

RAPID SCREENING AND DIAGNOSIS OF TUBERCULOSIS: A REAL CHALLENGE FOR THE MYCOBACTERIOLOGIST

F. ZAKHAM^{1,2,3}, M. AKRIM¹, M. EL MZIBRI⁴, A. BENJOUAD³, R. EL AOUAD^{1*} and M. M. ENNAJI^{2* ∞}

¹ Institut National d'Hygiène, Rabat, Morocco.

² Laboratoire de Virologie et Hygiène & Microbiologie, Faculté des Sciences et Techniques. Mohammedia, Morocco.

³ Laboratoire de Biochimie et Immunologie, Faculté des Sciences. Université Mohammed V-Agdal. Rabat. Morocco.

⁴ Unité de Biologie et Recherches Médicales, Centre National de l'Energie, des Sciences et Techniques Nucléaires. Rabat. Morocco.

*My M. ENNAJI and R. ELAOUAD share senior authorship in this study (equal contribution).

Abstract

Tuberculosis (TB) is an infectious, devastating and contagious disease, which infects third of the global population worldwide with high rates of incidence in the developing countries, where the health care providers face a serious problem and a real challenge during their clinical practice for controlling and preventing the transmission of this illness. Indeed the first step of control is the correct diagnosis and the initiation of the drug treatment regimen at the early stage of infection, which mandate the rapidity of screening and the accuracy of laboratory testing. In this paper we aim to highlight the different actual techniques, regarding the rapid screening and diagnosis of tuberculosis.

Key words: Mycobacterim tuberculosis MTB, Bacteriological techniques, Molecular techniques, Diagnosis, Identification.

Article information

Received on October 2, 2011 Accepted on January 13, 2012

Corresponding author
Tel: + 212 6 61 74 88 62
Fax: +212 5 23 31 53 53
E-mail:m.ennaji@yahoo.fr

INTRODUCTION

Tuberculosis (TB) is an infectious, devastating and contagious disease caused by a *Mycobacterium*, called Koch s' bacillus (KB).

This disease is an ancient infection which affected the human being since millennia and that had been documented and detected in Egyptian mummies in several studies, either by direct conventional microscopic examination (111) or by molecular techniques (67,112).

Furthermore, tuberculosis is still a major threatening of humanity especially in developing countries and according to the last reports of The World Health Organization (WHO), it is estimated that one-third of the global population is infected with tuberculosis and that approximately 8.9- 9.9 million new cases of tuberculosis arise annually and over 1.3 million deaths among HIV-negative people and 0.38 million deaths among HIV-positive people (105). In almost cases; the causal agent of human tuberculosis is *Mycobacterium tuberculosis* (MTB). However TB can be caused by other Mycobacteria in some cases with special conditions (10), these Mycobacteria are belonging to the members of *Mycobacterium tuberculosis* complex (MTBc), (15, 85, 86) which include:

- *Mycobacterium africanum*: That can provoke human tuberculosis, principally in the west of Africa (18).
- Mycobacterium bovis: which infects Badgers, cattle,

deer, elephants, goats, lions, seals, etc (15) and can spread to humans through inhalation of infectious droplet and by ingestion of raw milk. Furthermore, *M. bovis* has been associated with extrapulmonary tuberculosis in infants and children, generally occurring due to the consumption of milk, which had not been pasteurized or boiled, from infected cattle (93), especially in the HIV infected infants (37). Therefore the zoonotic risk for human represents a serious problem, mostly for those living at the animal-human interface (61).

- *Mycobacterium bovis*, Bacille Calmette–Guérin (*BCG*): this has been largely used as a vaccine against human tuberculosis (6, 19) and can be obtained by the attenuation of *M.bovis* and deletion of the RD1 region (15).
- *Mycobacterium microti*: which infects voles, Cats, dogs (15, 82) and human as reported recently in immunocompetent patients in France by Panteix et al, 2010 (71).
- *Mycobacterium canetti*: which infects human in limited geographical location, in the horn of Africa (24).
- *Mycobacterium pinnipedii*: that infects seals, sea lions and marine mammals (8, 45).
- *Mycobacterium caprae*: which can infect domestic animals such as goats, sheep, ewes (60), camels, horses, pigs, dogs, cats (16), wild animal species (80) and human being.

Furthermore, it has been demonstrated that these members are sharing a common ancestor in their evolutionary events (34, 110) and has been settled that *M. tuberculosis* arose from *M. bovis* and *M. tuberculosis* emerged approximately 10–15,000 years ago, when the bovine tubercle bacillus was transmitted to the mankind (15, 34).

It is worth mentioning that there are other mycobacteria called atypical mycobacteria or non tuberculosis mycobacteria (NTM).

These mycobacteria are ubiquitous in the environment and in extreme circumstances (immunosuppression, HIV infection, underlying diseases.....etc), some of them become pathogenic for humans and can induce opportunistic infections or mycobacterioses (30). These mycobacteria often are described based on their growth rate and pigmentation with and without exposure to light (5). The last group of mycobacteria is represented by *M leprae*, the causal agent of leprosy in humans and characterized by the inability to be cultured *in vitro* (42).

Although the diagnosis of TB can be made by different techniques: radiological, clinical and immunological techniques, the identification of causative organism MTB in the clinical sample is the most accurate and reliable for the final decision of tuberculosis and for initiating the drug treatment regimen (17). In this paper we aim to outline the different actual techniques regarding the rapid screening and diagnosis of tuberculosis.

SCREENING AND DETECTION OF THE COM-PLEX Mycobacterium tuberculosis (MTBc)

Diagnosis of the latent tuberculosis

In 2005, the CDC guidelines for controlling the tuberculosis and the reduction of the mortality and morbidity cases due to this horrible illness, one of the most important strategies for the achievement of this gaol is the identification of the persons with latent TB infection (LTBI), especially those who are at high risk for potentially active TB disease (3).

The diagnosis of LTBI has habitually been based upon results of tuberculin skin testing or Mantoux test (56). This test involves an intradermal injection of the Purified Protein Derivative (PPD) or the tuberculin (2). The response typically appears a day or two after the injection and consists of a raised, red, and indurated area in the skin, which then disappears as the antigen degraded (5, 10). This indicates the presence of antibodies or lymphocytes that are specific for that antigen (cellular immunity).

Moreover, the immunological tests (the QuantiFERON-TB Gold® and TSPOT®- TB tests) which are whole blood interferon gamma release assays (IGRAs), are now other options for detecting LTBI and are potential tools for diagnosing LTBI (49, 62). These tests are based on the principle that T cells from most persons that have been infected with MTB will release IFN- γ when re-exposed to the same mycobacterial antigens (*in vitro*).In fact these immunological tests on peripheral blood alone can not differentiate between active and latent TB (51).

Diagnosis of active TB

It is important to know that tuberculosis can be diagnosed accurately by identifying the causative organism, MTB in the clinical sample (17) and the suspicion of TB disease in a patient requires the completion more thorough medical examinations:

Radiological Examination: The radiological diagnosis can highlight the pulmonary form of TB and the chest X ray is the most traditional technique for the screening of TB (51). Although the presence of abnormality findings in the conventional radiography is not decisive for the TB infection (29, 39), the cavitation is still the most remarkable sign of the active TB or the post primary infection and can indicate the severity of disease (58).

Bacteriological examination: Generally, the investigation of the tubercle bacilli can be done on pulmonary samples after their decontamination, though it can also be performed on the other extrapulmonary specimens or other body fluids (Urine, cerebrospinal fluid, semen, gastric liquid.....etc) and the diagnosis of MTB can be achieved by:

Microscopic examination

The smear microscopy is the first step and the key of bacteriological diagnosis of TB. However the smear microscopy can not distinguish between viable and dead microorganism and does not differentiate between the species of mycobacteria (35), Moreover it can only detect acidfast bacilli in concentrations of 10,000 organisms per ml or more (109), but from an economical view the conventional microscopy is still the most useful tool or the sole tool in the low income countries (88), where the diagnosis of smear negative tuberculosis poses a serious problem for the health care providers, especially in the HIV co infected patients (9, 84). In fact there are different staining methods, but the widely used technique is the Ziehl-Neelsen method (13), which lack sensitivity and require the good expert technicians for the investigation about the bacillus in different fields on the smear (56). The problem of sensitivity can be improved by the concentration by centrifugation of the specimens after adding the disinfectant NaOCl as demonstrated by Gebre et al., in different developing countries (27). Nevertheless the sensitivity of the microscopical examination has been developed in the industrial countries by the utility of the Fluorescence microscopy (88), which provides more accurate results.

• Culture

The culture is the gold standard for the diagnosis and detection of TB (72). Most laboratories use solid medium for the isolation of MTB. After homogenizing and decontaminating the specimen, inoculation the media by means of a pipette delivering around 0.2ml as recommended by WHO (106). Two media are used for MTB growth, Middle brook's medium which is an agar based medium and Lowenstein-Jensen medium which is an egg based medium. Both types of media contain inhibitors to keep contaminants from out-growing MTB and the culture should be examined during 4-6 weeks to get visual colonies on either type of media. It is noteworthy to mention that there are also new liquid techniques that have been developed to shorten the time of culturing, comparing with traditional techniques of culturing on solid medium, such as: BAC-

Table 1.	Some of the mor	phological and bio	chemical properties	of tubercle bacilli.
----------	-----------------	--------------------	---------------------	----------------------

Mycobacterial strain	Host	Colony Morphology	Consumption of Oxygen	<u>Urease h</u> at 3 h	ydrolysis at 18 h	PZA	ТСН	Niacin accumulation	Nitrate reduction
M.tuberculosis	Humans	eugonic	aerophilic	-	+	S	R	+	+
M.bovis	Wild and domestic animals	dysgonic	Micro aerophilic	-	+	R	S	-	-
M. bovis BCG		eugonic	Micro aerophilic	+	+	R	S	-	-
M. africanum	Humans in the West of Africa	dysgonic	Micro aerophilic	-	+	S	R/S	+/-	+/-
M. microti	Wild and domestic animals	eugonic	aerophilic	-	+	S	S	+	-
M.canetti	Humans in the horn of Africa	Very smooth, eugonic	aerophilic	+	+	R	R	+	+
M.caprae	Wild and domestic animals	eugonic	aerophilic	-	+	S	S	+	-
M.pinnipedii	Seals, sea lions	eugonic	aerophilic	-	+	S	S	+	-

TCH: thiophen-2-carboxylic hydrazide, PZA: pyrazinamide, R: resistant, S: sensitive

TEC 460 TB, BacT/ALERT 3D and BACTEC MGIT 960, ESP II culture system (1, 65, 73, 96). Although of the rapidity of liquid media in culturing mycobacteria, the solid medium still have the advantage of enabling the differentiation of mycobacterial growth and contamination, even more the colonial morphology, production of pigments, rates of growth and the optimal temperature of growth can help in the identification and the discrimination between rapid and slow growing mycobacteria (50). Table1 shows some of the colonial morphology, the production of pigments and oxygen consumption for the differentiation among the complex MTB. Therefore it is recommended to combine both of solid and liquid medium for the best recovery of mycobacteria (87).

• Phenotypic and biochemical identification

Even though their consumption of time and cumbersomeness, the biochemical identification is still useful in the developing countries for the differentiation among MTB complex and other mycobacteria, particularly the niacin test (26) and due to the large number of tests in this topic, we can not mention them in detail and briefly passing through the most important utilized phenotypic and biochemical tests, we can point out: Catalase, Niacin test, Nitrate reduction, Aryl sulphatase, Tween80 analysis, Urease Activity, Pyrazinamide (PZA), Iron Uptake, Growth inhibition by Thiophene 2 carboxylic acid Hydrazide (TCH), Growth on 5% sodium chloride, ß glucosidase, tellurite reduction (31, 52).

Levy-Frebault *et al.*, had evaluated 8 rapid biochemical and enzymatic tests for the identification of 18 species of mycobacteria (niacin, catalase, nitrate reductase, β glucosidase, urease, penicillinase, trehalase and cephalosporinase) and they found that those tests were able in some cases to discriminate between closely related species (54).

Table 1 show also the most used biochemical tests for the phonotypical and biochemical differentiation among the complex MTB quoted from (15, 20).

• Drug susceptibility testing DST

After the detection and the identification of MTB, the DST is the main analysis to be performed for better management of TB, using different anti tuberculosis agents.

The most used method of DST is the proportional method, adjusted from the method described by Canetti (12). This technique consists of observing the mycobacterial growth on the Löwenstein-Jensen medium containing different concentrations of tested antibiotics, this method is currently the method of choice for estimating drug resistance but it takes approximately four weeks for the final assessment. This period can be halved by the implementation of the DST on the BACTEC liquid media (33, 38, 98). There are also different commercially colorimetric methods for performing the DST; the Reszurin test is one of the low cost, rapid and accurate tests for the detection of drug resistance of MTB strains (53).

Molecular Examination: Nowadays, there are many molecular techniques are commercially available which have decreased the time for the diagnosis, detection, identification of MTB and drug susceptibility pattern (44). However, they have an excellent sensitivity and specificity when used from a culture, these techniques have currently insufficient sensitivity when applied directly to respiratory and other samples (46), these tests are numerous and we can list the most important tests:

• DNA Amplification by PCR, including Real Time PCR

The utilisation of PCR for the detection of MTB in clinical samples has been reported and commercially available amplification and detection kits as well as manual in-house methods are also applied in routine diagnostic laboratories (28, 40, 55, 63, 75-77, 83, 104, 107) and its reliability has been questioned (68). Moreover, the paucibacilary nature of specimens (sputum, biopsies, pus and body fluids) was a challenge for the detection of this microorganism.

The insertion sequence IS 6110 (7, 22, 23, 91) 16S rRNA (14, 48, 64) and hsp 65 (47) are the most common targets used for the MTB diagnosis in the clinical specimens. Additionally there are different types of PCR-based assays have been developed and modified for this purpose, the Real-time PCR is one of the promising tools with high sensitivity for the rapid identification of different mycobacterial species, with the advantage of possible identification and detection of a given target sequence directly from clinical specimens (95).

The Multiplex PCR is also a potential tool for distinguishing between the pathogenic species of mycobacteria and it is supposed to be simple, rapid, cost effective and superior to the traditional methods (30). Recently, Warren et al., have developed a new multiplex PCR for the differentiation the members of MTBC by the amplification of genomic regions of difference (RD1, RD1^{mic}, RD2^{seal}, RD4, RD9, RD12) (103). The PCR-restriction endonuclease analysis (PRA) had been used and evaluated for the differentiating between 39 pathogenic rapid growing mycobacteria (RGM) by Wang et al., and they found good results (102), in addition of the fast identification comparing with conventional method and it could be used into the clinical laboratory setting, particularly for patients who are suffering of infection due to pathogenic RGM and according to Varma-Basil et al., the PCR-RFLP was recently used for the direct identification of MTB in the clinical specimens and could offer a considerable benefit for clinician for their chemotherapy choice (101).

• Nucleic acid Probe

The DNA probe is one of the efficient methods for the identification of MTB members from pure culture (66) and the most used DNA probes in the routine laboratories are the AccuProbe for the rapid identification of MTB.

Badak *et al.*, demonstrated that the AccuProbe allows the accurate and rapid identification of MTB when applied directly on the positive MB/BacT broth (4). Furthermore it can also be used for the identification of other non tuberculosis mycobacteria (97)

• In situ Hybridization

The fluorescence hybridization *in situ* by using Peptide Nucleic Acid Probes has been recently demonstrated a good results for the identification of the members of the MTBC and the differentiation tuberculosis and non tuberculosis mycobacteria, especially in the liquid culture (21, 36, 70).

Automated Sequencing

Genetic sequencing techniques have progressively become useful tools for mycobacterial differentiation (74) and sequencing of a fragment of conserved genes such as 16S rRNA (32, 81, 108) or hsp65 (78, 79, 90) are the most sensitive methods for identification of a large number of mycobacterial species. Recently a single step sequencing technique has been applied for the identification of the eight closely related members of the complex MTB, called the Exact Tandem Repeat D or the ETR-D sequencing (20). Importantly, sequencing is also used for DST to characterize the genetic mutations associated with resistance to antituberculosis drugs.

• Strain typing and DNA fingerprinting

Tuberculosis epidemiology has been clarified significantly by the development of molecular biological techniques which allow the relatively unambiguous identification of a particular clinical isolate (5). The restriction fragment length polymorphism (RFLP) using the insertion sequence IS6110 has become the standard international method for fingerprinting isolates of *M. tuberculosis* (62, 100). The IS6110 is a transposable element present in the members of MTB complex in multiple copies (up to 25 copies) (92, 94) except *M. bovis* BCG which harbours a single copy (68) and absent in other mycobacteria. Furthermore, due to its high numerical and positional polymorphism, has become a widely used marker in the epidemiological studies (57, 59, 69), identification (99) and phylogenetic analysis (94). In the last decade many methods for typing of clinical strains of MTB were developed, the most commonly used methods; the spoligotyping and MIRU-VNTR.

The spoligotyping relies on the analysis of a unique chromosomal region of the genome with high polymorphism, called DR or direct repeat and contains of 36 bp that are separated by non repetitive DNA spacers (41), the order of spacers is identical in all mycobacterial strains, but their presence or absence varies from one isolate to another (Figure 1).

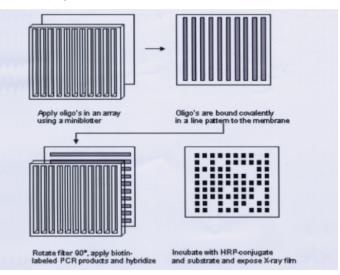


Figure 1. Steps of Spoligotyping method.

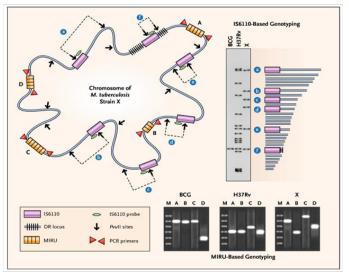


Figure2. Chromosome of MTB (X) strain, genotyping of *M. bovis* BCG, H37Rv MTB strain on the basis of repeated units MIRUs. On the top: a chromosome of MTB strain, the three lower panels show the results of genotyping based on MIRUs. The MIRUS contain repeated units; the analysis of MIRUS involves a PCR amplification followed by electrophoresis to look for the number and size of the elements repeated in 12 independent loci, each with one repeated sequence. The sizes of molecular weight marker (M) and PCR products (A, B, CD) BCG, H37Rv and X strains are given. The specific sizes of the different MIRUS in each strain are the result of a distinct fingerprint of the strain.

	Cultu	Culture based techniques	
Technique	Principle	Advantages	Limitations
Culture based techniques	Detection of bacterial growth after	Gold standard	Cumbersome and takes a long time (up to 8 weeks) especially on solid media.
(MTB detection, identification and DST)	inoculation of clinical specimens on media culture	pigmentation of colonies can help in the detection, identification of MTB and DST testing	The presence of viable bacteria is necessary and it is not always possible, especially in treated people.
	Moleci	Molecular based Techniques	
Technique	Principle	Advantages	Limitations
PCR and various PCR techniques:	Detection of the presence of MTB genomic	High specificity.	Higher cost and limited availability. Variable sensitivity.
Real time PCR	DNA in clinical	Fast results.	Inferior sensitivity for non respiratory
Multiplex PCRetc	samples after amplification	Allows identification and investigation of genetic resistance patterns	specimens. Does not allow ruling out tuberculosis
Nucleic acid Probe	Detection of a complementary target	Rapid identification of MTBC members from pure culture.	The sensitivity of MTB detection in clinical specimen has been questioned.
		Differentiation between MTB and NTM	
In situ Hybridization	Fluorescence hybridization of the Bacterial DNA with Peptide Nucleic Acid Probes	Identification of MTBC members Differentiation between MTB and NTM especially in liquid culture.	High cost and necessitate a good expert skills.
Automated Sequencing	The determination of the nucleotides order in the genes	Rapid Identification of a large number of mycobacterial species	Higher cost is the main limitation and good expertise in the analysis of sequences
Strain typing and DNA fingerprinting	The discrimination between mycobacterial strains based on polymorphism of the insertion sequence IS6110 and repetitive	The IS 6110 is the standard international method.	The IS 6110 is the standard international method, but this technique is difficult to perform.
Techniques (RFLP Spoligotyping and MIRU	DNA elements such as the polymorphic GC-rich sequence (PGRS) and the direct-repeat (DR) region.	The strain typing and DNA fingerprinting help in the epidemiological studies	The spoligotyping and MIRU-VNTR must be combined for better discrimination and differentiation between strains.

Table 2. Culture and Molecular based techniques (Principles, advantages and limitations)

MIRUs (Mycobacterial Interspersed Repetitive Units) are loci in the MTB genome that contain variable numbers of tandem repeats (VNTRs) (25). MIRU-VNTR typing based on PCR amplification targeted areas and determining the number of repetitions of the unit. The end result is a numeric code corresponding to the 12-digit number of repeats observed each chromosomal locus (66) (Figure 2). Recently a standardized method based on analysis of 15 MIRU loci instead of 12, with a discriminatory power has been proposed as a new standard for epidemiological studies and 24 loci was anticipated as a method of high-resolution for phylogenetic studies (89).

• Microarray analysis

The microarray analysis or the DNA chips are a collection of labeled DNA probes fixed on a solid surface, after the hybridization with the DNA in question, the intensity can be computed and fluorescent image can be visualised (66).

The microarray of the mycobacterial genom provided a new insight of understanding and measuring the genes expression on multiple regions on the genome, which can be exploited for improving drugs, vaccines, and diagnostics tools for controlling mycobacterial diseases (11, 43).

CONCLUDING REMARKS

The screening of TB can be performed by different techniques: radiologic, clinical, immunological, bacteriological and molecular techniques. However the final decision of the infection of TB can be merely completed by the identification of MTB.

The conventional techniques of MTB identification are based on the bacteriological examinations which are time consuming. However in the over last decades, different molecular techniques have been developed and provided excellent, rapid and accurate results.

The main limitation of their utilization is the high cost of their application in routine analysis and in conclusion, the culture for MTB is irreplaceable but molecular techniques are optional to save the life of patients in the high suspected cases of tuberculosis and briefly the principles, main advantages and limitations of culture and molecular based techniques have been summarized in Table 2.

REFERENCES

1. Anargyros, P., Astill, D. S. and Lim, I. S. Comparison of improved BACTEC and Lowenstein-Jensen media for culture of mycobacteria from clinical specimens. *J. Clin. Microbiol.* 1990, **28** (suppl 6):1288-91.

2. Arias Guillen, M., Palomar, R. and Arias, M. Advances in the diagnosis of latent tuberculosis infection in patients receiving renal replacement therapy. *Nefrologia* .2011, **31**(suppl 2):137-41.

3. ATS. Controlling tuberculosis in the United States: recommendations from the American Thoracic Society. CDC, and the Infectious Diseases Society of America. 2005, **54:** 15.

4. Badak, F. Z., Goksel, S., Sertoz, R., Nafile, B., Ermertcan, S., Cavusoglu, C. and Bilgic, A. Use of Nucleic Acid Probes for Identification of Mycobacterium tuberculosis Directly from MB/BacT Bottles. *J. Clin. Microbiol.* 1999, **37**(suppl 5):1602-05.

5. Baron, S. In: *Medical Microbiology*. Galveston (TX):University of Texas. Medical Branch, Texas. 1996. NCBI bookshelf.

6. Bastos, R. G., Borsuk, S., Seixas, F. K. and Dellagostin, O. A. Recombinant Mycobacterium bovis BCG. *Vaccine*. 2009, **27**(suppl 47): 6495-503.

7. Ben Kahla, I., Ben Selma, W., Marzouk, M., Ferjeni, A., Ghezal, S. and Boukadida, J. Evaluation of a simplified IS6110 PCR for the rapid diagnosis of Mycobacterium tuberculosis in an area with high tuberculosis incidence. *Pathologie Biologie*. 2011, **59** (suppl 3):161-5.

8. Bigi, F., Garcia-Pelayo, M., Nuñez-García, J., Peralta, A., Caimi, K., Golby, P., Hinds, J., Cataldi, A., Gordon, S. and Romano, M. Identification of genetic markers for Mycobacterium pinnipedii through genome analysis. *FEMS Microbiol Lett.* 2005. **15**(suppl 2):147-52.

 Borgdorff, M. W., Floyd, K. and Broekmans, J. F. Interventions to reduce tuberculosis mortality and transmission in low- and middle-income countries. *Bull World Health Organ*. 2002, **80** (suppl 3): 217-27.
Brooks, G., Butel, J. and Morse, S. In: *Jawetz, Melnick, Adelberg's Medical Microbiology*, 21st edition ed. Lange Medical book. 1998. PP. 279-283.

11. Butcher, P. D. Microarrays for Mycobacterium tuberculosis. *Tuber-culosis.* (Edinburgh, Scotland). 2004, **84** (suppl 3-4):131-7.

12. Canetti, G., Fox, W., Khomenko, A., Mahler, H., Menon, N., Mitchison, D., Rist, N. and Smelev, N. Advances in techniques of testing mycobacterial drug sensitivity, and the use of sensitivity tests in tuberculosis control programmes. *Bull World Health Organ*. 1969, **41**: 21-43.

13. Cheesbrough, M. In: *District laboratory practice in tropical countries*. Cambridge University Press.2000.

14. Clarridge, J. E., Shawar, R. M., Shinnick, T. M. and Plikaytis, B. B. Large-scale use of polymerase chain reaction for detection of Mycobacterium tuberculosis in a routine mycobacteriology laboratory. *J. Clin. Microbiol.* 1993, **31**(suppl 8): 2049-56.

15. Cole, S. T. Comparative and functional genomics of the Mycobacterium tuberculosis complex. *Microbiology*. 2002, **148** (suppl 10):2919-28.

16. Cvetnic, Z., Spicic, S., Katalinik-Jankovic, v., Marjanovic, S., Obrovac, M., Benic, M., Mitak, M. M. and Pavlik, I. Mycobacterium caprae infection in cattle and pig son one family farm in Croatia: a case report. *Vet Med.* 2006, **51**(suppl 11):523–31.

17. da Silva Rocha, A., da Costa Leite, C., Torres, H. l. M., de Miranda, A. B., Pires Lopes, M. r. Q., Degrave, W. M. and Suffys, P. N. Use of PCR-restriction fragment length polymorphism analysis of the hsp65 gene for rapid identification of mycobacteria in Brazil. *J. Microbiol. Methods*. 1999, **37**(suppl 3):223-9.

18. Davies, P. D. O., and Pai, M. The diagnosis and misdiagnosis of tuberculosis [State of the art series. Tuberculosis. Edited by I. D. Rusen. Number 1 in the series]. *Int. J. Tuberc. Lung Dis.* 2008, **12**(suppl 11):1226-34.

19. De Wit, D., Steyn, L., Shoemaker, S. and Sogin, M. Direct detection of Mycobacterium tuberculosis in clinical specimens by DNA amplification. *J. Clin. Microbiol.* 1990, **28**(suppl 11):2437-41.

20. Demers, A.-M., Mostowy, S., Coetzee, D., Warren, R., van Helden, P. and Behr, M. A. Mycobacterium africanum is not a major cause of human tuberculosis in Cape Town, South Africa. *Tuberculosis*. (Edinburgh, Scotland). 2010, **90** (suppl 2):143-4.

21. Dietrich, G., Viret, J.-F. and Hess, J. r. Mycobacterium bovis BCGbased vaccines against tuberculosis: novel developments. *Vaccine*. 2003,**21** (suppl 7-8):667-70.

 Djelouadji, Z., Raoult, D., Daffa, M. and Drancourt, M. A Single-Step Sequencing Method for the Identification of Mycobacterium tuberculosis Complex Species. *PLoS Negl Trop Dis*. 2008, 2(suppl 6):e253.
Drobniewski, F. A., More, P. G. and Harris, G. S. Differentiation of Mycobacterium tuberculosis Complex and Nontuberculous Mycobacterial Liquid Cultures by Using Peptide Nucleic Acid-Fluorescence In Situ Hybridization Probes. *J. Clin. Microbiol*. 2000, 38(suppl 1): 444-7.
Eisenach, K. D., Crawford, J. T. and Bates, J. H. Repetitive DNA sequences as probes for Mycobacterium tuberculosis. *J. Clin. Micro-* biol. 1988, 26 (suppl 11):2240-5.

25. Eisenstein, B. I. The Polymerase Chain Reaction. A new method of using molecular genetics for medical diagnosis. *N. Engl. J. Med.* 1990, **322**(suppl 3):178-83.

26. Fabre, M., Hauck, Y., Soler, C., Koeck, J.-L., van Ingen, J., van Soolingen, D., Vergnaud, G. and Pourcel, C. Molecular characteristics of Mycobacterium canettii the smooth Mycobacterium tuberculosis bacilli. *Infect. Genet. Evol.* 2011, **10** (suppl 8):1165-73.

27. Frothingham, R., and Meeker-O'Connell, W. A. Genetic diversity in the Mycobacterium tuberculosis complex based on variable numbers of tandem DNA repeats. *Microbiology*. 1998, **144**(suppl 8):1189-96.

28. Gadre, D., Mahajan, M., Singh, N., Agarwal, D. and Talwar, V. Niacin test for mycobacteria: a comparative study of two methods. *Ind. J. Tub*.1995, **42**:225-6.

29. Gebre, N., Karlsson, U., Jonsson, G., Macaden, R., Wolde, A., Assefa, A.and Miorner, H. Improved microscopical diagnosis of pulmonary tuberculosis in developing countries. *Trans R Soc Trop Med Hyg.* 1995, **89** (suppl 2):191-3.

30. Gillellamudi, **S.** Role of Urinary PCR in Diagnosis of Genitourinary Tuberculosis. *Glob. J. Med. Res.* 2010, **10** (suppl 2):2-5.

31. González-Martín, J., García-García, J., Anibarro, L., Vidal, R., Esteban, J., Blanquer, R., Moreno, S. and Ruiz-Manzano, J. Consensus document on the diagnosis, treatment and prevention of tuberculosis. *Arch Bronconeumol.* 2010, **46** (suppl 5):255-74.

32. Gupta, S., Bandyopadhyay, D., Paine, S. K., Banerjee, S., Bhattacharya, S., Gachhui, R. and Bhattacharya, B. Rapid identification of mycobacterium species with the aid of multiplex polymerase chain reaction (PCR) from clinical isolates. *Open Microbiol J.* 2010, **4**:93-7.

33. Gupte, S. In: *Short Textbook of medical microbiology*, 7th edition ed, New Delh. 1999.P: 264-83.

34. Han, X. Y., Pham, A. S., Tarrand, J. J., Sood, P. K. and Luthra, R. Rapid and Accurate Identification of Mycobacteria by Sequencing Hypervariable Regions of the 16S Ribosomal RNA Gene. *Am. J. Clin. Pathol.* 2002, **118** (suppl 5):796-801.

35. Hanna, B. A., Ebrahimzadeh, A., Elliott, L. B., Morgan, M. A., Novak, S. M., Rusch-Gerdes, S., Acio, M., Dunbar, D. F., Holmes, T. M., Rexer, C. H., Savthyakumar, C. and Vannier, A. M. Multicenter Evaluation of the BACTEC MGIT 960 System for Recovery of Mycobacteria. *J. Clin. Microbiol*.1999, **37** (suppl 11):748-52.

Hewinson, R. G., Vordermeier, H. M., Smith, N. H., and Gordon, S. V. Recent advances in our knowledge of Mycobacterium bovis: A feeling for the organism. *Vet. Microbiol.* 2006, **112** (suppl 2-4):127-39.
Hobby, G. L., Holman, A. P., Iseman, M. D., and Jones, J. M. Enumeration of Tubercle Bacilli in Sputum of Patients with Pulmonary *Tuberculosis.* 1973, **4**: 94-104.

38. Hongmanee, P., Stender, H. and Rasmussen,O. F. Evaluation of a Fluorescence In Situ Hybridization Assay for Differentiation between Tuberculous and NontuberculousMycobacterium Species in Smears of Lowenstein-Jensen and Mycobacteria Growth Indicator Tube Cultures Using Peptide Nucleic Acid Probes. *J. Clin. Microbiol.* 2001, **39** (suppl 3): 1032-35.

39. Houde, C., and Dery, P. Mycobacterium bovis sepsis in an infant with human immunodeficiency virus infection. *Pediatr. Infect. Dis.J.*1998, **7:**810–12.

40. Huang, T.-S., Lee, S. S.-J., Tu, H.-Z., Huang, W.-K., Chen, Y.-S., Huang, C.-K., Wann, S.-R., Lin, H.-H.and Liu, Y.-C. Use of MGIT 960 for rapid quantitative measurement of the susceptibility of Mycobacterium tuberculosis complex to ciprofloxacin and ethionamide. *J. Antimicrob. Chemother.* 2004, **53** (suppl 4):600-3.

Jeong, Y. J., and Lee, K. S. Pulmonary Tuberculosis: Up-to-Date Imaging and Management. *Am. J. Roentgenol.* 2008, **191** (suppl3):834-44.
Jonas, V., Alden, M. J., Curry, J. I., Kamisango, K., Knott, C. A., Lankford, R., Wolfe, J. M. and Moore, D. F. Detection and identification of Mycobacterium tuberculosis directly from sputum sediments by

amplification of rRNA. *J. Clin. Microbiol.* 1993, **31**(suppl 9):2410-16. 43. Kamerbeek, J., Schouls, L., Kolk, A., van Agterveld, M., van Soolingen, D., Kuijper, S., Bunschoten, A., Molhuizen, H., Shaw, R., Goyal, M.and van Embden, J. Simultaneous detection and strain differentiation of Mycobacterium tuberculosis for diagnosis and epidemiology. *J. Clin. Microbiol.* 1997, **35** (suppl 4):907-14.

44. Kaplan, G., and Cohn, Z. A. 1986. The immunobiology of leprosy. *Int Rev Exp Pathol.* 1986, **28:**45-78.

45. Kendall, S. L., Rison, S. C. G., Movahedzadeh, F., Frita, R. and Stoker, N. G. What do microarrays really tell us about M. tuberculosis? *Trends. Microbiol.* 2004, **12** (suppl 12):537-44.

46. Kessler, H. H. Molecular diagnosis of mycobacteria. *Wien Med Wochenschr* 2003, **153**(suppl 15-16):336-41.

47. Kiers, A., Klarenbeek, A., Mendelts, B., Van Soolingen, D. and Koter, G. Transmission of Mycobacterium pinnipedii to humans in a zoo with marine mammals. *Int. J.Tuberc. Lung Dis.* 2008, **12**(suppl 12):1469-1473.

48. Kim, J. Y., Ferraro, M. J. and Branda, J. A. False-Negative Results Obtained with the Gen-Probe Amplified Mycobacterium tuberculosis Direct Test Caused by Unrecognized Inhibition of the Amplification Reaction. *J. Clin. Microbiol.* 2009, **47**(suppl 9):2995-2997.

49. Kim, K., Lee, H., Lee, M.-K., Lee, S.-A., Shim, T.-S., Lim, S. Y., Koh, W.-J., Yim, J.-J., Munkhtsetseg, B., Kim, W., Chung, S.-I., Kook, Y.-H. and Kim, B.-J. Development and Application of Multiprobe Real-Time PCR Method Targeting the hsp65 Gene for Differentiation of Mycobacterium Species from Isolates and Sputum Specimens. *J. Clin. Microbiol.* 2010, **48** (suppl 9):3073-80.

 Kox, L. F., van Leeuwen, J., Knijper, S., Jansen, H. M. and Kolk, A.
H. PCR assay based on DNA coding for 16S rRNA for detection and identification of mycobacteria in clinical samples. *J. Clin. Microbiol.* 1995, **33**(suppl 12): 3225-33.

51. Lalvani, A., and Pareek, M. A 100 year update on diagnosis of tuberculosis infection. *Br. Med. Bull.* 2010, **93:** 69-84.

52. Lambi, E. A. In: *Medium selection and incubation for the isolation of mycobacteria.*, 1992, vol. 1. American Society for Microbiology, Washington D.C.

53. Lange, C., and Mori, T. Advances in the diagnosis of tuberculosis. . *Respirology*. 2010, **15** (suppl 2):220–240.

54. Leao, S., Martin, A., Mejia, G., Palomino, J., Robledo, J., Telles, M. A. S. and Portaels, F. In: *Practical handbook for the phenotypic and genotypic identification of mycobacteria*. 2005.

55. Lemus, D., Martin, A., Montoro, E., Portaels, F. and Palomino, J. C. Rapid alternative methods for detection of rifampicin resistance in Mycobacterium tuberculosis. *J. Antimicrob. Chemother.* 2004, **54** (suppl 1):130-3.

56. Lévy-Frébault, V., Grandry, J. and David, H. Evaluation of rapid tests for the identification of mycobacteria. *J Med Microbiol.* 1982, **15** (suppl 4): 575-77.

57. Li, X. J., Wu, Q. X. and Zeng, X. S. Nontuberculous mycobacterial cutaneous infection confirmed by biochemical tests, polymerase chain reaction-restriction fragment length polymorphism analysis and sequencing of hsp65 gene. *Br. J. Dermatol.* 2003, **149** (suppl 3):642-6.

58. Lima, S. S. S., Clemente, W. T., Palaci, M., Rosa, R. V., Antunes, C. M. d. F. and Serufo, J. C. Conventional and molecular techniques in the diagnosis of pulmonary tuberculosis: a comparative study. *J. Bras Pneumol.* 2008, **34** (suppl 12):1056-62.

59. Mark, D., and Perkins, M. New diagnostic tools for tuberculosis. *Int J tuberc Lung Dis.* 2000, **4**(suppl 12):182-188.

60. Mazurek, G. H., Cave, M. D., Eisenach, K. D., Wallace, R. J., Bates, J. H.and Crawford, J. T. Chromosomal DNA fingerprint patterns produced with IS6110 as strain-specific markers for epidemiologic study of tuberculosis. *J. Clin. Microbiol*.1991, **29** (suppl 9):2030-33.

61. McAdams, H. P., Erasmus, J. and Winter, J. A. Radiologic manifestations of pulmonary tuberculosis. *Radiol. Clin. North. Am.* 1995, **33** (suppl 4):655-78.

62. McEvoy, C. R. E., Falmer, A. A., van Pittius, N. C. G., Victor, T. C., van Helden, P. D. and Warren, R. M. The role of IS6110 in the evolution of Mycobacterium tuberculosis. *Tuberculosis*. (Edinburgh, Scotland). 2007, **87** (suppl 5):393-404.

63. Mendoza, M., Juan, L., Menandez, S., Ocampo, A., Mourelo, J., Saez, J. L., Domanguez, L., Gortazar, C., Garcia Marin, J. F. and Balseiro, A. Tuberculosis due to Mycobacterium bovis and Mycobacterium caprae in sheep. *Vet. J.* 2011, 191(suppl 2):267-9.

64. Michel, A. L., Maller, B. and van Helden, P. D. Mycobacterium bovis at the animal"human interface: A problem, or not? *Vet. Microbiol.* 2011, **140** (suppl 3-4):371-81.

65. Morris, A. *Mycobacteriology:* Laboratory Methods and Standards. Guidelines for Tuberculosis Control in New Zealand. 2003.

66. Nagesh, B. S., Sehgal, S., Jindal, S. K. and Arora, S. K. Evaluation of Polymerase Chain Reaction for Detection of Mycobacterium tuberculosis in Pleural Fluid. Chest. 2001, **119** (suppl 6):1737-41.

67. Nakano, N., Wada, R., Yajima, N., Yamamoto, N., Wakai, Y. and Otsuka, H. Mycobacterial infection of the musculoskeletal tissues: the use of pathological specimens for identification of causative species by PCR-direct sequencing of 16S rDNA. *Jpn. J. Infect. Dis.* 2010, **63** (suppl 3): 188-91.

68. Nazish, F. Newer diagnostic techniques for tuberculosis. *Respiratory Medicine CME* 2009, **2:**151–4.

69. Neonakis, I. K., Gitti, Z., Krambovitis, E. and Spandidos, D. A. Molecular diagnostic tools in mycobacteriology. *J. Microbiol. Methods*. 2008, **75** (suppl 1):1-11.

70. Nerlich, A. G., Haas, C. J., Zink, A., Szeimies, U. and Hagedorn H. G. Molecular evidence for tuberculosis in an ancient Egyptian mummy. *Lancet*, 1997, **350** (suppl 9088):1404.

71. Noordhoek, G. T., van Embden, J. D. A. and Kolk, A. H. J. Questionable Reliability of the Polymerase Chain Reaction in the Detection of Mycobacterium Tuberculosis. *N. Engl. J. Med.* 1993, **329** (suppl 27):2036-36.

72. Otal, I., Martin, C., Vincent-Levy-Frebault, V., Thierry, D. and Gicquel, B. Restriction fragment length polymorphism analysis using IS6110 as an epidemiological marker in tuberculosis. *J. Clin. Microbiol.* 1991, **29** (suppl 6):1252-54.

73. Padilla, E., Manterola, J., Rasmussen, O., Lonca, J., Domínguez, J., Matas, L., Hernández, A.and Ausina, V. Evaluation of a fluorescence hybridisation assay using peptide nucleic acid probes for identification and differentiation of tuberculous and non-tuberculous mycobacteria in liquid cultures. *Eur. J. Clin. Microbiol. Infect. Dis.* 2002, **19** (suppl 2):140-5.

74. Panteix, G., Gutierrez, M. C., Boschiroli, M. L., Rouviere, M., Plaidy, A., Pressac, D., Porcheret, H., Chyderiotis, G., Ponsada, K., Van Oortegem, M., Salloum, S., Cabuzel, S., Bauls, A. L., Van de Perre, P. and Godreuil, S. Pulmonary tuberculosis due to Mycobacterium microti: a study of six recent cases in France. *J. Med. Microbiol.* 2011, **59** (suppl 8):984-9.

75. Phelan, E., El-Gammal, A. and O'Connor, T. In: *Tuberculosis,* Encyclopedia of Environmental Health. 2011, p. 408-17,

76. Piersimoni, C., Scarparo, C., Callegaro, A., Tosi, C. P., Nista, D., Bornigia, S., Scagnelli, M., Rigon, A., Ruggiero, G. and Goglio, A. Comparison of MB/BacT ALERT 3D System with Radiometric BACTEC System and Lowenstein-Jensen Medium for Recovery and Identification of Mycobacteria from Clinical Specimens: a Multicenter Study. *J. Clin. Microbiol.* 2001, **39** (suppl 2):651-7.

77. Rafi, A., and Naghily, B. Efficiency of Polymerase Chain Reaction for the diagnosis of tuberculous meningitis. *Med J.Islam. Acad. Sci.* 1998, **11**(suppl 4):117-20.

78. Rebollo, M. J., San Juan Garrido, R., Folgueira, D., Palenque, E., Daz-Pedroche, C., Lumbreras, C. and Aguado, J. M. Blood and urine samples as useful sources for the direct detection of tuberculosis by

polymerase chain reaction. *Diagn. Microbiol. Infect. dis.* 2006, **56** (suppl 2):141-6.

79. Restrepo, B. I., Gomez, D. I., Shipley, G. L., McCormick, J. B. and Fisher-Hoch, S. P. Selective enrichment and detection of mycobacterial DNA in paucibacillary specimens. *J. Microbiol. Methods.* 2006, **67** (suppl 2):220-9.

80. Ringuet, H., Akoua-Koffi, C., Honore, S., Varnerot, A., Vincent, V., Berche, P., Gaillard, J. L. and Pierre-Audigier, C. hsp65 Sequencing for Identification of Rapidly Growing Mycobacteria. *J. Clin. Microbiol.* 1999, **37** (suppl 3):852-7.

81. Rodríguez, S., Bezos, J., Romero, B., de Juan, L., Álvarez, J., Castellanos, E., Moya, N., Lozano, F., Javed, M., Sáez-Llorente, J., Liébana, E., Mateos, A., Domínguez, L. and Aranaz, A. Mycobacterium caprae infectionin livestock and wildlife, Spain. Spanish Network on Surveillance and Monitoring of Animal Tuberculosis. *Emerg. Infect. Dis.*2011, **17** (suppl 3):532-5.

82. Rogall, T., Wolters, J. R., Flohr, T. and Bottger, E. C. Towards a Phylogeny and Definition of Species at the Molecular Level within the Genus Mycobacterium. *Int. J. Syst. Bacteriol.* 1990, **40** (suppl 4):323-330.

83. Rufenacht, S., Bogli-Stuber, K., Bodmer, T., Jaunin, V. F., Jmaa, D. C. and Gunn-Moore, D. A. Mycobacterium microti infection in the cat: a case report, literature review and recent clinical experience. *J. Feline. Med. Surg.* 2011, **13** (suppl3):195-204.

84. Saltini, C. Direct amplification of Mycobacterium tuberculosis deoxyribonucleic acid in paucibacillary tuberculosis. *Eur. Respir. J.* 1998, **11**(supl 6):1215-17.

85. Siddiqi, K., Lambert, M.-L. and Walley, J. Clinical diagnosis of smear-negative pulmonary tuberculosis in low-income countries: the current evidence. *Lancet Infect. Dis.* 2003, **3** (suppl 5):288-96.

86. Smith, N. H., and Upton, P. Naming spoligotype patterns for the RD9-deleted lineage of the Mycobacterium tuberculosis complex; *Infect. Genet. Evol.* 2011. (In press).

87. Soo, P.C., Horng, Y.T., Hsueh, P.R., Shen, B.J., Wang, J.Y., Tu, H.H., Wei, J.R., Hsieh, S.C., Huang, C.C. and Lai, H.C. Direct and Simultaneous Identification of Mycobacterium tuberculosis complex (MTBC) and Mycobacterium tuberculosis (MTB) by Rapid Multiplex nested PCR-ICT assay. *J. Microbiol. Methods.* 2006, **66** (suppl 3):440-8.

88. Stager, C. E., Libonati, J. P., Siddiqi, S. H., Davis, J. R., Hooper, N. M., Baker, J. F. and Carter, M. E. Role of solid media when used in conjunction with the BACTEC system for mycobacterial isolation and identification. *J. Clin. Microbiol.* 1991, **29** (suppl 1):154-7.

89. Steingart, K. R., Henry, M., Ng, V., Hopewell, P. C., Ramsay, A., Cunningham, J., Urbanczik, R., Perkins, M., Aziz, M. A.and Pai, M. Fluorescence versus conventional sputum smear microscopy for tuberculosis: a systematic review. *Lancet Infect. Dis.* 2006, **6** (suppl 9):570-581.

90. Supply, P., Allix, C., Lesjean, S., Cardoso-Oelemann, M., Rch-Gerdes, S., Willery, E., Savine, E., de Haas, P., van Deutekom, H., Roring, S., Bifani, P., Kurepina, N., Kreiswirth, B., Sola, C., Rastogi, N., Vatin, V., Gutierrez, M. C., Fauville, M., Niemann, S., Skuce, R., Kremer, K., Locht, C. and van Soolingen, D. Proposal for Standardization of Optimized Mycobacterial Interspersed Repetitive Unit-Variable-Number Tandem Repeat Typing of Mycobacterium tuberculosis. *J. Clin. Microbiol.*2006, **44** (suppl 12):4498-510.

91. Swanson, D. S., Pan, X.and Musser, J. M. Identification and subspecific differentiation of Mycobacterium scrofulaceum by automated sequencing of a region of the gene (hsp65) encoding a 65-kilodalton heat shock protein. *J. Clin. Microbiol.*. 1996, **34** (suppl 12): 3151-9.

92. Takahashi, T., Tamura, M., Takahashi, S. N., Matsumoto, K., Sawada, S., Yokoyama, E., Nakayama, T., Mizutani, T. Takasu, T. and Nagase, H. Quantitative nested real-time PCR assay for assessing the clinical course of tuberculous meningitis. *J. neuro.sci.* 2007, **255** (suppl 5):69-76.

93. Thierry, D., Cave, M. D., Eisenach, K. D., Crawford, J. T. Bates, J.H., Gicquel, B. and Guesdon, J. L. IS6110, an IS-like element of Mycobacterium tuberculosis complex. *Nucleic. Acids. Res.* 1990, 18 (suppl 1):188.

94. Thoen, C., LoBue, P. and de Kantor, I. The importance of Mycobacterium bovis as a zoonosis. *Vet. Microbiol*.2006, **112** (suppl 2-4):339-45.

95. Thorne, N., Borrell, S., Evans, J., Magee, J., Garcaa de Viedma, D., Bishop, C., Gonzalez-Martin, J., Gharbia, S. and Arnold, C. IS6110based global phylogeny of Mycobacterium tuberculosis. *Infect. Genet. Evol*.2011, **11** (suppl 1):132-8.

96. Tobler, N. E., Pfunder, M., Herzog, K., Frey, J. E. and Altwegg, M. Rapid detection and species identification of Mycobacterium spp. using real-time PCR and DNA-Microarray. *J. Microbiol. Methods.* 2006, **66** (suppl 1):116-24.

97. Tortoli, E., Benedetti, M., Fontanelli, A. and Simonetti, M. T. Evaluation of Automated BACTEC MGIT 960 System for Testing Susceptibility of Mycobacterium tuberculosis to Four Major Antituberculous Drugs: Comparison with the Radiometric BACTEC 460TB Method and the Agar Plate Method of Proportion. *J. Clin. Microbiol* 2002, **40** (suppl 2):607-10.

98. Tortoli, E., Cichero, P., Piersimoni, C., Simonetti, M. T., Gesu, G. and Nista, D. Use of BACTEC MGIT 960 for Recovery of Mycobacteria from Clinical Specimens: Multicenter Study. *J. Clin. Microbiol.* 1999, **37**(suppl 11):3578-82.

99. Tortoli, E., Simonetti, M. T.and Lavinia, F. Evaluation of reformulated chemiluminescent DNA probe (AccuProbe) for culture identification of Mycobacterium kansasii. *J. Clin. Microbiol*.1996, **34** (suppl 11):2838-40.

100. van Embden, J. D., Cave, M. D., Crawford, J. T., Dale, J. W., Eisenach, K. D., Gicquel, B., Hermans, P., Martin, C., McAdam, R.and Shinnick, T. M. Strain identification of Mycobacterium tuberculosis by DNA fingerprinting: recommendations for a standardized methodology. *J. Clin. Microbiol.* 1993, **31**(suppl 2):406-9.

101. van Soolingen, D., Hermans, P. W., de Haas, P. E., Soll, D. R. and van Embden, J. D. Occurrence and stability of insertion sequences in Mycobacterium tuberculosis complex strains: evaluation of an insertion sequence-dependent DNA polymorphism as a tool in the epidemiology of tuberculosis. *J. Clin. Microbiol.* 1991, **29** (suppl 11):2578-86.

102. Varma-Basil, M., Pathak, R., Singh, K., Dwivedi, S., Garima, K., Kumar, S., Sharma, D., Dhiman, B. and Bose, M. Direct early identification of Mycobacterium tuberculosis by PCR-restriction fragment length polymorphism analysis from clinical samples. *Jpn. J. Infect. Dis.* 2010, **63** (suppl 1):55-7.

103. Wang, S., Tay, L.and Sng, L. Rapid identification of pathogenic rapidly growing mycobacteria by PCR-restriction endonuclease analysis. *Ann Acd Med Singapore*. 2005, **34**(suppl 1):137-140.

104. Warren, R. M., Gey van Pittius, N. C., Barnard, M., Hesseling, A., Engelke, E., de Kock, M., Gutierrez, M. C., Chege, G. K., Victor, T. C., Hoal, E. G.and van Helden, P. D. Differentiation of Mycobacterium tuberculosis complex by PCR amplification of genomic regions of difference [Short Communication]. *Int. J. Tuberc. Lung Dis.* 2006, **10** (suppl 7):818-822.

105. WHO Report. Global Tuberculosis Control: epidemiology, strategy, financing WHO/ HTM/TB/ 2010, 300. . WHO Report.

106. WWW.WHO.INT/EMC. Guidelines for speciation within the Mycobacterium tuberculosis complex. Emerging and other Communicable Diseases, Surveillance and Control. 1996.

107. Yam, W.C., Yuen, K.Y., Kam, S.Y., Yiu, L.S., Chan, K.S., Leung, C.C., Tam, C.M. Ho, P.O., Yew, W.W., Seto, W.H.and Ho, P.L. Diagnostic application of genotypic identification of mycobacteria. J. *Med. Microbiol.* 2006, **55** (suppl 5):529-36.

108. Yam, W. C., Cheng, V. C. C., Hui, W. T., Wang, L. N., Seto, W. H. and Yuen, K. Y. Direct detection of Mycobacterium tuberculosis in clinical specimens using single-tube biotinylated nested polymerase chain reaction-enzyme linked immunoassay (PCR-ELISA). *Diagn. Microbiol. infect. dis.*2004, **48** (suppl 4):271-5.

109. Yeager, H., Lacy, J. J., Smith, L. and Le Maistre, C. Quantitative studies of mycobacterial populations in sputum and saliva. *Am. Rev. Respir. Dis.* 1967, **95**:998-1004.

110. Zakham, F., Belayachi, L., Ussery, D., Akrim, M., Benjouad, A., El Aouad, R. and Ennaji, M. Mycobacterial species as Case study of comparative genome analysis. *Cell. Mol. Biol.* 2011, **57**:1462-69.

111. Zimmerman, M. R. Pulmonary and osseous tuberculosis in an Egyptian mummy. *Bull. N.Y. Acad. Med.* 1977, **55** (suppl 6):604-8.

112. Ziskind, B., and Halioua, B. La tuberculose en ancienne. *Rev. Mal. Respir.* 2007, **24** (suppl 10): 1277-83.