

Programme

Sunday 25 June

12.00-14.00 **Registration**

14:00-16:00

New regimens for TB and TPP to shape the future of TB treatment

Chairs: Daniela Maria Cirillo, San Raffaele Scientific Institute, Milan; Philip Supply, Univ. Lille, CNRS, Inserm, CHU Lille, Institut Pasteur de Lille, U1019 - UMR 9017 - CIIL - Center for Infection and Immunity of Lille

<u>GL01</u> Samuel Schumacher, WHO, Geneva Target Regimen Profiles (TRPs) for TB treatment - VIRTUAL

<u>GL02</u> **Francesca Conradie**, *WITS HEALTH, University of the Witwatersrand, South Africa* TB universal regimens; pros and cons for adults and pediatric population

<u>GL03</u> Christian Leinhardt, WHO, French Institute for Research on Sustainable Development (IRD), Montpellier

New regimens, new TB drugs: what to expect? TPP for TB regimens

<u>GL04</u> **Saskia Den Boon,** *WHO* Target Product Profiles for Tests for TB Treatment Monitoring and Optimization

16:00-16:30 Coffee break

16:30-17:00

Student mini-symposium on new drugs and DR TB (5 min flash talks)

Chairs: **Stefan Niemann**, Forschungszentrum Borstel; **Silva Tafaj**, University Hospital "Shefqet Ndroqi", Tirana

<u>P38</u> **Marco Schiuma**, Department of Biomedical & Clinical Sciences "Luigi Sacco", Università degli Studi di Milano, Italy.

Rifampicin and isoniazid dosage adjustment according to TDM and acetylator status: a single centre prospective observational study

<u>P63</u> Jihad Snobre, Mycobacteriology Unit, Biomedical Sciences, Institute of Tropical Medicine (ITM), Antwerp

Exploring the impact of mutations in Rv0678 gene on bedaquiline resistance in Mycobacterium tuberculosis: insights from computational biostructural proteomics

<u>P61</u> **Ilariaa lannucci,** *Universita Vita-Salute San Raffaele, Milan* In vitro susceptibility testing of GSK656 against Mycobacterium tuberculosis complex isolates to establish the epidemiological cut-off values and MIC distribution

<u>P08</u> Emilie Rousseau, Molecular and Experimental Mycobacteriology, Research Center Borstel, Mutation rates in strains of different Mycobacterium tuberculosis lineages associated with emergence of multi-drug resistant tuberculosis



<u>P30</u> **Darshaalini Nadarajan**, *National and Supranational Reference Laboratory for Mycobacteria, Research Center Borstel, Leibniz Lung Center, Borstel, Germany* Prospective evaluation of targeted next-generation sequencing of Mycobacterium tuberculosis complex strains in routine diagnostics in Germany.

<u>P35</u> Virginia Batignani, San Raffaele Scientific Institute Xpert MTB/XDR assay for the rapid diagnosis of TB resistance. A country wide cross sectional observational prospective study from Pakistan

17:00-18.45 Opening session

Chairs: Daniela Maria Cirillo, San Raffaele Scientific Institute, Milan; Silva Tafaj, University Hospital "Shefqet Ndrogi", Tirana

<u>GL05 Opening Keynote</u> **Silvia Bino**, *Head of Infectious Diseases, Institute of Public Health* High priority and emerging pathogens in Albania

GL06 Gertrud Meissner Award presented by S. Niemann

GL07 Gardner Middlebrook Award presented by BD

Monday 26 June

08:00-09:00 Registration 09:00-10:30 Host pathogens interaction in *M* tuberculosis Chairs: Leen Rigouts, Institute of Tropical Medicine, Antwerp, Matthias Merker, Research Center Borstel GL08 Margarida Saraiva, Department of Microbiology and Immunology, McGill University Study of host pathogen interactions in TB by using an in clinico to in vitro to in vivo approach GL09 Stephanie Boisson-Dupuis, Rockefeller University, NYC Novel genetic etiologies in susceptibility to tuberculosis OR01 Sarah Danchuk, McGill University, Montreal Understudied and overlooked: Characterizing Mycobacterium orygis OR02 Paolo Miotto, San Raffael Scientific Institute Mycobacterial extracellular vesicles (MEVs) as a novel option in bladder cancer therapy OR03 Issy Schiavi, St. George's University of London Mycobacterial interactions promote Vy9V δ 2 T cells to target and kill cancer cells OR04 Jana Schoenfeld, Research Center Borstel, Germany Uncovering epigenetic changes in early-stage MTBC-infected macrophages 10:30-11:00 Coffee break



11:00-12:45

Resistance to new antitubercular drugs and clinical implications

Chairs: **Francesca Conradie**, University of Witwatersrand, Johannesburg; **Philip Supply**, Univ. Lille, CNRS, Inserm, CHU Lille, Institut Pasteur de Lille, U1019 - UMR 9017 - CIIL - Center for Infection and Immunity of Lille

<u>GL10</u> **Claudio Köser**, *Cambridge University* The X(DR)-Files – I want to believe

<u>OR05</u> **Kurt Wollenberg**, *National Institute of Allergy and Infectious Diseases* Molecular evolutionary analysis of a clade of closely-related Delamanid-resistant Mycobacterium tuberculosis (M.tb) strains from Eastern Europe and Central Asia.

<u>OR06</u> **Annelies Van Rie**, *University of Antwerp* Bayesian probability of bedaquiline resistance to guide rifampicin-resistant tuberculosis treatment

<u>OR07</u> **Valeriu Crudu,** *State University of Medicine and Pharmacy, Chisinau, Moldova* Evolution of resistance to new drugs in high tuberculosis burden country.

<u>OR08</u> **Sonia Borrell**, *Swiss Tropical and Public Health Institute-University of Basel* Drug-specific differential culturability in diverse strains of Mycobacterium tuberculosis

OR09 Siavash Valafar, Chicago Medical School

Prognosis and Prevention of Antibiotic Resistance in Mycobacterium tuberculosis: the Isoniazid (INH) Case Study

12:45-13:30 **Lunch**

13:30-14:30 Poster Session 1

14:30-15:45

Future of next generation sequencing

Chairs: Kristin Kremer, KNCV Tuberculosis Foundation, Den Haag; Andrea Cabibbe, San Raffaele Scientific Institute, Milan

<u>GL11</u> **Philip Fowler**, *University of Oxford* Whole genome sequencing for tuberculosis: it works, how do we get it used more widely?

<u>OR10</u> **Vincent Rennie,** Family Medicine and Population Health (FAMPOP), Faculty of Medicine and Health Sciences, University of Antwerp

The MAGMA platform for global and equitable WGS-guided management of drug resistant TB and TB control

<u>OR11</u> **Maximilian Marin,** *Department of Biomedical Informatics, Harvard Medical School* Analysis of the limited Mtb pan-genome reveals potential pitfalls of pan-genome analysis approaches

OR12 Christophe Sola, INSERM UMR1137

TB-ANNOTATOR: A scalable web application that allows in-depth analysis of very large sets of publicly available Mycobacterium tuberculosis complex genomes.

15:45-16:15 Coffee break

16:15-17:30

Animal models to study mycobacterial infections

Chairs: **Margarida Saraiva**, *Department of Microbiology and Immunology, McGill University*; **Leen Rigouts**, *Institute of Tropical Medicine, Antwerp*

<u>GL12</u> **Pere-Joan Cardona Iglesias,** *Hospital Universitari Germans Trias i Pujol, Badalona* Mouse models to study TB pathogenesis

<u>GL13</u> **Nicola Lore**, *IRCCS San Raffaele Scientific Institute* Mouse models to study host-pathogens interaction in *M.abscessuss* lung infections

<u>OR13</u> **Maria Vidal Ramos**, Unitat de Tuberculosi Experimental, Microbiology Dept. Germans Trias i Pujol Research Institute and Hospital (IGTP-HUGTIP), Badalona Mycobacterium tuberculosis infecting Drosophila melanogaster: first insights of the new latent tuberculosis infection model.

17:30-19:00

Round Table: Bordering EU countries: Situation, challenges and way out (Availability and affordability of NGS technologies to control DR TB, Viral Diseases and AMR)

Chairs: Silvia Bino, Institute of Public Health, Tirana; Hasan Hafizi, University Hospital for Lung diseases, Tirana

Round table discussion



Tuesday 27 June

08:30-09:00 **Registration**

09:00-10:45 Host pathogens interaction in NTMs

Chairs: **Troels Lillebaek**, Statens Serum Institut, Copenhagen; **Eva Sodja**, University Clinic of Pulmonary and Allergic Diseases Golnik

<u>GL14</u> **Lucas Boeck**, *University Hospital Basel* Phenogenomic analyses: linking mycobacterial behaviours to molecular mechanisms

GL15 Stephen Leon Icaza, IPBS-Toulouse

The organoid revolution to assess mycobacterial pulmonary infections

<u>OR14</u> **Federico Di Marco,** San Raffaele Scientific Institute, Emerging Bacterial Pathogens Unit Single cells RNA sequencing of peripheral blood mononuclear cells reveals hyperinflammatory monocytes in patients with Mycobaterium abscessus pulmonary disease

<u>OR15</u> **Ivana Palucci,** *Catholic University of Sacred Heart, Rome* Cysteamine/Cystamine exert anti-Mycobacterium abscessus activity alone or in combination with amikacin.

<u>OR16</u> **Francesca Nicola**, *San Raffaele Scientific Institute* The spatial distribution of type 1 and type 17 immune transcriptomics profiles in murine models of chronic lung infection by opportunistic pathogens

10:45-11:15 Coffee break

11:15-13:00 Innovation in diagnostics

Chairs: Christophe Sola, Université Paris-Saclay; Paolo Miotto, San Raffaele Scientific Institute, Milan

<u>GL16</u> **Morten Ruhwald,** *FIND, Geneva* Future trends and innovation in diagnostics for TB

<u>OR17</u> **Onya Opota**, *Institute of Microbiology, Lausanne University Hospital and University of Lausanne* Nanomotion technology in combination with machine learning: a new approach for rapid antibiotic susceptibility test for Mycobacterium tuberculosis

<u>OR18</u> Leen Rigouts, Institute of Tropical Medicine, Antwerp, Belgium Successful Myocbacterium tuberculosis culture isolation from spiked tongue swabs processed by the Kudoh-Ogawa or cetylpyridinium chloride methods.

<u>OR19</u> **Faridath Massou**, *Laboratoire de Reference des Mycobacteries* Deeplex Myc/TB directly on sputum detects more mixed infections and heteroresistance compared to culture-based whole genome sequencing.

OR20 Margaretha de Vos, FIND, Geneva

Diagnostic accuracy of upper airway swabs and saliva with Xpert MTB/RIF Ultra for the detection of tuberculosis in adults

OR21 Kristin Kremer, KNCV Tuberculosis Foundation

The simple one-step stool processing method to diagnose tuberculosis is robust enough for global scale up



13.00-14.00 **Lunch**

14.00-15.00 Poster Session 2

15:00-16:15

Innovation in diagnostics (cont.)

Chairs: Leen Rigouts, Institute of Tropical Medicine, Antwerp, Belgium; Richard Anthony, National Institute for Public Health and the Environment (RIVM), Bilthoven

<u>OR22</u> Emilyn Costa, South African Medical Research Council Centre for Tuberculosis Research, Division of Molecular Biology and Human Genetics, Faculty of Medicine and Health Sciences, Stellenbosch University, Cape Town

Evaluating DNA extraction commercial kits from Mycobacterium tuberculosis clinical primary liquid (MGIT) culture for downstream sequencing applications

<u>OR23</u> **Miguel Moreno**, *Biomedicine Institute of Valencia IBV-CSIC* The role of MIC shifts as early markers of treatment failure in tuberculosis

OR24 Tim Bull, St. George's University of London

Ph neutral anti-microbial peptide-based decontamination of samples enhances recovery in culture of low load Mycobacterium tuberculosis

<u>OR25</u> **Erik Svensson,** International Reference Laboratory of Mycobacteriology, Statens Serum Institut, Copenhagen

Detection of Mycobacterium tuberculosis and resistance mutations in different sample types using FluoroType MTBDR v2. A study from Germany and Denmark.

OR26 Dmytro Butov, Kharkiv National Medical University

Consideration of the results of the Xpert MTB/RIF method on the treatment outcome of patients with M\XDR pulmonary tuberculosis during the COVID-19 epidemic in Kharkiv region, Ukraine

16:15-16:45 **Coffee break**

16:45-17:30 General Assembly



Wednesday 28 June

 09.30-11.00 Session Non tuberculous mycobacteria, epidemiology and more Chairs: Troels Lillebaek, Statens Serum Institut, Copenhagen; Dorte Bek Folkvardsen, Statens Serum Institut, Copenhagen GL17 Victor Næstholt Dahl, Aarhus University Hospital Global trends of pulmonary infections with nontuberculous mycobacteria OR27 Margo Diricks, Research Center Borstel Exploring the plasmidome of non-tuberculous mycobacteria OR28 Nils Wetzstein, Department of Internal Medicine, Infectious Diseases, University Hospital Frankfurt, Goethe University, Frankfurt am Main Genomic landscape of M. avium complex in Central Germany OR29 Xenia Iversen, International Reference Laboratory of Mycobacteria OR30 Sandra Salillas-Berges, Radboud University Medical Center Rifampicin substituted by clofazimine in the recommended therapy of Mycobacterium avium pulmonary disease: a hollow-fibre model study 11:00-11.30 Coffee break 11:30-12.30 Session Biology of Pathogen Chair: Erik Svensson, Statens Serum Institut, Copenhagen; Mireia Coscolla, University of Valencia OR35 Rina De Zwaan, National Institute for Public Health and the Environment Next-generation sequencing cluster typing; All single nucleotide polymorphisms are equal but some are more equal than others
Institut, Copenhagen GL17 Victor Næstholt Dahl, Aarhus University Hospital Global trends of pulmonary infections with nontuberculous mycobacteria OR27 Margo Diricks, Research Center Borstel Exploring the plasmidome of non-tuberculous mycobacteria OR28 Nils Wetzstein, Department of Internal Medicine, Infectious Diseases, University Hospital Frankfurt, Goethe University, Frankfurt am Main Genomic landscape of M. avium complex in Central Germany OR29 Xenia Iversen, International Reference Laboratory of Mycobacteriology, Statens Serum Institut, Copenhagen, Denmark Frozen in Time: Unlocking the History of Nontuberculous Mycobacteria OR30 Sandra Salillas-Berges, Radboud University Medical Center Rifampicin substituted by clofazimine in the recommended therapy of Mycobacterium avium pulmonary disease: a hollow-fibre model study 11.00-11.30 Coffee break 11:30-12.30 Session Biology of Pathogen Chair: Erik Svensson, Statens Serum Institut, Copenhagen; Mireia Coscolla, University of Valencia OR36 Rina De Zwaan, National Institute for Public Health and the Environment Next-generation sequencing cluster typing; All single nucleotide polymorphisms are equal but some are
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Next-generation sequencing cluster typing; All single nucleotide polymorphisms are equal but some are
OR31 Kerri Malone, EMBL-EBI Fine-scale evolution of Mycobacterium tuberculosis growth rate
OR32 Philip Supply, Univ. Lille, CNRS, Inserm, CHU Lille, Institut Pasteur de Lille, U1019 - UMR 9017 - CIIL - Center for Infection and Immunity of Lille CRISPR-Cas molecular memory in Mycobacterium canettii reveals the putative ancestral environmental origin of M. tuberculosis
OR34 Sladjana Prisic, University of Hawaii at Manoa From bad to worse: Does zinc limitation make M. tuberculosis more virulent?



12:30-13.30 Session Biology of Pathogen

Chair: Miguel Moreno, CSIC, Valencia; Violeta Valcheva, Bulgarian Academy of Sciences

OR35 Melanie Grobbelaar, Stellenbosch University

Evolution of drug resistance and treatment outcome within a longitudinal retrospective study – linking outcome to treatment.

OR33 Igor Mokrousov, St. Petersburg Pasteur Institute

Paleopathological and molecular evidence of tuberculosis in human skeletal remains from 18th-19th century Orthodox cemeteries in Irkutsk, Eastern Siberia

<u>OR37</u> **Joaquin Sanz**, *Universidad de Zaragoza - Instituto BIFI* Improving vaccine descriptions in model-based impact prognosis of new tuberculosis vaccines: removing arbitrariness and reducing bias.

OR38 Siavash Valafar, Chicago Medical School

Diversifying Evolution in Mycobacterium tuberculosis and Evasion of Molecular Diagnostics for Isoniazid (INH) Resistance is most prevalent in Asia

13:30-14.00

Poster Awards and Closing Ceremony

Chair: Daniela Maria Cirillo, San Raffaele Scientific Institute, Milan; Troels Lillebaek, Statens Serum Institut, Copenhagen; Silva Tafaj, University Hospital "Shefqet Ndroqi", Tirana



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