PROGRAM

2nd St. Petersburg Symposium on Tuberculosis and Mycobacteria: Molecular Approach

St. Petersburg, Russia
5-6 December 2018

WELCOME ADDRESS

Tuberculosis is both ancient and re-emerging disease and its impact on the global health and economy is serious and adverse. The causative agent, Mycobacterium tuberculosis is not only medically important pathogen that accompanied humans since their early evolution but an interesting biological species. The recent years continue to witness an impressive advance in molecular studies of M. tuberculosis and other mycobacterial species through implementation and wide use of new generation and omics approaches. This helped to better understand and revisit certain theories on phylogenomics of M. tuberculosis, its evolutionary paradigm and adaptive strategies, role of clinical relevance of its genetic diversity.

Back in the history, in September 2014, within St. Petersburg Ecological forum organized by Institute of Experimental Medicine, a Symposium on Tuberculosis and Mycobacteria took place. It was a one-day event organized by St. Petersburg Pasteur Institute and Institute of Phthisiopumonology. It was attended, along with Russian participants, by six renowned experts from Germany, UK, France, Sweden, and Japan. In my unhumble opinion, it was the first event on molecular tuberculosis research with such a visible international component ever hold in Russia.

More than three years later, I am pleased to announce that 2nd St. Petersburg Symposium on Tuberculosis and Mycobacteria: Molecular Approach will be hold on 5-6 December 2018. It will be a stand-alone part of the regular anniversary conference of St. Petersburg Pasteur Institute. International conference «Molecular aspects of epidemiology, diagnosis, prevention and treatment of infectious diseases» will be dedicated to the 110 years since establishment of the institute and 95 years since its naming after Louis Pasteur.

An extensive program of the Symposium will consist of invited lectures, as well as short oral presentations and poster sessions based on the abstracts received. The official language of all oral and poster presentations will be English (simultaneous Russian translation will be provided).

I cordially welcome all interested in the most recent advances in molecular research on tuberculosis and other mycobacteria, willing to acquire new knowledge, to share ideas and to network on future collaborations, to the beautiful city of St. Petersburg on 4-6 December 2018.

Igor MOKROUSOV
Symposium Chairman

2nd St. Petersburg Symposium on Tuberculosis and Mycobacteria: Molecular Approach

St. Petersburg, Russia, 5-6 December 2018

SYMPOSIUM CHAIRMAN: Igor Mokrousov (St. Petersburg Pasteur Institute, Russia)

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Prasit Palittapongarnpim (Mahidol University, Bangkok, Thailand)
Margarida Saraiva (Instituto de Investigacao e Inovacao em Saude, Porto, Portugal)
Hanna Soini (National Institute for Health and Welfare, Helsinki, Finland)
Dick van Soolingen (RIVM, Bilthoven, Netherlands)
Boris Vishnevsky (Research Institute of Phthisiopulmonology, St. Petersburg, Russia)

OFFICIAL LANGUAGE: English (simultaneous translation into Russian)

VENUE: Hotel Courtyard St. Petersburg Vasilyevsky, Conference Hall "Dmitrov" (2nd line of Vasilievsky Island, 61/30. St. Petersburg, Russia)

Website: http://pasteur110.ru/wp-content/Program-of-Symposium-eng.html

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5 December 2018

9:00-9:15	**Opening of the Symposium** **Igor Mokrousov,** Symposium Chairman **Areg A. Totolian,** Acad. of RAS, Director of St. Petersburg Pasteur Institute
Section**: Evolution and phylogenomics** Co-chairs*:* **Iñaki Comas** (Spain), **Igor Mokrousov** (Russia)	
9:15-9:40	**Iñaki Comas** (*Institute of Biomedicine, Valencia, Spain*) Genomic epidemiology of tuberculosis: from within host evolution to global migration patterns
9:40-10:05	**Tao Luo** (*Sichuan University, Chengdu, China*) Evolution and transmission of *Mycobacterium tuberculosis* resistance to fluoroquinolones
10:05-10:25	**Igor Mokrousov** (*St. Petersburg Pasteur Institute, Russia*) Clichés and dogmas in molecular TB research
10:25-10:45	**Egor Shitikov** (*Federal Research and Clinical Centre of Physical-Chemical Medicine, Moscow, Russia*) Role of IS*6110* in micro- and macroevolution of *Mycobacterium tuberculosis* Lineage 2
10:45-11:05	**Prasit Palittapongarnpim** (*Mahidol University and the National Science and Technology Development Agency, Bangkok, Thailand*) Bacterial WGS and host genome-wide SNP analysis of tuberculosis patients in Thailand
11:05-11:30	COFFEE-BREAK
Section**: Whole-genome sequencing and personalized medicine** Co-chairs*:* **Vlad Nikolayesvkyy** (UK), **Dario Garcia de Viedma** (Spain)	
11:30-11:55	**Dick van Soolingen** (*National Institute for Public Health and the Environment, Bilthoven, The Netherlands*) International validation of analysis pipelines for Whole Genome Sequencing data of *Mycobacterium tuberculosis* isolates
11:55-12:20	**João Perdigão** (*Universidade de Lisboa, Portugal*) Looking inside the forest: from classical genotyping of *Mycobacterium tuberculosis* to Whole Genome Sequencing in high multidrug resistance settings
12:20-12:45	**Hanna Soini** (*National Institute for Health and Welfare, Helsinki, Finland*) WGS in routine diagnostics of tuberculosis – prediction of drug resistance and genotyping
12:45-13:00	**Anzaan Dippenaar** (*Stellenbosch University, Cape Town, South Africa*) Whole genome sequencing sheds light on the transmission dynamics of a multi-drug resistant *Mycobacterium tuberculosis* outbreak over 23 years in a high incidence setting
13:00-14:00	LUNCH
14:00-15:00	POSTER SESSION
13:00-15:00	**Satellite event:** 2nd meeting of the Consortium "Fight Against TB in Central and Eastern Europe" (FATE). Co-chairs: Tomasz Jagielski (Poland), Igor Mokrousov (Russia)
15:00-15:25	**Dario Garcia De Viedma** (*Clinical Microbiology and Infectious diseases Department, Gregorio Marañón University Hospital; CIBER Enfermedades Respiratorias CIBERES, Madrid, Spain*) Simplifying NGS approaches to optimize tracing of transborder spread of *Mycobacterium tuberculosis*
15:25-15:45	Diaem **Bhupinder Hundle** (*Oxford Nanopore Technologies, UK*) Through the Nanopore – An Introduction to Nanopore Sequencing. Actual aspects for epidemiology and diagnosis.
15:45-16:05	Applied Maths **Margo Diricks** (*Applied Maths, St-Martens-Latem, Belgium*) Whole genome sequence based resistance prediction and molecular typing of *Mycobacterium tuberculosis* complex (MTBC) strains in BioNumerics
16:05-16:30	COFFEE-BREAK
Section**: Molecular epidemiology and molecular diagnostics** Co-chairs*:* **Olga Narvskaya** (Russia), **Dick van Soolingen** (Netherlands)	
16:30-16:50	**Aleksei Korobitsyn** (*WHO Global TB Program, Geneva, Switzerland*) Global WHO policies on molecular methods for TB diagnosis
16:50-17:10	**Renate Ranka** (*Latvian Biomedical Research and Study Centre; Riga Stradiņš University, Latvia*) Molecular epidemiology of tuberculosis in Latvia
17:10-17:30	**Yuriy Skiba** (*Aitkhozhin Institute of Molecular Biology and Biochemistry; Almaty Branch of National Center for Biotechnology at Central Reference Laboratory, Almaty, Kazakhstan*) Molecular epidemiology of tuberculosis in Kazakhstan, 2006-2018
17:30-17:45	**Andrei Gabrielian** (*National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville MD, USA*) TB Portals Program: Data-driven multi-national consortium against drug-resistant tuberculosis
17:45-18:00	**Silva Tafaj** (*University Hospital "Shefqet Ndroqi" Tirana, Albania*) Molecular epidemiology of TB in Albania

18:00-18:15	**Anna Vyazovaya** (*St. Petersburg Pasteur Institute, Russia*) Population structure of Mycobacterium tuberculosis in Russian regions bordering EU countries
18:15-18:30	**Tatiana Umpeleva** (*Ural branch of National Medical Research Center of Tuberculosis and Infectious Diseases, Ekaterinburg, Russia*) Molecular features of *Mycobacterium tuberculosis* strains from patients living in closed city in the Ural region, Russia
18:30-18:45	**Imane Chaoui** (*Centre National de l'Energie, des Sciences et Techniques Nucléaires, Rabat, Morocco*) Genotyping of multidrug and pre-extensively drug-resistant *Mycobacterium tuberculosis* isolates from a high TB incidence area in Morocco
18:45	Discussion

6 December 2018

Section**: Nontuberculous mycobacteria** Co-chairs*:* **Alexander Apt** (Russia), **Tomotada Iwamoto** (Japan)	
9:30-9:55	**Alexander Apt** (*Central Institute for Tuberculosis, Moscow, Russia*) *Mycobacterial avium* triggered disease: host genetics and immunity in mouse models
9:55-10:20	**Tomotada Iwamoto** (*Kobe Institute of Health, Japan*) Genomics and local adaptation of *Mycobacterium avium*
10:20-10:40	**Vlad Nikolayevskyy** (*Imperial College, London UK*) Development of the External Quality Assessment scheme for non-tuberculous Mycobacteria drug susceptibility testing in European Union
10:40-11:00	Syntol **Vera Ustinova** (*Central Tuberculosis Research Institute & Syntol, Moscow, Russia*) Prevalence and diversity of nontuberculous mycobacteria in different regions of the Russian Federation
11:00-11:30	COFFEE-BREAK
11:30-11:55	**Tomasz Jagielski** (*University of Warsaw, Poland*) Molecular typing of *Mycobacterium kansasii* - a global perspective
11:55-12:10	**Sara Truden** (*University Clinic of Respiratory and Allergic Diseases Golnik, Slovenia*) Emerging opportunistic pathogen *Mycobacterium abscessus* in Slovenia: molecular analysis of resistance genes compared to MIC method
12:10-12:30	**Laura Rindi** (*University of Pisa, Italy*) Genetic diversity and drug resistance of *Mycobacterium avium* in Italy

12:30-14:30	LUNCH (13:00-14:00) & POSTER SESSION
Section**: Virulence and resistance 1** Co-chairs*:* **Margarida Saraiva** (Portugal), **Roland Brosch** (France)	
14:30-14:55	**Roland Brosch** (*Institut Pasteur, Paris, France*) Update on virulence factors in Mycobacteria
14:55-15:20	**Oleg Ogarkov** (*Scientific Center for Family Health and Human Reproduction Problems, Irkutsk, Russia*) Polymicrobial biofilm formation as a possible cause of unexpected defaulted treatment of pulmonary tuberculosis
15:20-15:45	**Margarida Saraiva** (*Instituto de Investigação e Inovação em Saúde; Universidade do Porto, Portugal*) Functional relevance of Mycobacterium tuberculosis diversity: from genotypes to immune responses and disease severity
15:45-16:00	**An Van den Bossche** (*Sciensano, Brussels, Belgium*) RNA-based drug susceptibility testing of *Mycobacterium tuberculosis*
16:00-16:30	COFFEE-BREAK
Section**: Virulence and resistance 2** Co-chairs*:* **Danila Zimenkov** (Russia), **Scott Heysell** (USA)	
16:30-16:55	**Jim Werngren** (*Supranational reference laboratory for TB & Public Health Agency, Sweden*) Drug resistance in *Mycobacterium tuberculosis*: from phenotypic MIC-analysis to WGS for routine DST
16:55-17:15	**Maria Alvarez Figueroa** (*Central Research Institute for Epidemiology, Moscow, Russia*) Analysis of gene mutations associated with MDR among *Mycobacterium tuberculosis* strains isolated in Moscow region
17:15-17:35	**Richard Anthony** (*National Institute for Public Health and the Environment Bilthoven, The Netherlands*) Could the new insights into PZA resistance provide route to shorter more effective TB therapy?
17:35-17:55	**Danila Zimenkov** (*Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia*) Advances in the study of molecular basis of resistance to new anti-TB drugs
17:55-18:15	**Scott Heysell** (*University of Virginia, Charlottesville, USA*) *M. tuberculosis* drug resistance mutations and understanding of pharmacokinetics/ pharmacodynamics: treatment and care implications
18:15	**Concluding remarks**

POSTER SESSION

2.1.	**Performance of GeneXpert MTB/RIF in the diagnosis of extrapulmonary tuberculosis in Morocco** Aainouss A. [1,2], G. Momen[2], K. Bennani[3], A. Lamaammal[2], F. Chtioui[2], M. Messaoudi[2], J. Mouslim[1], M. Khyatti[2], M.D. El Messaoudi[2] *[1] Faculté des Sciences Ben M'Sik, Casablanca, Morocco ; [2] Institut Pasteur du Maroc, Casablanca, Morocco ; [3] Direction de l'épidémiologie et lutte contre les maladies, Ministry of Health, Morocco*
2.2.	**Genetic diversity of multidrug-resistant *Mycobacterium tuberculosis* isolates in Pakistan** Bakuła Z. [1], M. Pleń[1], H. Javed[2], H.J. Hashmi[2], Z. Tahir[3], K. Roeske[1], N. Jamil[2], T. Jagielski[3] [1]Department of Applied Microbiology, Institute of Microbiology, Faculty of Biology, University of Warsaw, Poland; [2]Department of Microbiology and Molecular Genetics, University of the Punjab, Lahore, Pakistan; [3]Provincial TB Control Program, Lahore, Pakistan
2.3.	**The correlation between levels of phenotypic resistance and genotypic mutations of *Mycobacterium tuberculosis*** Ciobanu N. [1], S. Alexandru[1], D. Chesov[1], A. Codreanu[1], C. Lange[2], V. Crudu[1] *[1]Phthisiopneumology Institute, Chisinau, Moldova; [2]Research Center Borstel, Germany*
2.4.	**Emergence of bedaquiline resistance after completion of bedaquiline-based drug-resistant TB treatment: a case study from South Africa** de Vos M. [1], S Ley[1], B Derendinger[1], A Dippenaar[1], M Grobbelaar[1], A Reuter[2], J Daniels[2], S Burns[3], G Theron[1], J Posey[3], R Warren[1], H Cox[4] *1 DST/NRF Centre of Excellence in Biomedical Tuberculosis Research / SAMRC Centre for Tuberculosis Research, Division of Molecular Biology and Human, Faculty of Medicine and Health Science, Stellenbosch University, South Africa; 2Médecins Sans Frontières, Operational Centre Brussels (OCB), Khayelitsha Project, Cape Town, South Africa; 3 Division of Tuberculosis Elimination, National Center for HIV/AIDS, Viral Hepatitis, STD, and TB Prevention , Centers for Disease Control and Prevention, 1600 Clifton Road , Atlanta , Georgia 30329 , United States.; 4 Institute of Infectious Disease and Molecular Medicine and Division of Medical Microbiology, Department of Pathology, Faculty of Health Sciences, University of Cape Town, South Africa*
2.5.	**A 15-year spatiotemporal analysis of *Mycobacterium tuberculosis* lineages 1 and 2 in Chiang Rai, Thailand** A. Disratthakit[1], P. Palittapongarnpim[2,3], P. Ajawatanawong[2], N. Smittipat[3],S. Mahasirimongkol[1], R. Miyahara[4],H. Yanai[5,6], N. Yamada[7], S. Nedsuwan[8], W. Imasanguan[8], P. Kantipong[8], B. Chaiyasirinroje[5], S. Bupachat[5], P. Ananpradit[5], P. Piboonsiri[1], W. Ruengchai[2], T. Juthayothin[3], J. Phelan[9], J. Parkhill[10], T.G. Clark[9],M.L. Hibberd[9], K. Tokunaga[4] [1] Department of Medical Sciences, Ministry of Public Health, Thailand; [2] Department of Microbiology, Faculty of Science, Mahidol University, Thailand; [3] National Centre for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Thailand; [4] Department of Human Genetics, Graduate School of Medicine, the University of Tokyo, Japan; [5] TB-HIV Research Foundation, Thailand; [6] Fukujuji Hospital, Japan Antituberculosis Association (JATA), Japan; [7] Research Institute of Tuberculosis, JATA, Japan; [8] Chiangrai Prachanukroh Hospital, Ministry of Public Health, Thailand; [9] London School of Hygiene and Tropical Medicine, UK; [10] Welcome Trust Sanger Institute, Hinxton, UK
2.6.	**Molecular-genetic methods of detection of tuberculosis and its drug resistance in Arkhangelsk region in 2017** Eliseev P.I. [1], I.V. Tarasova [2], A.O. Mariandyshev[1] *[1]Northern State Medical University, Arkhangelsk, Russia; [2]Arkhangelsk Regional Antituberuclosis Dispensary, Arkhangelsk*
2.7.	**Detection of extracellular *Mycobacterium tuberculosis* small RNAs** Fursov M.V., T.I. Kombarova, I.A. Dyatlov, V.D. Potapov *State Research Center for Applied Microbiology and Biotechnology, Obolensk*
2.8.	**Genotypes of *Mycobacterium tuberculosis* isolates from different organs of patients with generalized TB and HIV-coinfection** Gerasimova A. [1], A. Vyazovaya[1], M. Mayskaya[2], I. Mokrousov[1], O. Narvskaya[1,3] *[1]St. Petersburg Pasteur Institute, St. Petersburg, Russia; [2] City Pathoanatomical Bureau, St. Petersburg, Russia; [3] Research Institute of Phthisiopulmonology, St. Petersburg*
2.9.	**In vitro activity of Bedaquiline against non-tuberculous mycobacteria** Godino I.T.[1,2], F. Boutachkourt[2], D.A. Aguilar-Ayala[3], O. Vandenberg[4], V. Mathys[5], E. Tortoli[6], J.C. Palomino[7], N. Lounis[8], H. Rodriguez Villalobos[2], A. Martin[2] *[1]Talentum Jaén Program, Jaén, Spain; [2]Laboratory of Medical Microbiology, Université Catholique de Louvain (UCL) & Cliniques Universitaires Saint-Luc, Brussels, Belgium; [3]Departamento de Microbiologia, Escuela Nacional de Ciencias Biologicas, Instituto Politecnico; Nacional, Mexico,D.F., Mexico; [4]Laboratoire des Hôpitauxuniversitaires de Bruxelles (LHUB-ULB), Brussels, Belgium ; [5]Belgian Reference Laboratory for Tuberculosis and Mycobacteria, Sciensano, Brussels, Belgium; [6]Emerging Bacterial Pathogens Unit, IRCCS San Raffaele Scientific Institute, Milan, Italy; [7]Independent mycobacteriology expert, Antwerp, Belgium; [8]Janssen Infectious Diseases, Beerse, Belgium*
2.10.	**Physiological impact of the evolution of the *rpoB* mutation** Grobbelaar M [1], SL Sampson[1], GE Louw[2], PD van Helden[1], A Van Rie[3] and RM Warren[1] *[1]DST-NRF Centre of Excellence for Biomedical Tuberculosis Research; 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; [2]Institute of Infectious Diseases and Molecular Medicine, University of Cape Town, Cape Town, South Africa; [3]Global Health Institute, Epidemiology and Social Medicine, Faculty of Medicine, University of Antwerp, Antwerp, Belgium*
2.11.	**Utility of whole genome sequencing of *Mycobacterium tuberculosis* complex isolates in practice** Jajou R.[1], A. de Neeling[1], S. Lipworth[2], T. Walker[2], R. Anthony[1], D. van Soolingen[1] *[1]National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands; [2]Nuffield Department of Medicine, University of Oxford, John Radcliffe Hospital, Oxford, UK*

2.12.	**Minor genetic determinants of second-line injection drugs resistance in *Mycobacterium tuberculosis*** Jou R.[1,2,3], E.V. Kulagina[4], W.T. Lee[1,2], E.Yu. Nosova[5], J.Y. Weng[1,2], O.V. Antonova[4], W.H. Lin[1,2], A.I. Isakova[5], M.H. Wu[1,2], D.V. Zimenkov [4] *[1]Tuberculosis Research Center, Taiwan Centers for Disease Control, Taipei, Taiwan; [2]Diagnostics and Vaccine Center, Taiwan Centers for Disease Control, Taipei, Taiwan; [3]Institute of Microbiology and Immunology, National Yang-Ming University, Taipei, Taiwan; [4]Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow, Russia; [5]The Moscow Research and Clinical Center for Tuberculosis Control of the Moscow Government Health Department, Moscow, Russia*
2.13.	**Prevalence of nontuberculous *Mycobacterium spp*. strains isolated from clinical specimens at North Estonia Medical Centre in 2001-2017** Levina K. *North Estonia Medical Centre, Tallinn, Estonia*
2.14.	**The influence of the H2 complex on *Mycobacterium avium* infection in mice** Linge I. A. [1], E. S. Petrova[1], E. V. Kondratieva[1], A. S. Apt[1, 2] *[1]Central Institute for Tuberculosis, Moscow, Russia; [2] Lomonosov Moscow State University, Moscow*
2.15.	**Epidemiological of Extrapulmonary Tuberculosis in Albania 2010-2016** Mema D.[1], P.Kapisyzi[1], S.Tafaj[1], D.Mema[2], S.Bala[1], H.Hafizi[1] *[1] University Hospital " Shefqet Ndroqi" Tirana; [2] Center of primary health care nr.2, Tirana, Albania*
2.16.	**Genetics and Social Determinants of TB related death from tuberculosis patients in the Northern Thailand** Miyahara R.[1], H. Yanai[2], S. Mahasirimongkol[3], L. Toyo-oka[1] K. Tokunaga[1] *[1]Department of Human Genetics, Graduate School of Medicine, The University of Tokyo, Japan; [2]Fukujuji Hospital, Japan Anti-Tuberculosis Association, Kiyose, Japan; [3]Medical Genetics Center, Medical Life Sciences Institute, Department of Medical Sciences, Ministry of Public Health, Nonthaburi, Thailand*
2.17.	**Analysis of secondary resistance of *Mycobacterium tuberculosis* to second-line anti-tuberculosis drugs in Casablanca** Momen G. [1,2], A. Aainoussi[2] , A. Lamaammal[2], F. Chtioui[2], M. Messaoudi[2], M Blaghen[1], M.D. El Messaoudi[2], M. Khyatti[2] *[1] Faculté des Sciences Ain Chok, Casablanca, Morocco ; [2] Institut Pasteur du Maroc, Casablanca, Morocco*
2.18.	**Population structure of *Mycobacterium tuberculosis* isolates from TB-HIV coinfected patients in Omsk region, West Siberia, Russia** Pasechnik O. ***[1], A. Vyazovaya[2], I. Mokrousov[2]*** *[1] Omsk State Medical University, Omsk, Russia; [2] St. Petersburg Pasteur Institute, St. Petersburg*
2.19.	**The implementation of next-generation sequencing for epidemiological studies and drug resistance investigations in micro-epidemics involving pediatric tuberculosis patients** Pole I. [1,2], I. Ozere[2,3], I. Norvaisa[2], R. Ranka [1,3] *[1] Latvian Biomedical Research and Study Centre; [2] Riga East University Hospital, Centre of Tuberculosis and Lung Diseases; [3] Riga Stradiņš University, Riga, Latvia*

2.20.	**NGS determination of mycobacterial trans-renal DNA as potential tool of clinical diagnostic** Sinkov V. [1], O. Ogarkov[1,2], A. Plotnikov[3], S. Zhdanova[1], N. Belkova[4], M. Koscheev[5], S. Heysell[6] *[1]SC FHHRP, Irkutsk, Russia; [2]ISMACE, Irkutsk, Russia; [3]ICIS UD RAS, Orenburg, Russia; [4]LIN SB RAN Irkutsk, Russia; [5]RTBH, Irkutsk, Russia; [6]UVA, Charlottesville, VA, USA*
2.21.	**Next-generation sequencing of drug resistant *Mycobacterium tuberculosis* strains – first Slovenian experience** Sodja E. [1], N. Toplak[2], S. Koren[2], M. Kovač[2], S. Truden[1], M. Žolnir-Dovč[1] *[1]University Clinic of Respiratory and Allergic Diseases Golnik, Golnik, Slovenia; [2]Omega doo., Ljubljana, Slovenia*
2.22.	**Single nucleotide polymorphisms in *hsp65* and *MACPPE12* genes of *Mycobacterium avium* subsp. *hominissuis*** Starkova D. [1], T. Iwamoto[2], A. Vyazovaya[1], V. Molchanov[3], V. Zhuravlev[4], B. Vishnevsky[4], O. Narvskaya[1,4] *[1] St. Petersburg Pasteur Institute, St. Petersburg, Russia; [2] Department of Infectious Diseases, Kobe Institute of Health, Kobe, Japan; [3] St. Petersburg State Chemical Pharmaceutical University, St. Petersburg, Russia; [4] St. Petersburg Research Institute of Phthisiopulmonology, St. Petersburg*
2.23.	**Molecular characterization of *Mycobacterium bovis* isolates from cattle in Bulgaria** Valcheva V. [1], T. Savova-Lalkovska[2], A. Dimitrova[2], H. Najdenski[1], M. Bonovska[1] *[1]The Stephan Angeloff Institute of Microbiology, BAS, Sofia, Bulgaria; [2] National Diagnostic and Research Veterinary Medical Institute, Sofia, Bulgaria*
2.24.	**Molecular epidemiology of tuberculosis in Eastern Siberia and Far East** Zhdanova S.N. [1], M.K.Vinikurova[2], A.A. Yakovlev [3], O.B. Ogarkov[1,4] *[1]Scientific Center of Family Health and Human Reproduction, Irkutsk, Russia; [2]Phthisiatry Research and Practice Center, Yakutsk, Russia; [3]Vladivostok State Medical University, Vladivostok ,Russia; [4]Branch of the Educational Institution of Further Professional Education «Russian Medical Academy of Continuing Professional Education», Irkutsk*
2.25.	**Molecular epidemiology of tuberculosis in Mongolia: sources and pathways of MDR *Mycobacterium tuberculosis* strains** Zhdanova S.N.[1], T. Oyuntuya[2], M.V. Badleeva[3], O.B. Ogarkov[1,4] [1]Scientific Center of Family Health and Human Reproduction, Irkutsk, Russia; [2]National Center for Infectious Diseases, Ulaanbaatar, Mongolia; [3]Buryat State University, Ulan-Ude, Russia; [4]Branch of the Educational Institution of Further Professional Education «Russian Medical Academy of Continuing Professional Education», Irkutsk, Russia
2.26.	**Prevalence of extensively drug-resistant tuberculosis: a descriptive study in the Omsk region** Yarusova I.V.[1], A.I. Blokh[2], O.A. Pasechnik[2] *[1]Clinical Antituberculosis Dispensary (Omsk), [2]Omsk State Medical University, Omsk, Russia*

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