ESM Annual Meeting, Tirana Albania, 25-28 June 2023 Poster List

Number	Title	Category	Presenter
P01	Characterization of novel double-reporter strains of Mycobacterium abscessus for drug discovery: a study in mScarlet	Animal and in vitro model to study mycobacterial infections	C M Bento, *Instituto de Investigação e Inovação em Saúde, Universidade do Porto, Portugal / IBMC – Instituto de Biologia Molecular e Celular, Universidade do Porto, Portugal / Programa Doutoral em Biologia Molecular e Celular (MCBiology), Instituto de Ciências Biomédicas Abel Salazar da Universidade do Porto, Portugal / ICBAS – Instituto de Ciências Biomédicas Abel Salazar da Universidade do Porto, Portugal*
P02	A quantitative method for the study of HIV-1 and Mycobacterium tuberculosis co-infection	Animal and in vitro model to study mycobacterial infections	S Donnellan, *Edinburgh Napier University*
P03	Drosophila melanogaster as a model for the characterization of host-pathogen interactions of rapid growing Mycolicibacterium manresensis.	Animal and in vitro model to study mycobacterial infections	M Arch, *Institut d'Investigació en Ciències de la Salut Germans Trias i Pujol*

P04	Phylogenetically related Mycobacterium tuberculosis isolates with wild type rpoB and rifampicin resistance levels around the critical concentration	Biology of the pathogen	P Lempens, *Institute of Tropical Medicine Antwerp / University of Antwerp*
P05	The Mycobacterium tuberculosis complex pangenome is small and driven by (sub-)lineage specific regions of difference	Biology of the pathogen	M Behruznia, *Department of Biosciences, Nottingham Trent University, Notttingham, UK*
P06	Effect of Iron and carbon sources on in-vitro transcriptional responses to growth arrest of Mycobacterium tuberculosis	Biology of the pathogen	J A Cárdenas-Pestana, *University of Zaragoza*
P07	Multi-omics portrait of VirR protein function in cell wall remodeling and vesiculogenesis in Mycobacterium tuberculosis	Biology of the pathogen	J Bertol, *University of Zaragoza*
P08	Mutation rates in strains of different Mycobacterium tuberculosis lineages associated with emergence of multi-drug resistant tuberculosis	Biology of the pathogen	E Rousseau, *Molecular and Experimental Mycobacteriology, Research Center Borstel, Borstel, 23845, Germany*
P09	Rifampicin tolerance and growth fitness among isoniazid-resistant clinical Mycobacterium tuberculosis isolates: an in-vitro longitudinal study.	Biology of the pathogen	S Vijay, *Oxford University Clinical Research Unit, Ho Chi Minh City, Vietnam / Centre for Tropical Medicine and Global Health, Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom / Theoretical Microbial Ecology, Friedrich Schiller University, Jena, Germany*
P10	Non-redundant Pangenome construction of Mycobacterium tuberculosis	Biology of the pathogen	Y Zhou, *Chinese CDC - Center for Disease Control and Prevention / Radboud University MC*

P11	Comparison of 13 software tools to detect structural variation in Mycobacterium tuberculosis	Biology of the pathogen	Y Zhou, *Chinese CDC - Center for Disease Control and Prevention / Radboud University MC*
P13	Assessment of circulating mitochondrial cell-free DNA dynamics in patients with tuberculosis: pilot study	Biomarkers and biology of the host	L Freimane, *Latvian Biomedical Research and Study Centre, Riga, LV – 1067, Latvia*
P14	Evaluating immunological parameters in human fluids for diagnostic purposes in Tuberculosis.	Biomarkers and biology of the host	G Gloria Guerrero M, *University Autonome of Zacatecas*
P15	GENOTUBE, a high-throughput tool for exploring the genetic diversity of pathogenic mycobacteria	Future of next gen sequencing	G Refregier, *Université Paris-Saclay, CNRS, AgroParisTech, Ecologie Systématique et Evolution, 91190, Gif-sur-Yvette, France*
P16	Demonstration of nanopore sequencing for the detection of tuberculosis and other infectious diseases in low-and-middle-income countries	Future of next gen sequencing	K Kremer, *KNCV Tuberculosis Foundation*
P17	Early positive culture: what is in a name?	Future of next gen sequencing	E C Conceicao, *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, South Africa*
P18	Evaluation of whole-genome sequencing of Mycobacterium tuberculosis isolates in clinical laboratory	Future of next gen sequencing	E Sodia, *University Clinic Golnik*

P19	Implementation and evaluation of the ABL-DeepChek 13-Plex Assay for diagnosis of antibiotic resistant tuberculosis	Future of next gen sequencing	V Mohr, *Molecular and Experimental Mycobacteriology, Research Center Borstel, Germany / National Tuberculosis Reference Laboratory, Research Center Borstel, Germany*
P21	Exploring the potential of Oxford Nanopore Technologies for Mycobacterium tuberculosis sequencing: an assessment of R10 flowcells and V14 chemistry	Future of next gen sequencing	A Dippenaar, *University of Antwerp*
P22	Beyond the clone: A new ancestor for Mycobacterium tuberculosis and implications for host-specific genomic events	Future of next gen sequencing	P Ruiz-Rodriguez, *I2SysBio, University of Valencia – FISABIO Joint Unit, 46980 Paterna, Spain*
P23	Determining the situation of drug-resistance Tuberculosis in the South of Mozambique by using whole genome sequencing for the first time	Future of next gen sequencing	C Mariner-Llicer, *Instituto de Biomedicina de Valencia (CSIC)*
P24	MAGMA – A novel bioinformatics pipeline developed for integration of WGS in clinical care and tuberculosis control	Future of next gen sequencing	V Rennie, *Family Medicine and Population Health (FAMPOP), Faculty of Medicine and Health Sciences, University of Antwerp, Wilrijk, Belgium*
P25	Rapid detection of IS1081 of Mycobacterium bovis using CRISPR/Cas12a system combined with recombinase polymerase amplification	Innovation in diagnostics	S H Son, *Animal and Plant Quarantine Agency*
P26	Spatial clustering of rifampicin-resistant tuberculosis and dominant clone in Rwanda: implications for targeted case finding	Innovation in diagnostics	I Cuella Martin, *Mycobacteriology Unit, Department of Biomedical Sciences, Institute of Tropical Medicine, Antwerp, Belgium*

P27	Evaluating the performance of the novel Xpert MTB/XDR assay in detecting fluoroquinolone hetero-resistance	Innovation in diagnostics	A Dippenaar, *Institute of Tropical Medicine, Antwerp / University of Antwerp*
P28	The microbiological confirmation of leprosy patients with tongue swabs exhibits a lower sensitivity compared to nasal swabs	Innovation in diagnostics	L Krausser, *University of Antwerp, Belgium / Institute of Tropical Medicine, Antwerp, Belgium / Research Foundation Flanders (FWO), Brussels, Belgium*
P29	Validation and implementation of thin-layer agar for direct Mycobacterium tuberculosis testing for bedaquiline resistance: a promising technique to increase access in low-resource settings.	Innovation in diagnostics	I Cuella Martin, *Unit of Mycobacteriology, Institute of Tropical Medicine, Antwerp, Belgium*
P30	Prospective evaluation of targeted next-generation sequencing of Mycobacterium tuberculosis complex strains in routine diagnostics in Germany.	Innovation in diagnostics	D Nadarajan, *National and Supranational Reference Laboratory for Mycobacteria, Research Center Borstel, Leibniz Lung Center, Borstel, Germany*
P31	Validation of Capilia TB-Neo for identifying M. tuberculosis complex in culture isolates	Innovation in diagnostics	S Chung, *Singapore General Hospital*
P32	Mechanical lysis is critical to ensure optimal yield of DNA from mycobacterial cells	Innovation in diagnostics	R de Zwaan, *National Institute for Public Health and the Environment*
P33	Evaluation of a new rapid kit for MALDI-TOF MS Mycobacteria identification	Innovation in diagnostics	A Camaggi, *AOU Maggiore della Carità, Laboratory of Microbiology and Virology, Novara, Italy*
P34	Evaluation of a new molecular assay for tuberculous and nontuberculous mycobacteria rapid detection in clinical samples	Innovation in diagnostics	A Camaggi, *AOU Maggiore della Carità, Laboratory of Microbiology and Virology, Novara, Italy*

P35	Xpert MTB/XDR assay for the rapid diagnosis of TB resistance. A country wide cross sectional observational prospective study from Pakistan	Innovation in diagnostics	V Batignanim, *San Raffael Scientific Institute*
P36	The PEOPLE trial on post exposure prophylaxis for leprosy	Innovation in therapy for Mycobacteria	E Hasker, *Institute of Tropical Medicine, Antwerp*
P37	Serratia sp. clusters in bronchoalveolar lavage specimens from patients with tuberculosis and non-tuberculous mycobacterial lung diseases	Innovation in therapy for Mycobacteria	M Belheouane, *Evolution of the Resistome, Research Center Borstel, Borstel, Germany*
P38	Rifampicin and isoniazid dosage adjustment according to TDM and acetylator status: a single centre prospective observational study	Innovation in therapy for Mycobacteria	M Schiuma, *Department of Biomedical & Clinical Sciences "Luigi Sacco", Università degli Studi di Milano, Italy*
P39	Search for conserved sites in Mycobacterium tuberculosis DNA gyrase	Innovation in therapy for Mycobacteria	D Zygala-Pytlos, *Laboratory of Genetics and Physiology of Mycobacterium, Institute of Medical Biology, Polish Academy of Sciences, Lodz, Poland / The Bio-Med-Chem Doctoral School of the University of Lodz and Lodz Institutes of the Polish Academy of Sciences, University of Lodz, Lodz, Poland*
P40	Single nucleotide variation catalogue from clinical isolates mapped on tertiary and quaternary structures of ESX-1 related proteins reveals critical regions as putative Mtb therapeutic targets	Innovation in therapy for Mycobacteria	O Tzfadia, *Institute for Tropical Medicine / University of Antwerp*
P46	In Vitro Activity of Tedizolid and Omadacycline in Nontuberculous Mycobacteria	NTM	D Satana, *Istanbul University, Istanbul Faculty of Medicine, Department of Medical Microbiology*

P47	Research of In Vitro Activity of Bedaquiline In Nontuberculous Mycobacteria	NTM	D Satana, *Istanbul University, Istanbul Faculty of Medicine, Department of Medical Microbiology*
P48	Mouse models to study host-pathogens interaction in Mycobacterium abscessus lung infections.	NTM	N Lorè, *San Raffaele Scientific Institute*
P49	New method for fast and direct Mycobacteria identification from positive blood culture	NTM	A Camaggi, *AOU Maggiore della Carità, Laboratory of Microbiology and Virology - Novara, Italy*
P50	Identification and specie-typing of nontuberculous mycobacteria among sputum samples of presumed and diagnosed drug-resistant tuberculosis patients in Ghana, a 10-year retrospective laboratory analysis	NTM	E T Abbew, *Institute of Tropical Medicine, Antwerp / University of Antwerp / Cape Coast Teaching Hospital, Ghana*
P51	Phenotypic drug susceptibility patterns of Mycobacterium avium complex clinical isolates in Russia	NTM	D Starkova, *St Petersburg Pasteur Institute, St Petersburg, Russia*
P52	Is M. saskatchewanense misidentified as M. intracellulare using the DNA STRIP technology-based method?	NTM	F Bisognin, *IRCCS Azienda Ospedaliero-Universitaria di Bologna / Alma Mater Studiorum, University of Bologna*
P54	Whole genome sequencing analysis for confirmation of suspected Mycobacterium avium laboratory cross-contamination	NTM	S Mok, *Irish Mycobacteria Reference Laboratory, St. James's Hospital / Trinity College Dublin*
P55	Host specific in vitro virulence of different Mycobacterium tuberculosis ecotypes	Other	M Coscolla, *I2SysBio, University of Valencia-FISABIO Joint Unit, 46980 Paterna, Spain*

P56	BCCM/ITM: a public repository for safe and easy accessible quality-assured mycobacterial strains and services	Other	L Rigouts, *BCCM/ITM, Institute of Tropical Medicine, Antwerp, Belgium / Mycobacteriology Unit, Institute of Tropical Medicine, Antwerp, Belgium*
P57	Clusters of multidrug-resistant Mycobacterium tuberculosis strains from newly-diagnosed patients in Northwest Russia	Other	A Vyazovaya, *St Petersburg Pasteur Institute, St Petersburg, Russia*
P58	Comprehensive Quality Assurance Intervention for Reliable Drug Susceptibility Testing Results for TB in Armenia	Other	S Andres, *National and World Health Organization Supranational Reference Laboratory for Mycobacteria, Research Center Borstel, Leibniz Lung Center, Borstel, 23845, Germany*
P59	Is stool a good specimen for diagnosing pulmonary tuberculosis in a high resource setting?	Other	D B Folkvardsen, *International Reference Laboratory of Mycobacteriology, Statens Serum Institut, Copenhagen, Denmark*
P60	Shikimic acid amides as promising antitubercular agents – synthesis and in vitro studies	Resistance to new drugs	V Valcheva, *The Stephan Angeloff Institute of Microbiology, Bulgarian Academy of Sciences*
P61	In vitro susceptibility testing of GSK656 against Mycobacterium tuberculosis complex isolates to establish the epidemiological cut-off values and MIC distribution	Resistance to new drugs	I Iannucci, *Universita Vita-Salute San Raffaele, Milan, Italy*
P62	The Niger rifampicin-resistant tuberculosis treatment approach is safer than the WHO bedaquiline/linezolid-containing 9-month regimen	Resistance to new drugs	M B Souleymane, *Damien Foundation, Niamey, Niger*

P63	Exploring the impact of mutations in Rv0678 gene on bedaquiline resistance in Mycobacterium tuberculosis: insights from computational biostructural proteomics	Resistance to new drugs	J Snobre, *Mycobacteriology Unit, Biomedical Sciences, Institute of Tropical Medicine (ITM), Antwerp, Belgium / Doctoral School of Life Sciences & Medicine, Vrije Universiteit Brussel , Brussels, Belgium / Internal Medicine Department, UZ Brussel, Brussels, Belgium*
P64	Prolonged heating should be avoided during the preparation of Delamanid containing Middlebrook 7H11 medium	Resistance to new drugs	P Rupasinghe, *Unit of Mycobacteriology, Department of Biomedical Sciences, Institute of Tropical Medicine, Antwerp, Belgium*
P65	Screening for non-fixed/mixed single nucleotide polymorphisms (SNPs) in serial Mycobacterium tuberculosis isolates during treatment for MDR-TB, the emergence of sugI mutations in patients receiving d-cycloserine.	Resistance to new drugs	R M Anthony, *National Tuberculosis Reference Laboratory, Centre for Infectious Disease Control, National Institute for Public Health and the Environment (RIVM), 3721BA Bilthoven, The Netherlands*
P66	11-year trend in antibiotic consumption in Albania and the implications for the future	Resistance to new drugs	I Hoxha, *University of Medicine Tirana*
P67	Genotypic diversity of strains of Mycobacterium tuberculosis isolated from TB patients from high burden MDR-TB country	Resistance to new drugs	N Ciobanu, *Institute of Phthisiopneumology, Chisinau, Moldova / State Medical and Pharmaceutical University, Chisinau, Moldova*
P68	Elucidating drug tolerance and resistance mechanisms of M. tuberculosis using evolutionary medicine principles	Resistance to new drugs	T Walz, *Research Center Borstel*

P69	Use of M. tuberculosis genome sequencing to determine relapse and reinfection in a phase 2 prevention of recurrent tuberculosis vaccine trial	Sequencing in accession countries	A M Cabibbe, *San Raffaele Scientific Institute*
P70	Whole genome sequencing from clinical primary Mycobacterium tuberculosis liquid cultures: pushing the boundaries	Sequencing in accession countries	A Dippenaar, *University of Antwerp*
P71	Performance of targeted and whole genome sequencing for routine genotypic drug resistance profiling of Mycobacterium tuberculosis	Sequencing in accession countries	A Dippenaar, *University of Antwerp*
P72	Advancing TB Diagnosis in Sub-Saharan Africa: A Roadmap for Next-Generation Sequencing Implementation	Sequencing in accession countries	L de Araujo, *Molecular Mycobacteriology, Research Center Borstel - Leibniz Lung Center, Borstel, 23845, Germany*
P73	SARS-CoV-2 lineages and Variants Of Concern in patients from a university hospital in Tirana, Albania, January-February 2021	Sequencing in accession countries	S Tafaj, *Microbiology Department National TB Reference Laboratory, University Hospital "Shefqet Ndroqi", Tirana, Albania*
P74	A Virtual Molecular Biology Training Program for DNA Extraction and Whole Genome Sequencing of Mycobacterium tuberculosis Clinical Isolates	Sequencing in accession countries	A Dippenaar, *University of Antwerp*
P75	Household and community-based transmission of Mycobacterium tuberculosis in Harare, Zimbabwe	Transmission and public health epidemiology	M Chipinduro, *Biomedical Research and Training Institute, Harare, Zimbabwe / Midlands State University, Gweru, Zimbabwe*

P76	Transmission and drug resistance surveillance by whole-genome sequencing in a population-based cohort in Southern Mexico	Transmission and public health epidemiology	F J Martínez-Martínez, *Instituto de Biomedicina de Valencia (IBV-CSIC)*
P77	Epidemiology of infections caused by Tuberculous and Non-Tuberculous Mycobacteria in the province of Pavia: a 12-year comparative analysis	Transmission and public health epidemiology	M Siciliano, *U.O.C. Microbiologia e Virologia, Dipartimento Medicina Diagnostica, Fondazione IRCCS Policlinico San Matteo, Pavia, 27100, Italy*
P78	WGS-based genetic diversity assessment of LAM genotype M. tuberculosis strains among the tuberculosis outbreaks in distant Latvian counties	Transmission and public health epidemiology	D Sadovska, *Latvian Biomedical Research and Study Centre, Riga, Latvia / Riga Stradins University, Riga, Latvia*
P79	Relative competitive fitness of Mycobacterium tuberculosis outbreak strains isolated in Poland	Transmission and public health epidemiology	K Strus, *Institute of Medical Biology, Polish Academy of Sciences*
P80	Impact of Mycobacterium tuberculosis complex strain diversity on tuberculosis transmissions in a cosmopolitan low-incidence setting	Transmission and public health epidemiology	N Ullrich, *Molecular and Experimental Mycobacteriology, Research Center Borstel, Borstel, 23845, Germany*
P81	Transmission of drug resistant tuberculosis in Mozambique	Transmission and public health epidemiology	I Barilar, *Molecular and Experimental Mycobacteriology, Research Center Borstel, Borstel Germany / German Center for Infection Research, Partner Site Hamburg-Lübeck-Borstel-Riems, Borstel, Germany*
P82	Interrogation of an Multi Drug Resistant Tuberculosis outbreak using Whole Genome Sequencing	Transmission and public health epidemiology	E Streicher, *Stellenbosch University*