Basis of Immunology and immunophysiopathology of infectious diseases

Jointly organized by Institut Pasteur in Ho Chi Minh City and Institut Pasteur with kind support from ANRS & Université Pierre et Marie Curie

January 24 – February 5, 2005 at the Institut Pasteur in Ho Chi Minh City, Vietnam

Organisateurs :	Dr. Truong Xuan Lien & Pr. Pierre-André Cazenave			
Coordinateur :	Adrien Six			
Equipe enseignante :	Muriel Almoussa, Institut Pasteur			
	Pierre-André Cazenave, Univeristé Paris 6			
	Jean-Luc Guesdon, Institut Pasteur			
	Jacques Louis, Institut Pasteur			
	Sylviane Pied, CNRS			
	Daniel Scott-Algara, Institut Pasteur			
	Adrien Six, Université Paris 6			

Practical workshop

on

Cytokines quantification

- Quantification of cytokine gene expression (RT-PCR, evaluation of mRNA)

- Measurement of cytokine concentration (ELISA)

Muriel Almoussa, Jean-Luc Guesdon, Daniel Scott-Algara

The purpose of this practical workshop is to determine the cytokine levels by two different methods: mRNA quantitative RT-PCR and ELISA technique.

The objective of this 3-day lab session is to demonstrate the power and the limits of these two approaches, which can be applied in both basic and clinical research.

In this manual, you will find a detailed protocol for the experimental steps that will be carried out during the workshop, as well as some reference information on the techniques, protocols, reagents and equipment.

I - Isolation of mouse splenocytes

- 1. Mice are killed.
- 2. In a hood, the animals are dissected and the spleen is taken.
- 3. The spleens are dilacerated in a Petri dish containing 5 ml of RPMI and 5% FCS using two sterile polished glass slides.
- 4. The cell suspension is transferred to a 15 ml tube containing 5 ml of RPMI and 5% FCS.
- 5. After 5 minutes on ice, the cell suspension is decanted to a new 15 ml tube.
- 6. Centrifuge (5 minutes at 300 x g) at 4° C.

II - Lysis of erythrocytes

- 1. Decant the supernatant.
- 2. Disrupt the cell pellet by "racking" the tube.
- 3. Resuspend the cells in M-lyse buffer that has been diluted to 1X strength with sterile distilled water and quickly vortex the tube.

Note: We recommend using 2 ml of 1X M-Lyse solution per processed spleen (approximately 1 ml of 1X H-Lyse per 25 million splenocytes).

4. Incubate the cells at room temperature until red cell lysis is complete (10 minutes).

This is easily observed by a darkening in colour of the fluid and clearing of turbidity. Exposure to M-lyse Buffer for longer periods (i.e. 30 minutes) will reduce cellular viability and decrease the total yield of leukocytes.

5. Wash the cells by filling the tube with 1X Wash Buffer

Note: Wash Buffer must be diluted with sterile water to 1X strength prior to use.

6. Centrifuge the cells for 10 minutes at 200 x g. Resuspend the cells in 1ml of 1X column wash buffer.

III - Isolation of the T cells

1. For each column to be used, prepare 20 ml of 1X column wash buffer by mixing 2.0 ml of 10X column wash buffer with 18 ml of sterile distilled water.

Columns have a maximum cell loading capacity of 100×10^6 total cells.

- 2. The column is placed in a column rack or ring stand. The top cap of the column is removed first to avoid drawing air into the bottom of the column. Next, the bottom cap is removed. The fluid within the column is allowed to drain into a waste receptacle. During this process the outside of the column tip should be rinsed with 70% alcohol to ensure sterile column processing.
- 3. The column content is then washed with a total of 6 ml of 1X column wash buffer and this eluate is also allowed to drain into the waste receptacle. The column is now ready to be loaded with cells.
- 4. The waste receptacle is replaced with a sterile 15 ml centrifuge tube.
- 5. After the column buffer has drained down to the level of the white filter, the 1 ml cell suspension is applied to the top of the column. The cells will enter the column and displace the wash buffer contained in the column, which is collected in the sterile centrifuge tube.
- 6. The cells, now suspended within the column, are incubated at room temperature for 10 minutes.
- 7. After the incubation step, T cells are eluted from the column with 4 aliquots (2 ml each) of 1X column wash buffer.
- 8. The collected T cells are centrifuged at 250 x g for 5 minutes.
- 9. Discard the supernatant and resuspend the pellet in 10 ml of RPMI containing 5% FCS.
- 10. Count cells on a hemocytometer using Trypan blue.

IV - Culture of the T cells

- 1. Add 10 ml of cells suspension at 10^6 / ml in a culture flask.
- 2. Add PMA (Phorbol ester) at 10 ng/ml final concentration and Ionomycin at 500 ng/ml final concentration.
- 3. Incubate at 37° C with 5% CO₂ for either 4 hours (for RT-PCR method) or overnight (for ELISA method).

V - **RNA** preparation

- 1. After 4 hr incubation, count cells on a hemocytometer using Trypan blue.
- 2. Calculate the volume of the suspension corresponding to 10 millions cells.
- 3. Pour the suspension in a sterile 15 ml tube.
- 4. Centrifuge the suspension for 5 minutes at 1200 rpm.

Special precautions must be observed to avoid degradation of mRNA by RNases. Reagents and plastic- or glassware that contact the RNA sample should first be treated with diethyl pyrocarbonate (DEPC) to inactivate any contaminating RNases and then autoclave according to standard procedures. Gloves must be worn to avoid sample contamination with nucleases shed from the skin. Filter pipette tips must be used.

- 5. Discard the supernatant.
- 6. Resuspend the pellet in 1ml Trizol and pour the suspension into a 1.5 ml Eppendorf tube.
- 7. Keep the tube at room temperature for 5 minutes.
- 8. Add 200 µl chloroform; use a chemical hood and new gloves.
- 9. Mix vigorously the tube for 15 seconds.
- 10. Keep for 2-3 minutes on the bench.
- 11. Centrifuge for 15 minutes at 4° C at maximum speed of 12 000 g.
- 12. Pipette the clear superior aqueous phase (about 500-600 μ l) into a new tube, keep the first tube.
- 13. Add 500 µl isopropanol into the new tube, mix and keep at room temperature for 10 minutes.
- 14. Centrifuge for 10 minutes at +4° C, 12 000 g maximum.
- 15. Transfer the supernatant in an another Eppendorf tube and wash the pellet by adding 1ml Ethanol (75 % in 0.1 % DEPC treated water) onto the pellet. Mix.
- 16. Centrifuge for 5 minutes at +4° C, 7 500 g.
- 17. Transfer the supernatant in another Eppendorf tube and the pellet is then dried under vacuum for 5 10 minutes.
- 18. Resuspend the pellet in 50 µl DEPC treated water
- 19. Put the tube in a heating block (55° C 60° C) for 5 10 minutes.
- 20. Quantify the RNA using a spectrophotometer (260 nm). Blank the spectrophotometer with water. Read the RNA sample at 260 nm and 280 nm. Calculate the purity of the sample by dividing the 260 reading by the 280 reading. An $A_{260/280}$ ratio of at least 1.8 is required. Multiply the 260 reading by 37 to obtain the concentration of the RNA in μ g/ml.

21. The RNA preparation are stored frozen at -20° C or preferably at -70° C.

VI - cDNA synthesis

MMLV reverse transcriptase is used in the first-strand cDNA reaction to generate cDNA from mRNA. Prior to first-strand cDNA synthesis the mRNA suspended in RNase-free water is heated to remove any secondary structure which could hinder the reaction.

1. Use 200 ng to 1 μ g RNA for the first-strand reaction.

Prepare the following reaction in a 200 μ l microcentrifuge tube.

mRNA	Xμl
RNase free water	Xμl
Oligo dT primers (100 µM)	0.5 µl
Total Volume	32.6 µl

- 2. Heat the mRNA at 65° C for 5 minutes and cool immediately on ice. Start the first-strand cDNA reaction (bellow) within 2 minutes of placing on ice.
- 3. During the incubation make the master solution using the table below.

dNTP (25 mM)	0,4 µl
5X buffer	10 µ1
DTT 0.1M	5 µl
RNASin	1 µl
RT-MMLV	1 µl
Total Volume	17,4 µl

Mix the solution by inversion, then spin the tube at 1000 x g for 5 seconds.

- 4. Transfer 17.4 µl of the master solution to the first-strand reaction tube.
- 5. Incubate for 70 minutes at 37° C.
- 6. Stop the reaction by incubating 15 minutes at 70° C. Then store the tube at 4° C.

Alternatively the whole reaction can be carried out using a thermal cycler. Use the following programme:

1 cycle of: 65° C for 5 minutes Pause 1 cycle of: 37° C for 70 minutes, 70° C for 15 minutes, hold at 4° C.

VII - PCR Amplification

The first-strand cDNA is used as a template for PCR amplification to generate cytokine specific DNA fragment. IFN γ mRNA will be the target mRNA during the workshop (Fig. 1, Fig. 2).

It may be a good idea to quantitate a house-keeping gene mRNA as well as target mRNA. This will correct for unequal amounts of mRNA in total RNA. Good house-keeping genes are β -actin, APRT, HPRT or glucose-6-phosphate dehydrogenase.

Note: β -actin and G6PD are high expression, HPRT and APRT are low expression. Standardize with a housekeeping gene which is similar to the expression of the gene of interest.

Since there may be some variability in the quality of RNA extraction from day-to-day, try to extract all samples to be analyzed in the same run, if possible.

During the workshop, we will use G3PDH mRNA as housekeeping gene mRNA (Fig. 3).

- 1. Label one tube as IFNγ, a second tube as positive control, a third tube as negative control and a fourth tube as G3PDH.
- 2. Add the reagents shown below to the appropriate tubes.

IFNγ

Sterile distilled water	39.6 µl	
10X PCR buffer (without MgCl ₂)	5 µl	
MgCl ₂ (50 mM)	1.5 µl	
dNTP (25 mM)	0.4 µl	
Primers 1 et 2 (7.5 µM each)	2 µl	
Taq DNA polymerase (5 units/µl)	0.5 µl	
First-strand reaction	1 µl	
Total Volume	50 µl	
Positive control		
Sterile distilled water	39.6 µl	
10X PCR buffer (without MgCl ₂)	5 µl	
MgCl ₂ (50 mM)	1.5 μl	
dNTP (25 mM)	0.4 µl	
Primers 1 et 2 (7.5 µM each)	2 µl	
Taq DNA polymerase (5 units/µl)	0.5 μl	
dsDNA positive control	1 µl	
Total Volume	50 µl	

Negative control

Sterile distilled water	40.6 µ1
10X PCR buffer (without MgCl ₂)	5 µl
MgCl ₂ (50 mM)	1.5 µl
dNTP (25 mM)	0.4 µl
Primers 1 et 2 (7.5 µM each)	2 µl
Taq DNA polymerase (5 units/µl)	0.5 µl
Total Volume	50 µl

G3PDH

Sterile distilled water	33.4 µl
10X PCR buffer (without MgCl ₂)	5 µl
MgCl ₂ (50 mM)	2 µl
dNTP (25 mM)	0.1 µl
Primer 1 (10 µM), Fig. 4	2 µl
Primer 2 (10 µM), Fig. 4	2 µl
Taq DNA polymerase (5 units/µl)	0.5 µl
First-strand reaction	5 µl
Total Volume	50 µl

- Mix gently with a micropipette and spin the tubes at 1000 x g for 5 seconds. Overlay
 each reaction with 50 µl of mineral oil only if the addition of mineral oil is a
 requirement for your thermal cycler.
- 4. Place the tube in a thermal cycler and immediately run the following program:

IFNγ

1 cycle of:	94° C for 4 minutes
30 cycles of:	94° C for 45 seconds
	55° C for 45 seconds
	72° C for 45 seconds
1 cycle of:	72° C for 10 minutes
Hold at 4°C	

G3PDH

1 cycle of:	94° C for 2 minutes
30 cycles of:	94° C for 30 seconds
	61° C for 45 seconds
	72° C for 45 seconds
1 cycle of:	72° C for 10 minutes
Hold at 4°C	

VIII - Agarose gel electrophoresis of PCR amplified DNA fragment

Agarose gel electrophoresis of aliquots of the PCR products alongside a known amount of a standard PCR fragment provides a visual estimate of the relative amounts of the IFN γ or G3PDH fragments based on their band intensities in an ethidium bromide-stained gel. It is important that the tubes with PCR products are not opened in the room where the PCR is set-up. Take tubes to a separate room.

- 1. Prior to use, prepare a 1.2 % agarose gel in 1X TBE containing 0.5 μ g/ml ethidium bromide with wells sufficient to accomodate 15 μ l samples.
- 2. Add 2 μ l of the 6X loading dye to 10 μ l of each amplification reaction.
- 3. Load each sample and 5 μ l of Smart Ladder into separate wells of the agarose gel and electrophorese at 100 V for 1 hour.
- 4. Take a photograph with film that produces a positive image (Polaroid Type 66).
- **5.** Proceed with data analysis (see example Fig. 5).

	Size of the PCR fragment
IFNγ DNA fragment	384 bp
G3PDH DNA fragment	450 bp
Positive control	300 bp

Figure 1: Mouse Interferon *γ* mRNA sequence.

```
1207 bp
LOCUS
            XM_125899
                                               mRNA
                                                       linear ROD 24-FEB-2003
DEFINITION Mus musculus interferon gamma (Ifng), mRNA.
ACCESSION
            XM 125899
            XM 125899.2 GI:28501526
VERSION
SOURCE
           Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
            1 (bases 1 to 1207)
 AUTHORS NCBI Annotation Project.
  TTTLE
            Direct Submission
  JOURNAL
            Submitted (17-FEB-2003) National Center for Biotechnology
            Information, NIH, Bethesda, MD 20894, USA
            MODEL <u>REFSEQ</u>: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence
COMMENT
            (NT_039501) using gene prediction method: BLAST, supported by mRNA
            evidence.
            Also see:
                Documentation of NCBI's Annotation Process
            On Feb 24, 2003 this sequence version replaced gi: 20866206.
FEATURES
                     Location/Qualifiers
     source
                     1..1207
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db xref="taxon:10090"
                     /chromosome="10"
                     1..1207
     gene
                     /gene="Ifng"
                     /db_xref="LocusID:15978"
                     /db_xref="MGI:107656"
                     109..576
     CDS
                     /gene="Ifng"
                     /codon_start=1
                     /product="interferon gamma"
                     /protein_id="XP_125899.1"
                     /db_xref="GI:20866207"
                     /db_xref="LocusID:15978"
                     /db_xref="MGI:107656"
                     /translation="MNATHCILALQLFLMAVSGCYCHGTVIESLESLNNYFNSSGIDV
                     EEKSLFLDIWRNWQKDGDMKILQSQIISFYLRLFEVLKDNQAISNNISVIESHLITTF
                     FSNSKAKKDAFMSIAKFEVNNPQVQRQAFNELIRVVHQLLPESSLRKRKRSRC"
                     148..558
     misc_feature
                     /gene="Ifng"
                     /note="IFN-gamma; Region: Interferon gamma"
                     /db_xref="CDD:pfam00714"
        1 atagetgeea teggetgaee tagagaagae acateagetg ateetttgga eeettgaet
       61 tgagacagaa gttctgggct tctcctcctg cggcctagct ctgagacaat gaacgctaca
      121 cactgcatct tggctttgca gctcttcctc atggctgttt ctggctgtta ctgccacggc
      181 acagtcattg aaagcctaga aagtctgaat aactatttta actcaagtgg catagatgtg
      241 gaagaaaaga gtctcttctt ggatatctgg aggaactggc aaaaggatgg tgacatgaaa
      301 atcctgcaga gccagattat ctctttctac ctcagactct ttgaagtctt gaaagacaat
      361 caggecatea geaacaacat aagegteatt gaateacaee tgattaetae ettetteage
      421 aacagcaagg cgaaaaagga tgcattcatg agtattgcca agtttgaggt caacaaccca
      481 caggtccagc gccaagcatt caatgagetc atccgagtgg tccaccaget gttgccggaa
      541 tccagcctca ggaagcggaa aaggagtcgc tgctgattcg gggtggggaa gagattgtcc
      601 caataagaat aattctgcca gcactatttg aatttttaaa tctaaaccta tttattaata
      661 tttaaaacta tttatatqqa qaatctattt taqatqcatc aaccaaaqaa qtatttataq
      721 taacaactta tatgtgataa gagtgaattc ctattaatat atgtgttatt tataatttct
      781 gtctcctcaa ctatttctct ttgaccaatt aattattctt tctgactaat tagccaagac
      841 tgtgattgcg gggttgtatc tgggggtggg ggacagccaa gcggctgact gaactcagat
      901 tgtagcttgt acctttactt cactgaccaa taagaaacat tcagagctgc agtgaccccg
      961 ggaggtgctg ctgatgggag gagatgtcta cactccgggc cagcgcttta acagcaggcc
     1021 agacagcact cgaatgtgtc aggtagtaac aggctgtccc tgaaagaaag cagtgtctca
     1081 agagacttga cacctggtgc ttccctatac agctgaaaac tgtgactaca cccgaatgac
     1141 aaataactcg ctcatttata gtttatcact gtctaattgc atatgaataa agtatacctt
     1201 tgcaacc
```

Figure 2: Comparison between mouse and human Interferon γ sequences.

S1 Mouse MNATHCILALQLFLMAVS-GCYC Human .KY.SY...F..CIVLG.L.... 1 10 50 Mouse HGTVIESLES LNNYFNAGHS DV-EEKSLFLD IWRNWQKDGD MKILQSQIIS Human QDPYVKEA.N .KK...SSGI ..ADNGT...G .LK..KEES. R..M....V. 100 Mouse FYLRLFEVLK DNQAISNNIS VIESHLITTF FSNSKAKKDA FMSIAKFEVN Human ..FK..KNF. .D.S.QKSVE T.KEDMNVK. .NSN.K.R.D .EKLTNYS.T 110 Mouse NPQVQRQAFN ELIRVVHQLL PESSLRKRKR SRC Human DLN...K.IH ...Q.MAE.S .AAKTG.... .QM LFRGRRASQ

Figure 3: Mouse G3PDH gene sequence.

LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	M32599 M32599.1 GI:193423 glyceraldehyde-3-phosphate dehydrogenase. Mus musculus (house mouse)					
REFERENCE AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1228) Sabath,D.E., Broome,H.E. and Prystowsky,M.B.					
TITLE JOURNAL MEDLINE	Glyceraldehyde-3-phosphate dehydrogenase mRNA is a major interleukin 2-induced transcript in a cloned T-helper lymphocyte Gene 91 (2), 185-191 (1990) 91007274					
PUBMED COMMENT	2145197 Original source text: Mouse (strain C57BL/10J) adult lymphocyte, cDNA to mRNA, clones B7 and A3. Draft entry and computer-readable sequence for [Gene (1990) In press] kindly submitted					
FEATURES	by D.E.Sabath, 05-MAR-1990. Location/Qualifiers					
source						
	/organism="Mus musculus"					
	/mol_type="mRNA"					
	/strain="C57BL/10J"					
	/db_xref="taxon:10090"					
/cell_type="lymphocyte"						
	/dev_stage="adult"					
mRNA	<11228					
05.0	/product="GAPDH mRNA"					
CDS	471048					
	/note="glyceraldehyde-3-phosphate dehydrogenase" /codon start=1					
	/protein_id="AAA37659.1"					
	/db xref="GI:309243"					
	/translation="MVKVGVNGFGRIGRLVTRAAICSGKVEIVAINDPFIDLNYMVYM					
	FQYDSTHGKFNGTVKAENGKLVINGKPITIFQERDPTNIKWGEAGAEYVVESTGVFTT					
	${\tt MEKAGAHLKGGAKRVIISAPSADAPMFVMGVNHEKYDNSLKIVSNASCTTNCLAPLAK}$					
VIHDNFGIVEGLMTTVHAITATQKTVDGPSGKLWRDGRGAAQNIIPASTGAAKAVGK						
IPELNGKLTGMAFRVPTPNVSVVDLTCRLEKPAKYDDIKKVVKQASEGPLKGILGYTE DOVVSCDFNSNSHSSTFDAGAGIALNDNFVKLISWYDNEYGYSNRVVDLMAYMASKE"						
	DŐAASCRANSUSUSUSUSUSUSUSUSUSUSUSUSUSUSUSUSUSUSU					

ORIGIN						
1	acagccgcat	cttcttgtgc	agtgccagcc	tcgtcccgta	gacaaaatgg	tgaaggtcgg
61	tgtgaacgga	tttggccgta	ttgggcgcct	ggtcaccagg	gctgccattt	gcagtggcaa
121	agtggagatt	gttgccatca	acgacccctt	cattgacctc	aactacatgg	tctacatgtt
181	ccagtatgac	tccactcacg	gcaaattcaa	cggcacagtc	aaggccgaga	atgggaagct
241	tgtcatcaac	gggaagccca	tcaccatctt	ccaggagcga	gaccccacta	acatcaaatg
301	gggtgaggcc	ggtgctgagt	atgtcgtgga	gtctactggt	gtcttcacca	ccatggagaa
361	ggccggggcc	cacttgaagg	gtggagccaa	acgggtcatc	atctccgccc	cttctgccga
421	tgcccccatg	tttgtgatgg	gtgtgaacca	cgagaaatat	gacaactcac	tcaagattgt
481	cagcaatgca	tcctgcacca	ccaactgctt	agcccccctg	gccaaggtca	tccatgacaa
541	ctttggcatt	gtggaagggc	tcatgaccac	agtccatgcc	atcactgcca	cccagaagac
601	tgtggatggc	ccctctggaa	agctgtggcg	tgatggccgt	ggggctgccc	agaacatcat
661	ccctgcatcc	actggtgctg	ccaaggctgt	gggcaaggtc	atcccagagc	tgaacgggaa
721	gctcactggc	atggccttcc	gtgttcctac	ccccaatgtg	tccgtcgtgg	atctgacgtg
781	ccgcctggag	aaacctgcca	agtatgatga	catcaagaag	gtggtgaagc	aggcatctga
841	gggcccactg	aagggcatct	tgggctacac	tgaggaccag	gttgtctcct	gcgacttcaa
901	cagcaactcc	cactcttcca	ccttcgatgc	cggggctggc	attgctctca	atgacaactt
961	tgtcaagctc	atttcctggt	atgacaatga	atacggc <mark>tac</mark>	agcaacaggg	tggtggacct
1021	catggcctac	atggcctcca	aggagtaaga	aaccctggac	cacccacccc	agcaaggaca
1081	ctgagcaaga	gaggccctat	cccaactcgg	cccccaacac	tgagcatctc	cctcacaatt
1141	tccatcccag	acccccataa	taacaggagg	ggcctaggga	gccctcccta	ctctcttgaa
1201	taccatcaat	aaagttcgct	gcacccac			

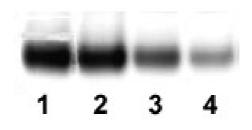
Figure 4: Primers used for G3PDH PCR amplification

primer GR: TCCACCACCCTGTTGCTGTA

primer GF: ACCACAGTCCATGCCATCAC

The size of the PCR fragment is 450 bp (566 - 1016).

Figure 5: Measurement of a RNA sample. The four bands are the standard bands. Lane 1: 250 pg; lane 2: 100 pg; lane 3: 50; lane 4: 25 pg.



The band intensities can be analyzed by ImageQuant software (Molecular Dynamics). A regression line is calculated or drawn.

Quantification of INFy by Enzyme Linked Immunosorbent Assay (ELISA)

- 1. After overnight culture, centrifuge the T cells suspension for 5 minutes at 1200 rpm at 4° C.
- 2. Transfer the supernatant in sterile 15 ml tubes. The tubes are stored at 4° C until quantification step.

Plate Preparation:

- 3. Dilute the Capture Antibody to the working concentration in PBS without carrier protein. Immediately coat a 96-well microplate with 100 µl per well of the diluted Capture Antibody. Seal the plate and incubate overnight at room temperature.
- 4. Aspirate each well and wash with Wash Buffer, repeating the process two times for a total of three washes. Wash by filling each well with Wash Buffer ($400 \ \mu$ L) using a squirt bottle, multi-channel pipette, manifold dispenser or autowasher.
- 5. Complete removal of liquid at each step is essential for good performance. After the last wash, remove any remaining Wash Buffer by aspirating or by inverting the plate and blotting it against clean paper towels.
- 6. Block plates by adding 300 μ l of Block Buffer to each well. Incubate at room temperature for a minimum of 1 hour.
- 7. Repeat the aspiration/wash as in step 4. The plates are now ready for sample addition.

Assay Procedure :

- 8. Add 100 μl of sample or standards in Reagent Diluent, or an appropriate diluent, per well. Cover with an adhesive strip and incubate 2 hours at room temperature.
- 9. Repeat the aspiration/wash as in step 4 of Plate Preparation.
- 10. Add 100 µl of the Detection Antibody, diluted in Reagent Diluent, to each well. Cover with a new adhesive strip and incubate 2 hours at room temperature.
- 11. Repeat the aspiration/wash as in step 2 of Plate Preparation.
- 12. Add 100 µl of the working dilution of Streptavidin-HRP to each well. Cover the plate and incubate for 20 minutes at room temperature. Avoid placing the plate in direct light.
- 13. Repeat the aspiration/wash as in step 4.
- 14. Add 100 µl of Substrate Solution to each well.
- 15. Incubate for 20 minutes at room temperature. Avoid placing the plate in direct light.
- 16. Add 50 μ l of Stop Solution to each well. Gently tap the plate to ensure thorough mixing.

17. Determine the optical density of each well immediately, using a microplate reader set to 450 nm. If wavelength correction is available, set to 540 nm or 570 nm. If wavelength correction is not available, subtract readings at 540 nm or 570 nm from the readings at 450 nm. This subtraction will correct for optical imperfections in the plate. Readings made directly at 450 nm without correction may be higher and less accurate.

Bibliography

Celi FS, Zenilman ME, Shuldiner AR. 1993: A rapid and versatile method to synthesize internal standards for competitive PCR. Nucleic Acids Research 21; p. 1047

Gilliland, G.S., Perrin, K. and Bunn, H.F. Competitive PCR for quantitation of mRNA. In: Innis et al. (eds.) PCR Protocols: A Guide to Methods and Applications, pp. 60-66, San Diego, CA, Academic Press, Inc., 1990.

Meuer S., Wittwer C., Nakagawara K.I., Rapid Cycle Real-Time PCR, Methods and Applications. Springer. 2001.

Rychlik, W. and Rhoads, R.E. (1989). A computer program for choosing optimal oligonucleotides for filter hybridization, sequencing and in vitro amplification of DNA. Nucl. Acids Res. 17: 8543-8551.

Schneeberger C, Speiser P, Kury F, Zeillinger R. 1995: Quantitative detection of reverse transcriptase-PCR products by means of a novel and sensitive DNA stain. PCR Methods and Applications 4; p. 234-238

Vanden Heuvel, J.P., Tyson, F.L. and Bell, D.A. (1993) Constructions of recombinant RNA templates for use as internal standards in quantitative RT-PCR. Biotechniques 14: 395-398.

Vanden Heuvel, J.P., Clark, G.C., Kohn, M.C., Tritscher, A.M., Greenlee, W.F., Lucier, G.W. and Bell, D.A. (1994) Dioxin-responsive genes: Examination of dose-response relationships using quantitative reverse transcriptase-polymerase chain reaction. Cancer Res. 54: 62-68.

Quantitative RT-PCR. Methods and Applications Book 3; Clontech Laboratories, Inc. 1993.

PCR quantitative. Techniques en Immunologie. Société Française d'Immunologie. Sonia Berrih-Aknin, ed. 2000.

Main materials required

Equipment

UV spectrophotometer.

Thermal cyclers.

Microcentrifuge with variable-speed control.

Microtiter plate reader.

Reagents and buffers

All water used in these protocols should be sterile, deionized, distilled water. All reagents, plastic- and glassware should be sterile

Ethanol (75 %) keep at - 20° C.

Isopropanol à 80 %.

Taq DNA Polymerase (GeneAmp, Perkin-Elmer Cetus).

10 X TBE buffer: 0.89 M Tris; 0.89 M boric acid; 20 mM EDTA ($pH \approx 8.3$).

Smart Ladder (Eurogentec).

Agarose NA (17-0554-01, -02, -03).

6X loading dye: 10 mM Tris-HCl (pH 7.6) containing 0.25 % bromophénol blue and xylene cyanol and 30 % glycerol.

MgCl₂ 25 mM (sterile aqueous solution).

dNTP (25 mM each dNTP in sterile water).

10X PCR buffer: 100 mM Tris-HCl, pH 8.3 (25°C), 500 mM KCl 0.01% (w/v) gelatine (Sigma, n°G2500).

TE buffer: 10 mM Tris-HCl (pH 8.0) et 0.1 mM EDTA.

Trizol (Invitrogen)

Microtiter paltes Maxisorb (Nunc, Danemark).

PBS: 0.15 M Sodium chloride containing 0.01 M phosphate buffer pH 7.4.

PBS-Tw: 0.15 M Sodium chloride containing 0.01 M phosphate buffer pH 7.4 and 0.05 % Tween 20.

PBS-Tw-BSA: PBS-Tw solution containing 0.1 % bovine albumin.

Enzyme-antibody conjugate diluted in PBS-BSA-Tw.

Peroxidase substrate: Tetramethyl benzidine and hygrogen peroxide.