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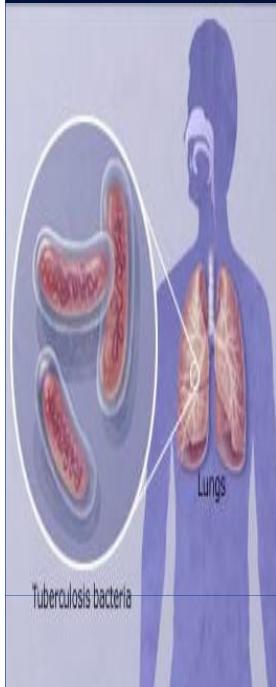
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Diagnostic potential of *M. tuberculosis*-specific proteins and peptides



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Bacteriology 2014



Publications >225

Impact Factor >480

Citations = >6400

h-index = 42

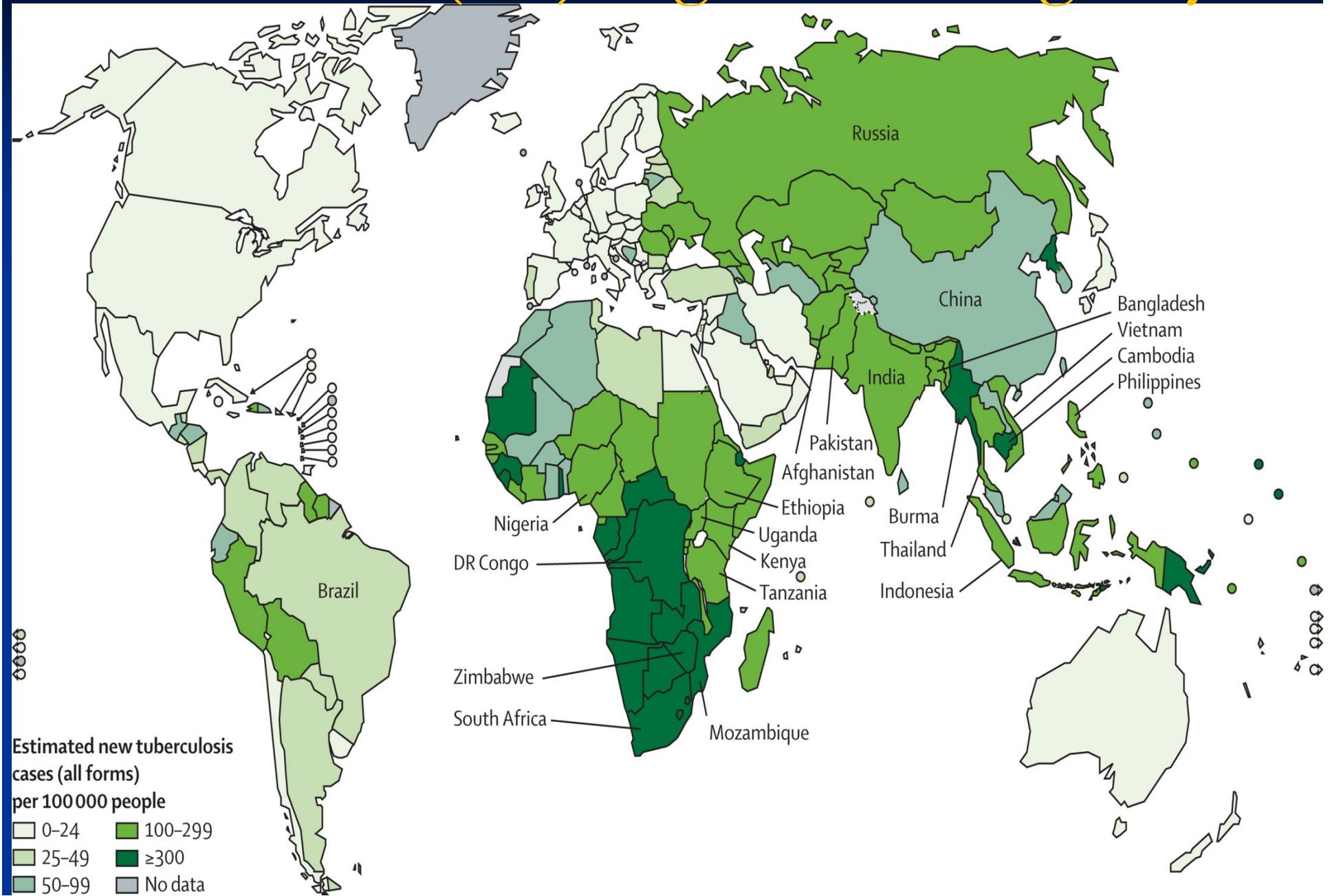
i10 index = 125

Theses supervisor
(n=28)

Theses examiner
(n=32)

Invited speaker >³100

Tuberculosis (TB): a global emergency



Tuberculosis: a global emergency

- TB is the second top most infectious killer of adults, after HIV/AIDS & is among the overall top 10 causes of death in the world
- Annually, 8-9 million people develop active TB disease and 1.3 million people die
- According to the WHO, almost 1/3rd of the world's population is latently infected with *M. tuberculosis*
- HIV and TB co-infection
- MDR and XDR TB
- Failure of BCG vaccine

What is required to control TB?

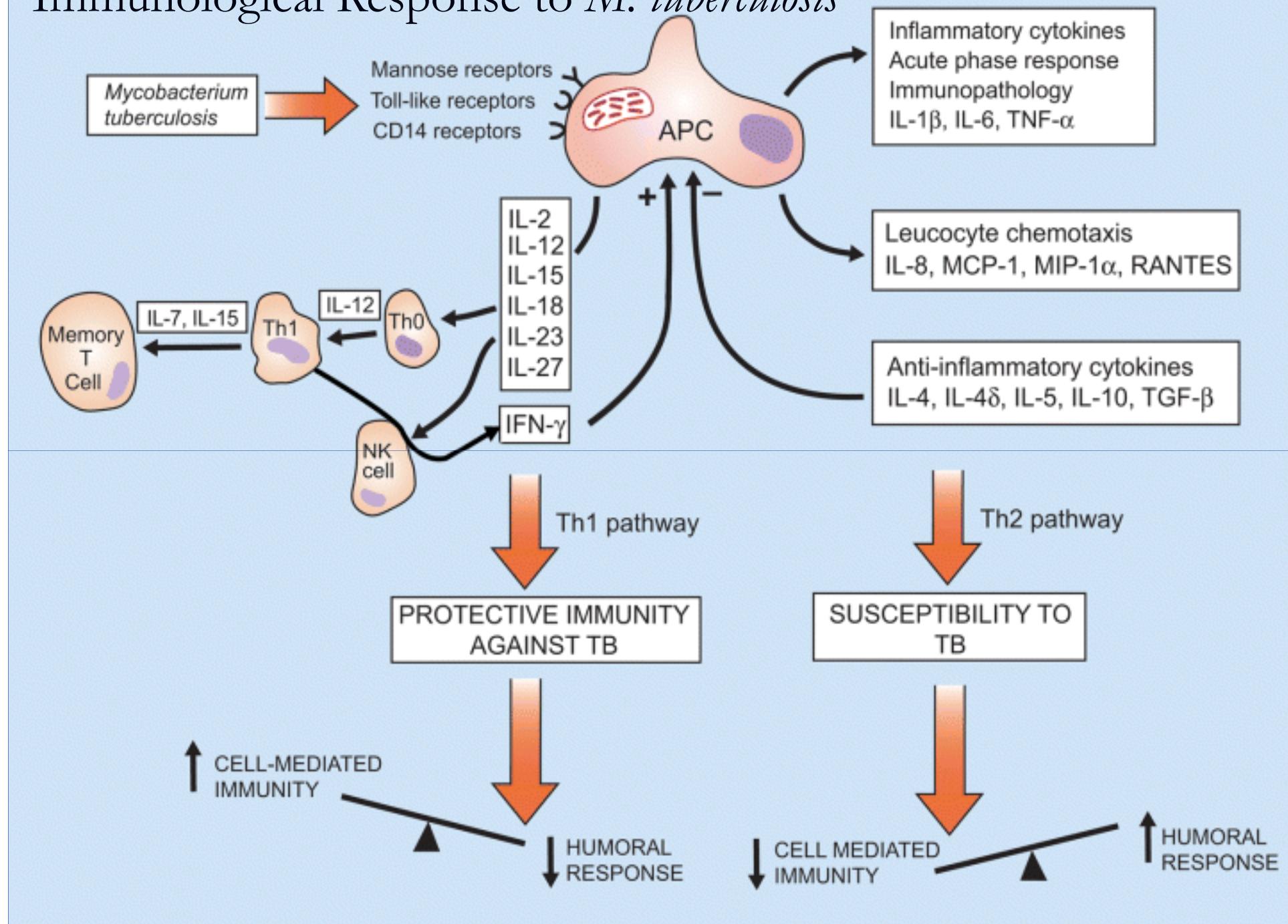
1. Specific diagnosis of both active and latent TB
2. New drugs
3. Effective vaccines

TB Diagnosis

1. Clinical symptoms
2. Chest X-ray
3. Microscopy and culture
4. Molecular methods
5. Immunological methods



Immunological Response to *M. tuberculosis*



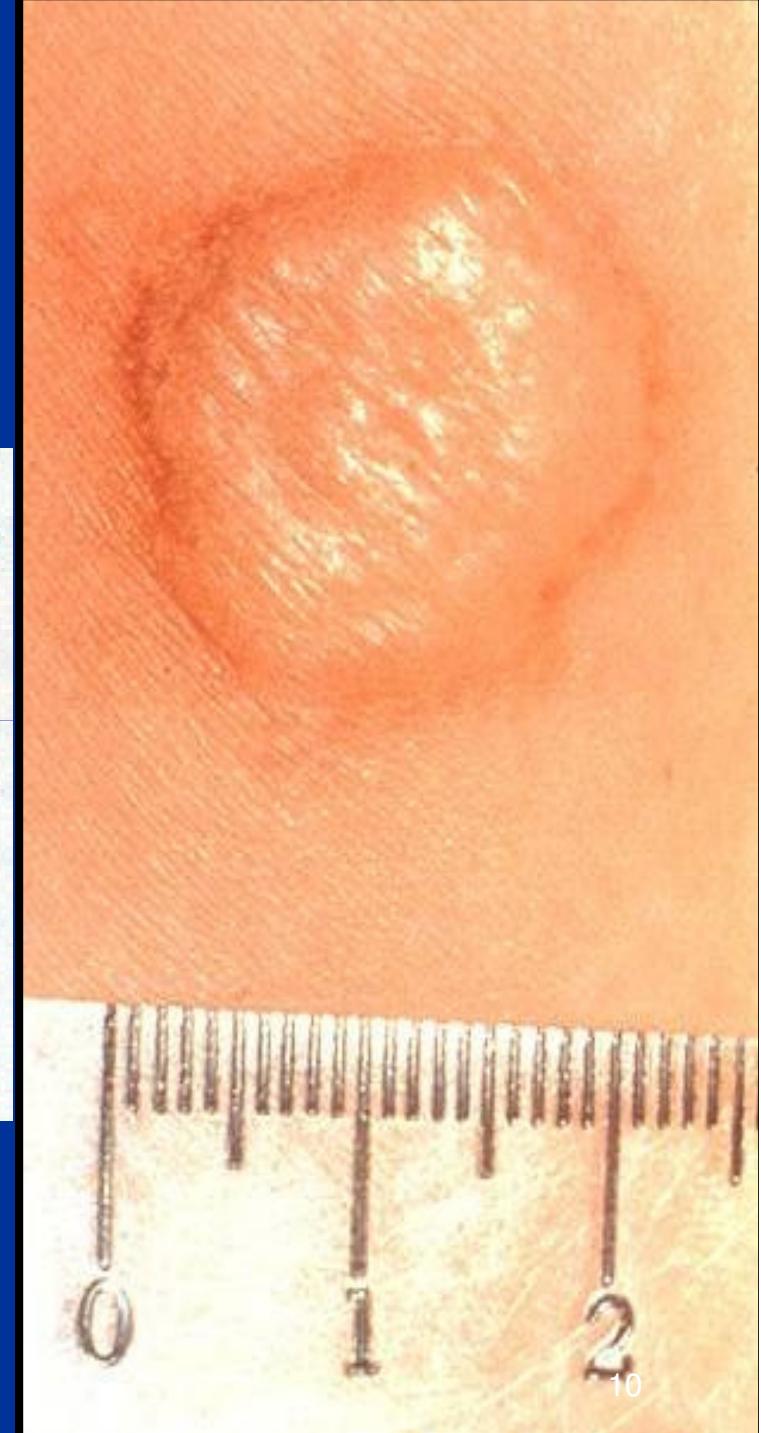
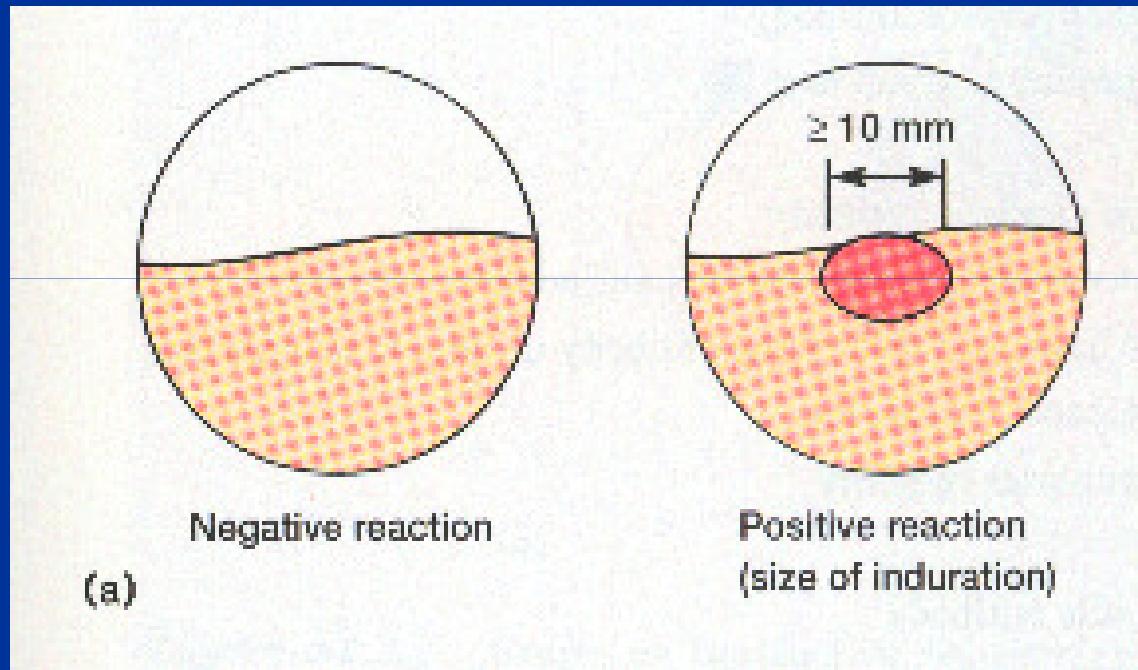
Immunological diagnosis of active and latent TB

- **Tuberculin Skin test (PPD Test)**

- ✓ Crude mixture of culture filtrate of *M. tuberculosis* which contains all types of molecules (species-specific as well as cross-reactive with other mycobacteria)
- ✓ Intra-dermal injection of 0.1 ml of PPD



✓ Immunological response (Erythema and induration) is measured after 48-72 h



Limitations of the tuberculin (PPD) Test:

Cannot distinguish between:

Active TB disease and

- ♣ Latent TB infection
- ♣ BCG vaccination
- ♣ Exposure to environmental mycobacteria



- ⦿ Thus, there is an overwhelming need to identify *M. tuberculosis*-specific antigens as
 - Specific diagnostic reagents

How to obtain *M. tuberculosis*-specific antigens?

■ Classical approach:

- Grow *M. tuberculosis* *in vitro*
- Purify single proteins using biochemical methods
- Test the purified proteins for immunological reactivity with patient's samples

Antigens identified using classical approach

- CFP10, ESAT-6 & TB7.7
- Currently used in CMI assays (IFN- γ response assay, IGRA) using peripheral blood cells from patients

These assays are costly, technically demanding & not affordable in TB endemic countries

Simple and cost-effective assays are required

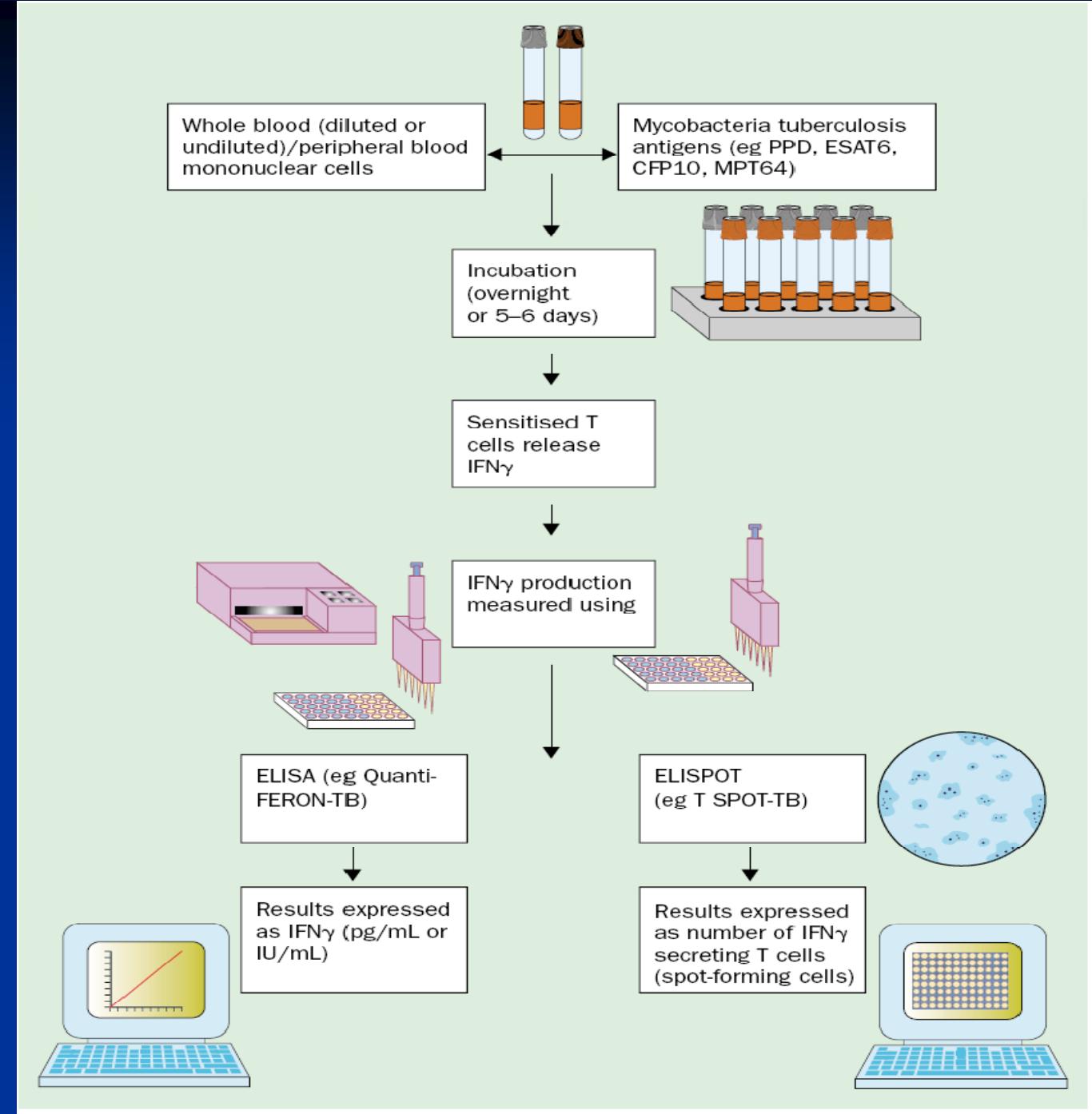
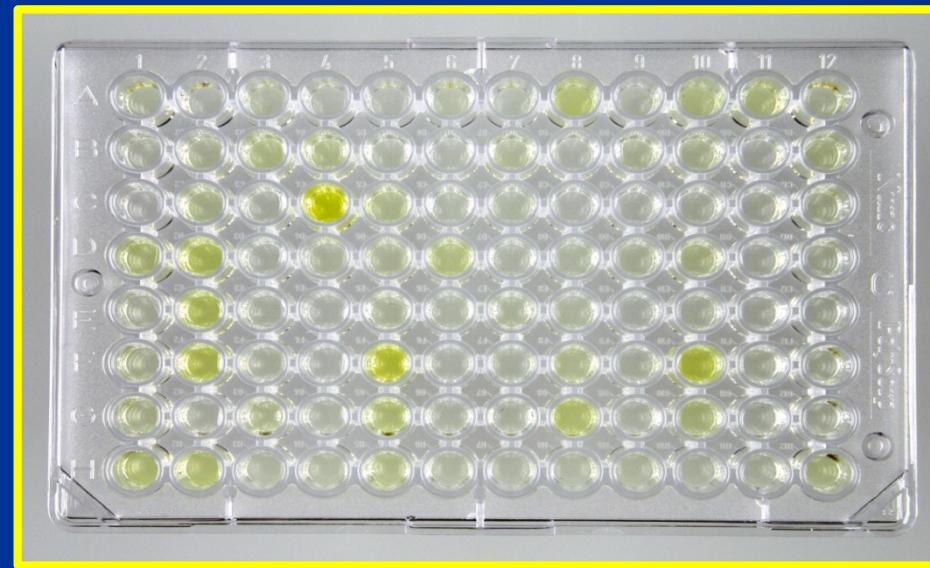


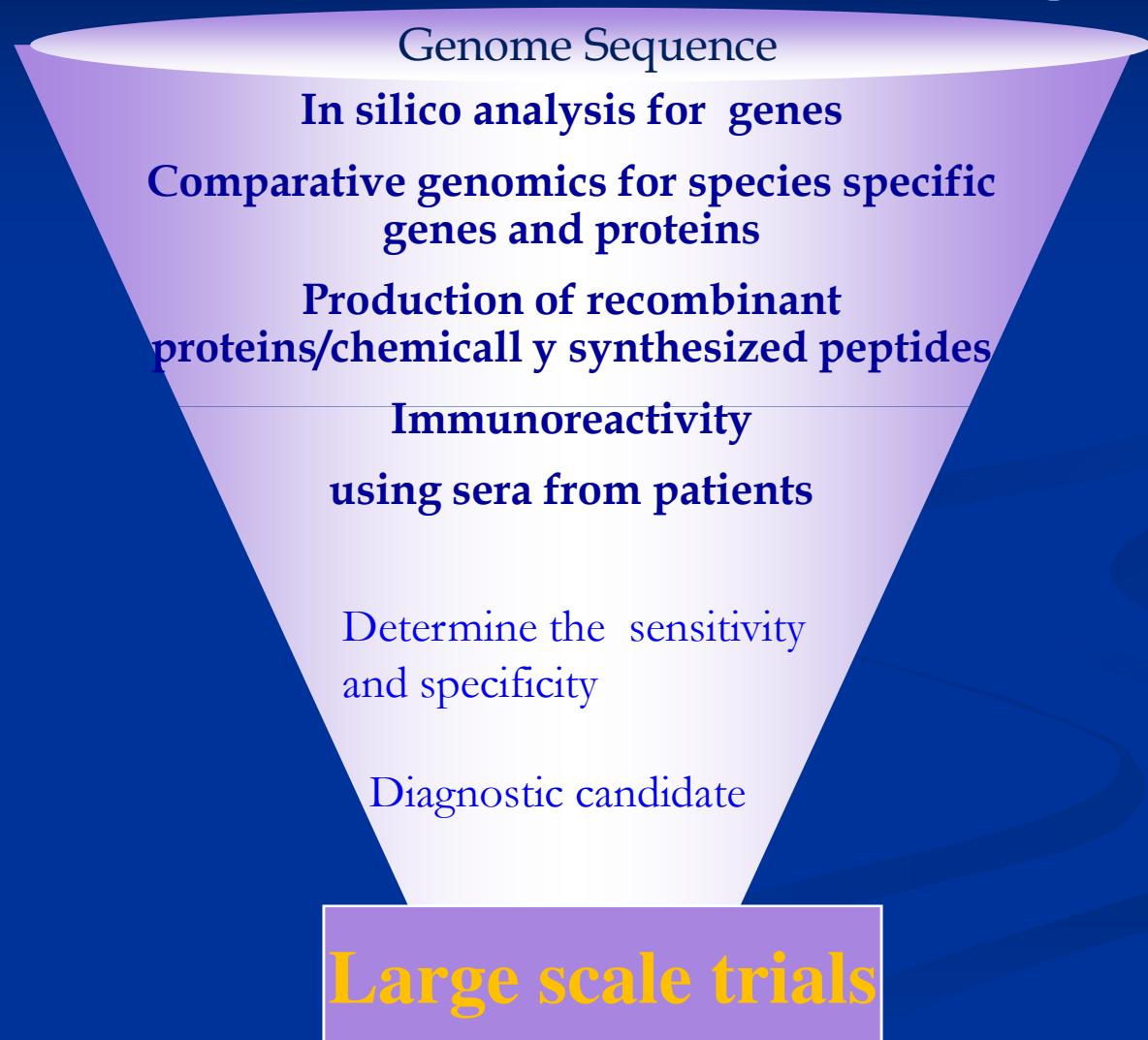
Figure 2. Overview of the interferon- γ (IFN- γ) assay technology.

Antibody assays

- Enzyme-Linked-Immunosorbent Assays (ELISA) to detect antibodies to *M. tuberculosis* components in serum samples
- Cost effective, easy to perform

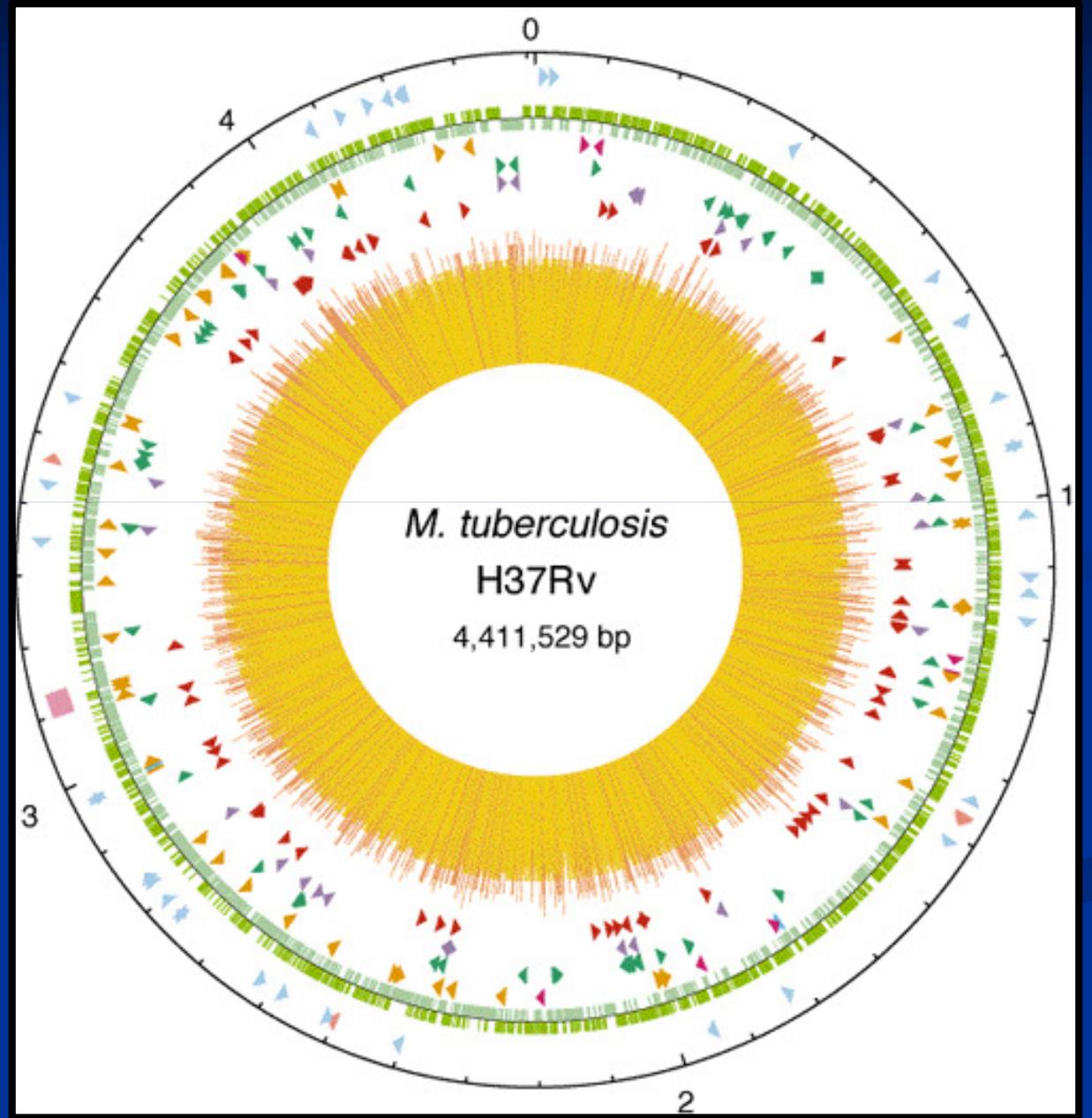


Diagnostic Development in Post Genomic Era: Reverse diagnostic

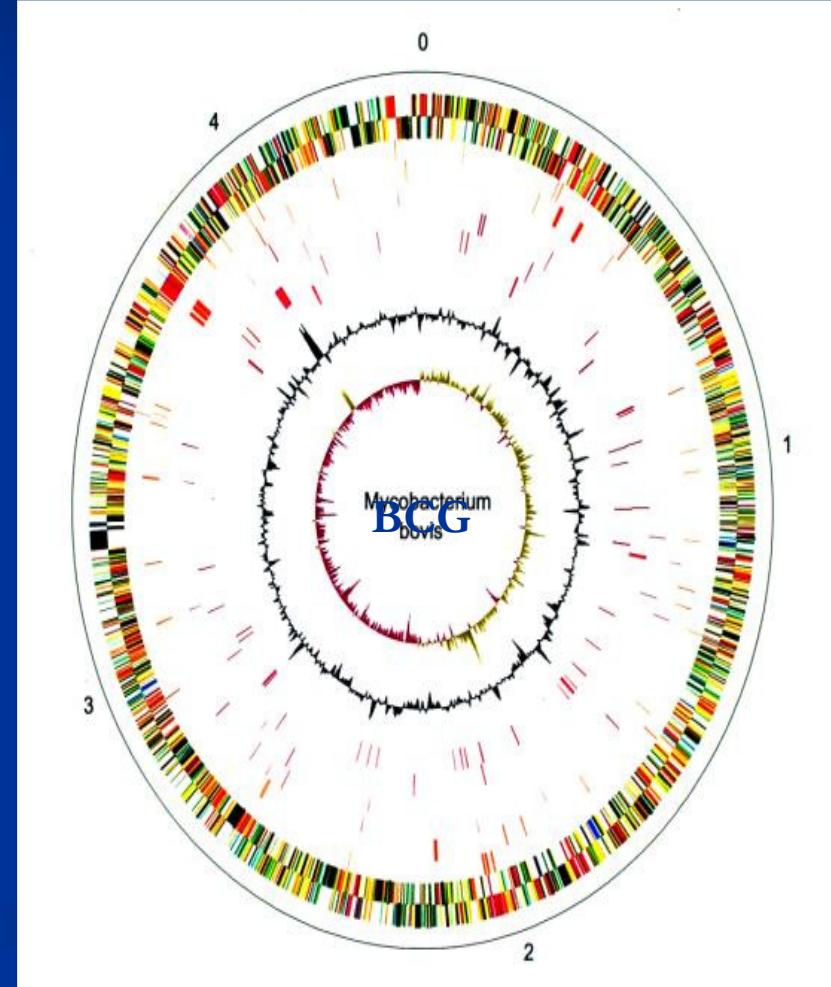
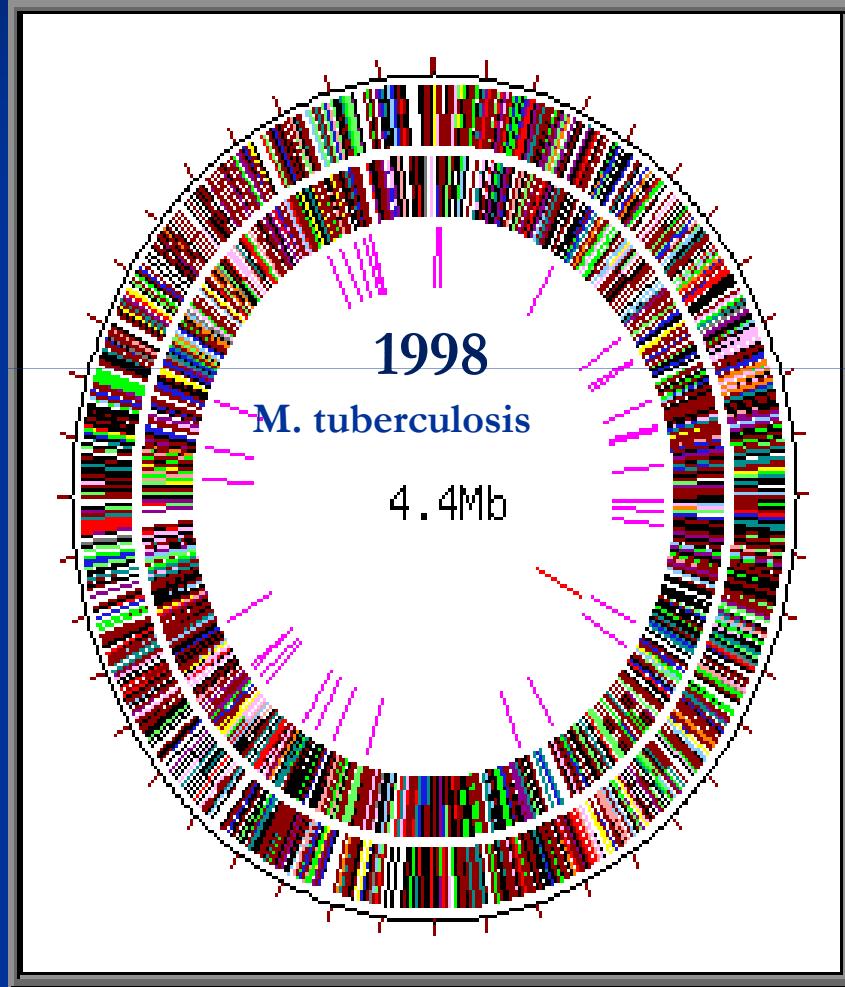


Complete genome sequence of *M. tuberculosis* and gene annotation

Genome: ca 4 MB
Genes: ca 4000

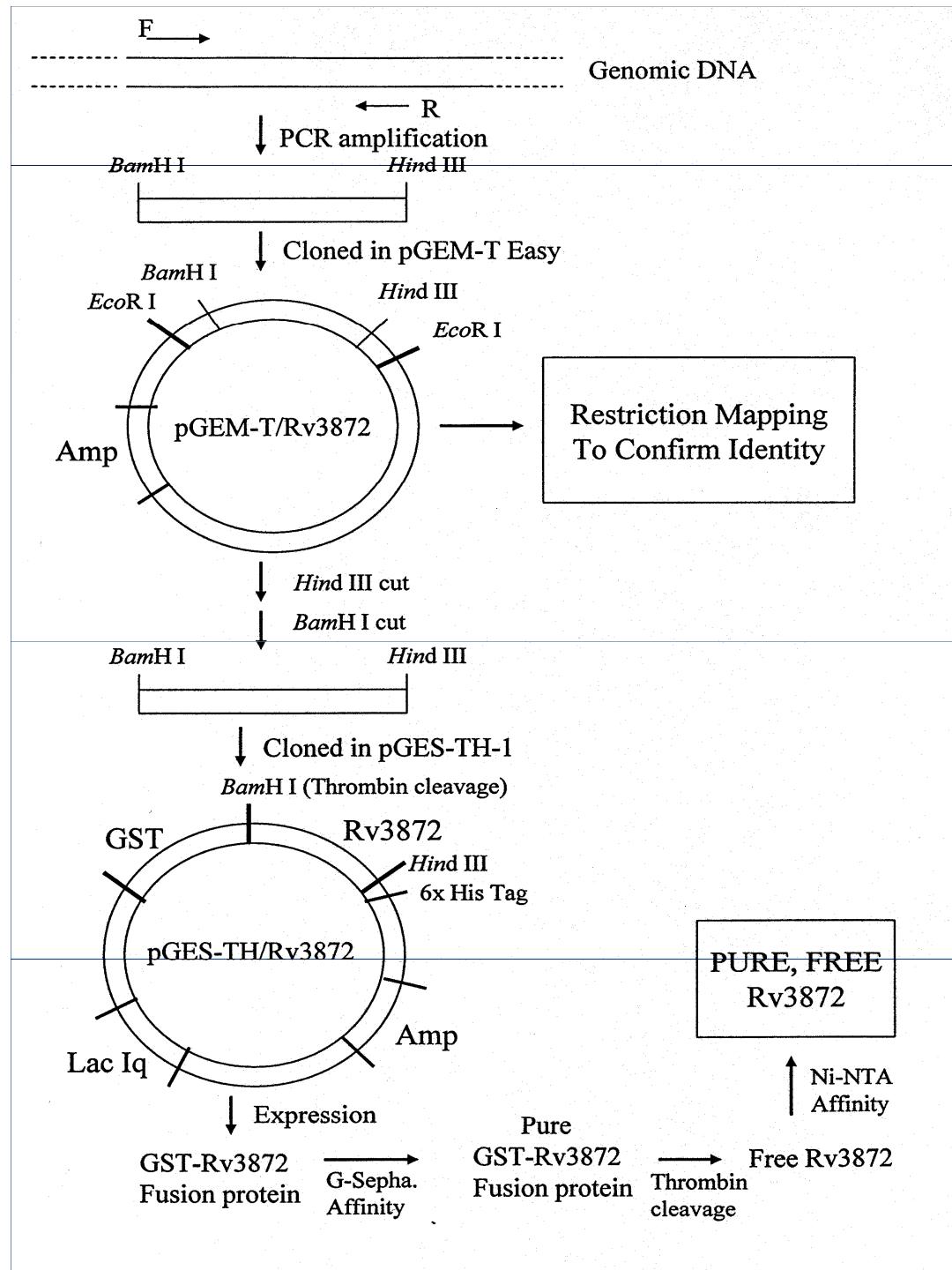


Genomic comparisons of *M. tuberculosis*, *M. bovis BCG* and other mycobacteria



Comparative genomics identified *M. tuberculosis* genomic regions absent in other mycobacteria

Region deleted	<i>M. tuberculosis</i>	<i>M. africanum</i>	<i>M. bovis</i>	BCG
RD1 (12 ORFs)	+	+	+	-
RD4 (3 ORFs)	+	-	-	-
RD5 (5 ORFs)	+	+	-	-
RD6 (11 ORFs)	+	+	-	-
RD7 (8 ORFs)	+	+	-	-
RD9 (7 ORFs)	+	-	-	-
RD10 (3 ORFs)	+	+	-	-
RD11 (5 ORFs)	+	+	-	-
RD12 (4 ORFs)	+	+	-	-
RD13 (16 ORFs)	+	+	+/-	-
RD15 (15 ORFs)	+	+	-	-



Recombinant proteins

- Only six of the 12 targeted RD1 proteins were obtained in purified form.

Inability to amplify full-length gene

Low level of expression

Degradation of the recombinant mycobacterial proteins by *E. coli* proteases

Presence of contaminating *E. coli* components in purified preparations

Overlapping synthetic peptides

P1 MTEQQWNFAGIEAAASAIQGNVTSI

P2 SAIQGNVTSIHSLLED**GKQSLTKLA**

P3 **EGKQSLTKLA**AAWGGS**GSEAYQGVQ**

P4 **SGSEAYQGVQ**QKWDA**TATELNNALQ**

P5

TATELNNALQNLARTISEAGQAMAS

P6

ISEAGQAMASTEGNVTGMFA

Synthetic peptides corresponding to proteins predicted in the RDs

RD	Protein	No. of proteins	No. of Peptides
RD1	Rv3871-Rv3878, ORFs 4, 8, 14 and 15	12	220
RD4	Rv0221- Rv0223	3	80
RD5	Rv3117- Rv3121	5	72
RD6	Rv1506c- Rv1516c	11	236
RD7	Rv2346c- Rv2353c	8	167
Total		39	775

Individual peptides were tested for antibody reactivity with pooled TB sera (n=10) in ELISA

Protocol of ELISA using TB sera of pool 1

Rows/ Wells	1	2	3	4	5	6	7	8	9	10	11	12
A	Blank	RD1ORF 8 P7	RD1ORF P6	RD1ORF 9 P14	RD1ORF 9 P22	RD1ORF 9 P30	RD1ORF9 P38	RD1ORF10 P2	RD1ORF10 P10	RD1ORF10 P18	RD1ORF10 P26	<u>RD1ORF1 0 P34</u>
B	Sera	RD1ORF 8 P8	RD1ORF P7	RD1ORF 9 P15	<u>RD1ORF9 P23</u>	RD1ORF 9 P31	RD1ORF9 P39	RD1ORF10 P3	RD1ORF10 P11	RD1ORF10 P19	RD1ORF10 P27	RD1ORF10 P35
C	CW	<u>RD1ORD 8 P9</u>	RD1ORF P8	RD1ORF 9 P16	<u>RD1ORF9 P24</u>	RD1ORF 9 P32	RD1ORF9 P40	<u>RD1O3RF 10 P4</u>	RD1ORF10 P12	<u>RD1ORF1 0 P20</u>	<u>RD1ORF1 0 P28</u>	RD1ORF10 P36
D	<u>CW+Sera</u>	RD1ORF 9 P1	RD1ORF P9	RD1ORF 9 P17	<u>RD1ORF9 P25</u>	RD1ORF 9 P33	RD1ORF9 P41	RD1ORF10 P5	RD1ORF3F1 0 P13	<u>RD1ORF1 0 P21</u>	<u>RD1ORF1 0 P29</u>	RD1ORF11 P1
E	RD1ORF8 P3	RD1ORF 9 P2	RD1ORF P10	RD1ORF 9 P18	RD1ORF 9 P26	RD1ORF 9 P34	RD1ORF9 P42	RD1ORF10 P6	RD1ORF5F1 0 P14	<u>RD1ORF1 0 P22</u>	<u>RD1ORF1 0 P30</u>	RD1ORF11 P2
F	RD1ORF8 P4	RD1ORF 9 P3	RD1ORF P11	RD1ORF 9 P19	RD1ORF 9 P27	RD1ORF 9 P35	RD1ORF9 P43	RD1ORF10 P7	<u>RD1OR7F 10 P15</u>	RD1ORF10 P23	<u>RD1ORF1 0 P31</u>	RD1ORF11 P3
G	<u>RD1ORF8 P5</u>	RD1ORF 9 P4	RD1ORF P12	<u>RD1ORF9 P20</u>	RD1ORF 9 P28	RD1ORF 9 P36	RD1ORF9 P44	<u>RD1ORF1 0 P8</u>	RD1ORF10 P16	RD1ORF10 P24	<u>RD1ORF1 0 P32</u>	RD1ORF11 P4
H	RD1ORF8 P6	<u>RD1ORF 9 P5</u>	RD1ORF P13	RD1ORF 9 P21	<u>RD1ORF9 P29</u>	<u>RD1ORF9 P37</u>	RD1ORF10 P1	RD1ORF10 P9	<u>RD1ORF1 0 P17</u>	<u>RD1ORF1 0 P25</u>	<u>RD1ORF1 0 P33</u>	<u>RD1ORF1 1 P5</u>

Blank ←
 Negative ←
 Ctrl ←
 Positive ←
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All 775 peptides were tested using the above protocol ₂₄

Results of ELISA test with pool 1 in terms of OD₄₀₅ values

Rows/ Wells	1	2	3	4	5	6	7	8	9	10	11	12
A	0.094	0.200	0.186	0.179	0.427	0.201	0.181	0.340	0.227	0.157	0.164	<u>0.818</u>
B	0.177	0.197	0.158	0.301	<u>0.546</u>	0.171	0.215	0.136	0.194	0.490	0.436	0.110
C	0.148	<u>1.154</u>	0.185	0.126	<u>0.975</u>	0.148	0.134	<u>0.922</u>	0.129	<u>0.578</u>	<u>0.919</u>	0.137
D	<u>0.676</u>	0.181	0.221	0.167	<u>0.951</u>	0.243	0.146	0.257	0.157	<u>1.147</u>	<u>1.142</u>	0.135
E	0.267	0.168	0.257	0.139	0.210	0.136	0.139	0.182	0.216	<u>0.759</u>	<u>0.710</u>	0.203
F	0.359	0.179	0.187	0.215	0.139	0.136	0.123	0.188	<u>0.515</u>	0.427	<u>0.679</u>	0.231
G	<u>>4</u>	0.165	0.234	<u>0.943</u>	0.360	0.154	0.133	<u>0.522</u>	0.395	0.190	<u>0.674</u>	0.377
H	0.364	<u>0.510</u>	0.186	0.232	<u>0.755</u>	<u>0.712</u>	0.302	0.229	<u>1.125</u>	<u>1.033</u>	<u>0.947</u>	<u>0.520</u>

E/C= OD₄₀₅ value with peptide + sera / OD₄₀₅ value with sera alone

E/C \geq 2 and OD405 values \geq 0.5 are shown in bold face and underlined

Results of ELISA with peptides (n=47) & sera of TB patients (pool 2)

Protein/Peptide	Mean OD ₄₀₅ values with peptide alone	Mean OD ₄₀₅ values with Sera+Peptide	E/C
RD1ORF2/P24	0.14	0.23	0.23/0.14=1.6
RD1ORF2/P25	>4	>4	>4/>4=1
RD1ORF2/P31	0.21	0.29	0.29/0.21=1.4
RD1ORF6/P2	0.18	0.33	0.33/0.18=1.8
RD1ORF7/P1	0.13	0.22	0.22/0.13=1.6
RD1ORF8/P4	>4	>4	>4/>4=1
RD1ORF8/P5	0.14	0.21	0.21/0.14=1.4
RD1ORF8/P6	0.10	0.17	0.17/0.10=1.6
RD1ORF8/P9	0.58	1.76	1.76/0.58=3
RD1ORF9/P5	0.41	0.45	0.45/0.41=1.1
RD1ORF9/P20	0.11	0.16	0.16/0.11=1.5
RD1ORF9/P23	0.27	0.47	0.47/0.27=1.7
RD1ORF9/P24	0.49	0.99	0.99/0.49=2
RD1ORF9/P25	0.30	0.59	0.59/0.30=1.9
RD1ORF9/P28	0.32	0.42	0.42/0.32=1.2
RD1ORF9/P29	1.5	0.89	0.89/1.5=0.61
RD1ORF9/P37	0.39	0.86	0.86/0.39=2.2
RD1ORF10/P4	1.8	1.5	1.5/1.8=0.83
RD1ORF10/P8	0.13	0.45	0.45/0.13=3.3
RD1ORF10/P15	0.48	0.56	0.56/0.48=1.1
RD1ORF10/P17	0.45	0.53	0.53/0.45=1.2
RD1ORF10/P19	0.35	0.45	0.45/0.35=1.2

Results of ELISA with peptides (n=11) & sera of TB patients (pool 3)

Protein/Peptide	Mean OD ₄₀₅ value with		E/C
	Peptide alone	Peptide+Sera	
RD1ORF8/ P9	0.65	1.5	<u>1.5/0.65=2.3</u>
RD1ORF9 /P24	0.41	1.3	<u>1.3/0.41=3.1</u>
RD1ORF9 /P37	0.41	0.34	0.34/0.41=0.85
RD1ORF10 /P28	1.3	1.5	1.5/1.3=1.1
RD1ORF11 /P14	0.28	0.48	0.48/0.28=1.7
RD1ORF14 /P10	0.86	0.69	0.69/0.86=0.8
RD4ORF2 /P5	1.7	1.8	1.8/1.7=1.03
RD6ORF3 /P17	0.45	1.0	<u>1.0/0.45=2.5</u>
RD6ORF5 /P10	0.51	1.4	<u>1.4/0.51=2.7</u>
RD6ORF10/ P18	0.32	0.45	0.54/0.32=1.7
RD6ORF11/ P26	0.45	1.4	<u>1.4/0.45=3.1</u>

Results of ELISA with peptides (n=5) & sera of TB patients (pool 3, and individual serum1-10)

Protein/Peptide	ELISA reactivity (E/C) with											No. of positive sera/total
	Pool 3	S1	S2	S3	S4	S5	S6	S7	S8	S9	s10	
RD1ORF8 /P9	<u>2.3</u>	1.6	1.4	1.7	1.7	1.7	<u>3</u>	1.4	1.5	1.2	1.1	1/10
RD1ORF9 /P24	<u>3.1</u>	<u>4.5</u>	<u>3.4</u>	1.9	1.7	<u>2.1</u>	<u>2.3</u>	<u>2.8</u>	<u>2.8</u>	<u>2.5</u>	<u>2.7</u>	<u>8/10</u>
RD6ORF3/ P17	<u>2.5</u>	<u>2.8</u>	<u>2.7</u>	<u>3.1</u>	<u>2.2</u>	<u>2.7</u>	<u>2.9</u>	<u>3.2</u>	1.5	1.7	1.1	<u>7/10</u>
RD6ORF5/ P10	<u>2.7</u>	<u>2.1</u>	1.9	<u>4.4</u>	<u>3.7</u>	<u>3.6</u>	<u>4.2</u>	<u>3.6</u>	<u>5.3</u>	<u>6.9</u>	<u>7.3</u>	<u>9/10</u>
RD6ORF1 1/P26	<u>3.1</u>	1.9	<u>3.6</u>	<u>5.7</u>	<u>2.8</u>	<u>2.1</u>	<u>3.1</u>	<u>2.2</u>	<u>2.7</u>	<u>2.9</u>	<u>3.2</u>	<u>9/10</u>

Results of ELISA with peptides (n=5) and sera of TB patients (pool 4, and individual serum 1-10)

Protein/Pep tide	ELISA reactivity (E/C) with										No. of positive sera/total	
	Pool 4	S1	S2	S3	S4	S5	S6	S7	S8	S9		
RD1ORF8 /P9	1	1.2	1.2	1	0.9	1	1	1.1	1.5	1.4	1.6	0/10
RD1ORF9 /P24	<u>3.4</u>	<u>4.5</u>	1.7	<u>2</u>	<u>2.7</u>	<u>3.2</u>	<u>2.2</u>	<u>2.2</u>	<u>2.1</u>	<u>2.9</u>	<u>4.8</u>	<u>9/10</u>
RD6ORF3/ P17	<u>3.5</u>	<u>3</u>	1.9	<u>2</u>	1.4	<u>2.2</u>	<u>11.3</u>	<u>5.9</u>	<u>2.6</u>	<u>2.8</u>	<u>4.6</u>	<u>8/10</u>
RD6ORF5/ P10	<u>3.3</u>	<u>3.4</u>	<u>5.9</u>	<u>7.8</u>	<u>4.9</u>	<u>7.7</u>	<u>3.4</u>	<u>2.6</u>	<u>2.1</u>	<u>3.5</u>	<u>2.2</u>	<u>10/10</u>
RD6ORF11 /P26	<u>2.4</u>	<u>2.2</u>	<u>2.6</u>	<u>3</u>	<u>4.5</u>	<u>3.1</u>	<u>5.6</u>	<u>3</u>	1.9	<u>5.3</u>	<u>2.5</u>	<u>9/10</u>

Results of ELISA with peptides (n=5) and sera of healthy subjects (pool, and individual serum 1-10)

Protein/Pep tide	ELISA reactivity (E/C) with											No. of positive sera/total
	Pool	seru m1	seru m2	seru m3	seru m4	seru m5	seru m6	seru m7	seru m8	seru m9	seru m10	
RD1ORF8 /P9	1.2	0.9	1.4	0.1	1.3	1	0.9	1.1	0.8	1.1	1	0/10
RD1ORF9 /P24	1.6	1.3	1.7	1.6	1.5	1.1	1.4	1.3	1.7	1.3	1.7	0/10
RD6ORF3/ P17	1.3	1.3	2.4	1.1	1.4	1.4	1.3	1.2	1.6	1.8	1.6	1/10
RD6ORF5/ P10	5.7	6.6	6.5	4.6	4.9	5.8	6.5	1.3	3.4	1.1	2.1	8/10
RD6ORF11 /P26	1.2	1.3	2.4	1.1	1	1	1.4	1.2	1.5	1.3	1.7	1/10

Consistent peptides' reactivity in terms of percentages

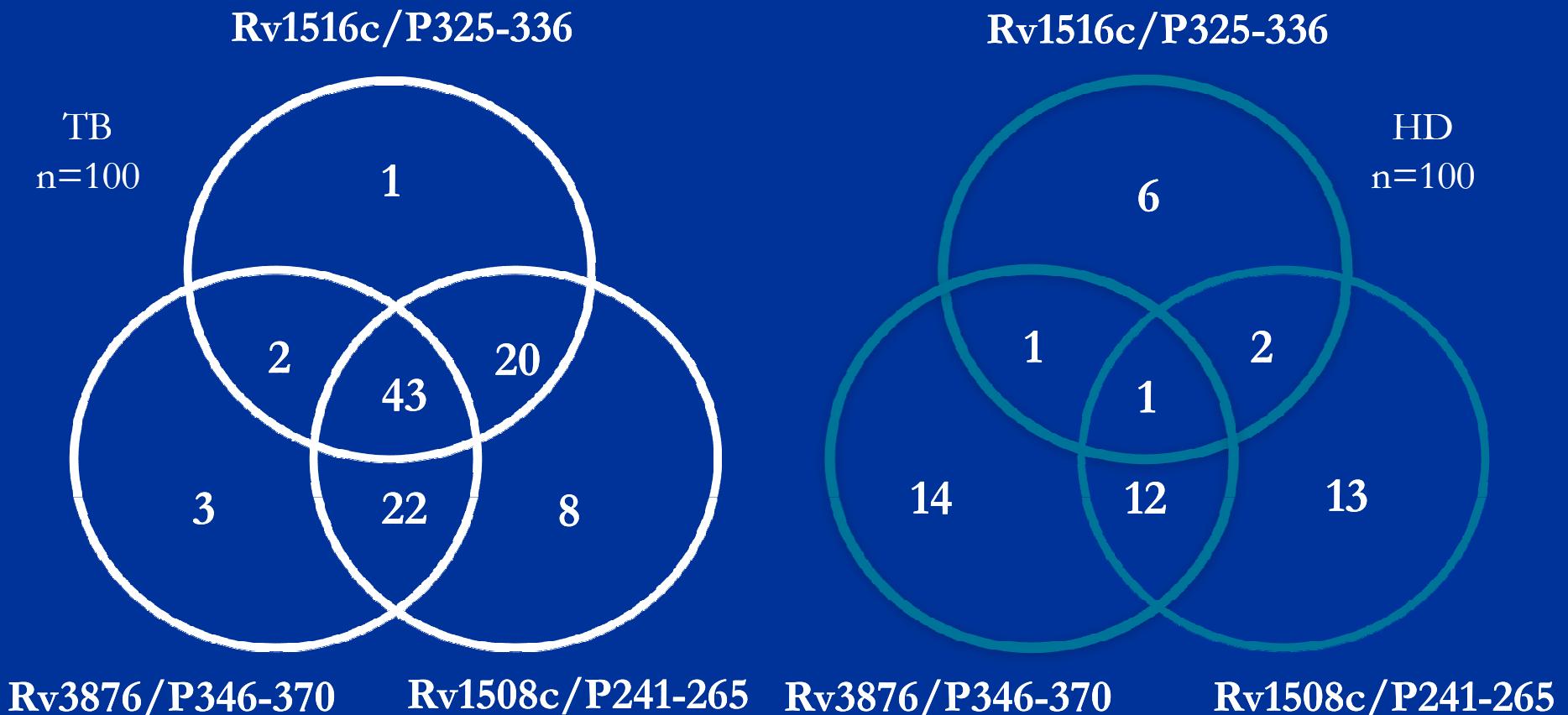
Peptides	TB patients' Sera	Healthy subjects' sera
RD1ORF9 (Rv3876)/P24	70%	28%
RD6ORF3 (Rv1508c)/p17	93%	28%
RD6ORF11 (Rv1516c)/P26	66%	10%
RD6ORF5 (Rv1510c)/P10	46%	50%

Results of BLAST search for sequence identity of immunodominant peptide aa 136-160 of RD6 protein Rv1510 in various strains of *M. tuberculosis* and other mycobacteria

Mycobacterial species and strains	Sequence	Identity
<i>M. tuberculosis</i> H37Rv, K85, CPHL_A, KZN 605, C, CDC1551, H37Ra, F11, KZN1435, T92, T85, str. Haarlem	Query 1 FVEGRWLSVGLLSVGVAGFCAQATL 25 FVEGRWLSVGLLSVGVAGFCAQATL Sbjct 127 FVEGRWLSVGLLSVGVAGFCAQATL 151	25/25 100%
<i>M. bovis</i> AF2122/97, BCG, Pasteur 1173P2	Query 1 FVEGRWLSVGLLSVGVAGFCAQATL 25 F E RWLSV LLS+G+AGFC ATL Sbjct 135 FAEARWLSVALLSIGLAGFCLHATL 159	10/25 72%
<i>M. avium</i> 104, paratuberculosis K-10	Query 1 FVEGRWLSVGLLSVGVAGFCAQATL 25 FVE R LSV LLSVG+AGFC ATL Sbjct 117 FVEARPLSVLLLGVLAGFCVHATL 141	19/25 76%
<i>M. smegmatis</i> str. MC2 155	Query 1 FVEGRWLSVGLLSVGVAGFCAQATL 25 FVE R LSV LLSVG+AGFC ATL Sbjct 129 FVESRALSVALLSVGLAGFCLHATL 153	19/25 76%
<i>M. sp.</i> KMS, <i>M. sp.</i> JLS	Query 1 FVEGRWLSVGLLSVGVAGFCAQATL 25 FVE RWLSV LLS G+AGFC ATL Sbjct 117 FVEARWLSVLLSAGLAGFCVHATL 141	19/25 76%
<i>M. marinum</i> , <i>M.</i> <i>ulcerans</i> Agy99	Query 1 FVEGRWLSVGLLSVGVAGFCAQATL 25 FVE RWLSVGLLSVG+AGFC ATL Sbjct 103 FVEDRWLSVGLLSVGLAGFCLHATL 127	21/25 84%
<i>M. kansasii</i> ATCC 12478	Query 1 FVEGRWLSVGLLSVGVAGFCAQATL 25 FVE RWLSVGLLSVG+AGFC ATL Sbjct 132 FVEARWLSVGLLSVGLAGFCLHATL 156	21/25 84%

Results of BLAST search for sequence identity of immunodominant peptide aa 361-372 of RD6 protein Rv1516c in various strains of *M. tuberculosis* and other mycobacteria

Mycobacterial species and strains	Sequence				Identity
<i>M. tuberculosis</i> H37Rv, H37Ra, F11, KZN 1435, str. Haarlem, CDC1551, C, 02 1987, 94 M4241A	Query 1	VWP SRLRRGCRA	12	Sbjct 362	VWP SRLRRGCRA 373 12/12 100%



- ✓ 87% with 2-3 peptides
- ✓ 12% with 1 peptide
- ✓ 1% didn't show reactivity

- ✓ 16% with 2-3 peptides
- ✓ 33% with 1 peptide
- ✓ 51% didn't show reactivity

Sensitivity, specificity, PPV, NPV and diagnostic accuracy of peptides 346-370 of Rv3876, 241-265 of Rv1508c and 325-336 of Rv1516c individually and in combination

Peptide	Sensitivity	Specificity	PPV	NPV	Diagnostic accuracy
346-370 of Rv3876	70%	72%	72%	71%	71%
241-265 of Rv1508c	93%	72%	77%	91%	82%
325-336 of Rv1516c	66%	90%	89%	74%	78%
≥Two peptides	87%	84%	84%	86%	85%

Epitope prediction by using the server ABCpred in the sequence of immunodominant peptide of Rv1510

Peptide	Predicted epitope	Prediction score
136-160 of Rv1510	FVEGRWLSVGLLSVGVAGFCAQATL	
	FVEGRWLSVGLLSVGVAGFC-----	0.65
	FVEGRWLSVGLLSVGVAG-----	0.74
	FVEGRWLSVGLLSVGV-----	0.57
	-----GLLSVGVAGFCAQATL	0.54
	-----SVGLLSVGVAGFCA---	0.65
	FVEGRWLSVGLLSV-----	0.58
	-----LSVGLLSVGVAG-----	0.55
	-----VGLLSVGVAG-----	0.57

Epitope prediction by using the server ABCpred in the sequence of immunodominant peptide of Rv3876

Peptide	Predicted epitope	Prediction score
346-370 of Rv3876	TQKSLRPAAKGPKVKKVKPQKPKAT	
	TQKSLRPAAKGPKVKKVKPQ-----	0.83
	-----PAAKGPKVKKVKPQKP---	0.78
	-----LRPAAKGPKVKKVK-----	0.70
	-----KGPKVKKVKPQKPK--	0.66
	-----GPKVKKVKPQKP---	0.80
	---LRPAAKGPKVKK-----	0.75
	TQKSLRPAAK-----	0.82
	-----PAAKGPKVKK-----	0.76

Epitope prediction by using the server ABCpred in the sequence of immunodominant peptide of Rv1508c

Peptide	Predicted epitope	Prediction score
241-265 of Rv1508c	ARGLERVVIFVTLGAAAIPAWGVID	
	-----VTLGAAAIPAWGVI-	0.81
	--LERVVIFVTLGAAAIP-----	0.72
	-----FVTLGAAAIPAWGVID	0.67
	-RGLERVVIFVTLGAAAIP-----	0.61
	----ERVVIFVTLGAAAIPAWGVI-	0.57
	-----VVIFVTLGAA-----	0.64
	ARGLERVVIF-----	0.62
	-----VVIFVTLGAAA-----	0.67
	--GLERVVIFVTLG-----	0.59
	-----VTLGAAAIPAWG---	0.51

Epitope prediction by using the server ABCpred in the sequence of immunodominant peptide of Rv1516c

Peptide	Predicted epitope	Prediction score
325–336 of Rv1516c	VWPSRLRRGCRA	
	VWPSRLRRGCRA	0.62
	VWPSRLRRGC--	0.62

The description of the proteins RD1 Rv3876, RD6 Rv1508c and RD6 Rv1516c using TubercuList server

Protein	Description
RD1 Rv3876 (666 aa)	Conserved hypothetical proline and alanine rich protein of unknown function
RD6 Rv1508c (599 aa)	Probable membrane protein, predicted to be in the GT-C superfamily of glycosyltransferases
RD6 Rv1516c (336 aa)	Probable sugar transferase, involved in cellular metabolism

Raising anti-peptide antibodies in rabbits and ELISA reactivity of sera to immunizing peptides

- Anti-RD1Rv3876, anti-RD6 Rv1508c and anti-RD6 Rv1516c antibodies were raised in 4-8 months rabbits against pools of 11 peptides of each protein

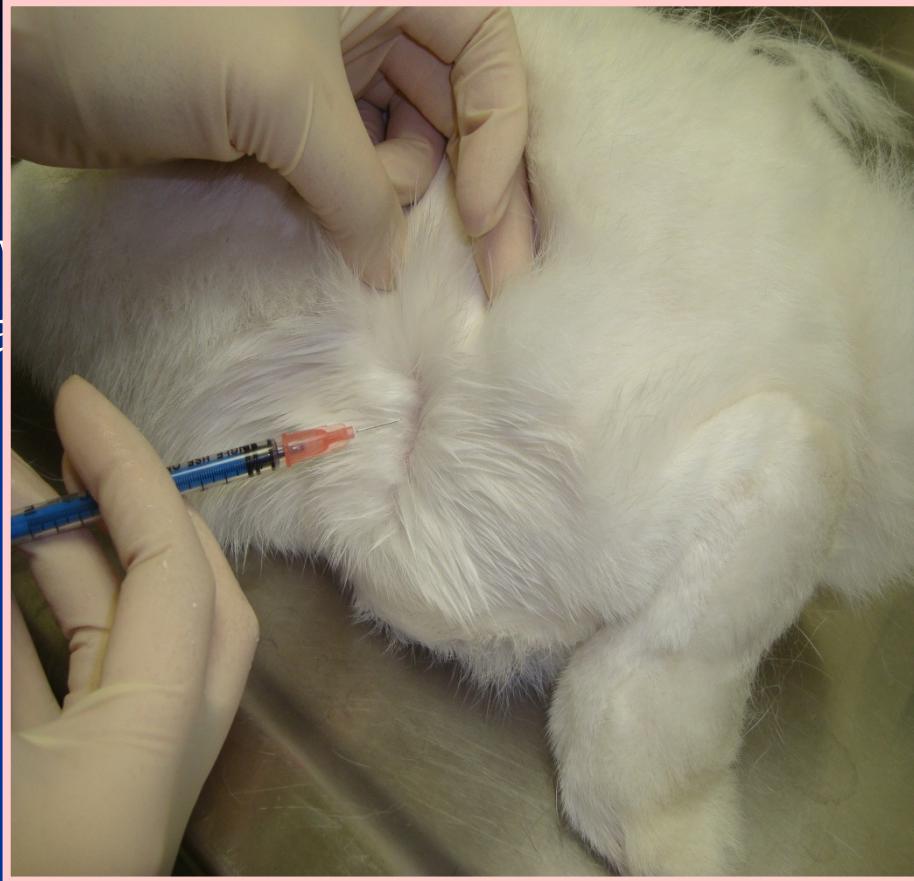
Rv3876	Amino acids sequence
P19	271 PAPLGQPRS YLAPP TRPAPTE PPPS 295
P20	286 RPAPTEPPPSPSPQR NSGR RAERRV 310
P21	301 NSGR RAERRVHPDLAAQHAAAQPDS 325
P22	316 AQHAAAQPDSITAATTGGRRRKRAA 340
P23	331 TGGRRRKRAAPDLDATQKSLRPAAK 355
P24	346 TQKSLRPAAKGPKVKKVKPQKPKAT 370
P25	361 KVKPQKPKATKPPKVVSQRGWRHWV 385
P26	376 VSQRGWRHWVHALTRINLGLSPDEK 40
P27	391 INLGLSPDEKYELDLHARVRRNPRG 415
P28	406 HARVRRNPRGSYQIAVVGLKGGAGK 430
P29	421 VVGLKGGAGK TTLTAALGSTLAQVR 445

Rv1516c	Amino acids sequence
P12	151 DWGMNIGRHCFS DYAMVAAAGI QPN 175
P13	166 MVAAAGI QPN PADYLISLPADYQPT 190
P14	181 ISLPADYQPTAVAAWAPARIPYAIF 205
P15	196 APARI PYAIFGLPSH WLGA PRL GLI 320
P16	211 WLGA PRL GLI CYLVAL TMAVI SPAI 235
P17	226 LTMAVISPAIWAARGARGLERVVIF 250
P18	241 ARGLERVVIFVTLGAAAIPA WGVID 265
P19	256 AAIPA WGVIDRGNSTGFVVPIALAY 280
P20	271 GFVVPIALAYFVALSRQRWGLATIT 295
P21	286 RQRWGLATITVILAVLVKPQFVVLG 310
P22	301 LVKPQFVVLGVVLLAARQWRWAGIG 325

Rv1508c	Amino acids sequence	
P16	211	YDDIPADVMPLDWYLHVRHAVHGDI 235
P17	226	HVRHAVHGDIAMLPDTMAVYRRHAQ 250
P18	241	TMAVYRRHAQGMWHNQVVDPPKFWL 265
P19	256	QVVDPPKFWLTQGPGLHAATFDAMLD 280
P20	271	HAATFDAMLDLFPGDPAREELIAVM 295
P21	286	PAREELIAVMADWILRQIANVPGPE 310
P22	301	RQIANVPGPEGRAALQETIARHPRI 325
P23	316	QETIARHPRIAMLALQHRGATPARR 340
P24	331	QHRGATPARRLKTQWRKLAAATPSR 355
P25	346	RKLAAATPSRRGLVDVWPSRLRRGC 370
P26	361	VWPSRLRRGCRA 385

Raising

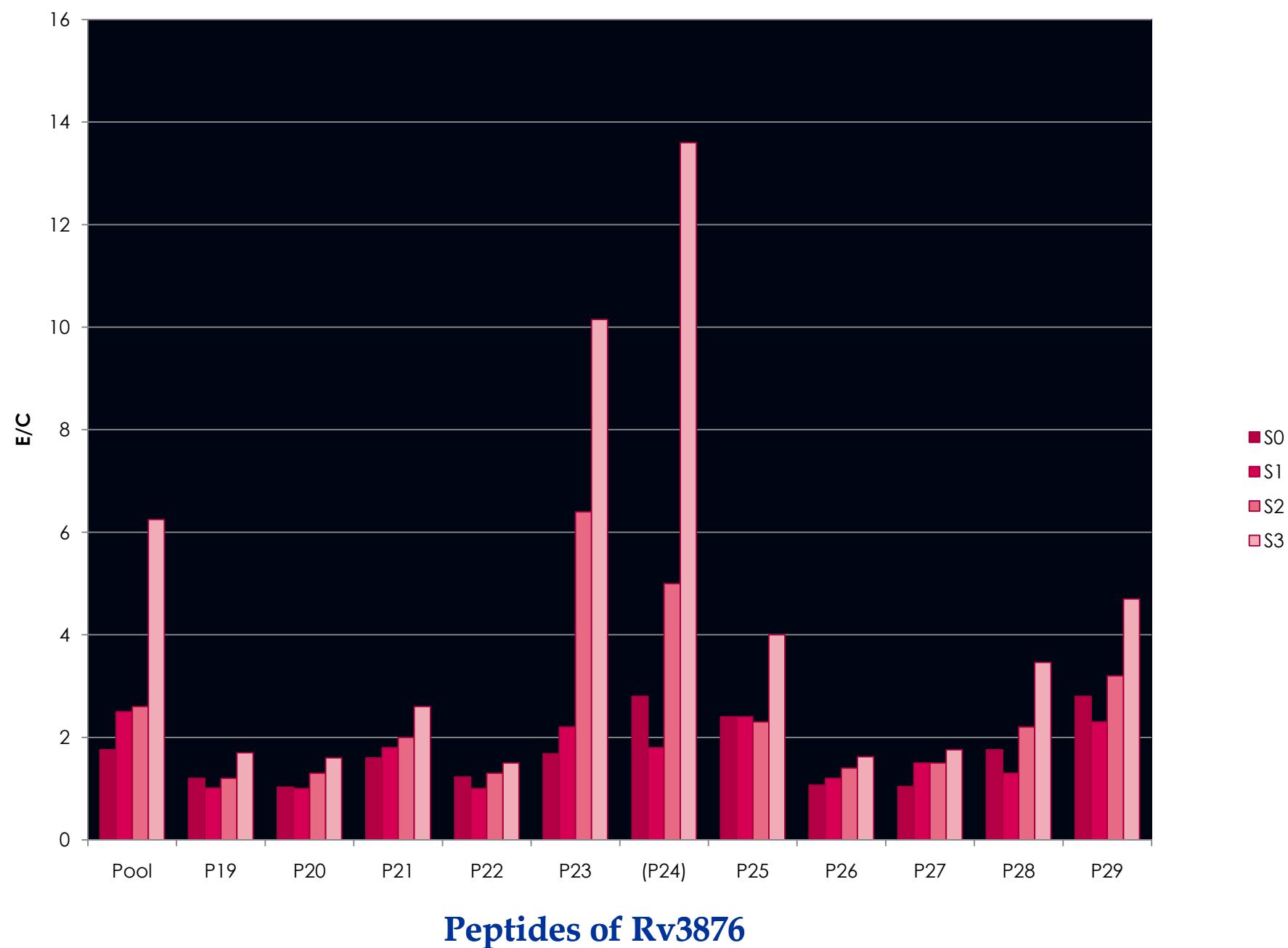
1. Peptides were emulsified with complete Freund's adjuvant and injected into rabbits

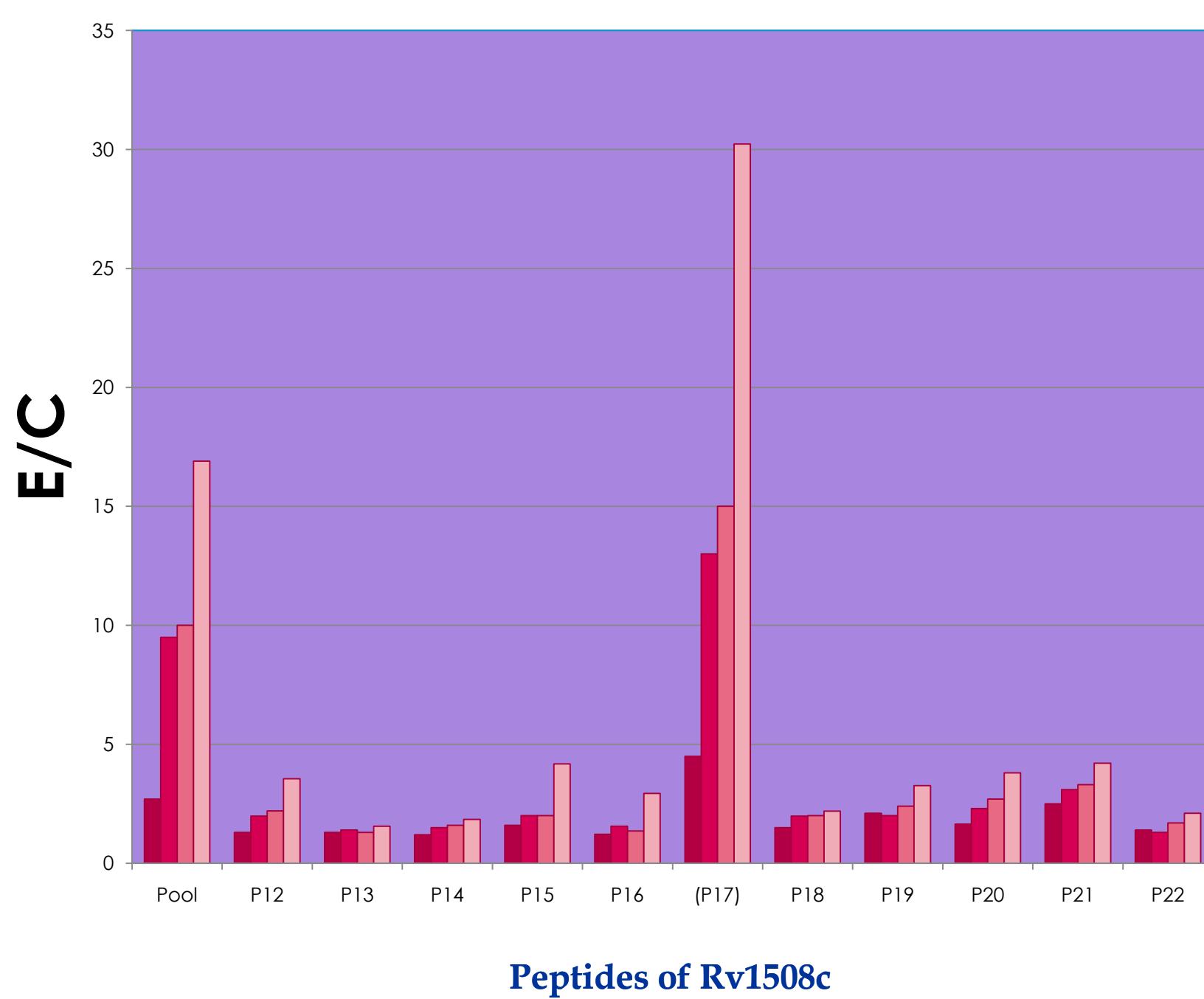


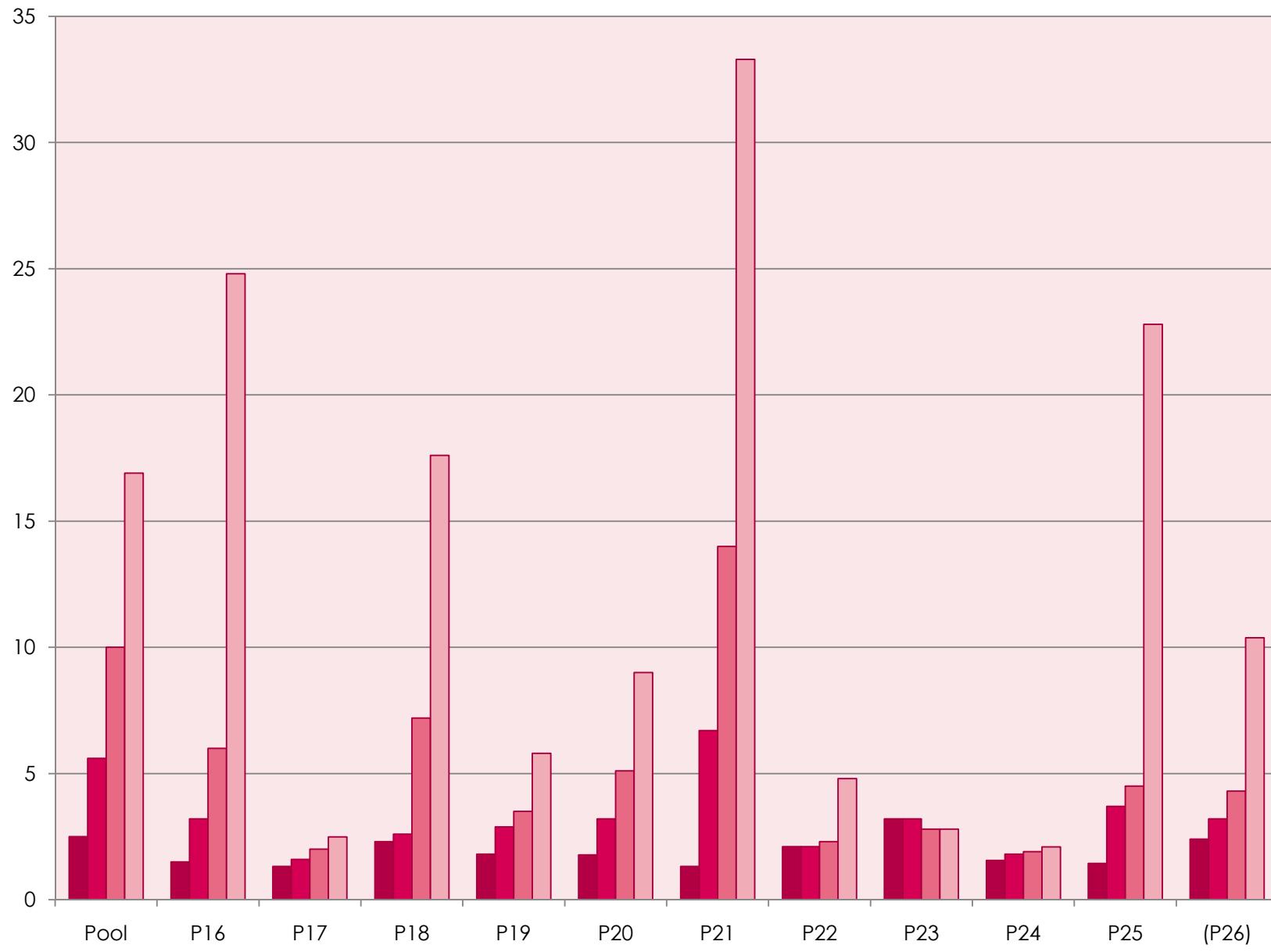
2. The rabbits were boosted with the same route and amount of emulsified pools of peptide after two weeks of the first immunization and after 1 month of the second immunization

Raising anti-peptide antibodies in rabbits protocol

1. Rabbits were bled from the ear vein before each immunization
2. Sera were used to test for antibody reactivity against the immunizing peptides using ELISA



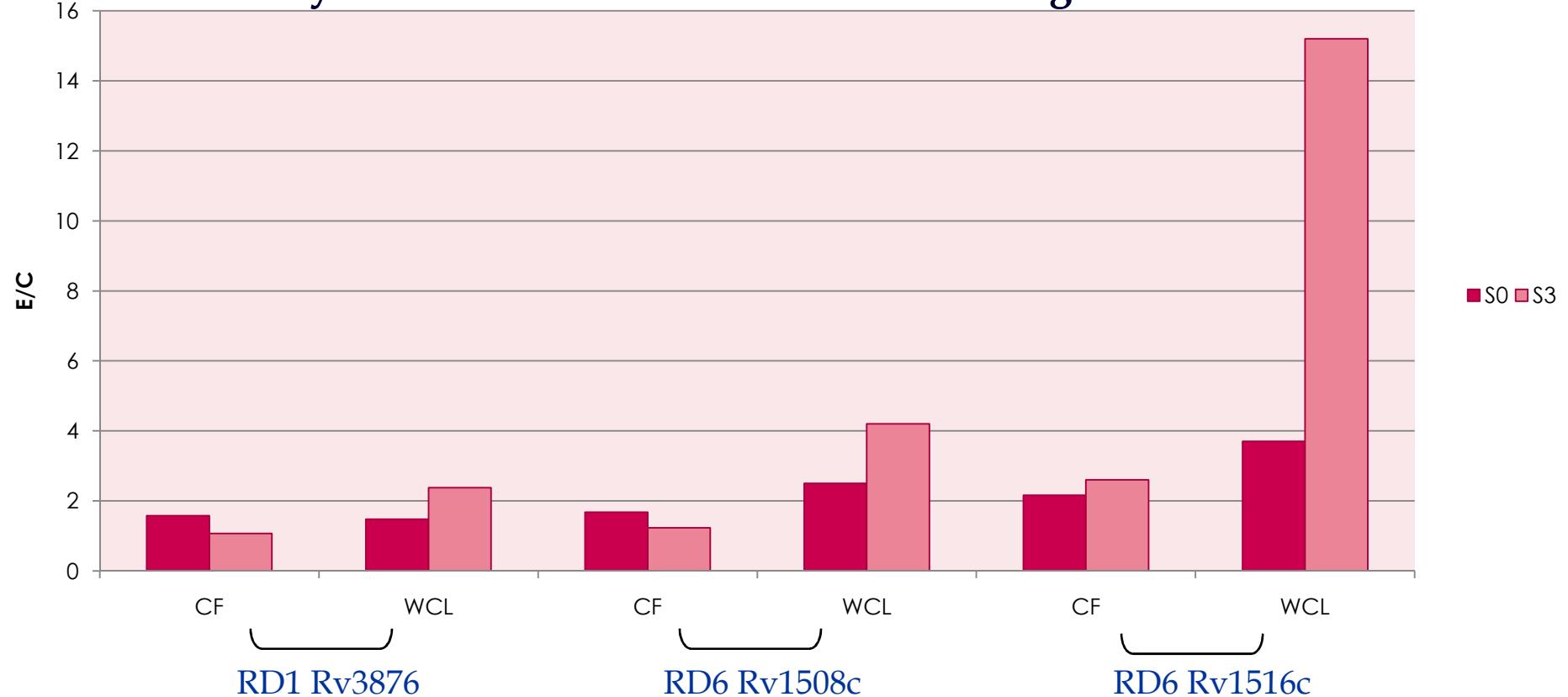




RD6ORF11 (Rv1516c)

Expression of RD1 Rv3876, RD6 Rv1508c and RD6 Rv1516c proteins in *M. tuberculosis*

ELISA reactivity of rabbits' sera with CF and WCL antigens of *M. tuberculosis*



Conclusions

- ✓ Three peptides, i.e. 346-370 of RD1 Rv3876, 226-250 of RD6 Rv1508c and 361-385 of RD6 Rv1516c, were found immunodominant and showed
- ✓ Strong antibody reactivity with sera of smear and culture positive pulmonary TB patients but weak reactivity with sera of healthy subjects from the community
- ✓ Thus suggesting their potential in the diagnosis of TB.

Conclusions

- ✓ Anti-peptides antibodies were successfully raised in rabbits by using pools of 11 peptides corresponding to each of the above three proteins
- ✓ All the three peptides found immunodominant with TB sera were also immunodominant with rabbits' sera.
- ✓ The probing of culture filtrates and whole cell lysates of *M. tuberculosis* with the anti-peptide antibodies confirmed their presence in the whole cell lysates, and thus their expression in *M. tuberculosis*.

Acknowledgments

- Collaborator: Prof. Raja'a Al-Attiyah
- Graduate Student: Noura Y Al-Khoudari
- Funding: Kuwait University, Research Sector grants YM08/07 and SRUL02/13

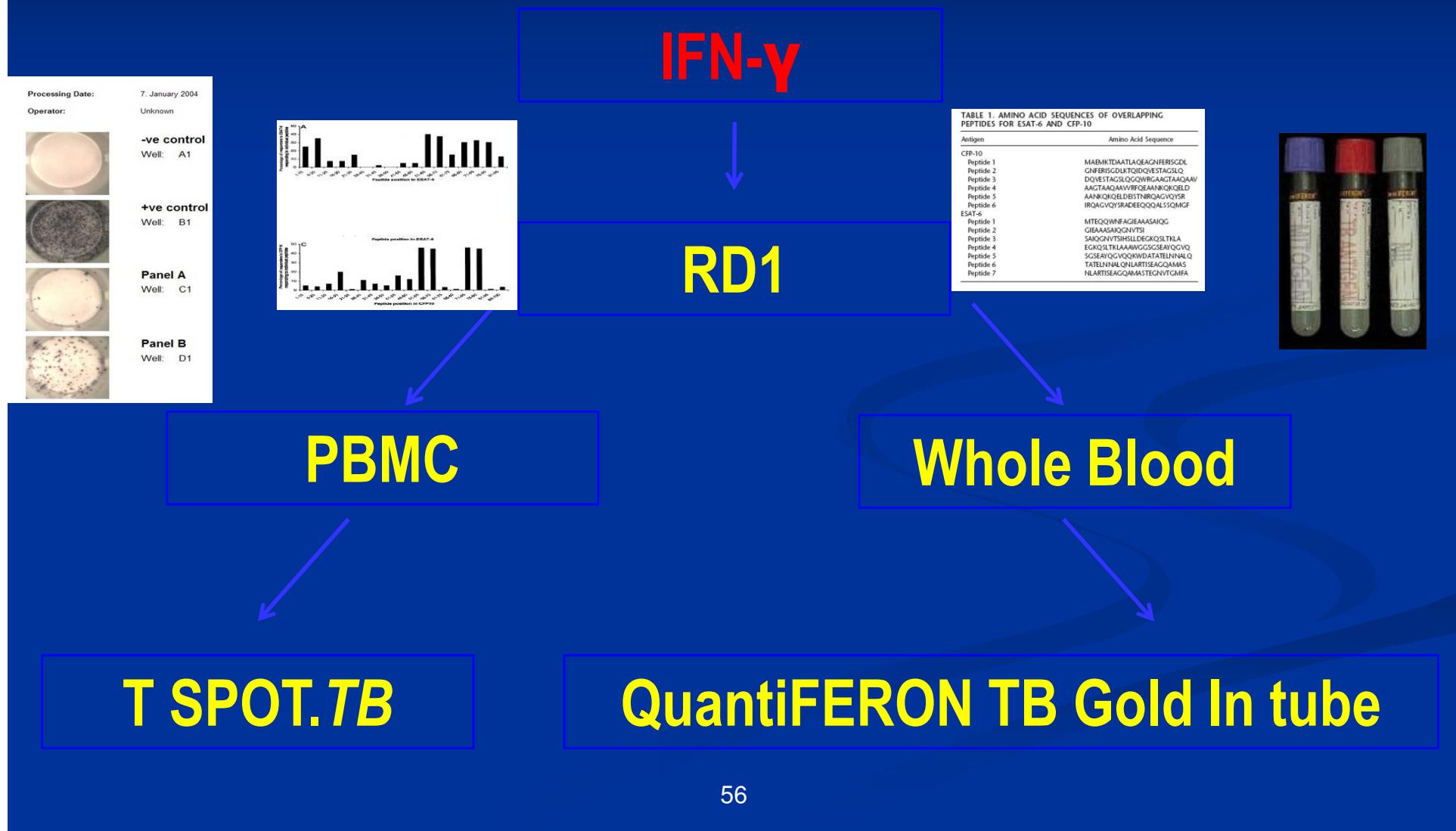
The work was performed at
Thanks for listening



THANKS



IGRA



TB Diagnosis

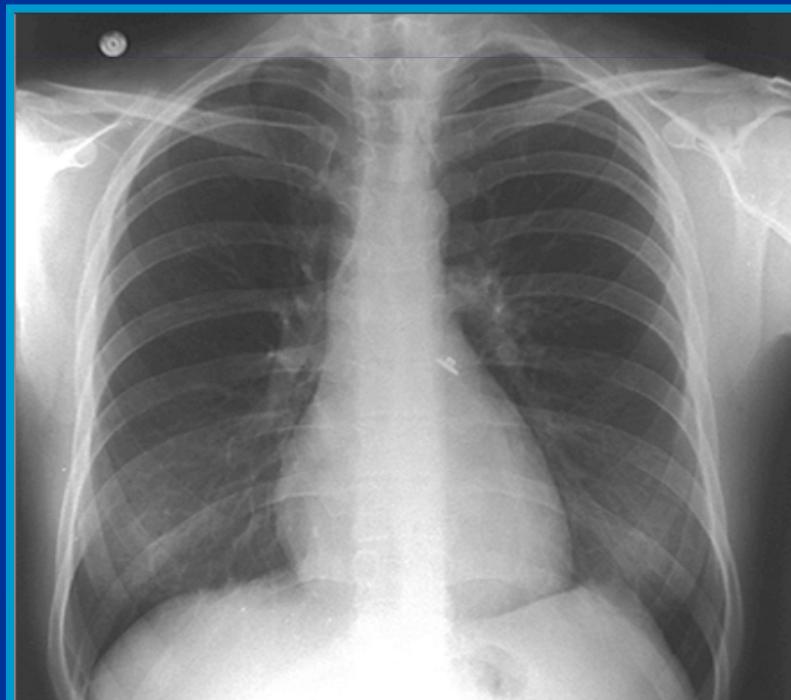
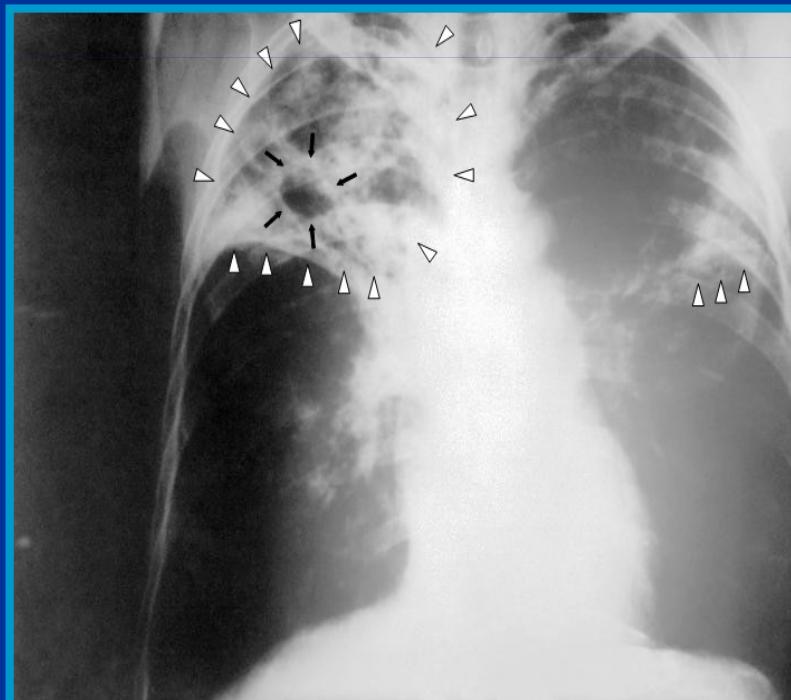
1. Clinical symptoms
2. Chest X-ray
3. Microscopy and culture
4. Molecular and immunological methods



1. Clinical symptoms

2. Chest X-ray

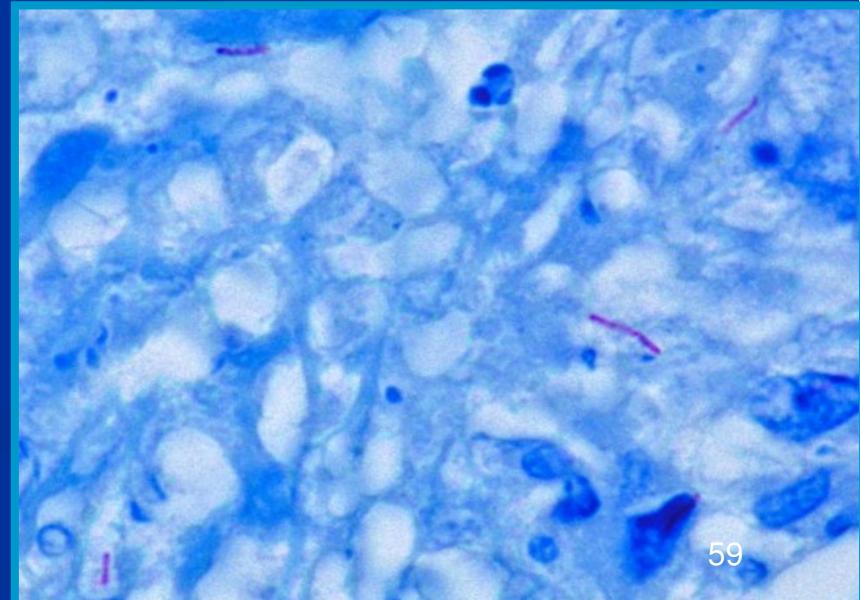
- Rule out diagnosis of active TB



3. Bacteriological examination

○ Microscopy

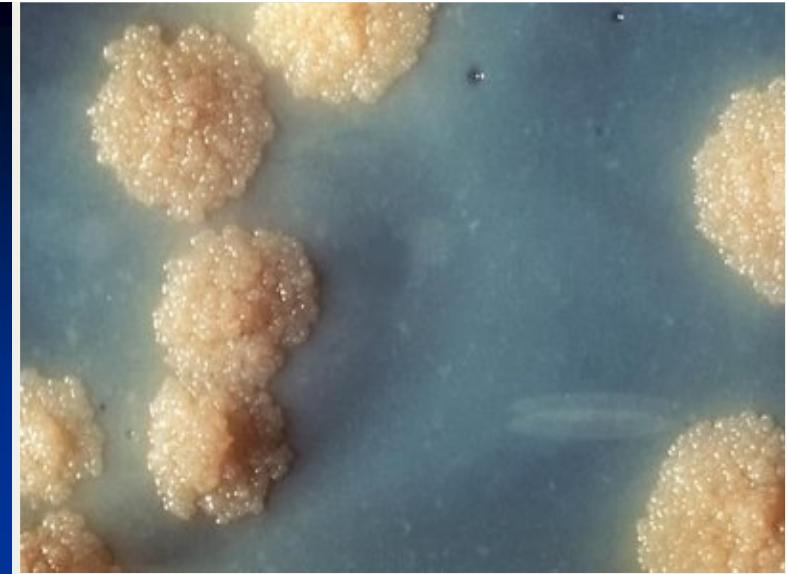
- ✓ Zeihl Neelsen stain, AFB
- ✓ Minimum of 10,000 organisms/ml
- ✓ If bacteria is detected, it doesn't identify the mycobacterial species



3. Bacteriological examination

○ Culture

- ✓ Middle Brook's medium
- ✓ Lowenstein-Jensen (LJ) medium
- ✓ 10 organisms/ml
- ✓ *M. tuberculosis* takes 4-6 weeks to get visible on media

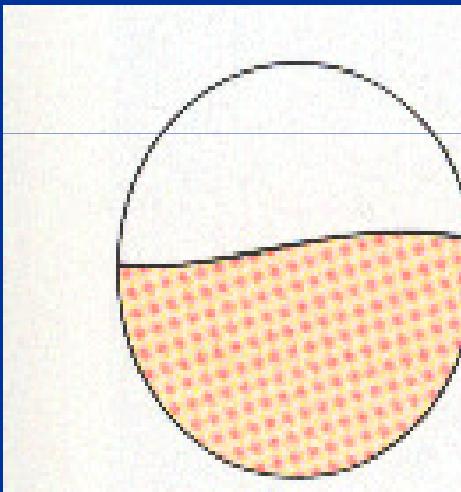
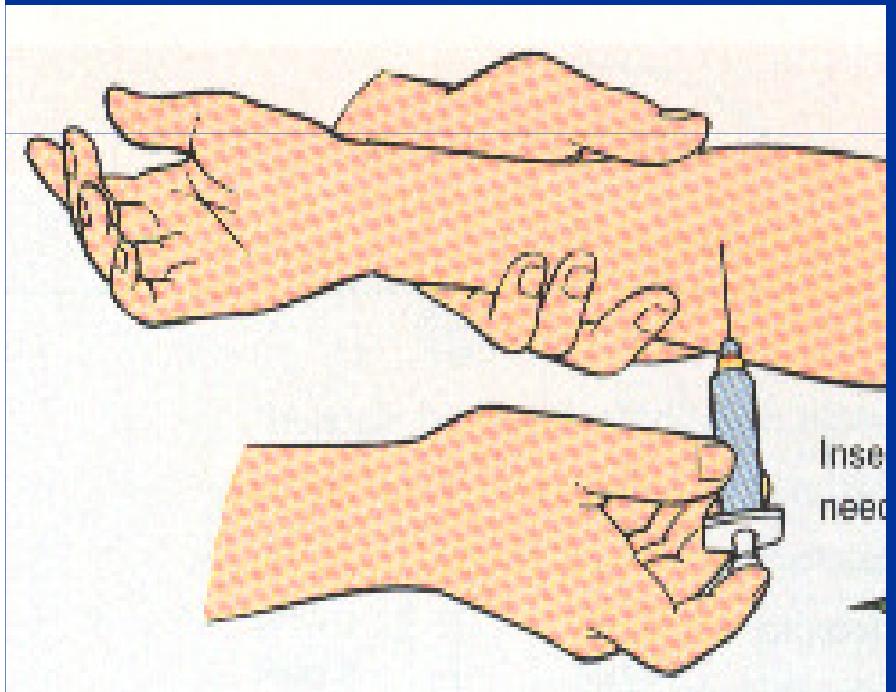


TB Diagnosis (active and latent)?

- Clinical symptoms
- Chest X-ray
- Microscopy and culture
- Molecular methods
- Immunological methods

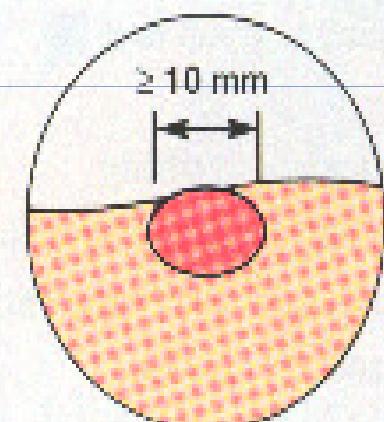


Tuberculin test (TST): Intradermal injection of the antigen in the forearm and reading of delayed type hypersensitivity responses after 48-72 h



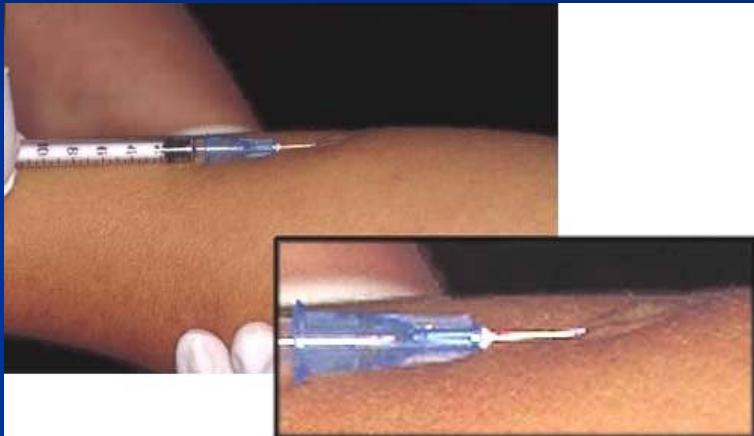
(a)

Negative reaction

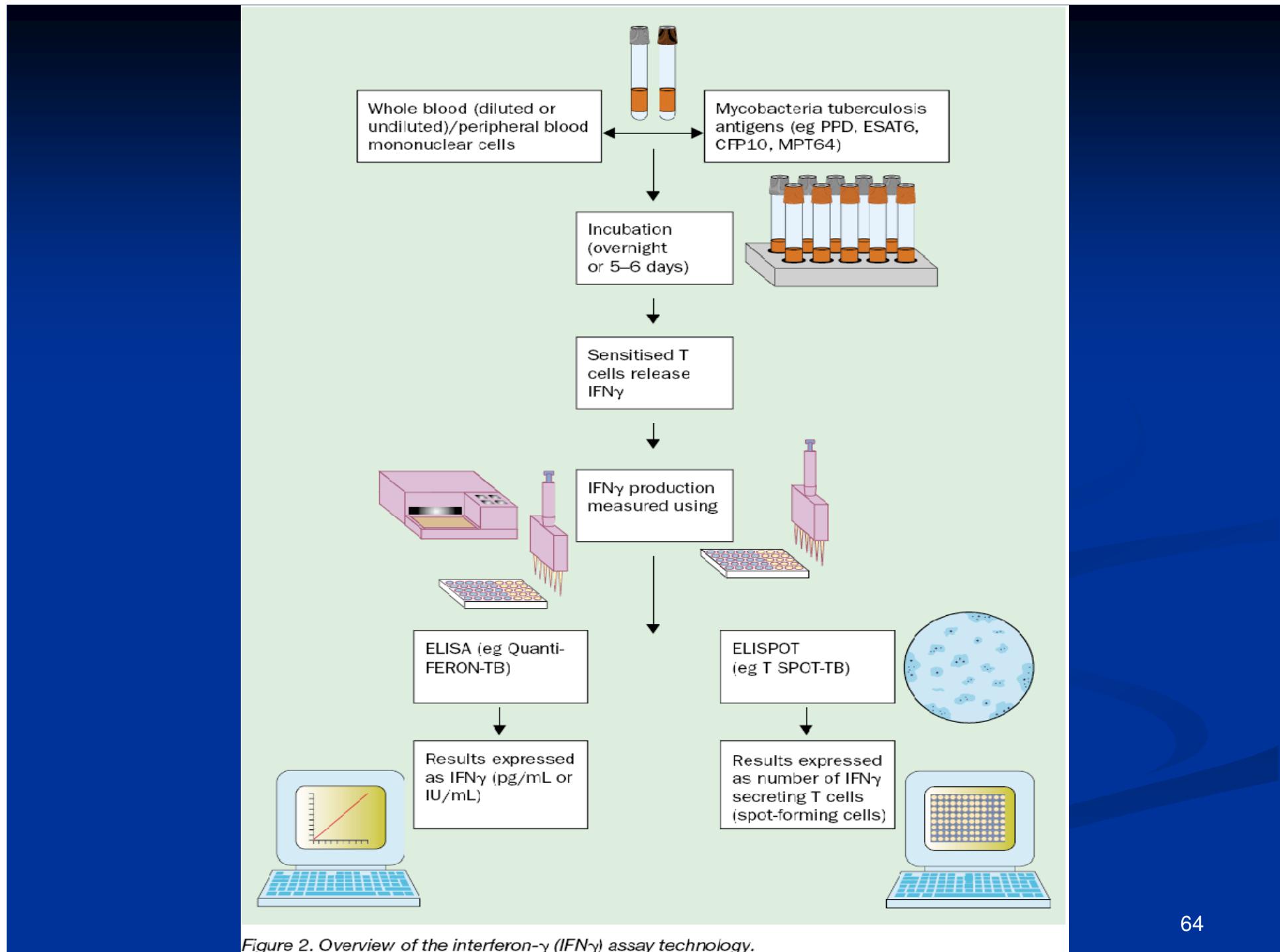


Positive reaction
(size of induration)

Limitations of the TST



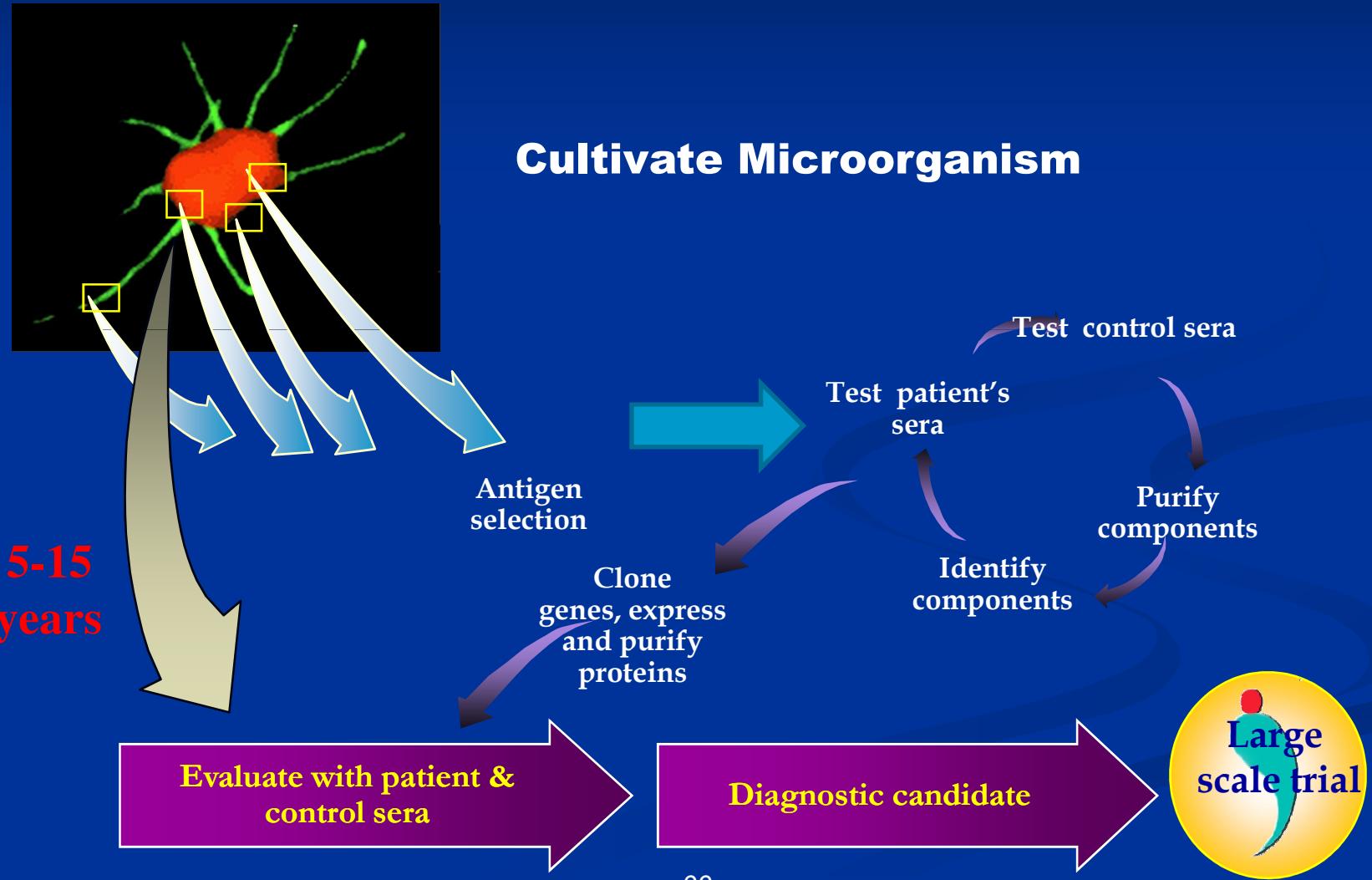
- Reagent:
 - Purified protein derivative (PPD) commonly shared among different Mycobacteria (*M. tuberculosis*, *BCG* and *atypical mycobacteria*)
- Variability:
 - Reproducibility in giving the test
 - Subjectivity in reading the test
- Logistics
 - Repeat visit needed
 - Wait for 3 days before result



Animal Work!



Diagnostic development In Pre-genomic era: Conventional approach



Results of BLAST search for sequence identity of immunodominant peptide aa 361-372 of RD6 protein Rv1516c in various strains of *M. tuberculosis* and other mycobacteria

Mycobacterial species and strains	Sequence				Identity
<i>M. tuberculosis</i> H37Rv, H37Ra, F11, KZN 1435, str. Haarlem, CDC1551, C, 02 1987, 94 M4241A	Query 1	VWP SRLRRGCRA	12	Sbjct 362	VWP SRLRRGCRA 373 12/12 100%

Results of BLAST search for sequence identity of immunodominant peptide aa 241-265 of RD6 protein Rv1508c in various strains of *M. tuberculosis* and other mycobacteria

Mycobacterial species and strains	Sequence	Identity
<i>M. tuberculosis</i> H37Rv, CDC1551, H37Ra, F11, KZN 605 K2M 1435, C, str. Haarlem, EAS054, '98-R604 INH-RIF- EM', KZN 4207, T17, GM 1503, EAS054, T85, T92, K85, T46, CPHLA, 021987	Query 1 LTMAVISPAIWAARGARGLERVVIF 25 LTMAVISPAIWAARGARGLERVVIF Sbjct 226LTMAVISPAIWAARGARGLERVVIF250	25/25 100%
<i>M. kansasi</i> ATCC 12478	Query 1 LTMAVISPAIWAARGARGLERVVIF 25 LT AV +PA+WAARGARGLERVV+F Sbjct 149 LTGAVFTPAPWAARGARGLERVVVF 173	20/25 80%
<i>M. marinum</i>	Query 1 LTMAVISPAIWAARGARGLERVVIF 25 L +AV++PA+WA RGARGLER+V F Sbjct 142 LVVAVLTPALWAVRGARGLERLVTF 166	17/25 68% 68

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