18. Total RNA Extraction from Virus



Hepatitis C Virus (HCV) RNA Extraction from Serum

Protocol





uickGene

Other

Detection of HCV virus RNA by RT-PCR / nested PCR



e, i f, j g, k h, l	: marker (100 bp ladder) : HCV negative normal human : HCV positive patient No.1 : HCV positive patient No.2 : HCV positive patient No.3
~ d	: QuickGene
~ h	: A company
- I	: B company

Hepatitis C RNA could be detected by RT-PCR / nested PCR method, using RNA prepared from serum of HCV infected patient with QuickGene.

Detection of HCV RNA

For 3 kinds of RNA obtained with QuickGene system, A company product and B company product, detection sensitivity of HCV RNA was examined using AMPLICOR detection system (hybridization method).



In comparison with B company, low reactivity of about 1/5 at maximum was found for 2 analytes among 3 analytes. On the other hand, meaningful difference in reactivity was not found for RNA prepared with QuickGene and A company product.

Regarding this sensitivity deviation from AMPLICOR, it is considered to be one cause that small fragments of decomposed RNA do not come into samples for QuickGene and A company product.

It was shown that HCV RNA in ordinary serum of patient can be detected with adequate sensitivity by serum RNA prepared with QuickGene. In QuickGene, troublesome operations such as isopropanol precipitation and collection by centrifugation which are contained in RNA preparation protocol of AMPLICOR are unnecessary and RNA preparation becomes easy.

Common protocol is usable for the following

HIV

Depending on sample and storage conditions, nucleic acid may not be extractable. Therefore, we cannot guarantee accurate data. The extracted nucleic acid contains unintended acid (ex: when extracting DNA, RNA is also extracted).



Norovirus RNA Extraction from Stool



Other

Inspection

PCR Method (approved by Ministry of Health, Labour and Welfare / Pharmaceuticals and Medical Devices 2007 Nov. 5)

http://www.mhlw.go.jp/topics/syokuchu/kanren/kanshi/031105-1.html

Common protocol is usable for the following

No Data

Depending on sample and storage conditions, nucleic acid may not be extractable. Therefore, we cannot guarantee accurate data. The extracted nucleic acid contains unintended acid (ex: when extracting DNA, RNA is also extracted).



Protocol B (TRC Method)

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RNA Extraction from Serum of HIV Patient and Human Serum which spiked HIV Virus Particle and Detection Limit of HIV RNA



Results

Other

 Refinement of HIV RNA from human serum which spiked HIV virus particle

Virus solution of HIV was added to normal human pool serum in concentrations in the table below. According to the above protocol, HIV RNA was detected quantitatively using AMPLICOR detection system (PCR-hybridization) for RNA preparted by use of QuickGene and RNA extracted by A company standard protocol.

Spiked virus amount	Calculated value(copy/ml)			
(number of virus particles/ml)	QuickGene	A company		
50,000	18623.6	30827		
5,000	2467	2471.2		
500	304.9	435.4		
50	-6.6	-2.6		

Depending on sample and storage conditions, nucleic acid may not be extractable. Therefore, we cannot guarantee accurate data. The extracted nucleic acid contains unintended acid (ex: when extracting DNA, RNA is also extracted).



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Abscissa axis : spiked virus particle amount Longitudinal axis : calculated HIV RNA amount

From above results, HIV RNA could be detected in detection sensitivity equivalent to A company using RNA extracted with QuickGene. The sensitivity was about several hundred virus particles/ml.

Refinement of HIV RNA from human serum which spiked HIV virus particle

RNA was prepared from pool serum (2 analytes of high titer and low titer) of HIV patient, using QuickGene, B company product and A company product, and HIV RNA was detected quantitatively with AMPLICOR detection system.



From above results, regarding HIV RNA detection for patient serum, the strongest response was obtained for A company product. Equivalent response was obtained for QuickGene and B company product, which was about 1/2 to 1/5 of A company product. This detection method aims calculation of order of copy number, and deviations of 1/2, 1/5 can be regarded as in error range between experiments. The 3 values are in the range of same order. So, they are equivalent from the point of view of detection sensitivity. Therefore, it was shown that HIV RNA can be detected from HIV patient serum quantitatively and in high sensitivity by this protocol using QuickGene.

Common protocol is usable for the following

HCV

Depending on sample and storage conditions, nucleic acid may not be extractable. Therefore, we cannot guarantee accurate data. The extracted nucleic acid contains unintended acid (ex: when extracting DNA, RNA is also extracted).



Total RNA Extraction from Influenza Virus Solution







Other

RT-PCR

RT-PCR was performed with AH3 type influenza-specific primer and B type influenza-specific primer for total RNA extracted from influenza virus solution using QuickGene system and Spin column method (A company).

Confirmation of virus type selectivity

Confirmation of virus RT-PCR



Electrophoresis condition : 2.0% agarose/1 x TAE

- M: 100 bp DNA Ladder
- 1 : AH3 type Influenza virus RNA
- 2 : B type Influenza virus RNA
- 3 : AH3 type Influenza virus RNA
- 4 : B type Influenza virus RNA

Primer : 1,2 AH3 type influenza-specific primer 3,4 B type influenza-specific primer

RT-PCR products were detected only with specific primer for each total RNA.

Electrophoresis condition : 2.0% agarose/1 x TAE

Spin column method (A company) AH3 type QuickGene 2 3 4 4 5 6 M 1 5 6 3 B type Spin column method QuickGene (A company) M 3 5 6 4 5 6 1 2 4 3



M: 100 bp DNA Ladder 1 : Influenza virus, 10⁶ pfu/ml 2 : Influenza virus, 10⁵ pfu/ml 3 : Influenza virus, 10⁴ pfu/ml 4 : Influenza virus, 10³ pfu/ml 5 : Influenza virus, 10² pfu/ml 6 : Influenza virus, 101 pfu/ml 7 : Negative control

RT-PCR products of AH3 type influenza and B type influenza were detected for each total RNA.

Common protocol is usable for the following

Measles Virus, Respiratory Syncytial (RS) Virus

Depending on sample and storage conditions, nucleic acid may not be extractable. Therefore, we cannot guarantee accurate data. The extracted nucleic acid contains unintended acid (ex: when extracting DNA, RNA is also extracted).



Total RNA Extraction from Measles Virus Solution







Other

RT-PCR

RT-PCR was performed with viral hemagglutinin (HA)-specific primer for total RNA extracted from measles virus solution using QuickGene system and Spin column method (A company).



Electrophoresis condition : 2.0% agarose/1 x TAE

M: 100 bp DNA Ladder 1 : Measles virus, 10⁵ pfu/ml 2 : Measles virus, 10⁴ pfu/ml 3 : Measles virus, 10³ pfu/ml 4 : Measles virus, 10² pfu/ml 5 : Negative control

RT-PCR products of HA were detected for each total RNA.

Common protocol is usable for the following

Influenza Virus, Respiratory Syncytial (RS) Virus





Total RNA Extraction from Plant virus



No Data

Common protocol is usable for the following

No Data





RH-7

Total RNA Extraction from Respiratory Syncytial (RS) Virus Solution







Other

RT-PCR

RT-PCR was performed with primer characteristic to G protein gene of RS virus for total RNA extracted from RS virus solution using QuickGene system and Spin column method (A company).



Electrophoresis condition : 2.0% agarose/1 x TAE

M: 100 bp DNA Ladder 1 : RC virus, 10^5 pfu/ml 2 : RC virus, 10^4 pfu/ml 3 : RC virus, 10^3 pfu/ml 4 : RC virus, 10^2 pfu/ml 5 : RC virus, 10^1 pfu/ml 6 : RC virus, 1 pfu/ml 7 : Negative control



RT-PCR products of G protein gene of RS virus were detected for each total RNA.

Common protocol is usable for the following

Measles Virus, Influenza Virus





RH-8

Total RNA Extraction from SARS Coronavirus (SARS-CoV) infected Cells







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The yield of viral RNA / Protein contamination: A260/280

Protocol	Yield (µg)	A260/280
QuiekCono	9.4	1.93
QuickGene	7.1	1.90
Spin column method	7.6	1.80
(A Company)	7.8	1.88

Other

RT-PCR

RT-PCR was performed with primer characteristic to E protein gene and M protein gene of SARS-CoV, *GAPDH* gene for total RNA extracted from SARS-CoV infected cells using QuickGene system and Spin column method (A company).



Electrophoresis condition : 2.0% agarose/1 x TAE

M: 100 bp DNA Ladder 1 : No.1 Noninfected Caco-2 cell 2 : No.2 SARS-CoV infected Caco-2 cell

RT-PCR products of E protein gene and M protein gene of SARS-CoV were detected for each total RNA of SARSCoV infected cell.

Common protocol is usable for the following

No data





Viral RNA Extraction from Simian Immunodeficiency Virus (SIV) Infected Cells



Results

The yield of viral RNA (µg)

	Experiment 1			Experiment 2			
Virus	mock	SIV clone 1	SIV clone 2	mock		SIV clone 2	
QuickGene-810	5.6	3.8	7.0	8.0	3.6	6.0	9.5
Spin column	-	-	-	7.1	0.8	4.5	4.7





Protein contamination : A260/280

	Experiment 1			Experiment 2			
Virus	mock	SIV clone 1	SIV clone 2	mock		SIV clone 2	
QuickGene-810	1.86	1.82	1.84	1.90	1.86	1.77	1.91
Spin column	-	-	-	1.92	1.66	1.82	1.88

Other

RT-PCR

AGE of RT-PCR with SIV-RNA isolated from SIV clone 1 or SIV clone 2 infected cells.

mock clone1 clone2 mock clone1 clone2 env GAPDH

Experiment 1: SIV-RNA detection from SIV clone 1 or SIV clone 2 infected cells.

458bp



588bp

Experiment 2: Comparison between QuickGene-810 and spin column SIVdone2 mock SIVcione2 mock





RT-PCR was performed on 1 µg of isolated total RNA.

RT-PCR amplification was performed succesfully using total RNA.

As SIV clone 2 has higher infectiouness than SIV clone 1, larger amount of SIV-RNA can be isolated from SIV clone 2 infected cells.

F: QuickGene-810 A : Spin column

Isolated S2V-RNA was used for RT-PCR template to amplify env and GAPDH gene.

Common protocol is usable for the following

No Data





KURABO

RH-10

VNN (Viral Nervous Necrosis) RNA Extraction from Tilefish





uickGene

Other

Inspection

RT-PCR : Amplification was performed on isolated RNA, targeting T4 region of RGNNV coat protein gene. Nested PCR : Amplification was performed using the primer specific to RG type among 4 genotypes of betanodavirus.

Sample : ovaries and eyeballs of 3 native tilefish P_{\downarrow} (each tissue was taken from the same individual)



Result : Amplification products similar to those of positive control were confirmed for ovaries of No.1, 2.

Sample : testes and eyeballs of 10 native tilefish (each tissue was taken from the same individual) Testes



Result : Amplification products were confirmed for testes of No.6 and eyeballs of No.2.

Common protocol is usable for the following

No Data

Depending on sample and storage conditions, nucleic acid may not be extractable. Therefore, we cannot guarantee accurate data. The extracted nucleic acid contains unintended acid (ex: when extracting DNA, RNA is also extracted).