

30 JUNE -  
3 JULY 2019



EUROPEAN SOCIETY OF  
MYCOBACTERIOLOGY

## Reliable Mycobacteria Diagnostics

**NEW: FluoroType® MTBDR – The 1<sup>st</sup> LiquidArray**

- **Novel technology:** The test system is based on the innovative **LiquidArray** technology. It thus enables reliable MDR-TB diagnostics within 2.5 hours only.
- **True MDR-TB testing:** Resistances to both first-line drugs, rifampicin and isoniazid, are reliably identified, as well as mono-resistances.
- **Reliable results:** The assay can detect silent mutations within the *rpoB* gene and therefore allows confidence when testing for resistance.

### Mycobacteria Product Series: Rapid, easy-to-use and cost-efficient!

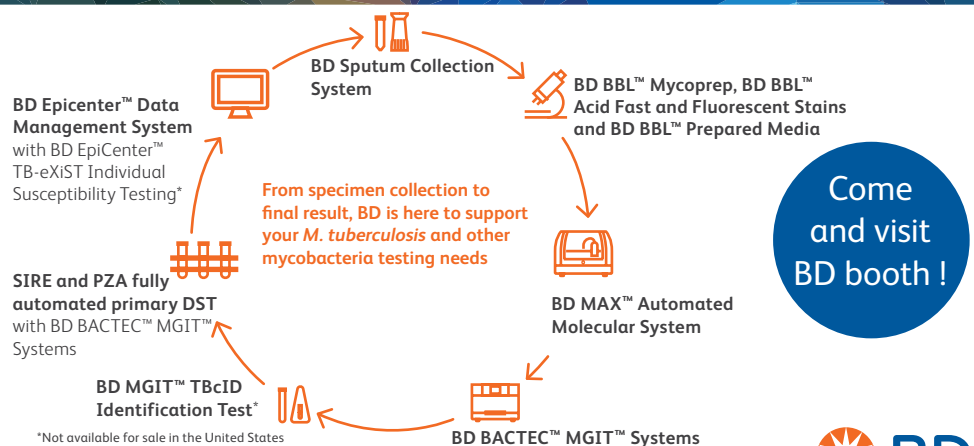
Perfect for TB screening	FluoroType® MTB
Perfect for MDR-/XDR-TB screening	FluoroType® MTBDR, GenoType MTBDR <sub>plus/sl</sub>
Perfect for NTM differentiation	GenoType CM <sub>direct</sub> , GenoType Mycobacterium CM/AS, GenoType NTM-DR



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## THE DIFFERENCE OF ONE INNOVATIVE PARTNER

DRIVING COMPREHENSIVE AND EFFECTIVE SOLUTIONS IN THE FIGHT TO END TB



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## General information

### Venue \*

The Westin Valencia  
Amadeo de Saboya, 16  
46010 Valencia  
+34 963 62 59 00

### Useful venue facts

- 500m from metro station Aragon \*
- Direct line from airport (metro Alameda \* - 25 minutes)
- Direct line from North Station (metro Xativa \* - 5 minutes)
- 1 change from Joaquin Sorolla station (15 minutes)

### Registration and information desk

Located at the congress entrance of the hotel.

Congress registration will open at 12:00 on Sunday 30 June and be open every day until Wednesday 3 July at 13:00.

### Wi-Fi access

**Network:** Westin

**Usuario / login:** ESM2019

**Contraseña / password:** ESM2019

### Social Media

Twitter: #ESMVal19

Facebook: @ESMycob

### Delegate list and abstracts

Electronic copies of the delegate list and the abstracts are available in 'My Congress Materials' in your ESM online account.

### Evaluation and certificate of attendance

We hope you enjoy the ESM annual congress. We really value your feedback and would be grateful if you could complete the survey, which you will be sent by email after the congress. You will be able to download your certificate of attendance from your online account from 15 July.

### For urgent enquiries

Please call Gaëlle Jamar, ESM Event Manager: +44 7766 475379  
[office@esmycobacteriology.eu](mailto:office@esmycobacteriology.eu)

\* See map on inside back cover

# It is our great pleasure and honour to welcome you to the 40<sup>th</sup> Annual Congress of the European Society of Mycobacteriology

**Last year saw the first UN General Assembly High-level Meeting on Ending TB. The outcome of the meeting put the spotlight on the need to speed up the adoption of the 2030 Agenda for Sustainable Development by increasing financial support from countries and industry, and by intensifying research into new tools for tuberculosis control.**

ESM is committed to the achievement of these goals through full alignment with the objectives of the European and global TB research agenda, and by enabling technology and knowledge transfer to those countries where tuberculosis represents an alarming public health issue.

After years of stagnation, the pipeline for promising TB diagnostics is now increasingly within reach. We expect that tests for incipient TB, biomarkers suitable for point of care diagnosis, and next-generation sequencing-based diagnostics for MDR-TB will become available within the next few years. In addition, we are

starting to see promising results in the vaccine field.

The ESM is a forum where not only state-of-the-art but also incipient research lines are presented and shared. In order to make progress in science, two conditions need to be fulfilled: the availability of funds, and the field of research being attractive to young and talented scientists. ESM has been instrumental in increasing the critical mass of basic and clinical scientists dedicated to this field of research and is committed to increasing their retention in the field by fuelling their scientific interests.

The ESM 2019 programme will address emerging issues like biomarkers, whole genome based diagnostics, epidemiology of tuberculosis and non-tuberculosis mycobacteria, new treatment regimens for MDR-TB, and ethical aspects of whole genome sequencing. At the same time, it will cover state-of-the-art topics on fundamental host and pathogen


biology and their translational potential to innovative control tools.

Valencia is the third most populous city in Spain and, as a result of being one of the largest cities in Europe during the XIV century and a prominent Mediterranean trading route, Valencia today sports a rich and diverse architectural and cultural landscape. The city is also well known as the birthplace of the paella, which can be enjoyed on one of the city's many beautiful beaches.

We are not only looking forward to a stimulating congress, but also to friendly and casual get-togethers in this beautiful environment.

We hope you enjoy this meeting.

Best regards,



Daniela M. Cirillo (President)



Iñaki Comas (Local)



Mireia Coscolla (Local)



## With special thanks to



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ASSOCIATION MANAGEMENT

## Sunday 30 June

12:00 Registration

14:00-16:00 **Workshop on host pathogen evolution**

**Chairs:** Mireia Coscollá, *University of Valencia*;  
Bouke de Jong, *Institute of Tropical Medicine, Antwerp*

14:00-14:30 **GL01**  
**Dissecting the genetic and evolutionary determinants of immune response variation in humans**  
Lluís Quintana Murci, *Institut Pasteur, Paris*

14:30-15:00 **GL02**  
**What can we learn from ancient horizontal gene transfer in *M. tuberculosis*?**  
Olivier Neyrolles, *IPSB, Toulouse*

15:00-15:30 **GL03**  
**Mycobacterial and host determinants of TB granuloma necrosis**  
Antonio Pagan, *University of Cambridge*

15:30-16:00 **OR01**  
**The impact of PE-PPE secretion on the evolution of the *Mycobacterium tuberculosis* complex**  
Louis Ates, *Amsterdam UMC, University of Amsterdam*

16:00-17:00 **Industry symposium**

16:00-16:30 **FT MTBDR VER2.0: LiquidArray technology predicts resistance to rifampicin and isoniazid with high accuracy in clinical specimens**  
Anzaan Dippenaar, *DST-NRF Centre of Excellence for Biomedical Tuberculosis Research | SAMRC Centre for Tuberculosis Research, Pretoria*



16:30-17:00 **TB control: issue and role of the diagnostic laboratory in a tertiary care university hospital**  
Onya Opota, *CHUV centre hospitalier universitaire vaudois*



17:00-17:30 Coffee break

## Sunday 30 June

17:30-20:00 **Opening session and awards**

**Chairs:** Daniela M Cirillo, Iñaki Comas

17:30-17:40 **Welcome from the organiser**  
Iñaki Comas, *Biomedicine Institute of Valencia (IBV)*

17:40-18:00 **Opening words from the President**  
Daniela M Cirillo, *San Raffaele Scientific Institute, Milan*

18:00-18:45 **GL04: Special Lecture**  
**What have we learned from the CRYPTIC consortium?**  
Derrick Crook, *University of Oxford*

18:45-19:15 **Presentation of Gertrud Meissner Award**  
by Stefan Nieman, *Research Center Borstel FZB*

19:15-19:45 **Presentation of Gardner Middlebrook Award**  
by Salman Siddiqi, *BD*

20:15 **Welcome reception at the Palau Alameda \***  
(Paseo Alameda corner with Arquitecto Mora, 2 -) \* See map on inside back cover

## Monday 1 July

09:00-10:30 **Biology of the host**  
**Chairs:** Pere Joan Cardona, *Institut Germans Trias i Pujol, Valencia*;  
Alexander Apt, *Central Tuberculosis Research Institute, Moscow*

09:00-09:30 **GL05**  
**Non-classical innate and adaptive immunity in host defence against *Mycobacterium tuberculosis* in humans**  
Tom Ottenhoff, *Leiden University Medical Centre*

09:30-09:50 **OR02**  
***Mycobacterium tuberculosis* modulates sialylation in the lung with an impact on disease susceptibility**  
Kaori Fonseca, *i3S, University of Porto*

09:50-10:10 **OR03**  
**The genetic architecture of the dynamic immune response to *M. tuberculosis* infection in human macrophages**  
Joaquín Sanz, *Institute BIFI for Bio-computation and Physics of Complex Systems, University of Zaragoza*



## Monday 1 July

10:10-10:30 **OR04**  
**TNF-alpha antagonists differentially induce TGF-beta1-dependent *Mycobacterium tuberculosis* reactivation in a human, *in vitro* granuloma model**  
 Ainhoa Arbués Arribas, *Swiss Tropical and Public Health Institute, Basel*

10:30-11:00  
 Coffee break

11:00-12:10 **One Health**  
**Chairs:** Thomas Kohl, *Research Center Borstel FZB*;  
 Jesús Gonzalo Asensio, *University of Zaragoza*

11:00-11:30 **GL06**  
***Mycobacterium tuberculosis* throughout Africa and different hosts using genomics**  
 Mireia Coscolla, *University of Valencia*

11:30-11:50 **OR05**  
**Exploring the role of the SigK regulon in the macrophage response to *Mycobacterium bovis* infection**  
 Alicia Smyth, *University College Dublin*

11:50-12:10 **OR06**  
**Combining genomics and epidemiology to analyse bi-directional transmission of *Mycobacterium bovis* in a multi-host system**  
 Joseph Crispell, *University College Dublin*

12:10-13:00 **Transmission**  
**Chairs:** Troels Lillebaek, *Statens Serum Institut*;  
 Dario Garcia de Viedma, *Gregorio Marañon Hospital, Madrid*

12:10-12:40 **GL07**  
**Diagnostic challenges that affect interruption of transmission**  
 Bouke de Jong, *Institute of Tropical Medicine, Antwerp*

12:40-13:00 **OR07**  
***M. tuberculosis* microvariation is common and is associated with rifampicin resistance and transmission: analysis of three years prospective universal sequencing in England**  
 David Wyllie, *University of Oxford*

13:00-14:00  
 Lunch

## Monday 1 July

14:00-15:00 **Poster session I**  
 Odd numbered posters (P001, P003, P005, P007 etc)



15:00-18:00 **Transmission**  
**Chairs:** Conor Meehan, *University of Bradford*;  
 Rana Jajou, *National Institute for Public Health and the Environment RIVM, Bilthoven*

15:00-15:30 **GL08**  
**Ten years and two thousand genomes: Insights from TB WGS in British Columbia, Canada**  
 Jennifer Gardy, *University of British Columbia's School of Population and Public Health, Vancouver*

15:30-15:55 **GL09**  
**TB precision epidemiology: Prospects and challenges of interpreting genomic data in a low burden country**  
 Anders Norman, *Statens Serum Institute, Copenhagen*

15:55-16:10 **OR08**  
**A descriptive analysis of tuberculosis meningitis associated mortality**  
 Michael Lauzardo, *University of Florida*

16:10-16:25 **OR09**  
**The frequency and rate of insertions and deletions in *Mycobacterium tuberculosis* during a single outbreak**  
 Maxime Godfroid, *Kiel University*

16:30-17:00  
 Coffee break

17:00-17:25 **GL10**  
**Beyond frontiers in TB: Transnational surveillance of transmission**  
 Dario Garcia de Viedma, *Hospital General Universitario Gregorio Marañon, Madrid*

17:25-17:40 **OR10**  
**Comparison of traditional field epidemiology and whole genome sequencing to understand tuberculosis transmission in a remote circumpolar**  
 Jennifer Guthrie, *University of British Columbia, Vancouver*

## Monday 1 July

17:40-17:55 **OR11**  
**Laboratory implementation of next generation sequencing in Kyrgyzstan to stop transmission of drug resistant tuberculosis in TB hospitals**  
 Vanessa Mohr, *Research Center Borstel*

**18:00-19:30**  
**Ethics lecture and round table**  
**Chair:** Annelies Van Rie, *University of Antwerp*

18:00-18:20 **GL11**  
**Ethical challenges in precision approaches to infectious disease: The case of phylogenetic tuberculosis sequencing?**  
 Eric Juengst, *UNC Chapel Hill*

18:20-19:00 **Round table discussion**  
 Jennifer Gardy - Annelies Van Rie - Bouke De Jong - Daniela Cirillo - Fernando González-Candelas - Dario Garcia de Viedma

**19:30**  
**Guided tour of Valencia**  
 Dinner at Convent Carmen \*  
 (Plaça del Portal Nou, 6): Depart from the venue, meet at the registration desk



\* See map on inside back cover

## Tuesday 2 July

**09:00-10:50**  
**Biology of the pathogen**  
**Chairs:** Igor Mokrousov, *Saint Petersburg Pasteur Institute*;  
 Louis Ates, *Amsterdam UMC*

09:00-09:30 **GL12**  
**How IS6110 transposition paved the way to construct the live attenuated TB vaccine MTBVAC?**  
 Jesús Gonzalo Asensio, *University of Zaragoza*

09:30-09:50 **OR12**  
**Adaptation through diversity: differential regulation of leaderless versus canonical translation in *Mycobacterium tuberculosis***  
 Anna Grabowska, *London School of Hygiene and Tropical Medicine, London*

09:50-10:05 **OR13**  
**Genome-wide functional characterization of non-coding RNAs in *Mycobacterium tuberculosis* using combinatorial CRISPR**  
 Thibault Barbier, *Department of Immunology and Infectious Diseases, Harvard T.H. Chan School of Public Health, Boston*

## Tuesday 2 July

10:05-10:20 **OR14**  
**Genome-wide mutational biases fuel transcriptional diversity in the *Mycobacterium tuberculosis* complex**  
 Alvaro Chiner-Oms, *Instituto de Biomedicina de Valencia IBV-CSIC*

10:20-10:35 **OR15**  
**Survival of *Mycobacterium tuberculosis* complex strains in the dormant state under hypoxic conditions is lineage-dependent**  
 Tobias Dallenga, *Research Center Borstel*

10:35-10:50 **OR16**  
**An ancestral lineage of the *Mycobacterium tuberculosis* complex discovered near the African Great Lakes, missing link between *M. canettii* and *M. tuberculosis sensu stricto***  
 Jean-Claude Ngabonziza Semuto, *Rwanda Biomedical Center, Kigali*

**10:50-11:20**

Coffee break

**11:20-13:05**

**Non tuberculosis mycobacteria**  
**Chairs:** Leen Rigouts, *Institute of Tropical Medicine, Antwerp*;  
 Stefan Nieman, *Research Center Borstel*

11:20-11:45 **GL13**  
**NTM epidemiology trends, which direction are we going?**  
 Troels Lillebaek, *Statens Serum Institute, Copenhagen*

11:45-12:15 **GL14**  
**NTM susceptibility test pitfalls and clinical implications**  
 Florian Maurer, *Research Center Borstel*

12:15-12:40 **OR17**  
**Reconstituting the genus *Mycobacterium***  
 Conor Meehan, *BCCM/ITM Mycobacterial Culture Collection, Institute of Tropical Medicine, Antwerp*

12:40-13:05 **OR18**  
**Identifying correlates of protection for a vaccine against *Mycobacterium ulcerans* infection in a low-dose murine challenge model**  
 Tim Stinear, *University of Melbourne*

**13:05-14:00**

Lunch

## Tuesday 2 July

**14:00-15:00** **Poster session II**  
Even numbered posters (P002, P004, P006, P008 etc)

**15:00-16:30** **New diagnostics and treatment concepts**  
**Chairs:** Vlad Nikolayevskyy, *Public Health England*;  
Maria Jesus Garcia, *Universidad Autonoma de Madrid*

15:00-15:30 **GL15**  
**TB diagnostics pipeline - Addressing the missing millions and enabling targeted therapy**  
Claudia Denking, *FIND & Center of infectious diseases, University of Heidelberg*

15:30-15:50 **OR19**  
**High percentage of mixed infections in a high MDR-TB country identified from lung surgery samples**  
Miguel Angel Moreno Molina, *Biomedicine Institute of Valencia - CSIC*

15:50-16:10 **OR20**  
**Targeting *Mycobacterium tuberculosis* with lipophilic efflux inhibitors exploring their dual activity: dissipation of the proton motive force and efflux inhibition**  
Diana Machado, *IHMT, Universidade Nova de Lisboa*

16:10-16:30 **OR21**  
**A new blood test to accelerate TB diagnosis**  
Marc Rodrigue, *BioMérieux*

**16:30-17:00** Coffee break

**17:00-18:00** **General assembly**

**18:30** **Buses depart to Albufera for tour of Albufera and dinner**  
Depart from the venue, meet at the registration desk

## Wednesday 3 July

**09:30-12:35** **New diagnostics and treatment concepts**  
**Chairs:** Daniela Cirillo, *San Raffaele Scientific Institute, Milan*;  
Vlad Nikolayevskyy, *Public Health England*

09:30-10:00 **GL16**  
**WHO guidelines on the path to modernize diagnosis, treatment and care of TB**  
Ernesto Jaramillo, *WHO, Geneva*

10:00-10:20 **OR22**  
**High frequency of bedaquiline resistance in programmatically-treated patients with unfavourable outcomes in Cape Town, South Africa**  
Brigitta Derendinger, *Faculty of Medicine and Health Sciences, Stellenbosch University*

10:20-10:40 **OR23**  
**Anti-tuberculosis activity of selected nitronaphtofuran compounds**  
Noelia Alonso Rodriguez, *Faculty of Mathematics and Natural Sciences, University of Oslo*

10:40-11:00 **OR24**  
**A portable real-time solution for next generation sequencing-based diagnosis of drug-resistant tuberculosis direct from clinical samples**  
Andrea Cabibbe, *San Raffaele Scientific Institute, Milan*

11:00-11:30 Coffee break

11:30-11:55 **GL17**  
**Relational sequencing TB (ReSeqTB) knowledge base: advances and future directions**  
Paolo Miotto, *San Raffaele Scientific Institute, Milan*

11:55-12:15 **OR25**  
**TB portals program: a multi-faceted global response to DR-TB threat.**  
Eric Engle, *National Institutes of Health, Bethesda, MD*

12:15-12:35 **OR26**  
**Whole genome sequencing to distinguish de-novo emergence or secondary infection of multi-drug resistant tuberculosis**  
Vijay Srinivasan

**12:35** **Poster awards & closing remarks**

## Partners

### Platinum



Cepheid is a leading molecular diagnostics company that is dedicated to improving healthcare by developing, manufacturing, and marketing accurate yet easy-to-use molecular systems and tests. By automating highly complex and time-consuming manual procedures, the company's solutions deliver a better way for institutions of any size to perform sophisticated genetic testing for organisms and genetic-based diseases. Through its strong molecular biology capabilities, the company is focusing on those applications where accurate, rapid, and actionable test results are needed most, in fields such as critical and healthcare-associated infections, sexual health, genetic diseases, virology and cancer.

[www.cepheid.com](http://www.cepheid.com)



Hain Lifescience GmbH is a manufacturer and distributor of *in vitro* diagnostics based in Nehren in the district of Tübingen. Our customers are medical laboratories worldwide. We are specialists in molecular genetic test systems and technical instruments for the detection of dangerous pathogens or hereditary diseases. The company was originally founded by David and Tobias Hain in 1986 as a mail order company offering laboratory supplies. Over the last 30 years the company developed steadily and successfully. Our overriding goal is to provide our customers in Germany and everywhere in the world with the best possible support.

[www.hain-lifescience.de](http://www.hain-lifescience.de)

### Silver



BD is one of the largest global medical technology companies in the world and is advancing the world of health by improving medical discovery, diagnostics and the delivery of care. The company develops innovative technology, services and solutions that help advance both clinical therapy for patients and clinical process for health care providers. BD and its 65,000 employees have a passion and commitment to help improve patient outcomes, improve the safety and efficiency of clinicians' care delivery process, enable laboratory scientists to accurately detect disease and advance researchers' capabilities to develop the next generation of diagnostics and therapeutics. BD has a presence in virtually every country and partners with organizations around the world to address some of the most challenging global health issues. BD helps customers enhance outcomes, lower costs, increase efficiencies, improve safety and expand access to health care.

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## Partners

### Silver



FISABIO Sequencing Service provides complete NGS solutions to our customers beginning with a free consultation with our experienced scientists regarding project design and initiation. We offer both standard and custom solutions for NGS library preparation, sequencing, and bioinformatics analysis support. Our experienced team is available to advise and help with your project at every step. We provide you with NGS services and capacities based on the market leading technologies:

Illumina Miseq; Illumine NextSeq500; MinION Oxford Nanopore; Sequel PacBIO (Soon, end of 2019)

We are involved since 2014 in several Mycobacterium sequencing (Whole genome sequencing and RNA-seq) and bioinformatics analysis projects:

Swiss tropical and public health institute; Universidade do Minho; Universidad de Zaragoza; IBV-CSIC (Biomedicine Institute of Valencia); Universidad de Valencia; (ITM) The Institute of Tropical Medicine, Belgium; National Centre for TB and Lung Diseases of Georgia; Pasteur Institute (Paris); GSK Global Health R&D Tuberculosis Unit

<http://fisabio.san.gva.es/en/fisabio>



QIAGEN is the leading global provider of Sample to Insight® solutions to transform biological materials into valuable molecular insights. QuantiFERON®-TB Gold Plus (QFT®-Plus) is the only TB test that offers >95% sensitivity, the highest specificity of any test for TB infection and innovative CD8+ T-cell technology.

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### Bronze



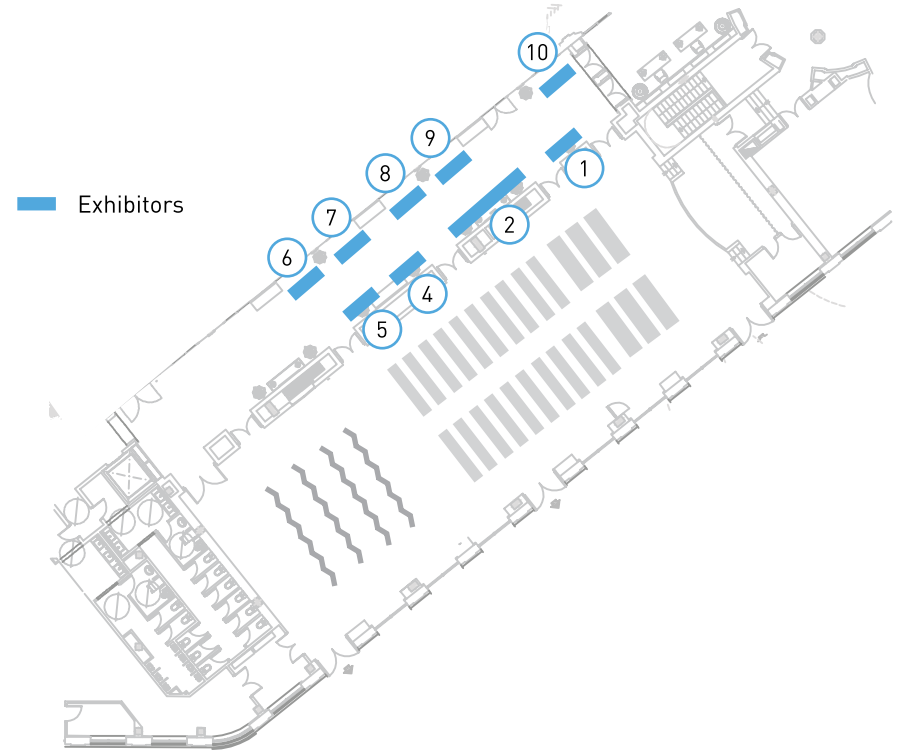
Oxford Nanopore Technologies has developed the world's first nanopore DNA and RNA sequencing devices. The MinION is a portable, real-time, long-read, low-cost device designed to bring easy biological analyses to anyone, whether in scientific research, education or real world applications such as disease/pathogen surveillance, environmental monitoring, food chain surveillance, self-quantification or microgravity biology. The GridION and PromethION devices serve users with larger projects or more samples. Oxford Nanopore Technologies products are currently for research use only.

[www.nanoporetech.com](http://www.nanoporetech.com)





## Westin ground floor: Exhibitors



FISABIO Sequencing Service provides complete NGS solutions to our customers beginning with a free consultation with our experienced scientists regarding project design and initiation. We offer both standard and custom solutions for NGS library preparation, sequencing, and bioinformatics analysis support. Our experienced team is available to advise and help with your project at every step. We provide you with NGS services and capacities based on the market leading technologies:

- Illumina Miseq
- Illumina NextSeq500
- MiniON oxford nanopore
- Sequel PacBIO (Soon, end of 2019)



We are involved since 2014 in several *Mycobacterium* sequencing (Whole genome sequencing and RNA-seq) and bioinformatics analysis projects.

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1		7	
2		8	
4		9	
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6			

## Partners

### Exhibitors



**Booth 9**  
BD



**Booth 7**

*Pioneering Diagnostics*

A world leader in the field of *in vitro* diagnostics for over 55 years, bioMérieux is present in 43 countries and serves more than 160 countries with the support of a large network of distributors. In 2018, revenues reached €2.4 billion, with over 90% of international sales.

bioMérieux provides diagnostic solutions (systems, reagents, software, services) which determine the source of disease and contamination to improve patient health and ensure consumer safety. Its products are mainly used for diagnosing infectious diseases. Its diagnostic solutions are also used for detecting microorganisms in agri-food, pharmaceutical and cosmetic products.

bioMérieux is listed on the Euronext Paris stock market.

[www.biomerieux.com](http://www.biomerieux.com)



**Booth 8**  
Cepheid



**Booth 4**

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**Booth 10**  
Fisabio

## Partners

### Exhibitors



**Booth 6**

A leading pioneer in sequencing, genotyping and bioinformatics since 2001, GenoScreen develops innovation programs that fuel its technological lead and drive the development of innovative services and products.

With GenoScreen, discover:

- Cutting-edge services in genomics, metagenomics and bioinformatics  
GenoScreen offers a wide range of solutions based on more than 18 years of experience and on a technological platform benefiting from the most powerful equipment.
- A key player in molecular microbiology research and innovation  
Involved in a wide range of research programs and projects, both public and private, GenoScreen develops a portfolio of analysis and control tools in genomics, metagenomics and molecular microbiology.
- A company at the service of Humankind and its environment  
The services and innovations developed by GenoScreen aim to meet the needs of academic and industrial researchers facing various problems in the health care of humans, animals, plants and the environment sectors.

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**Booth 2**  
Hain



**Booth 5**

Insmmed is dedicated to improving the lives of patients battling serious and rare diseases. Our mission is to develop novel, transformational therapies that make a real difference to patients.

[www.insmed.com](http://www.insmed.com)



**Booth 1**  
Qiagen

P011

**Genomic characterization of *Mycobacterium africanum* West-African 1 (Lineage 5)**  
C. N'Dira Sanoussi, *Laboratoire de Référence des Mycobactéries, Cotonou, Benin*

P013

**Uncovering the epitopes underlying the induction of varying adaptive immune responses by different *Mycobacterium tuberculosis* lineages**  
Carlos Magalhães, *University of Minho, Braga*

P015

**Exploring mechanisms of translation in the human pathogen, *Mycobacterium tuberculosis***  
Beth Sawyer, *London School of Hygiene & Tropical Medicine*

P017

**Ethambutol resistance: An interplay of efflux genes overexpression and genomic mutations**  
Mandira Varma-Basil, *University of Delhi*

P019

**Mechanisms of drug tolerance in *Mycobacterium tuberculosis***  
Annelies Van Rie, *University of Antwerp*

P021

**The role of *Mycobacterium tuberculosis* complex genetic variation and of macrophage phenotype during early stages of infection**  
Paolo Miotto, *IRCCS Ospedale San Raffaele, Milano*

P023

***M. tuberculosis* closely related variants with different transmission success also show different behaviour in an *ex vivo* infection model**  
Estefania Abascal, *Hospital General Universitario Gregorio Marañón, Madrid*

P025

**Genetic diversity of *Mycobacterium tuberculosis* Beijing strains in China**  
Yang Zhou, *Chinese Center for Disease Control and Prevention*

P027

**Primary multidrug-resistance and genotypic characterization of *Mycobacterium tuberculosis* strains circulating in North-West Russia**  
Anna Vyazovaya, *St. Petersburg Pasteur Institute*

P029

**Characterization of the intramacrophagic expression profile of the smallRNA ncRv0757c in different *Mycobacterium tuberculosis* lineages**  
Matteo Chiacchiaretta, *IRCCS Ospedale San Raffaele, Milano*

P031

**Genotypes and drug resistance of *Mycobacterium tuberculosis* from patients with HIV-associated tuberculosis in St. Petersburg, Russia**  
Alena Gerasimova, *St. Petersburg Pasteur Institute*

P033

**Ultrastructural comparison by electron microscopy of *M. tuberculosis* Beijing and Beijing-like genotypes isolated from Colombian patients**  
Martha Isabel Murcia Aranguren, *Universidad Nacional de Colombia*

P035

**Genome-based taxonomic workflow for defining new species within the *Mycobacterium* genus**  
Sari Cogneau, *Institute of Tropical Medicine Antwerp*

P037

**Comparison of drug susceptibility testing performed on TB specimens from HIV patients in a TB high-incidence country, locally and in a supranational reference laboratory**  
Dorte Bek Folkvardsen, *Statens Serum Institut, Copenhagen*

P039

**Homopolymers in *Mycobacterium tuberculosis*: A source for rapid adaptation?**  
Michaela Zwyrer, *University of Basel*

P041

**Gene panel for MTBC drug resistance detection by using next generation sequencing technologies**  
Carla Mariner Llicer, *Biomedicine institute of Valencia (IBV-CSIC)*

P043

**Emergence of bedaquiline resistance in *M. tuberculosis***  
Danila Zimenkov, *Russian Academy of Sciences, Moscow*

P045

**"Hole" genome sequencing: Illumina blind spots in the *M. tuberculosis* H37Rv genome**  
Faramarz Valafar, *San Diego State University*

P047

**Towards next generation diagnostics for tuberculosis: identification of novel molecular targets by large-scale comparative genomics**  
Galo Goig, *Institute of Biomedicine of Valencia*

P049

**Discordances between molecular assays for detection of rifampicin resistance in *Mycobacterium tuberculosis*: frequency, mechanisms and clinical impact**  
Michael Whitfield, *University of Antwerp*

P051

**Performance of the Deeplex®-MycTB kit on high quality DNA samples and on clinical samples for the detection of first- and second-line drug resistance in MTBC strains**  
Silke Feuerriegel, *Research Centre Borstel*

P053

**CAPTURE-XT -Isolation and concentration of *Mycobacterium tuberculosis* from sputum using a novel microfluidic-dielectrophoretic (DEP) technology to enable rapid diagnosis**  
Laura Katvars, *QuantuMDx, Newcastle*

P055

**Missed ethionamide resistance in South Africa**

Marisa Klopper, *Stellenbosch University, Cape Town*

P057

**Isoniazid resistance determination: challenges in practice**

Elizabeth Streicher, *Stellenbosch University, Cape Town*

P059

**Rapid detection of mycobacterial growth by fluorogenic media which can be used for rapid susceptibility testing**

Tanil Kocagoz, *Acibadem Mehmet Ali Aydinlar University, Istanbul*

P061

**High-dose isoniazid continues to contribute to treatment success in the majority of MDR-TB patients**

Pauline Lempens, *Institute of Tropical Medicine, Antwerp*

P063

**Unveiling the synergistic mechanisms of *M. tuberculosis* and HIV-1 through SPINET, a protein-protein interaction network analysis tool**

Ana Santos-Pereira, *University of Minho, Braga*

P065

**Identifying markers for high-dose INH treatment**

Annelies Van Rie, *University of Antwerp*

P067

**Development of a tuberculosis diagnostic kit based on next generation sequencing**

Maria Piñana, *Hospital Universitari Vall d'Hebron (HUVH), Barcelona*

P069

**Fluoroquinolone (hetero)resistant TB assessed by deep sequencing: a nationwide study**

Philip Supply, *Univ. Lille, CNRS, Inserm, CHU Lille, Institut Pasteur de Lille, U1019 - UMR 8204 - CILL*

P071

**Mycobacterial species identification from grown Middlebrook broth with VITEK®MS MALDI-TOF**

Ana Gil-Brusola, *Hospital Universitario y Politécnico La Fe, Valencia*

P073

**Identification of a highly successful MDR-TB clone transmitting in the high burden setting of Callao, Peru**

Christian Utpatel, *Research Centre Borstel*

P075

**Evaluation of the Xpert MTB/RIF Ultra (XTB-U) assay for Direct Detection of *Mycobacterium tuberculosis* (MTC) in selected respiratory specimens with minimal bacillary load**

Miguel José Martínez-Lirola, *Complejo Hospitalario Universitario Torrecárdenas, Almería*

P077

**Whole genome sequencing analysis to identify SNPs involved in bedaquiline and delamanid phenotypic resistance in *M. tuberculosis* clinical strains**

Simone Battaglia, *San Raffaele Scientific Institute, Milan*

P079

**Evaluation of GeneXpert MTB/RIF for detection of *Mycobacterium tuberculosis* complex and rifampicin resistance in non-respiratory clinical specimens at TB Lab in Rashid Hospital in Dubai**

Maya Habous, *Dubai Health Authority*

P081

**Evaluation of cyclopiazonic acid activity on *Mycobacterium tuberculosis* CtpF: potential target for anti-tubercular drugs**

Santos Ruiz, *Universidad Nacional de Colombia*

P083

**Transcriptional profiling of *Mycobacterium tuberculosis* suggests respiratory poisoning upon exposure to delamanid**

An Van den Bossche, *Sciensano, Brussels*

P085

***Mycobacterium tuberculosis* isolates subcultured on different growth media show no evidence of passage artifacts and remain representative of original clinical samples**

Charlotte Genestet, *CIRI, INSERM U1111, Université de Lyon*

P087

***In vitro* activity of Linezolid and Tedizolid against *Mycobacterium tuberculosis***

Pilar Ruiz-Martinez, *University of Córdoba*

P089

**New generation Interferon-Gamma Release Assay (QFT-PLUS): a possible tool to evaluate the response to treatment in active tuberculosis**

Paola Dal Monte, *University of Bologna*

P091

**Can we trust PZA DST? An investigation of EQA results from 7 NRLs and 13 clinical TB-laboratories**

Melles Haile, *Public Health Agency of Sweden, Solna*

P093

**Management of hazardous infectious waste in a Mycobacteria reference center**

Esther Vaquero-Alvarez, *University of Cordoba*

P095

**Application of superparamagnetic nanoparticles for fast, simultaneous and non-invasive diagnosis of tuberculosis and HIV infection**

Diana Machado, *Universidade Nova de Lisboa*

P097

**How well do routine molecular diagnostics detect rifampicin heteroresistance in *Mycobacterium tuberculosis*?**

Kamela Ng, *Institute of Tropical Medicine, Antwerp*

P099

**Whole-genome analysis of *Mycobacterium chimaera* as a potentially useful tool for description of outbreak associated to heater-cooler units (HCUs)**

Francesco Messina, *IRCCS, Rome*

P101

**Understanding the role and regulation of efflux pumps expression in an in-vitro evolved drug resistance *Mycobacterium***

Deepika Rai, *Indian Institute of Technology, Bombay*

P103

**Epidemiological typing of *Mycobacterium xenopi* by multilocus sequence typing**

Maria Teresa Tórtola Fernández, *Universitary Vall d'Hebron. UAB.Barcelona*

P105

**In vitro susceptibility of nontuberculous *Mycobacterium* (NTM) isolates to Tedizolid (TZD)**

Jenny Wee, *Singapore General Hospital*

P107

**Use of whole genome sequencing for investigating iatrogenic infections due to non-tuberculous mycobacteria**

Emmanuel Lecorche, *National Reference Center for Mycobacteria and Antimycobacterial Resistance, Paris*

P109

***Mycobacterium pseudoshottsii* in Italian marine water fish farms**

Davide Mugetti, *Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta – Torino*

P111

**Perception for risk and disease severity of NTM lung disease- physician survey in Germany, UK, Italy, France and the Netherlands**

Roald van der Laan, *Insmmed Europe*

P113

**Safety and toxicity study of the immunomodulatory agent *Mycobacterium brumae* in two different animal models**

Esther Julian, *Universitat Autònoma de Barcelona*

P115

**Performance of the GenoType CMdirect VER 1.0 assay on formalin fixed paraffin embedded (FFPE) biopsies: three case reports**

Anna Camaggi, *Maggiore della Carità University Hospital, Novara*

P117

**Emerging source of infection – *M. tuberculosis* in a rescue dog, a case report**

Silja Mentula, *National Institute for Health and Welfare, Helsinki*

P119

**Field application of antigen pre-coated blood collection tubes for the IFN- $\gamma$  assay for diagnosis of bovine tuberculosis**

Yun-Ho Jang, *Animal and Plant quarantine agency, Korea*

P121

**A phylogenomic perspective on a neglected infectious disease: tuberculosis by *Mycobacterium bovis* in North Brazil**

Marília Lima da Conceição, *PPGBPA, UEPA, Lisbon*

P123

**Multidrug resistant tuberculosis in Spain**

Sofia Samper, *Universidad de Zaragoza*

P125

**Population structure of *Mycobacterium bovis* in Germany: a long-term study using whole genome sequencing combined with conventional molecular typing methods**

Thomas Kohl, *Research Center Borstel*

P127

**Proposal for control of ventilation with low-cost sensors that use a standardized and open data management model based on the European FiWare standard**

Esther Vaquero-Alvarez, *University of Cordoba*

P129

**Evidence for Pleistocene zoonotic tuberculosis origins**

David Minnikin, *University of Birmingham*

P131

**Fast molecular approach for scrutiny of TB recurrences involving epidemic multidrug-resistant strains of *Mycobacterium tuberculosis***

Laura Perez-Lago, *Hospital General Universitario Gregorio Marañón, Madrid*

P133

**Expanded trans-national tracking of a Beijing strain successfully transmitted in France**

Laura Perez-Lago, *Hospital General Universitario Gregorio Marañón, Madrid*

P135

**Characterizing a TB outbreak in a prison in Costa Rica following non-standard laboratory approaches**

Laura Perez-Lago, *Hospital General Universitario Gregorio Marañón, Madrid*

P137

**WGS reveals a likely long-term prevalent status for a predominant Beijing strain in Colon, Panama**

Fermin Acosta, *Instituto de Investigación Sanitaria Gregorio Marañón, Madrid*

P139

**Phylogeny of modern Beijing clusters *M. tuberculosis* in Mongolia**

Svetlana Zhdanova, *Scientific Center of Family Health and Human Reproduction, Irkutsk*

P141

**Dynamic changes in MDR *M. tuberculosis* in northwestern Russia: an update from Russian-EU border region**

Igor Mokrousov, *St. Petersburg Pasteur Institute*

P143

**High rates of drug resistance and emerging *M. tuberculosis* clones in a specialised penitentiary facility in eastern Ukraine**

Vladyslav Nikolayevskyy, *Public Health England, Imperial College London*



## Poster session 1: Monday 1 July

TRANSMISSION OF TUBERCULOSIS

P145

**Genomic survey in Liberia reveals high burden of MDR-TB and multiple importation events**

Mariana Gabriela López, *Instituto de Biomedicina de Valencia*

P147

**Differences in tuberculosis transmission dynamics between two adjoining settings applying or not multidisciplinary intervention oriented by molecular epidemiology**

Miguel José Martínez-Lirola, *Complejo Hospitalario Universitario Torrecárdenas, Almería*

P149

**Elucidating the value of whole-genome sequencing for a rapidly spread outbreak analysis**

Sofia Samper, *Instituto Aragonés de Ciencias de la Salud*

P151

**Bridging WGS data with classical genotyping *Mycobacterium tuberculosis* profiles**

Guislaine Refrégier, *I2BC, CNRS-CEA, Université Paris-Saclay*

TRANSMISSION OF TUBERCULOSIS

P155

**Contribution of whole genome sequencing for the detection of tuberculosis transmission in healthcare settings: the experience of a french center**

Oana Dumitrescu, *University Hospital of Lyon*

P157

**Impact of *Mycobacterium tuberculosis* complex lineages as a determinant of disease phenotypes from an immigrant rich moderate tuberculosis burden country**

Sahal Al-Hojj Al-Nakhli, *King Faisal Specialist Hospital and Research Center, Saudi Arabia*

BIOLOGY OF THE HOST

P002

***Mycobacterium tuberculosis* associated with severe tuberculosis evades cytosolic surveillance systems to modulate IL-1 $\beta$  production**

Jeremy Sousa, *i3S, University of Porto*

P004

**The extraordinary impact of *Mycobacterium tuberculosis* in the Paleolithic predicts unprecedented population growth due to female protection against tuberculosis**

Pere-Joan Cardona, *Universitat Autònoma de Barcelona, CIBERES, Badalona*

P006

**Ex vivo characterization of CD56neg CD16pos NK cell subpopulation in active tuberculosis and latently infected subjects**

Nurhan Albayrak, *Université Libre de Bruxelles (ULB)*

P008

**Insights into lung microbiome dysbiosis in patients with active pulmonary tuberculosis**

Monica Ticlla, *Swiss Tropical and Public Health Institute, Basel*

P010

**The lipid environment modulates the stress response of *Mycobacterium tuberculosis***

Maria Jesus Garcia, *Autonoma University of Madrid*

BIOLOGY OF THE PATHOGEN

## Poster session 2: Tuesday 2 July

BIOLOGY OF THE PATHOGEN

P012

**Will the real pan-genome please stand up? Investigating the protein-coding regions of the *Mycobacterium tuberculosis* complex**

Christopher Beaudoin, *University of Cambridge*

P014

**Cryo-EM beauty and benefit for drug discovery and vaccine design: our achievements with T7SS in *Mycobacterium tuberculosis***

Peter J. Peters, *Maastricht University Medical Center*

P016

**Pinpointing genetic intra-host diversity of *Mycobacterium tuberculosis***

Charlotte Genestet, *CIRI, INSERM U1111, Université de Lyon*

P018

**Identification of putative compensatory mutations in *rpoA/C* suggests contribution to the fixation of RIF resistance in *M. tuberculosis***

Faramarz Valafar, *San Diego State University*

P020

**System multi-omics analysis of *Mycobacterium tuberculosis* Beijing B0/W148 cluster**

Egor Shitikov, *Federal Medical Biological Agency, Moscow*

P022

**An updated functional annotation of *Mycobacterium tuberculosis* reference strain H37Rv**

Faramarz Valafar  
San Diego State University

P024

**Resuscitation of BCG in blood samples of BCG vaccinated individuals**

Stefan Panaiotov, *National Center of Infectious and Parasitic Diseases, Sofia*

P026

**Predicting *Mycobacterium tuberculosis* population structure by MIRU-VNTR**

Yang Zhou, *Chinese Center for Disease Control and Prevention*

P028

***Mycobacterium tuberculosis* defective in the heavy metal transporter CtpA as a potential attenuation target**

Gina Marcela Lopez Ruiz, *Universidad Nacional de Colombia*

P030

**Typing of *Mycobacterium tuberculosis* by whole genome sequencing reveals a novel X3 lineage associated with multidrug resistance circulating in southeast Mexico**

Roberto Zenteno-Cuevas, *Universidad Veracruzana, Veracruz*

P032

**Virulence and immunopathology induced by *Mycobacterium tuberculosis* genotype Beijing and Beijing-like isolated in Colombia**

Martha Isabel Murcia Aranguren,  
*Universidad Nacional de Colombia*

P034

**Emergence of genetic variants in longitudinal *M. tuberculosis* isolates associated with increased minimum inhibitory concentrations of ethambutol**

Ha Vu Thi Ngoc, *Oxford University Clinical Research Unit & Ho Chi Minh City, Vietnam*

P036

**Insights on *Mycobacterium leprae* efflux pumps and their implications in drug resistance and virulence**

Diana Machado, *Universidade Nova de Lisboa*

P038

**Monitoring a multidrug-resistant *Mycobacterium tuberculosis* endemic genotype in Bulgaria**

Stefan Panaiotov, *National Center of Infectious and Parasitic Diseases, Sofia*

P040

**PE\_PGRS3 of *Mycobacterium tuberculosis* is specifically expressed at low phosphate concentration, and its arginine-rich C-terminal domain mediates adhesion and persistence in host tissues**

Michela Sali *Fondazione Policlinico Universitario A. Gemelli, IRCCS, Roma*

P042

**Near-untreatable TB: lessons learned and future directions**

Marisa Klopper, *Stellenbosch University, Cape Town*

P044

**Strong association of mutations known to confer resistance to three injectable drugs in a multinational analysis**

Faramarz Valafar, *San Diego State University*

P046

**LL37 derived peptides containing unnatural D amino acids and peptoid present inhibition Na<sup>+</sup>/K<sup>+</sup>, Cu<sup>+</sup> and Zn<sup>2+</sup> ATPases in mycobacterial plasma membrane and synergy in combination with isoniazid and kanamycin**

Sandra Chingaté López, *Universidad Nacional de Colombia*

P048

**Rifampin-nitazoxanide, but not rifampin-isoniazid-pyrazinamide-ethambutol kills dormant *Mycobacterium tuberculosis* in caseum mimicking conditions**

Lanfranco Fattorini, *Istituto Superiore di Sanità, Rome*

P050

**Evaluation of the FluoroType® MTBDR Version 2.0 assay for improved detection and differentiation of rifampicin and isoniazid resistance in *Mycobacterium tuberculosis* complex**

Anzaan Dippenaar, *Stellenbosch University, Cape Town*

P052

**Discovery of a new class of anti-tubercular antibiotic originating from the gut microbiota**

Dereje Abate Negatu, *National University of Singapore*

P054

***Mycobacterium smegmatis* as a model organism for *Mycobacterium tuberculosis*: are fast and slow that similar?**

F T Subtil, *The Francis Crick Institute*

P056

**Critical pulmonary tuberculosis: Identifying candidate molecular markers for diagnostic, prognostic and virulence.**

Gonzalo Greif, *Instituto Pasteur Montevideo, Montevideo*

P058

**First evaluation in routine use of the combination of GeneLeadVIII to extract and detect *Mycobacterium tuberculosis* (Mtb) DNA and Deeplex-MycTB to predict drug resistance and TB transmission in less than one week from clinical samples**

Wladimir Sougakoff, *National Reference Centre of Mycobacteria NRC MyRMA, Paris*

P060

**Exploring Bedaquiline resistance-associated genetic regions in clinical samples from a cohort study of Rifampicin resistant TB patients in South Africa**

Annelies Van Rie, *University of Antwerp*

P062

**Phenotypical and molecular characterization of streptomycin-resistant *M. tuberculosis* clinical isolates from a Portuguese cohort**

Deisy Rocha Silva, *University of Minho, Braga*

## Poster session 2: Tuesday 2 July

NEW DX AND TREATMENT CONCEPTS

P064

**Discordance across molecular and phenotypic methods for drug susceptibility testing of *Mycobacterium tuberculosis***

Nelly Ciobanu, *Phthisiopneumology Institute, Chisinau, Moldova*

P066

**Evaluation of new molecular test Allplex MTB/MDRe/XDRe Detection for rapid identification of drug resistance in *Mycobacterium tuberculosis***

Eva Sodja, *University Clinic Golnik, Slovenia*

P068

**Search for novel antituberculosis drug targets: Biotin biosynthesis pathway**

Mandira Varma-Basil, *University of Delhi*

P070

**MYCO-TB decontamination kit: evaluation of suitability for molecular biology and mycobacteria detection with extended time of incubation**

Giulia Lombardi, *S. Orsola-Malpighi University Hospital - University of Bologna*

P072

**Acquisition of cross-resistance to Bedaquiline and Clofazimine following treatment for tuberculosis**

Arash Ghodousi, *San Raffaele Scientific Institute, Milan*

P074

**TB1 and TB2 positivity rates with QuantiFERON-TB Gold Plus Assay**

Zeynep Saribas, *Hacettepe University, Ankara*

NEW DX AND TREATMENT CONCEPTS

P076

**How do Nipro line probe assays perform on the Hain Twincubator?**

Sarah Sengstake, *Institute of Tropical Medicine, Antwerp*

P078

**Application of nanopore sequencing for drug resistant prediction of *Mycobacterium tuberculosis* complex strains**

Francy Johanna Pérez Llanos, *Research Center Borstel*

P080

**Introducing a new target for specific detection of *Mycobacterium tuberculosis* complex using modified genome comparison method**

Reza Kamali Kakhki, *Mashhad University of Medical Sciences, Mashhad*

P082

**Bridging the TB data gap: Extracting rifampicin-resistance diagnostic test probe reactions from *Mycobacterium tuberculosis* whole genome sequence data**

Kamela Ng, *Institute of Tropical Medicine, Antwerp*

P084

**Molecular characterization of mutations associated with resistant tuberculosis in Northeast Brazil**

Luana Lima, *Evandro Chaga Institute, Anarindera, Para*

NEW DX AND TREATMENT CONCEPTS

P086

**Preliminary *in vitro* activity of linezolid and tedizolid against *Mycobacterium avium* complex**

Pilar Ruiz - Martinez, *Reina Sofia University Hospital-IMIBIC, Cordoba*

P088

**Comparison of two mapping algorithms for lineage and resistance prediction of MTBC samples**

Margo Diricks, *Applied Maths (bioMérieux)*

P090

**Sensitivity evaluation of LIAISON® QuantiFERON TB GOLD Plus assay, a new automated chemiluminescent immunoassay (CLIA) for diagnosis of tuberculosis infection**

Paola Mantegani, *San Raffaele Scientific Institute, Milan*

P092

**Preliminary comparison between BD MAX and Xpert MTB/RIF Ultra for rapid detection of *Mycobacterium tuberculosis* complex (MTB) in pulmonary and extrapulmonary specimens**

Anna Camaggi, *University Hospital, Novara*

P094

**Anti-tuberculosis treatment initiation within seven days of respiratory sample collection: the utility of the nucleic acid amplification test (NAAT) compared to acid-fast smear microscopy**

Marie Nancy Seraphin, *University of Florida*

## Poster session 2: Tuesday 2 July

NON TUBERCULOSIS MYCOBACTERIA

P096

**Evaluation of FluoroType MTBDR used for different specimen types**

Erik Svensson, *Statens Serum Institut, Copenhagen*

P098

**A pilot study of new external quality assessment applied to a tuberculosis microscopy laboratory network in Mexico**

Carolina Flores-Marroquin, *Institute of Diagnosis Reference Epidemiology, Mexico*

P100

**Genomic analysis of cardiac surgery-associated *Mycobacterium chimaera* infections in Northern Italy**

Arash Ghodousi, *San Raffaele Scientific Institute, Milan*

P102

**Each mycobacterium requires particular culture conditions to maximize its immunomodulatory and antitumoral effects**

Sandra Guallar Garrido, *Universitat Autònoma de Barcelona*

P104

**Whole genome sequencing (WGS) for the subspeciation of clinical isolates of *Mycobacterium abscessus* complex (MABC) in a clinical laboratory**

Jenny Wee, *Singapore General Hospital Pte Ltd*

P106

**Challenging features in mycobacteria identification by MALDI-TOF MS**

David Rodriguez Temporal, *Hospital Universitari de Bellvitge-IDIBELL, Hospitalet de Llobregat*

NON TUBERCULOSIS MYCOBACTERIA

## Poster session 2: Tuesday 2 July

NON TUBERCULOSIS MYCOBACTERIA

P108

**Invasive *Mycobacterium chimaera* infection after cardiac surgery: a case report**  
Agnese Denicolo, *The Romagna Hub Laboratory, Pievestina*

P110

**Underestimation of the pathogenic role of *Mycobacterium fortuitum* and its related species in fishes and humans**  
Davide Mugetti, *Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta – Torino*

P112

**Screening for NTM lung disease in adult non-CF adult bronchiectasis patients - physician survey in Germany, UK, Italy, France and the Netherlands**  
Roald van der Laan, *Universitätsklinikum Freiburg*

P114

**Tentative epidemiological cutoff values for *Mycobacterium kansasii*, *Mycobacterium xenopi* and *Mycobacterium marinum***  
Florian Maurer, *Research Center Borstel*

P116

**Evaluation of the Colour Test in inexperienced settings**  
Kadri Klaos, *Tartu University Hospital*

P118

**Evaluation of 8 VNTR loci and spoligotyping for molecular characterisation of *Mycobacterium bovis* and *Mycobacterium caprae* isolates from cattle in Bulgaria**  
Violeta Valcheva, *Bulgarian Academy of Sciences, Sofia*

P120

**The epidemiological situation of bovine tuberculosis in Korea**  
Yun-Ho Jang, *Animal and Plant quarantine agency, Korea*

ONE HEALTH

P122

**Outbreak of bovine tuberculosis by *Mycobacterium bovis* in cattle and buffalo in Northern Brazil**  
Karla Lima, *Universidade do Estado do Pará, Belém-PA*

P124

**Insights into the global phylogeography of *Mycobacterium bovis***  
Chloé Loiseau, *Swiss Tropical and Public Health Institute, Basel*

P126

**Etiology of mycobacterial infection in HIV-infected patients in Ukraine**  
Anna Barbova, *National Institute of Phthisiology and Pulmonology, Ukraine*

P128

**Direct DNA modified CTAB preparation from nasal exudate in live *M. bovis* infected cattle in Mexico provide with a valuable routine assay extrapolated to humans TB diagnostic test**  
Gloria Guerrero Manriquez, *Universidad Autonoma de Zacatecas*

P130

**Towards genotype resolution of mixed *Mycobacterium tuberculosis* infections in WGS analysis**  
Pedro Sola-Campoy, *Hospital General Universitario Gregorio Marañón, Madrid*

P132

**Unexpected findings of tuberculosis by the GeneXpert MTB/RIF method – case reports**  
Maria Mullerova, *CITYLAB, Prague*

P134

**Testing whole genome sequencing as gold standard to improve transmission tracing: a retrospective study in a low-burden region**  
Irving Cancino, *Biomedicine Institute of Valencia*

TRANSMISSION OF TUBERCULOSIS

P136

**Integrative transnational analysis to dissect non-obvious transmission events involving migrants**  
Laura Perez-Lago, *Hospital General Universitario Gregorio Marañón, Madrid*

P138

**The Emergence of *Mycobacterium tuberculosis* L4.5 in Lebanon shows a change of tuberculosis transmission dynamics**  
Khalidoun Masoud, *American University of Beirut*

P140

**Evolution of *Mycobacterium tuberculosis* complex strains during longitudinal transmission in a high drug resistant setting**  
Ivan Barilar, *Research Center Borstel*

P142

**Genotypic study using the MIRU-VNTR technique of clinical isolates of *Mycobacterium tuberculosis* in a cohort of patients with drug-resistant tuberculosis in Colombia 2012-2013**  
Lorena Alexandra & Argoty Chamorro, *Universidad Nacional de Colombia*

P146

**Different historical patterns underlie the *M. tuberculosis* Lineage 4 currently circulating in Vietnam and Indonesia**  
Philip Ashton, *Oxford University Clinical Research Unit & Ho Chi Minh City, Vietnam*

P148

**ECDC pilot study on the use of whole genome sequencing for MDR-TB surveillance in Europe: results of the first year of the project implementation**  
Elisa Tagliani, *San Raffaele Scientific Institute, Milan*

TRANSMISSION OF TUBERCULOSIS

## Poster session 2: Tuesday 2 July

P150

**Drug resistance landscape of *Mycobacterium tuberculosis* complex strains in Cameroon after successful introduction of the short course MDR-TB regimen**  
Matthias Merker, *Research Center Borstel*

P152

**Molecular epidemiology of *Mycobacterium tuberculosis* in urban Tanzania**  
Liliana K. Rutaiwa, *Swiss Tropical and Public Health Institute, Basel*

P154

**Whole genome sequencing provides additional insights into recurrent tuberculosis classified as endogenous reactivation by IS6110 DNA fingerprinting**  
Anzaan Dippenaar, *Stellenbosch University, Cape Town*

P156

***Mycobacterium tuberculosis* complex lineage 3 strains drive a pulmonary tuberculosis outbreak in Eastern Sudan**  
Yassir Shuaib, *Research Center Borstel*

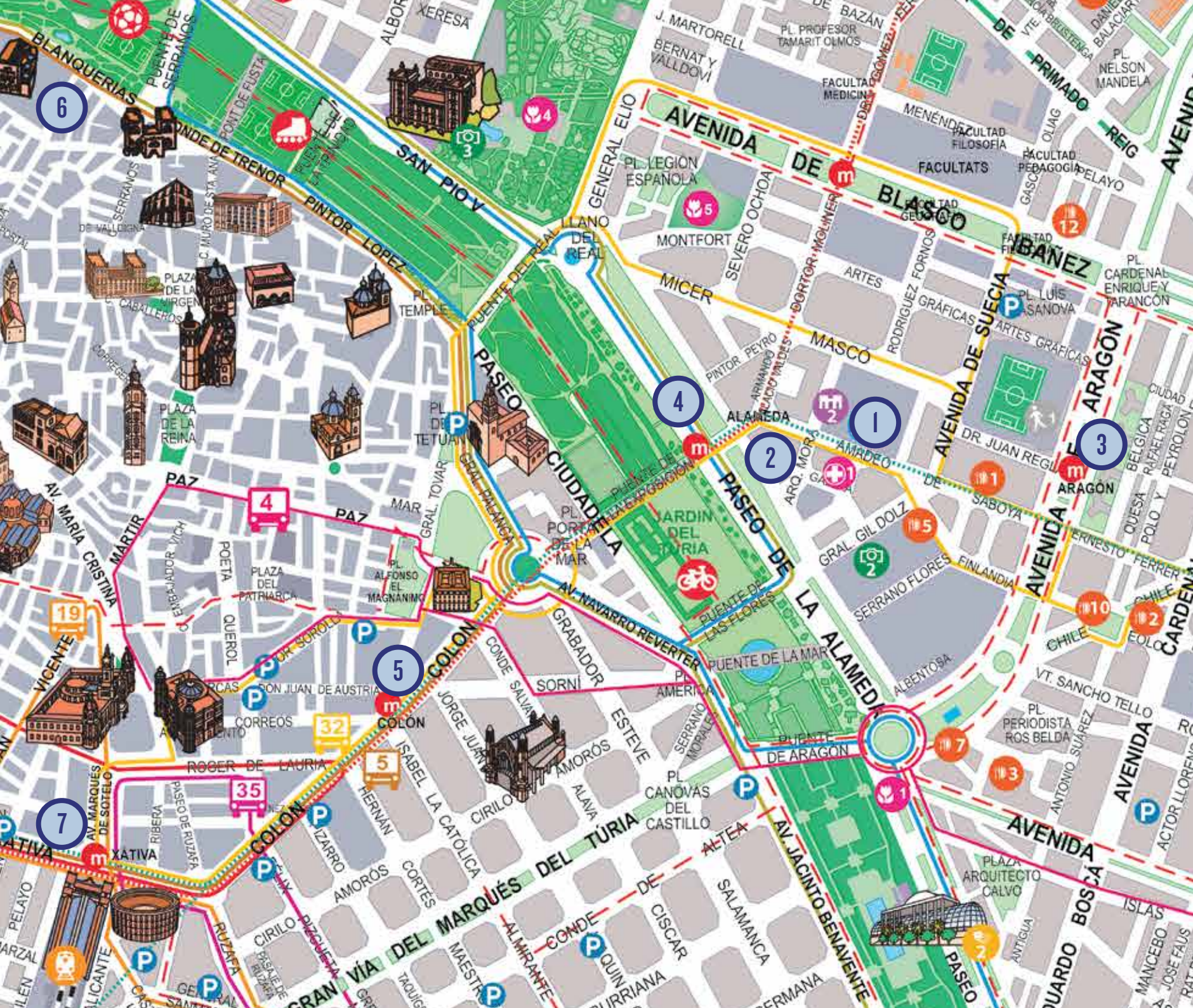
P158

**Genetic Lineages of *Mycobacterium tuberculosis* Display Distinctive Demographic and Migration Characteristics in Hawaii**  
James Douglas, *Affiliation University of Hawaii*

TRANSMISSION OF TUBERCULOSIS

ONE HEALTH





## Key locations



The Westin Valencia



Palau Alameda



Aragón Metro



Alameda Metro



Colón Metro



Convent Carmen



Xàtiva Metro



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