3	2	3
2010 ³⁰	27/6	51/15	36/10	0.93	4	2	3
2007 ³¹	37/23	108/47	44/61	0.01	4	2	3

HWE - NOS Newcastle-Ottawa Scale 0~4 1
 1 1 1 0~2 1 1 2 0~3

677C T
 TT CC OR=2.75 95%CI 1.35 5.59 =0.005
 2.5 TT CC+CT OR=2.52 95% CI 1.25 5.09 =
 0.010

Meta
 Begg s 3 5
 Bozok³³
 TT CC
 OR=2.34 95%CI 1.40 3.93 =0.001
 3

Meta
 T McCully³⁴ 1969 Hcy
 C677T Hcy
 Hcy

T
 32

2 Meta

Table 2 Summary of subgroup and meta-regression analysis results

			I ² %		Meta		
			OR	95CI			
T vs C	23	0.000 01	82	1.39	1.17,1.65	0.000 2	
TT vs CC	23	0.000 1	65	1.57	1.16,2.12	0.003	
TC vs CC	23	0.000 01	88	1.69	1.26,2.27	0.000 4	
TT+TC vs CC	23	0.000 01	84	1.53	1.21,1.94	0.000 5	
TT vs TC+CC	23	0.004	50	1.37	1.08,1.73	0.01	
T vs C	14	0.000 01	83	1.36	1.10,1.68	0.004	
TT vs CC	14	0.001	61	1.64	1.18,2.28	0.004	
TC vs CC	14	0.000 01	89	1.69	1.15,2.48	0.007	
TT+TC vs CC	14	0.000 01	84	1.44	1.09,1.91	0.01	
TT vs TC+CC	14	0.07	39	1.38	1.17,1.62	0.000 1	
T vs C	6	0.15	39	1.71	1.37,2.13	0.000 01	
TT vs CC	6	0.31	17	2.05	1.05,4.04	0.04	
TC vs CC	6	0.000 2	79	2.23	1.10,4.52	0.03	
TT+TC vs CC	6	0.000 8	76	2.25	1.18,4.29	0.01	
TT vs TC+CC	6	0.05	58	1.10	0.31,3.94	0.88	
T vs C	3	0.000 1	90	1.23	0.76,2.00	0.4	
TT vs CC	3	0.004	82	1.30	0.54,3.13	0.56	
TC vs CC	3	0.004	82	1.11	0.64,1.91	0.72	
TT+TC vs CC	3	0.000 2	88	1.19	0.63,2.24	0.59	
TT vs TC+CC	3	0.03	71	1.21	0.63,2.30	0.57	
TT vs CC	6	0.1	46	2.23	1.58,3.17	0.000 01	
50 TT+TC vs CC	6	0.000 01	88	2.38	1.20,4.74	0.01	
TT vs CC	8	0.000 01	81	1.77	0.91,3.44	0.09	
50~60 TT+TC vs CC	8	0.000 01	87	1.49	0.96,2.33	0.08	
TT vs CC	6	0.71	0	1.10	0.88,1.39	0.4	
60 TT+TC vs CC	6	0.006	69	1.18	0.88,1.60	0.27	

Hcy

35

C677T

Hcy

37

28%³⁶ C T C677T

MTHFR

3

Hcy

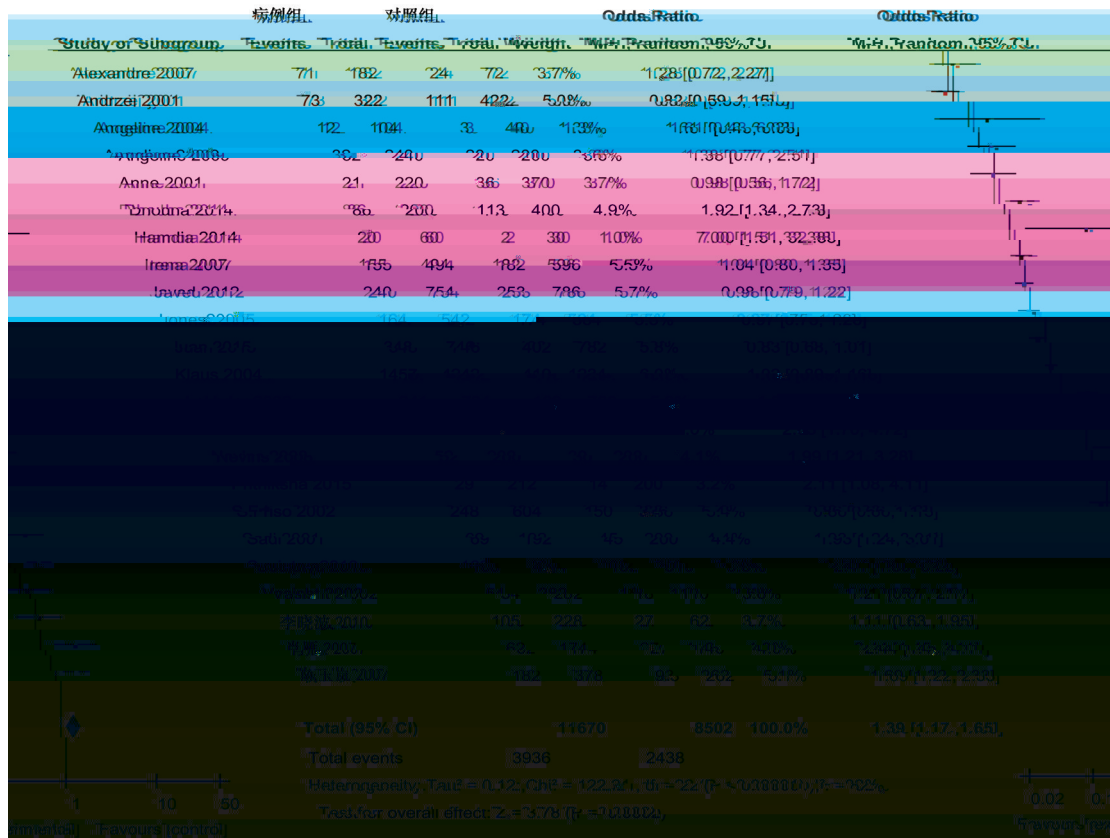
Hcy

Meta

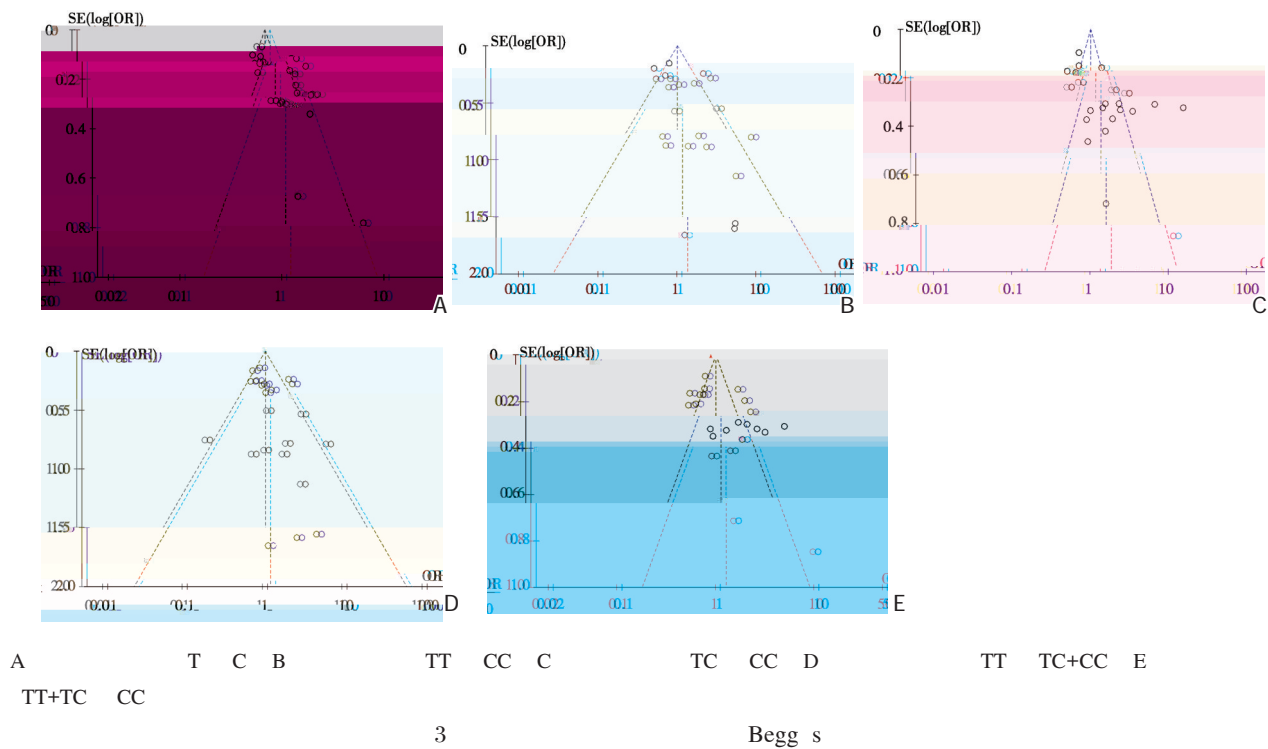
Hcy

Meta

Hcy



2 C677T Meta
 Figure 2 The meta analysis of the association between the gene polymorphism C677T and cardiovascular disease allele model



3 Begg's
 Figure 3 Begg's Funnel plot of publication biases on various genetic model

- 1
23
3
- C677T
T
- 1 . MTHFR C677T
J .
2014 40 6 409-410.
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reagent for clinical isolates of MTB, the DNA of 48 EMB resistance, 46 EMB sensitive but resistance to other drugs and 7 sensitive to four drugs of MTB were extracted and amplified gene sequence. The amplified products were then sequenced and analyzed the gene sequence of each MTB, compared with H37Rv standard strain in Genbank, the mutation sites, the form and the frequency of gene were analyzed. Results 17 different mutant forms were found in 101 strains of MTB gene. 53 strains of MTB mutated in the gene, 46 strains of which were EMB resistant, 7 were EMB sensitive; 48 strains of MTB were wild type in the gene, 2 strains of which were EMB resistant, 46 were EMB sensitive. There were significant differences in the drug resistance positive rates of EMB between mutation and wild type ($\chi^2=68.95$, $P<0.01$). There were 51 strains MDR in 101 MTB, including 42 strains of mutation, and 9 strains of wildtype, the mutation rate of gene was significantly different between MDR and non-MDR ($\chi^2=36.9$, $P<0.01$). Conclusion 306 mutation is moderately related to EMB resistance in MTB, mutation of gene is highly associated with EMB resistance and MDR-TB, the gene can be used as a marker for the detection of MDR-TB, which could be used guideline for clinical drug use.

[KEY WORDS] ; gene; Mutation; Ethambutol; MDR

2013
85.5
multi-
drug resistant MDR 5.4
MDR 1
MDR 1.1
MDR 2013 1 2014 5
9 038 MTB
ethambutol EMB MTB 2 243 865 BD
EMB MGIT 960 SIRE EMB
48 5.55% 48/865 EMB
MTB - - 46 4 7 101

1.2
2 MTB
MTB EMB BD MGIT 960
SIRE ri-
fampin RFP isonicazide INH EMB
3 Morkrouslv 4 streptomycin SM
306 EMB 1 mg/L 0.1 mg/L 5 mg/L 1 mg/L
48.3% EMB 32.5% EMB R S MDR
MTB 306 306 2

1.3
EMB MTB 1 mL 80°C 60
285Phe Leu 330Phe Val 630Thr Ile 4-6 min 13 300 rpm 10 min 1 mL
306 EMB MTB 13 300 rpm 10 min
50 µL
MTB 3 297 bp 100°C×10 min 13 300 rpm
EMB 10 min PCR

1.4 306 27 26 306
 EMB 1 306
 M.tuber- MTB EMB 497 Q K Q H Q
 culosis H37Rv GenBank ac- P 406 328 354 330 319 405 1 024 521
 cession no. NC_000962 MTB EMB 246 679 113
 3 297 bp PCR 5'-3' 534 MTB EMB 201
 AATCAGGCTCCAGACGC 5'-3' 306 MTB EMB
 TACCGAGCAGCATAGGAG PCR 609 330 MTB
 1 94°C 1 min 2 94°C 30 s EMB 246 497 Q R 573
 3 58°C 30 s 4 72°C 210 s 5 MTB EMB
 2 ~ 4 30 6 72°C 7 min 7 12°C 2
 Sanger 2.3 EMB
 DNASTAR Lasergene 101 53 MTB
 46 EMB
 86.8% 46/53 7 EMB
 13.2% 7/53 48 MTB
 1.5 EMB 2 MTB EMB
 SPSS 19.0 4.2% 2/48 46
 MTB EMB
 <0.05 MTB EMB
 2 MTB EMB MTB
 2.1 EMB 3
 101 MTB 48 2.4 MDR-TB
 EMB 53 EMB MDR 51 4 101 MDR-TB 51
 20 1 MDR-TB 42
 1 101 MTB 82.3% 42/51 MDR-TB 9
 17.6 % 9/51 MDR-TB
 Table 1 Results of drug sensitivity of 101 strains of MTB
 by ratio method

	EMB =48		EMB =53	
	R	S	R	S
RFP	40	8	19	34
INH	47	1	19	34
SM	40	8	38	15

2.2 17 tbdreamdb 7 306 406 534 46/48 MTB EMB
 328 497 Q K Q R 1 024 EMB
 tbdreamdb MTB 113 EMB
 201 246 319 330 354 405 573 521 609 679 EMB
 Q497P Q497H 2

[REDACTED]			
[REDACTED]			
			13
embB306	ATG->ATC	M306I	2
	ATG->ATA	M306I	7
	ATG->CTG	M306L	1
[embB306	ATG->GTG	M306V	
embB534	GAC->GAT	D534D	2
embB497]	CAG->CCG	Q497P	
[embB306	ATG->GTG	M306V	
[REDACTED]			
			1
[embB306	ATG->ATA	M306I	
[REDACTED]			
			1
	GGC->GCC	G406A	2
embB246	GGC->CGC	G246R	1
embB521	GAG->GCG	E521A	2
embB534	GAC->GAT	D534D	2
embB354	GAC->GCC	D354A	1
[embB354	GAC->GCC	D354A	
			1
embB534]	GAC->GAT	D534D	
embB328	GAT->TAT	D328Y	2
	GAT->GGT	D328G	1
[embB328	GAT->GGT	D328G	
			1
embB406]	GGC->GCC	G406A	
embB113	GCG->GTG	A113V	1
embB679	GCC->ACC	A679T	
embB1024	GAC->AAC	D1024N	
embB497	CAG->AAG	Q497K	
	CAG->CGG	Q497R	
[embB534	GAC->GAT	D534D	
embB497]	GAC->GAT	Q497H	
embB405	GAG->GAC	E405D	
embB330	TTC->TCC	F330S	
[embB330	TTC->ATC	F330I	
embB609]	CTG->CGG	L609R	
embB319	TAT->CAT	Y319H	
	TAT->TCT	Y319S	
[embB246	GGC->CGC	G246R	
embB497	CAG->CGG	Q497R	
embB573]	CGG->TGG	R573W	

3 *embB* *embB* MTB EMB
 Table 3 Analysis of drug resistance of EMB between *embB* gene mutation and wild type in MTB(strains)

	EMB	EMB	MTB	EMB	c ²	df	
	46	7	53		68.95	1	<0.01
	2	46	48				
	48	53	101				

SPSS 19.0 <0.05 df

4 MDR-TB
 Table 4 Results of MDR-TB drug sensitivity

	EMB			<i>embB</i>			<i>embB</i>			MDR TB			
	MDR TB			MDR TB									
	RFP	INH	EMB SM	RFP	INH	SM	RFP	INH	SM	RFP	INH	EMB	SM
<i>embB306</i>	3		18	21									
<i>embB497</i>	1		2	3									
<i>embB406</i>			3	3									
<i>embB405</i>			1	1									
<i>embB328</i>			3	3									
<i>embB330</i>			2	2									
<i>embB319</i>			2	2									
<i>embB246</i>													
<i>embB534</i>						1							1
<i>embB573</i>													
<i>embB679</i>					1								1
<i>embB113</i>					1								1
<i>embB201</i>													
<i>embB354</i>	1		1	2									
<i>embB1024</i>	1			1									
<i>embB521</i>													
<i>embB609</i>													
none							3	5		1	9		
	6		32	38	2	2	4	3	5	1	9		
306	MDR-TB			306	328	406	MDR-TB			406			
330	609	MDR			330								

54.2% 26/48

MDR

95.8% 46/48

MDR

MTB EMB

MDR-TB

Shi¹³

306

306

MTB

EMB

EMB

MDR

MTB

EMB

EMB

MTB

27%~

306

87%

306

8-9 14-15

MTB

EMB

96.3%

26/27

98.1%

306

27

52/53

306

EMB

49.3% 27/53

306

306

MTB

EMB

306

MTB

EMB

MTB

EMB^{13 15-17}

306

306

MTB

EMB

MTB

EMB

5 MDR-TB
Table 5 Analysis of MDR-TB between gene mutation and wild type(strains)

	MDR TB	MDR TB		²	df	P
<i>embB</i>	42	11	53	36.9	1	<0.01
<i>embB</i>	9	39	48			
	51	50	101			

SPSS 19.0

<0.05

df

15%^{13 15 22 24}

Safi¹⁸ MDR 306

EMB 3 RFP 306

INH SM 306

MTB MDR 81.5% 22/27 306

MDR²⁰ 306

MDR-TB MTB

306 MDR 43.1% 22/51

306 MDR-TB

306 MDR 82.3%

42/51 306

MDR 306

MDR-TB

EMB MDR-TB

406 497 MTB EMB

MDR 406 497 406 497 328 354 1024

306 2 81.3% 39/48 328 354 1024

¹⁵ 406 EMB 100% 5/5 EMB

MDR 80% 4/5 497 EMB 405 521 330 319 534 246 113 679

83.3% 5/6 MDR 83.3% 5/6 406 497 201 609 573 MTB EMB

EMB MDR

406 497 EMB tbdreamdb tb-

^{13 15 21-25} 406 497 dreamdb ^{13-15 21-24 27}

MTB EMB²³ 406 EMB MDR

497 EMB 406 MTB EMB

497 306 MTB EMB MDR

306 EMB MDR

Xu¹⁵ EMB MTB 306 EMB MDR

406 497 MDR-TB

MDR- 406 497

TB 406 497 5%~ EMB MDR-TB

354 1024 319 330 405 521 EMB MDR
 MDR-TB
 306 497 406 328
 EMB
 900~1500
 Shi¹³
 EMB
 EMB ethambutol resistance
 determining region ERDR
 MTB EMB MDR
 EMB MTB

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 2013 32 2 13-17.
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• •

EGFR KRAS

1

2

next generation sequencing NGS
108

1-2

3

4-5

2015B020233009

1.

510665

2

510515

E mail yxzb@schu.com

chain reaction qPCR
 quantitative polymerase
 qPCR

brary kit 2.0
 DNA
 DNA
 DNA
 PCR

PI
 DNA
 10 G

200 pmol/μL
 800 pmolDNA
 Ion PI™ Template OT2 Kit v3
 PCR
 PCR

200 Kit
 Ion PI™ Hi-Q™ Sequencing
 DA8600

loading
 =Qubit ng/μL × 10⁷/ 200 ×

DNA
 Ion Torrent
 7-8

660×2
 1.3.3

Torrent source
 Variant Caller Coverage Analysis

1

1.1

QIAamp® DNA FFPE Tissue Kit
 Ion Ampliseq™ library kit 2.0
 Ion PI™ Template OT2 Kit v3
 Ion PI™ Hi-Q™ Sequencing
 200 Kit
 Life Technology
 Nuclease-Free Water
 Life Technologies

5%
 5%

Hotspot

DA8600
 ABI 3500

1.2

2013	2015	
108	58	50
35	88	

1.3

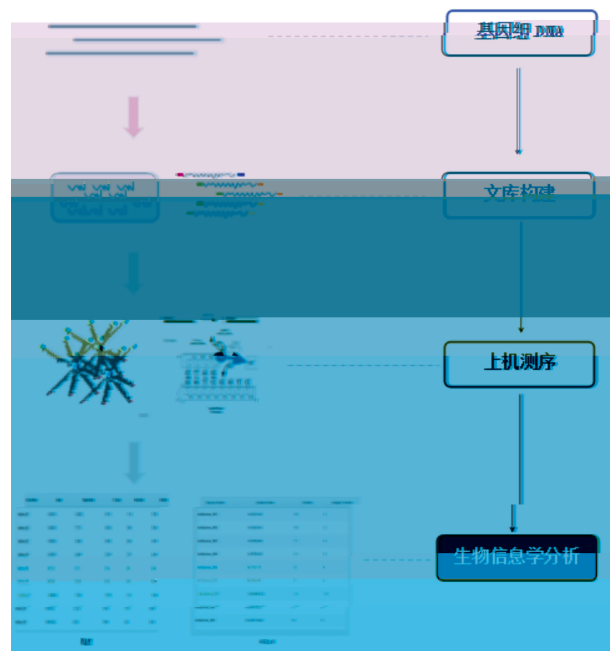
1.3.1 DNA
 QIAamp® DNA FFPE Tissue Kit
 DNA

1.3.2 DNA
 DNA
 4

DNA

1

Ion Ampliseq™ li-



1

Figure 1 Progress of NGS

COSMIC ID		Gly12Val	4	Gly13Asp	4
COSM		Gly12Ala	2	Gly12Ser Gly12Arg	1
	Novel	Gly12Asp	1	Gly12Cys	1
Coverage Analysis			18~21		2
		87		21	L858R
		15	E746_A750del	3	L747-
1.3.4		T751del	V769_D770ins	ASV	1
108	FFPE	G719S	S768I	1	75
			33	Gly12Asp	
1.3.1	DNA PCR	15	Gly12Cys	5	Gly12Val 4
	PCR	Gly13Asp	4	Gly12Ala	2
ABI 3500		Gly12Ser	Gly12Arg	1	Gly12Asp
1.3.5		Gly12Cys	1	1	
		10			
		2.2	2		
				2	
		21		87	
			0		0
2					
2.1					
		108			
			87		
		21	L858R	15	
E746_A750del	ELREA	3	L747-T751del		100%
V769_D770ins	ASV	1	G719S	33	2 75
S768I	1				0
		75	33	0	
Gly12Asp	15	Gly12Cys	5		100%

Table 1 Sequencing results in detail

COSMIC ID					
NBE1					-
NBE2					-
NBE3	L858R	2573 T G	COSM6224	L858R	2573 T G
NBE4	Gly12Ala	35G C	COSM522	Gly12Ala	35G C
NBE6					-
NBE7					-
NBE9	E746-A750del 1	2235-2249 del 15	COSM6223	E746-A750del 1	2235-2249 del 15
NBE10	Gly13Asp	38G A	COSM532	Gly13Asp	38G A
NBE12					-
NBE15				L858R	

2

Table 2 NGS results in detail

								COSMIC	
NBE1	chr1	162741794	C	T	Heterozygous	55.6	Novel	-	ON_DDR2_5
	chr4	1807894	G	A	Homozygous	100	Novel	-	CHP2_FGFR3_3
	chr7	55228053	A	T	Homozygous	100	Novel	-	ON_EGFR_2A
	chr17	7577548	C	T	Heterozygous	49.9	Hotspot	COSM6932	CHP2_TP53_6
NBE2	chr1	162741794	C	T	Heterozygous	48.1	Novel	-	ON_DDR2_5
	chr2	212812097	T	C	Homozygous	100	Novel	-	CHP2_ERBB4_1
	chr4	1807894	G	A	Homozygous	100	Novel	-	CHP2_FGFR3_3
	chr7	55228053	A	T	Homozygous	100	Novel	-	ON_EGFR_2A
	chr17	7577547	C	A	Heterozygous	44.6	Hotspot	COSM11196	CHP2_TP53_6
	chr17	7579472	G	C	Heterozygous	67.3	Novel	-	CHP2_TP53_2
NBE3	chr2	212812097	T	C	Homozygous	100	Novel	-	CHP2_ERBB4_1
	chr4	1807894	G	A	Homozygous	100	Novel	-	CHP2_FGFR3_3
	chr7	55228053	A	T	Homozygous	100	Novel	-	ON_EGFR_2A
	chr7	55259515	T	G	Heterozygous	46.3	Hotspot	COSM6224	CHP2_EGFR_8
	chr17	7578190	T	C	Heterozygous	36.2	Hotspot	COSM10758	CHP2_TP53_5
	chr17	7579472	G	C	Heterozygous	95.2	Novel	-	CHP2_TP53_2
NBE4	chr4	1807894	G	A	Homozygous	100	Novel	-	CHP2_FGFR3_3
	chr7	55228053	A	T	Homozygous	100	Novel	-	ON_EGFR_2A
	chr7	140481402	C	T	Heterozygous	1.9	Hotspot	COSM461	CHP2_BRAF_1
	chr10	89624218	C	G	Heterozygous	48.7	Hotspot	COSM5915	CHP2_PTEN_1
	chr12	25398284	C	G	Heterozygous	36.9	Hotspot	COSM522	CHP2_KRAS_1
	chr17	7577538	C	T	Heterozygous	2.3	Hotspot	COSM10662	CHP2_TP53_6
	chr17	7579472	G	C	Heterozygous	95.8	Novel	-	CHP2_TP53_2
NBE6	chr1	162741794	C	T	Heterozygous	49.9	Novel	-	ON_DDR2_5
	chr2	212812097	T	C	Heterozygous	64.5	Novel	-	CHP2_ERBB4_1
	chr3	41266137	C	T	Heterozygous	58	Hotspot	COSM5667	CHP2_CTNNB1_1
	chr3	178952085	A	G	Heterozygous	30.8	Hotspot	COSM775	CHP2_PIK3CA_10
	chr4	1807894	G	A	Homozygous	100	Novel	-	CHP2_FGFR3_3
	chr7	55228053	A	T	Homozygous	100	Novel	-	ON_EGFR_2A
	chr7	140453155	C	T	Heterozygous	26.4	Hotspot	COSM27639	CHP2_BRAF_2
	chr17	7578401	G	T	Heterozygous	6.8	Novel	-	CHP2_TP53_4
	chr17	7579472	G	C	Heterozygous	95	Novel	-	CHP2_TP53_2
	chr17	7579473	G	C	Heterozygous	3.7	Novel	-	CHP2_TP53_2

2.3

DNA

2

5

3

2 6

18~21

2 3

108

- 9-10 2014
National Comprehensive Cancer Network
NCCN
-TKI
-TKI 10
21
75 TKI
11
25%
12
13-14 3
15
16
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NGS

1 1 1 2

sequencing NGS HBV HBV YMDD next generation

Sanger NGS 100 YMDD

88 HBV YMDD 12 Sanger NGS 100 HBV YMDD

NGS HBV HBV

NGS HBV

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ABSTRACT Objective To explore the feasibility of HBV resistance mutation detection by next generation sequencing (NGS) technology as well as to examine the correlation of the patient's gender with his or her YMDD mutation. Thus, it can provide a reference for clinical diagnostic agents. **Methods** NGS technology was used in this study to detect the HBV YMDD mutation from 100 collected cases of clinical samples. These results were compared with the Sanger sequencing results, which is the gold standard for clinical detection. **Results** In these 100 cases of HBV samples, 88 cases of HBV YMDD wild type and 12 cases YMDD resistant mutation were detected. The sequencing results were the same as the Sanger sequencing results. **Conclusions** The results of this study showed NGS technology can be used to detect HBV resistance mutations. Furthermore, the patient's gender has no significant correlation with the HBV resistance mutations.

KEY WORD NGS; HBV; Resistance gene mutations

hepatitis B virus HBV¹

World Health Orga- 2015 7

nization WHO 2.4 9 000²

80 HBV

2015B020233009

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E mail yxxzb@schu.com

Lamivudine

LAM 3TC

cDNA
3-4 HBV

HBV
5 HBV

1.3.3					1	2		
1.3.3.1					1.3.4			
	1.3.2	DNA		200				
pmol/L								PCR-
1.3.3.2							2014	3401444
	Ion PI™	Hi - Q™	OT2 Reagents	200 kit	100			NGS
	Life Technologies			Ion One				
Touch™	2.0 System	Life Technologies			2			
1.3.3.3	DA8600				2.1	HBV YMDD		
	Ion PI™	Hi-Q™	Sequencing	200 Kit	Life	NGS		100
Technologies						HBV	HBV YMDD	88
						HBV YMDD	12	YIDD
						YVDD	4	Sanger
							100%	3
		1		6 µL	2.2	HBV YMDD		
						HBV	YMDD	59
			2			29	HBV	8
6 µL						4		
				3	0.05	4		
		3	HBV			NGS		

Table 3 The results of HBV drug-resistance gene sequencing

Allele Call						
11	YVDD	Homozygous	739A	G	YVDD	GTG
17	YIDD	Homozygous	741G	T	YIDD	ATT
21	YVDD	Homozygous	739A	G	YVDD	GTG
25	YIDD	Homozygous	741G	T	YIDD	ATT
28	YIDD	Homozygous	741G	T	YIDD	ATT
44	YIDD	Homozygous	741G	T	YIDD	ATT
48	YIDD	Homozygous	741G	T	YIDD	ATT
51	YIDD	Homozygous	741G	T	YIDD	ATT
54	YVDD	Homozygous	739A	G	YVDD	GTG
73	YIDD	Heterozygous	741G	T	YIDD	ATT
89	YIDD	Heterozygous	741G	T	YIDD	ATT
90	YVDD	Heterozygous	739A	G	YVDD	GTG

Absent Hot Spot coverage 6 Absent

4 H₀= ²_{0.05 1} =3.84 >0.05 H₁ H₀
 HBV H₁= HBV HBV HBV
²=1.950 4<

4 HBV		DNA	
Table 4 The correlation between patients gender and HBV YMDD mutation		88	100
			12
YMDD	59	29	
YIDD	8	4	
YVDD			

2.3 2

100 HBV

12 HBV

4 HBV

NGS

YIDD 8

YMDD 88

100%

5

Sanger

88 HBV

8 YIDD

4 YVDD

12.0%⁷

12

4

NGS

$$a/ a+c = 100\% \times d/ b+d = 100\% \times a+d / b+c$$

$$=12/ 12+0 \times 100\%= 100\%$$

$$=88/ 0+88 \times 100\%= 100\%$$

$$= 12+88 /100 \times 100\%= 100\%$$

3

NGS 100

NGS

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DELL370 MoticamPro205C

thinprep cytologic

test TCT DNA 40% 3 DNA
 1 DNA DNA Index DI 1 DNA
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image cytometer DNA-ICM 88.3% 100% TCT 5% 4C
 81.4% 3 DI>2.5

90.4%²⁻³ 145 4-5

TCT DNA-ICM 1.4 TCT DNA-ICM
 DNA SPSS 17.0

1

1.1

2013 8 2015
 8 145 65 80
 22~85 55 TCT

DNA-ICM

1.2

LBP

DNA

1.3

1.3.1 TCT

3 000 rpm/min 5 min
 30 s 12
 mL 5 min
 5 mL
 30 s 4 95% 10
 min 2 - hematoxylin-
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 2

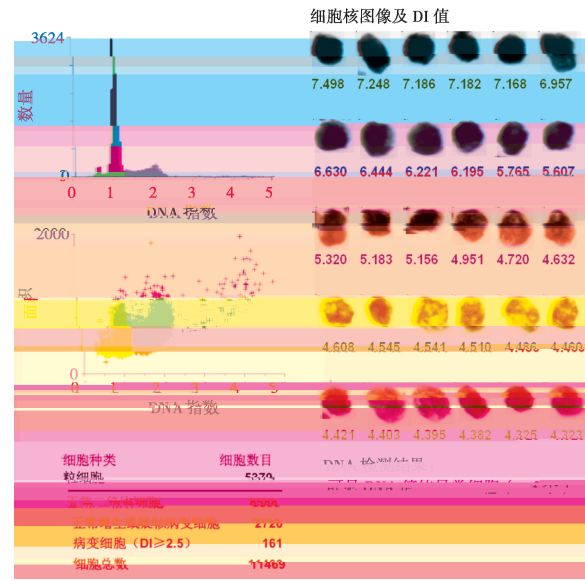
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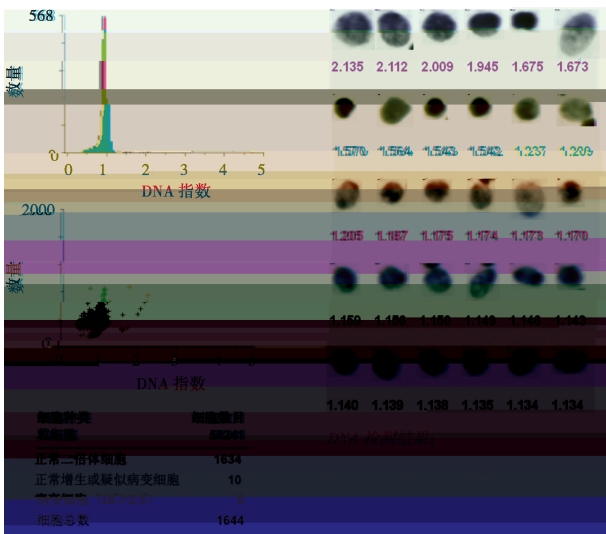
1 HE ×200

Figure 1 The positive results of TCT in patients with malignant peritoneal effusion HE ×200



3 DNA

Figure 3 Malignant peritoneal effusion in patients with DNA times physical examination



2 DNA

Figure 2 Benign peritoneal effusion in patients with cell DNA times physical examination

2 TCT DNA-ICM

Table 2 Comparison of TCT DNA-ICM and histopathology

	TCT		DNA-ICM	
	+	-	+	-
+	32	7	36	3
-	6	13	2	17
	38	20	38	20

ROC curve AUC 0.94 2 area under AUC 0.90 0.75

ROC TCT AUC 2 DNA-ICM 4

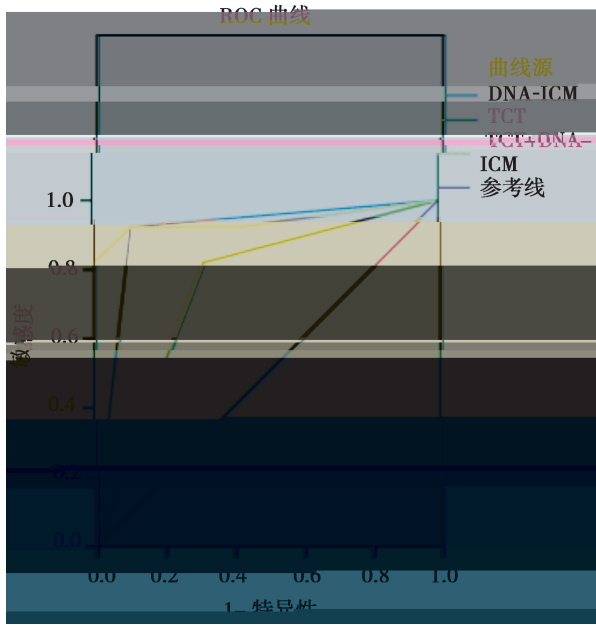
2.2 TCT DNA-ICM

58	39	14	18
4	3		
19	TCT	DNA-ICM	
	TCT	DNA-ICM	
84.21%	32/38	94.74%	36/38
65%	13/20	85%	17/20
			2
			0.01
TCT	DNA-ICM		2

Logistic

3

RNA DNA
-ICM 6-8



4 TCT DNA-ICM 2
ROC

Figure 4 ROC curve analysis TCT DNA-ICM and two kinds of methods combination for detection

	TCT			
81.4%		90.4%	DNA-ICM	
		88.3%		100% ²⁻³
2				
	ROC			145
	TCT		DNA-ICM	
84.21%	32/38	94.74%	36/38	
65%	13/20	85%	17/20	TCT
DNA-ICM	2			Logistic
				ROC
				ROC
	DNA-ICM	TCT	ROC	2
				2

2 DNA-ICM TCT
2

DNA-ICM TCT 37
DNA-ICM DNA DNA
2

TCT 20
90

TCT

DNA-ICM

DNA

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\bar{x}		\pm	0.05	AFP ALB
	c^2		SOD	
95	0.05	0.05	0.05 TP	
2			AFP SOD	0.05 TP
2.1	AFP TP ALB SOD		ALB	
		AFP TP	0.05	
ALB SOD			AFP ALB SOD	0.05 TP
				0.05
			1	

Table 1 Compared concentrations of AFP TP ALB and SOD among the 4 groups

	AFP ng/mL	TP g/L	ALB g/L	SOD U/mL
100	185.66±43.25*	65.21±7.07*	23.12±2.15*	53.46±15.68*
50	105.73±38.79*#	67.38±8.65*	29.33±5.41*	115.62±37.42*#
50	47.06±95.29*#	72.31±3.98	35.95±2.77*#	117.82±19.85*#
50	8.51±2.72	73.15±3.95	41.13±2.71	130.55±22.97

* 0.05 # 0.05

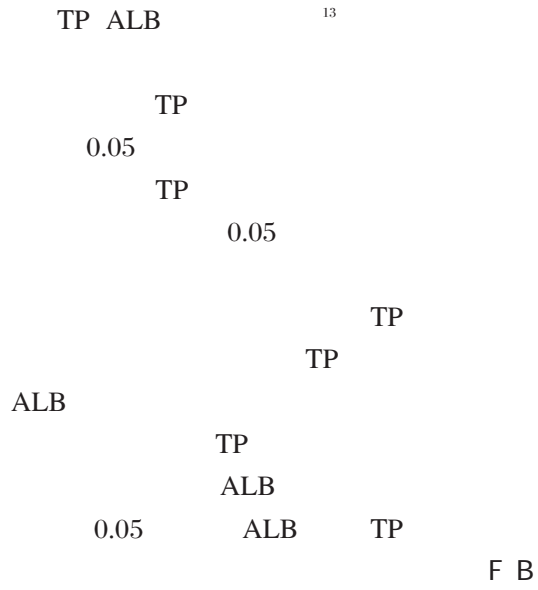
2.2	AFP TP ALB SOD			
		AFP TP	8 AFP	
ALB SOD		3		AFP
		2		
			AFP	
3	AFP ALB SOD		35~40	
	0.05 TP	3	9	3
	0.05		AFP	
2	AFP TP ALB SOD		AFP	
	n %		0.05	

Table 2 The abnormal rate of AFP/TP/ALB/SOD in each group of hepatopathy patients n %

	AFP	TP	ALB	SOD
100	100(100)	36 36	90(90)	93 93
50	47(94)	13 26	43(86)	18 36
50	39(78)	9 18	16(32)	11 22
c^2	24.88	4.95	63.66	88.14
	0.000	0.084	0.000	0.000

3			AFP	
			TP	
		ALB ¹¹	TP ALB	
		57 ~68	TP ALB	12

TP ALB



• •

1 2 3

regression equation was $Y=0.120+0.966X$. The specificity samples test result was normal. Conclusion Darui LH-CLIA Kit is a valuable diagnostic kit for clinic application.

[KEY WORDS] Luteinizing hormone (LH); Chemiluminescent immunoassay (CLIA); Kit

15 44 16.6% 11.9% 730
7 ~10 1-3 8
hormone LH luteinizing

1.1.2 LH
C1 4~6 IU/L C2 32~48 IU/
L C3 72~96 IU/L

1.1.3
18 50
64 28
63 64 64
283 15 37
52 283

follicle stimulating hormone FSH 10
thyroid stimulating hormone
TSH 10 human cho-
rionic gonadotropin HCG 10
rheumatoid factor RF 10 anti
nuclear antibodies ANA 10
human anti mouse antibody HAMA 10
10 10 10

2 LH
1.1.4 Ca-

ris200
1.2
1.2.1

1.2.2

LH
1
1.1
1.1.1

9-10

TSH 10 FSH 10 HCG 10
RF 10 ANA 10
HAMA 10 10 10

10

2.4

3

Dr. *
23

LH

15

Bland-Altman

LH

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3 221

HPV 13

human papilloma virus HPV 13
2012 4 2014 2
PCR SPSS 16.0
3 221 HPV 13 33.7% 650
22.8% 2 571 36.5% 18~22 23~44 45~80 HPV 13
** 14.7% 21.2% 37.9% 44 33 ž

3 221
HPV HPV
13

1

1.1

2012 4 2014 2

-20°C

1.2

SLAN-9P PCR
HPV

1.3

1.5 mL 13 000 rpm 5 min 1 mL
1 mL
1 mL
13 000 rpm 5 min 100
µL 10 min 13 000
rpm 5 min PCR

1.4 PCR

94°C 2 min
93°C 2 min
62°C 31 s 40 60°C

1 HPV13 %
Table 1 The distribution of 13 high-risk types in different sex %

	16	18	31	33	35	39	45	51	52	56	58	59	68
	0.99	0.37	0.56	0.22	0.06	0.28	0.12	0.31	0.25	0.28	0.71	0.4	0.03
	5.7	2.1	1.63	1.24	1.71	3.19	0.17	2.88	6.53	3.19	5.21	1.67	1.09

>0.05

<0.05

>0.05

>0.05

<0.05

HPV13

3

14.7% 21.2% 37.9% 3

2 HPV13 %

Table 2 The distribution of 13 high-risk types in different age groups in female %

	16	18	31	33	35	39	45	51	52	56	58	59	68
A	5.88	2.94	2.94	0	0	0	0	8.82	11.7	0	5.88	2.94	0
B	5.88	2.45	1.25	1.08	1.31	3.19	0.51	2.85	5.47	3.08	4.16	1.42	1.03
C	6.27	5.50	2.17	1.66	2.69	3.58	0	2.81	8.70	3.84	7.42	2.3	1.28

3 HPV13 %

Table 3 The distribution of 13 high-risk types in different age groups in male %

	16	18	31	33	35	39	45	51	52	56	58	59	68
A	1.64	0	3.28	0	0	0	1.64	3.28	3.28	0	1.64	0	0
B	4.59	1.72	2.49	1.15	0.26	1.15	0.57	0.96	0.96	1.34	3.63	2.1	0.19
C	10.6	4.55	4.55	1.52	0	3.03	0	4.55	1.52	1.52	3.03	3.03	0

2.4 HPV13

3 221

2 426

3

HPV

885

HPV

DNA

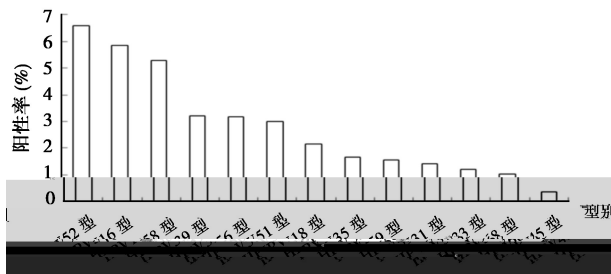
36.5%

2 HPV13

HPV52 HPV16 HPV58

5%

3%



2 HPV13

Figure 2 The distribution of 13 high-risk types in Cervical disease

HPV

HPV

HPV

HPV

20%~46%⁵

3 221

1 086

33.7%

⁵

3 221

HPV13

HPV16

HPV52

HPV58

HPV56

HPV39

HPV16

HPV52

HPV58

5%

	3%				2 426
	HPV			94.4%	HPV
	6 HPV16			38.7%	HPV16
7					HPV
8	HPV16				10
	HPV16	6		HPV	HPV
CIN		210	9		
HPV52	58	HPV16			HPV
		10			
3 221					HPV13
HPV					HPV
HPV16		HPV58			
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	HPV				7
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PCR

polymerase chain reaction PCR
PCR digital polymerase chain
reaction dPCR
PCR quantitative real-time PCR qPCR

PCR dPCR

JIANG Xiwen , ZHU Xiaoya, GAO Xiujie, ZHOU Qiwei
(DaAn Gene CO., Ltd. of SunYat-sen University, Guangzhou, Guangdong, China, 510665)

[ABSTRACT] Polymerase chain reaction (PCR) is the foundation of molecular biology and the core technology for virus nucleic acid detection of human infectious, which can be used for qualitative and quantitative analysis of nucleic acid. Digital PCR is a new the c

PCR digital polymerase chain reaction 1-6
dPCR 90
1
7-8 qPCR
PCR quantita-
tive real-time PCR qPCR Ct 9
Ct

510665

E mail yuanyecat@vip.sina.com

				200 copies/mL	2 000		1985
	200 copies/mL			HIV	2014		
qPCR				49.7			34.4 ²⁰
¹⁰⁻¹³ dPCR				AIDS			
						highly active anti-retroviral	
qPCR		¹⁴⁻¹⁶		therapy HAART		AIDS	
				orah ²¹			2013 Deb- HIV
PCR		dPCR			HIV		
				30 h			18
¹⁷		dPCR					HIV DNA
				0.005%	HIV RNA	HIV	
qPCR	200 ¹⁸				ddPCR		
		dPCR			HAART		
					HIV DNA		HIV
					2-LTR HIV		
1 dPCR						HIV	
					ddPCR	HIV DNA	2-LTR
PCR		Vogelstein				HIV DNA	
¹⁹				qPCR	5	2-LTR	
		PCR		qPCR	20 ²²		ddPCR
2		dPCR chip digital		2-LTR HIV			
PCR cdPCR		FluidigmBioMark™HD				²³	
Life Technologies QuantStudio™3D		PCR			ddPCR		
	PCR					HIV-1 RNA CA HIV-1 RNA	
	Bio-Rad RainDance				Kiselinova ²⁴ 44	HIV	
dPCR	droplet digital PCR	ddP-			CA HIV-1 RNA		
CR				ddPCR			
	Bio-Rad QX200	2	RainDance				
100~1 000				PCR	PCR		
						dPCR	
	cdPCR			dPCR			
2 dPCR				2.2 dPCR		hepatitis B virus	
				HBV			
2.1 dPCR		human immuno-		HBV			
deficiency virus HIV		acquired im-		HBV			World
1981				Health Organization WHO			

HBV 20 100
HBV
hepatocellular carcinoma HCC
²⁵⁻²⁶ Huang ²⁷ ddPCR
HBV HCC HBV
DNA
-fetoprotein AFP

HBV HCC
ddPCR qPCR HBV DNA

PCR
Ct
cccD-
NA HBV
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HBV
cccDNA
DNA cccDNA
NA qPCR
CR 1 ng/
2.3 dPCR
HCV hepatitis C virus
HCV / 6 // H

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HSV CE

HSV
35 Azizi 36 dPCR
HSV-1 AV529-19
UL5 UL29 HSV
AV529-19 dP-
dPCR
dPCR

3

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PCR
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dPCR
mi-RNA dPCR
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QuantaLife PCR
Bio - Rad PCR
QX100 2
Rain Dance Technology 2012 RainDrop™
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3 dPCR Bio-RadQX100

dPCR

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• •

1 2 2
hepatitis C HC
3

1.7 5' 3'
HCV 95%
3 010~3 033
hepatocellular carcinoma HCC 10 3
core pro-
2 teins C 1 envelope protein 1 E1
hepatitis C virus HCV 2 envelope protein 2 E2 6
non-structural protein2~5B NS2~NS5B
HCV
3 HCV RNA 9.5 kb HCV

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E-mail sluo815@gmail.com

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1.2 HCV

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1

HCV

50~70

real-time

polymerase chain reaction real-time PCR

HCV RNA

HCV

4

1.1 HCV

HCV

HCV

RNA

HCV

5-8

HCV

HCV

HCV RNA

8-11

PCR

RNA 1/10

HCV

12

The Architect HCV Ag

HCV

3~20 000 fmol/L HCV

food and drug admin-

istration FDA

HCV RNA

HCV

HCV

lowest limit of detection LLOD

HCV RNA 500~3 000 IU/mL

13

: 5

response-guided therapy RGT

,

H

: 5

14

HCV

NS3 NS4

NS3

NS4

HCV

HCV

9

A : 5

15

HCV				2.1		real-time PCR	
				DNA		RNA	
dry blood method DBS		HCV RNA		PCR		PCR	
PCR		real-time PCR		DBS		PCR	
		FDA					
		18		PCR		Taq 5'-3'	
HCV mL ¹⁹		HCV FDA		1 000 IU/		DNA	
		16		HCV			
		20		PCR			
		Abbott i-STAT System					
		FDA		HCV		23	
ciency virus HIV		human immunodeficiency virus		2 HCV RNA		HCV	
HBV HCV ²¹				ART		COBAS AmpliPrep/COBAS TaqMan	
1.4				HCV		COBAS AmpliPrep/COBAS TaqMan HCV test	
				CAP/CTM		ART	
				HCV		CAP/CTM	
				HCV		24	
				PCR		12 IU/mL	
				50~100 IU/mL ²⁵		real-time PCR	
DNA		22		real-time PCR		RNA	
				HCV			
				2.2		real-time transcription mediated amplification	
						real-time TMA	
2				RNA		T7 RNA	
						HCV	
				RNA		TMA	
				PCR		real-time	
al-time PCR		re-				HCV ²³	
						real-time PCR	
HCV						5~10 IU/mL	
						real-time	

PCR 1 3 HCV
2 4 HCV real-time

TMA

24

2.3

25

RNA

26 &

- time PCR ³⁰
- NS3 NS4
- NS3 NS4
- HCV
- HCV
- HCV
- 90%
HCV
- NS4
- NS3
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J .
2011 18 2 134-136.

1 2 1 3

[] hepatitis B virus, HBV
 hepatocellular carcinoma, HCC HBV
 HBV HCC
 HCC

woodchuck hepatitis virus, WHV
 HBV HCC
 HBV HCC
 HCC

[]

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[ABSTRACT] Hepatitis B virus (HBV) is a widespread human pathogen that can cause hepatitis, cirrhosis, and hepatocellular carcinoma (HCC). HBV infection has been a serious threat to human health, especially in China and Southeast Asian countries. The pathogenesis, diagnosis and treatment of chronic hepatitis B and HBV caused HCC are still very challenging. Currently, understanding of the pathogenesis and diagnosis of viral hepatitis, liver cirrhosis post hepatitis, and HCC are largely dependent on the animal model system, and the choice of a well-established animal model is the basis in accomplishment of the study. The features of woodchuck body weight, the size of its liver, the pathogenesis of the hepatitis B virus it carries, and the progress of the disease course are very similar to those of human hepatitis B virus, thus, the woodchuck is a very useful animal model in hepatitis B virus infection and in the study of the development, pathogenesis, diagnosis, and treatment of hepatitis B and HCC. Therefore, the woodchuck hepatitis B virus animal model enables us to have a better understanding of the complex relationship between HBV infection and HCC. It will also promote a better prevention and treatment strategy for hepatitis B infection. In this paper, recent reports in the application of the woodchuck animal model in the field of hepatitis B and HCC will be summarized.

[KEY WORDS] Woodchuck; Hepatitis B virus; Animal model; Hepatocellular carcinoma

1. 530021
 2. 530023
 3. 14263

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hepatitis B virus HBV HCC

hepatocellular carcinoma HCC 2 WHV

2 4 000 4.5 kg

620 000 HBV 6.5 kg 56 cm

HCC 1 3

HCC woodchuck 10 5 kg

hepatitis virus WHV HBV 1 500 1978 WHV HCC HBV

HCC WHV

HCC 4

1 3 HBV

HBV HBV DNA HBV

HBV HBV HBV

HBV 5 WHV HBV

2 HBV WHV HBV HBV

HBV 6 HBV HCC

HBV 7

DNA HBV 4

4.1 WHV HBV WHV

WHV DNA HCC 24

HBV 30~32

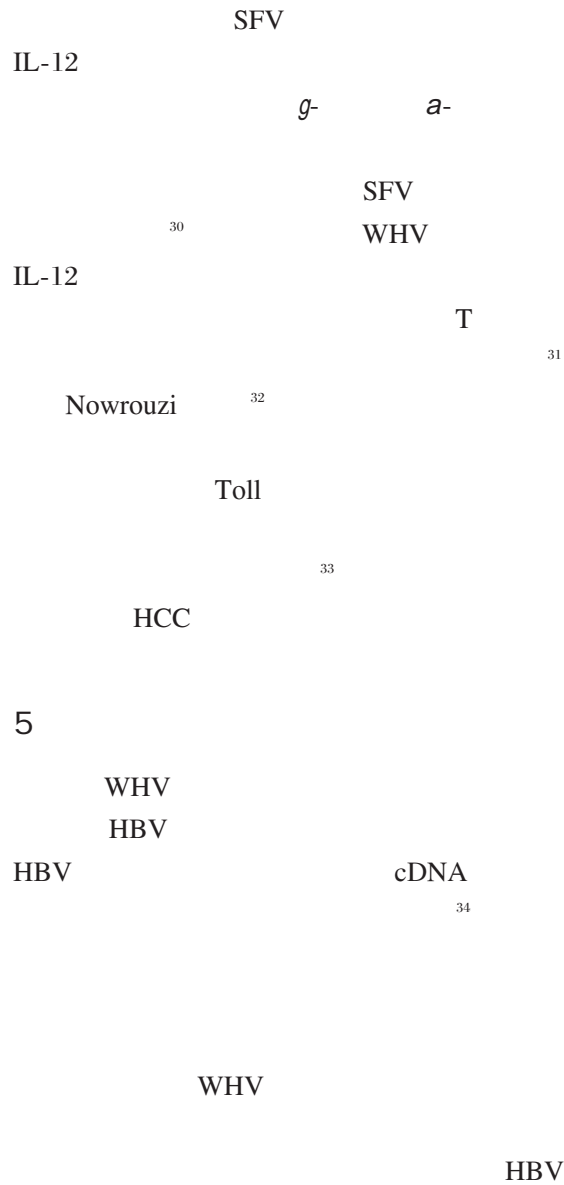
65% 3 WHV WHV7 WHV8 WHV

HCC 2~4 WHVNY WHV7 8

HCC WHV7P1 60%~75%

2 50% HCC 4
100% HCC
HBV 9
WHV
e HCC e
HBV
WHV
e
4.2 HCC
4.2.1
HBV HBV WHV HBV
10
WHV
WHV
11
primary occult infection POI
T
T
12 Mulrooney-
Cousins 13 10
10 100 WHV POI
DNA <
100~200 copies/mL
WHV WHV

lipoproteins
 18 apo-
 1 HCC
 WHV
 20 HBV
 A
 matrix metalloproteinases
 MMPs HCC
 MMPs
 WHV
 WHV
 MMPs
 MMPs
 HCC
 HCC
 22
 4.3
 4.3.1
 HBV
 HCC
 HCC
 HBV
 HCC
 magnetic resonance imaging MRI
 23 29 Semliki semliki
 rus SFV
 12 IL-12 WHV HCC
 23-24
 MRI
 DNA
 cccDNA
 25
 1
 3 + T



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[ABSTRACT] Carcinoma of unknown primary (CUP) is a heterogeneous group of patients whose primary sites cannot be found when the cancer has metastasized. It is one of the ten most common malignancies and the fourth most common cause of cancer-related death worldwide. The prognosis of patients with CUP is usually poor for those receiving empiric treatments. Identification of the primary site can ease the patient's anxiety and improve long-term survival with the help of more specific therapies. The current diagnostic approaches constitute clinical evaluation, medical imaging and histopathological examination. With the rapid evolution of the molecular biology and bioinformatics technology, genomic testing has shown great potential and has been gradually used for CUP diagnosis in clinic. In this article, a general description of the diagnostic approaches for CUP will be presented.

KEY WORDS Carcinoma of unknown primary CUP Molecular diagnostics Genomic testing

carcinomas of unknown primary CUP 60 2.8% CUP

15% 80% 30% 3~4 6-7

1/3 CUP¹ CUP

CUP 3%~5% 4 CUP

311188

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prehensive Cancer Network NCCN CUP

8-9
55%~85%

2 cm
10-11

12-13 CUP

CUP

30%
10 14
15%
50%

X
computed tomography CT
positron emission computed tomogra-
phy PET

CUP

2

CUP

1

2.2

21

CUP

CT
magnetic resonance imaging MRI

15-16

CUP CT MRI

20%

4.5
4.7%¹⁷

CUP

18-19

18F
fluorine 18 fluoro-2-deoxy-d-glucose 18F-FDG

reverse transcriptase polymerase chain reac-
tion RT-PCR CUP 92

PET

18F-FDG

PET
PET CT

396

194

18F-FDG PET/CT

9.1

12.5

16

22

18F-FDG PET/CT

CUP

24%~53%²³ 18F-FDG PET/CT

17 20

18F-FDG PET/CT

11

2

37% 84% 84%²⁴

PET/

CT

2.1

National Com-

2.3

	CUP				GCD-
		1	FP15	mammaglobin	
	2		TTF1 CK7+CK20-	HEPAR1	
			RCC	thyrobolulin	
		CUP	TG /TTF1	PLAP/OCT4	
	3		CDX2	CK7-CK20+	
			WT1/PAX8	A chromo-	
			granin A CgA	synaptophysin	
	4			leukocyte common	
			antigen LCA		1
				CUP	1 15 21
		1			

Table 1 Immunohistochemical markers for the diagnosis of carcinoma of unknown primary

S100 Melan-A HMB45				
actin	vimentin	S100	desmin	
LCA				
CK5/6 p63	calretinin	mesothelin	WT1 D2-40	
CK20 CK7 CDX2	villin CK7			
HEPAR1 CD10				
CK7 CK20 TTF1				
CK7 CK20 P63 CK5/6				
TTF1 CgA	synaptophysin			
CK7 ER/PR GCDFP15		CEA		
CK7 ER WT1	mesothelin			
ER PR CEA	vimentin			
CEA	vimentin p16 ER/PR			
CK20 CK5/6 p63	thrombomodulin			
PSA CK7 CK20 PAP				
CK7 CK20 CA19-9 MUC5-AC	mesothelin	DPC4		
RCC CD10	vimentin	CEA		
	alpha-Inhibin	Melan-A CK7 CK20	calretinin	
PLAP OCT4				
TG TTF1				

4

CUP

65.6%²⁵

Dennis

13

10

88%

TTF1 CDX2

3

RNA

3

CUP

3%~

5%

CUP

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中山大学达安基因股份有限公司依托中山大学雄厚的科研平台,以分子诊断技术为切入点,集研发、生产、销售为一体,专注于分子诊断试剂、仪器的研发、生产和销售,是国内领先的分子诊断试剂、仪器研发、生产、销售企业。



一、 行业优势

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