

Poster Session I: October 17, 2022  
Epidemiological Cues and Bridging Silos

| Control Number                 | Poster board no. | Presentation Start       | Presentation End         | Duration (in mns) | Title   | Author Block  |
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| <a href="#">2022-A-148-NGS</a> | 101              | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120               | Status of public <i>Candida auris</i> whole genome assemblies                           | <b>A. R. Gener</b> <sup>1</sup> , P. Hemarajata <sup>2</sup> ;<br><sup>1</sup> Association of Public Health Laboratories; Los Angeles County Public Health Laboratories, Los Angeles, CA, <sup>2</sup> Los Angeles County Public Health Laboratories, Los Angeles, CA.  |
| <a href="#">2022-A-185-NGS</a> | 102              | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120               | Management of Wastewater Data and Dashboard Development for SARS-CoV-2 Variant Tracking | <b>C. H. Bias</b> <sup>1</sup> , T. Kayikcioglu <sup>2</sup> , J. Amirzadegan <sup>1</sup> , P. Ramachandran <sup>2</sup> , R. Timme <sup>2</sup> , M. Balkey <sup>2</sup> ;<br><sup>1</sup> Oak Ridge Institute for Science and Education/Center for Food Safety and Applied Nutrition, Food and Drug Administration, College Park, MD, <sup>2</sup> Center for Food Safety and Applied Nutrition, Food and Drug Administration, College Park, MD. |
| <a href="#">2022-A-161-NGS</a> | 103              | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120               | AusTrakka - integrated pathogen genomics across Australia and New Zealand               | <b>C. Sloggett</b> , S. Carswell, V. Phu, T. Hoang, T. Seemann, B. Howden; Microbial Diagnostic Unit Public Health Laboratory at the Peter Doherty Institute and University of Melbourne, Melbourne, AUSTRALIA.   |

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| <a href="#">2022-A-188-NGS</a> | 104 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | The Mercury Workflow Series and Terra_2_NCBI: Bioinformatics Solutions to Facilitate Genomic Data Submission to NCBI & GISAID for Public Health Laboratories | <b>S. M. Wright</b> <sup>1</sup> , F. J. Ambrosio <sup>1</sup> , K. G. Libuit <sup>1</sup> , D. Park <sup>2</sup> , J. Sevinsky <sup>1</sup> ; <sup>1</sup> Theiagen Genomics, Highlands Ranch, CO, <sup>2</sup> Broad Institute, Cambridge, MA. |
| <a href="#">2022-A-44-NGS</a>  | 105 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Single cell microbial sequencing for global surveillance of AMR  | <b>B. AVOT</b> ; DTU, Lyngby, DENMARK.   |
| <a href="#">2022-A-54-NGS</a>  | 106 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Prediction of antimicrobial resistance and associated whole genome analysis for Salmonella Heidelberg isolated from Minnesota in 10 years                    | <b>J. Haan</b> <sup>1</sup> , D. Boxrud <sup>2</sup> ; <sup>1</sup> Minnesota Department of Health, St. Paul, MN, <sup>2</sup> Centers for Disease Control and Prevention, Atlanta, GA.  |
| <a href="#">2022-A-64-NGS</a>  | 107 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | What Organisms Are Found in Culture-negative Periprosthetic Joint Infections? Insights with Next Generation Sequencing                                       | <b>C. M. Baker</b> , K. Goswami, S. Tarabichi, E. Chisari, J. Parvizi; Rothman Orthopaedics, Philadelphia, PA.   |
| <a href="#">2022-A-57-NGS</a>  | 108 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | A Unified molecular epidemiology approach for the utilization of SARS-CoV-2 whole genome sequencing, a state public health perspective                       | <b>X. Wang</b> , J. Garfin, N. Lehnertz, S. Seys, S. Meyer, K. Como-Sabetti, S. Vetter, R. Lynfield; Minnesota Department of Health, Saint Paul, MN.   |
| <a href="#">2022-A-66-NGS</a>  | 109 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | In-silico discovery of uncategorized anti-microbial resistance genes   | <b>M. Hallgren</b> ; Technical University of Denmark, National Food Institute, Kongens Lyngby, DENMARK.  |
| <a href="#">2022-A-76-NGS</a>  | 111 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Molecular Epidemiology of the First NDM-1-   | <b>S. B. Namugenyi</b> , J. L. Dale, J. Garfin, M. Plumb, B. VonBank, S. O'Malley,   |

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|                               |     |                          |                          |     | Producing <i>Klebsiella pneumoniae</i> Outbreak in Minnesota   | R. Lynfield, P. Snippes Vagnone, X. Wang; Minnesota Department of Health, Saint Paul, MN.   |
| <a href="#">2022-A-78-NGS</a> | 112 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Identification of candidate antimicrobial resistance determinants in Enterococcus using machine learning                                     | <b>J. Kim</b> <sup>1</sup> , T. A. McAllister <sup>2</sup> , R. G. Beiko <sup>1</sup> ;<br><sup>1</sup> Dalhousie University, Halifax, NS, CANADA, <sup>2</sup> Agriculture and Agri-Food Canada, Lethbridge, AB, CANADA.   |
| <a href="#">2022-A-84-NGS</a> | 113 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Clinical Utility of Whole Genome Sequencing of AMR Pathogens and its benefits to Infection Prevention and Control and Antibiotic Stewardship | <b>A. C. Materna</b> , S. Beisken, J. Weinberger, P. Májek, L. Lueftinger, I. Ferreira, T. Weinmeier; Ares Genetics GmbH, WIEN, AUSTRIA.  |
| <a href="#">2022-A-88-NGS</a> | 114 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Lack of Host Sex Effect on <i>Brugia pahangi</i> Gene Expression   | <b>C. Holt</b> <sup>1</sup> , S. Baumberger <sup>2</sup> , R. E. Bromley <sup>1</sup> , B. C. Sparklin <sup>1</sup> , J. Mattick <sup>1</sup> , S. Ott <sup>1</sup> , L. Sadzewicz <sup>1</sup> , L. J. Tallon <sup>1</sup> , J. M. Foster <sup>3</sup> , M. L. Michalski <sup>2</sup> , J. C. Dunning Hotopp <sup>1</sup> ;<br><sup>1</sup> University of Maryland, Baltimore, Baltimore, MD, <sup>2</sup> University of Wisconsin, Oshkosh, Oshkosh, WI, <sup>3</sup> New England Biolabs, Ipswich, MA. |
| <a href="#">2022-A-99-NGS</a> | 115 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Ribavirin therapeutic as a mutagen of Crimean-Congo haemorrhagic fever virus (CCHFV) genome in clinical samples                              | <b>N. Wand</b> <sup>1</sup> , J. D'Addiego <sup>1</sup> , N. Elaldi <sup>2</sup> , K. Osman <sup>1</sup> , B. Koksai Bagci <sup>3</sup> , E. Kennedy <sup>1</sup> , A. Nur Pektas <sup>4</sup> , E. Hart <sup>1</sup> , G. Slack <sup>1</sup> , R. Hewson <sup>1</sup> ;<br><sup>1</sup> UK Health Security Agency, Porton, Salisbury, UNITED   |

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|                                |     |                          |                          |     |   | KINGDOM, <sup>2</sup> Cumhuriyet University Faculty of Medicine, Sivas, TURKEY, <sup>3</sup> Cumhuriyet University, Faculty of Health Sciences, Sivas, TURKEY, <sup>4</sup> Cumhuriyet University, Advanced Technology Application and Research Centre, Sivas, TURKEY.  |
| <a href="#">2022-A-104-NGS</a> | 116 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Wastewater Based Genomic Surveillance of SARS CoV 2 in Karachi City, Pakistan                                 | <b>W. Khan</b> , S. Kanwar, F. Kabir, F. Aziz, N. Ansari, U. Mehmood, F. Jehan, M. I. Nisar; The Aga Khan University, Karachi, PAKISTAN.  |
| <a href="#">2022-A-107-NGS</a> | 117 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Characterizing Consequences of X:Autosome Fusions in Onchocercidae Through Secondary Analysis of RNA-seq Data | <b>K. A. Hackbarth</b> <sup>1</sup> , E. S. Haag <sup>2</sup> , J. C. Dunning Hotopp <sup>3</sup> ; <sup>1</sup> University of Maryland, Maryland, MD, <sup>2</sup> University of Maryland, College Park, MD, <sup>3</sup> University of Maryland School of Medicine, Baltimore, MD.  |
| <a href="#">2022-A-109-NGS</a> | 118 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Molecular Surveillance of Monkeypox in the District of Columbia   | S. V. Nguyen <sup>1</sup> , E. L. Vaughn <sup>1</sup> , <b>J. H. Doss</b> <sup>1</sup> , M. Adjei <sup>1</sup> , C. Williams <sup>1</sup> , M. Mann <sup>1</sup> , A. Cabello <sup>1</sup> , S. Byfield <sup>1</sup> , L. Sealey <sup>1</sup> , S. Merid <sup>1</sup> , R. Blackwell <sup>1</sup> , E. Zelaya <sup>1</sup> , M. Doucette <sup>2</sup> , L. Gagne <sup>2</sup> , D. Payne <sup>1</sup> , J. A. Kiehlbauch <sup>1</sup> , J. R. Hauser <sup>1</sup> ; <sup>1</sup> DC Department of Forensic Sciences Public Health Laboratory, Washington, DC, <sup>2</sup> Massachusetts Department of Public Health, Boston, MA. |

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| <a href="#">2022-A-103-NGS</a> | 119 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | $\beta$ -Lactamase Alleles in <i>Acinetobacter</i> and <i>Pseudomonas</i> : How do they stack up?   | <b>A. R. Mack</b> , A. M. Hujer, R. A. Bonomo; Case Western Reserve University & Louis Stokes Cleveland Department of Veterans Affairs Medical Center, Cleveland, OH.   |
| <a href="#">2022-A-130-NGS</a> | 120 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Genome Wide Association Studies (GWAS) to predict Cryptic Carbapenem Resistance Mechanisms in <i>Klebsiella pneumoniae</i> Detected in Italy  | A. Cornacchia <sup>1</sup> , <b>A. Chiaverini</b> <sup>1</sup> , A. Janowicz <sup>1</sup> , G. Centorotola <sup>1</sup> , M. Saletti <sup>1</sup> , S. Chiatamone Ranieri <sup>2</sup> , A. Di Pasquale <sup>1</sup> , C. Cammà <sup>1</sup> , F. Pomilio <sup>1</sup> ; <sup>1</sup> Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Teramo, ITALY, <sup>2</sup> Operative Unit of Clinical Pathology and Microbiology, ASL of Teramo, Teramo, ITALY. |
| <a href="#">2022-A-132-NGS</a> | 121 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Whole Genome Sequencing Study on <i>Listeria monocytogenes</i> Clinical Strains: 9 Years of Surveillance in Umbria and Marche Regions (Italy) | F. Guidi <sup>1</sup> , <b>M. Torresi</b> <sup>1</sup> , G. Centorotola <sup>1</sup> , A. Chiaverini <sup>1</sup> , E. Rocchegiani <sup>2</sup> , F. Pomilio <sup>1</sup> , G. Blasi <sup>2</sup> ; <sup>1</sup> Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Teramo, ITALY, <sup>2</sup> Istituto Zooprofilattico Sperimentale dell'Umbria e delle Marche "Togo Rosati", Perugia, ITALY.   |
| <a href="#">2022-A-139-NGS</a> | 122 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Genomic Sequencing of <i>Bacillus cereus</i> Group Strains Isolated in Conjunction with 2020 Welder Anthrax Cases in the United States        | <b>L. M. Carroll</b> <sup>1</sup> , C. K. Marston <sup>2</sup> , C. B. Kolton <sup>2</sup> , C. A. Gulvik <sup>2</sup> , J. E. Gee <sup>2</sup> , Z. P. Weiner <sup>2</sup> , J. Kovac <sup>3</sup> ; <sup>1</sup> EMBL, Heidelberg, GERMANY, <sup>2</sup> Centers for Disease Control and Prevention, Atlanta, GA, <sup>3</sup> Pennsylvania State   |

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|                                |     |                          |                          |     |   | University, University Park, PA.  |
| <a href="#">2022-A-135-NGS</a> | 123 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Genomic Epidemiology of SARS-CoV-2 Transmission among University Students in Western Pennsylvania   | <b>V. Rangachar Srinivasa</b> , M. P. Griffith, K. D. Waggle, L. Zhu, J. W. Marsh, D. Van Tyne, L. H. Harrison, E. Martin; University of Pittsburgh, Pittsburgh, PA.  |
| <a href="#">2022-A-153-NGS</a> | 125 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Genomic epidemiology and population structure of <i>Campylobacter jejuni</i> in Peru  | W. Quino, J. Caro-Castro, D. Flores-Leon, <b>R. G. Gavilan</b> ; Instituto Nacional de Salud, Lima, PERU.   |
| <a href="#">2022-A-155-NGS</a> | 126 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Genomic Instability Patterns of Gastric Cancer Between Different Location, and Interaction Cancer Cells - Microbiota Using Next Generation Sequencing | <b>V. Ymelong Ghokeng</b> , C. Gnimpiaba, S. Tonlio Kenfack, C. Gnimpieba Kassep, I. Etikan; Near East University, Nicosia / TRNC, CYPRUS.  |
| <a href="#">2022-A-156-NGS</a> | 127 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Nanopore adaptive sampling enriches for target antibiotic resistance genes in soil microbial communities  | <b>D. Wrenn</b> , D. M. Drown; University of Alaska Fairbanks, Fairbanks, AK.   |
| <a href="#">2022-A-162-NGS</a> | 128 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Genomic Analysis of Novel Dog-Bite-Associated, Fastidious, Gram-negative Bacilli from Multiple Patient Specimens                                      | <b>B. M. Liu</b> <sup>1</sup> , M. A. Fisher <sup>2</sup> ; <sup>1</sup> Univ of Utah / ARUP; Children's National Hospital / George Washington University, Washington, DC, <sup>2</sup> Univ of Utah / ARUP, SLC, UT.                               |
| <a href="#">2022-A-163-NGS</a> | 129 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | SARS-CoV-2 Evolution Within Immunocompromised Individuals: An Origin of Variants?   | <b>D. Lemmer</b> <sup>1</sup> , P. Montfort <sup>1</sup> , W. T. Porter <sup>1</sup> , C. Hepp <sup>1</sup> , S. Dadwal <sup>2</sup> , D. Engelthaler <sup>1</sup> ; <sup>1</sup> TGen North, Flagstaff, AZ, <sup>2</sup> City of Hope, Duarte, CA. |

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| <a href="#">2022-A-170-NGS</a> | 130 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | A Novel Approach to Characterizing and Sequencing Influenza A from Rapid Tests                             | D. Erickson <sup>1</sup> , D. Lemmer <sup>1</sup> , Z. Barrand <sup>1</sup> , K. Simmons <sup>1</sup> , P. Hawkinson <sup>1</sup> , B. Brock <sup>1</sup> , <b>K. H. Sheridan</b> <sup>2</sup> , M. Valentine <sup>1</sup> , H. Centner <sup>1</sup> , D. Engelthaler <sup>1</sup> , C. Hepp <sup>1</sup> ;<br><sup>1</sup> TGen North, Flagstaff, AZ, <sup>2</sup> TGen North, Ashburn, AZ.   |
| <a href="#">2022-A-173-NGS</a> | 131 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Disease surveillance and outbreak investigations using AusTrakka, a national genomic surveillance platform | <b>C. Lam</b> <sup>1</sup> , M. Wilmot <sup>2</sup> , P. Andersson <sup>2</sup> , T. Hoang <sup>3</sup> , S. Nguyen <sup>4</sup> , K. Horan <sup>3</sup> , A. Arnott <sup>5</sup> , L. Leong <sup>6</sup> , T. Seeman <sup>2</sup> , A. V. Jennison <sup>7</sup> , V. Sintchenko <sup>1</sup> , B. P. Howden <sup>2</sup> ;<br><sup>1</sup> Centre for Infectious Diseases and Microbiology- Public Health-Institute of Clinical Pathology and Medical Research, Westmead, NSW, AUSTRALIA, <sup>2</sup> Microbiological Diagnostic Unit Public Health Laboratory, The University of Melbourne, at The Peter Doherty Institute for Infection and Immunity, Melbourne, VIC, AUSTRALIA, <sup>3</sup> Microbiological Diagnostic Unit Public Health Laboratory, The Department of Microbiology and Immunology, The University of Melbourne at The Peter Doherty Institute for Infection and Immunity, Melbourne, VIC, AUSTRALIA, <sup>4</sup> Forensic and Scientific Services, Queensland Health, |

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|                                |     |                          |                          |     |   | Brisbane, QLD, AUSTRALIA, <sup>5</sup> Centre for Infectious Diseases and Microbiology Laboratory Services, NSW Health Pathology–Institute of Clinical Pathology and Medical Research, Westmead, NSW, AUSTRALIA, <sup>6</sup> Public Health Laboratory, Microbiology and Infectious Diseases, SA Pathology, Adelaide, SA, AUSTRALIA, <sup>7</sup> Public Health Microbiology, Queensland Public Health and Infectious Diseases Reference Genomics (Q-PHIRE Genomics), Forensic and Scientific Services, Brisbane, QLD, AUSTRALIA. |
| <a href="#">2022-A-176-NGS</a> | 132 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | The Utility of Next-Generation Sequencing in Revision Total Joint Arthroplasty                        | <b>C. Baker</b> , S. Tarabichi, E. Chisari, K. Goswami, G. S. Goh, J. Parvizi; Rothman Orthopaedics, Philadelphia, PA.  |
| <a href="#">2022-A-177-NGS</a> | 133 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Genetic Diversity of USA300 Strains: Y2K to the Present   | <b>E. A. Felton</b> <sup>1</sup> , S. J. Kennedy <sup>1</sup> , J. K. Jackson <sup>1</sup> , E. Cella <sup>2</sup> , T. Azarian <sup>2</sup> , L. N. Shaw <sup>1</sup> ;<br><sup>1</sup> University of South Florida, Tampa, FL, <sup>2</sup> University of Central Florida, Orlando, FL.   |
| <a href="#">2022-A-56-NGS</a>  | 134 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Transcriptomic Signature for the identification of Drug-Susceptible <i>Mycobacterium tuberculosis</i> | <b>H. Poonawala</b> <sup>1</sup> , S. Kuchibhotla <sup>2</sup> , K. Zhang <sup>3</sup> , M. R. Farhat <sup>3</sup> ;<br><sup>1</sup> Tufts Medical Center, Boston, MA, <sup>2</sup> Harvard College, Cambridge, MA, <sup>3</sup> Harvard Medical School, Boston, MA.  |



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| <a href="#">2022-A-181-NGS</a> | 135 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | <p>Evaluation of the ONT MinION Mk1C platform vs Illumina MiSeq for the epidemiological surveillance of SARS-CoV-2 in the Northern Metropolitan Area of Barcelona, Spain</p> | <p><b>A. C. Pelegrin</b><sup>1</sup>, D. Panisello Yagüe<sup>1</sup>, L. Soler<sup>1</sup>, A. E. Bordoy<sup>1</sup>, S. Martínez-Puchol<sup>1</sup>, G. Clara<sup>1</sup>, S. González-Gómez<sup>1</sup>, A. Paris de León<sup>1</sup>, A. Blanco<sup>1</sup>, M. Noguera<sup>2</sup>, M. Armengol<sup>3</sup>, O. Francino<sup>4</sup>, I. Blanco<sup>5</sup>, V. Saludes<sup>1</sup>, P. Cardona<sup>1</sup>, E. Martró<sup>1</sup>;<br/> <sup>1</sup>Microbiology Department, Laboratori Clínic Metropolitana Nord, Germans Trias i Pujol University Hospital, Germans Trias i Pujol Research Institute (IGTP), Badalona, Spain, Badalona, SPAIN, <sup>2</sup>IrsiCaixa AIDS Research Institute, Germans Trias i Pujol Research Institute (IGTP), Badalona, SPAIN, <sup>3</sup>Translational Genomics Unit, IGTP, Badalona, SPAIN, <sup>4</sup>Facultat de Veterinària, Universitat Autònoma de Barcelona, Bellaterra, SPAIN, <sup>5</sup>Clinical Genetics Department, Laboratori Clínic Metropolitana Nord, Germans Trias i Pujol University Hospital, Badalona, SPAIN.</p> |
| <a href="#">2022-A-150-NGS</a> | 136 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | <p>Evaluating the detection of <i>Mycobacterium tuberculosis</i> heteroresistance by Whole Genome Sequencing</p>   | <p>S. Danchuk<sup>1</sup>, <b>O. Solomon</b><sup>1</sup>, T. Kohl<sup>2</sup>, S. Niemann<sup>2</sup>, D. van Soolingen<sup>3</sup>, J. van Ingen<sup>4</sup>, M. Behr<sup>1</sup>;<br/> <sup>1</sup>McGill University, Montreal, QC, CANADA, <sup>2</sup>Molecular</p>   |

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|                                |     |                          |                          |     |   | and Experimental Mycobacteriology, Research Center Borstel, Borstel, GERMANY, <sup>3</sup> National Institute for Public Health and Environment, Bilthoven, NETHERLANDS, <sup>4</sup> Radboud University Medical Centre, Nijmegen, NETHERLANDS.   |
| <a href="#">2022-A-101-NGS</a> | 137 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Genotyping of isolates from children with tuberculosis in a tertiary care hospital in Mexico                  | <b>D. Manzano</b> , J. A. Ferrer, I. V. Diaz, A. G. Bravo, P. Saltigeral, M. Macias; INSTITUTO NACIONAL DE PEDIATRIA, MEXICO, MEXICO.   |
| <a href="#">2022-A-195-NGS</a> | 138 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Comparing Genomic Methods for <i>Salmonella</i> Enteritidis   | <b>S. Holtsmark Nielsen</b> , P. Gyomose, E. Litrup; Statens Serum Institut, Copenhagen, DENMARK.   |
| <a href="#">2022-A-194-NGS</a> | 139 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Modularizing SARS-CoV-2 Bioinformatics Solutions for Adaptability to Other Pathogens of Public Health Concern | <b>F. J. Ambrosio</b> <sup>1</sup> , C. J. Kapsak <sup>1</sup> , N. Hull <sup>2</sup> , K. G. Libuit <sup>1</sup> , J. R. Sevinsky <sup>1</sup> ; <sup>1</sup> Theiagen Genomics, Highlands Ranch, CO, <sup>2</sup> APHL, Silver Spring, MD.  |
| <a href="#">2022-A-25-NGS</a>  | 141 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Utility of Whole Genome Sequencing in Diagnosis of Mono- and Polyresistant Tuberculosis                       | <b>M. Dohál</b> <sup>1</sup> , I. Porvazník <sup>2</sup> , M. Škereňová <sup>3</sup> , J. Mokry <sup>4</sup> ; <sup>1</sup> Department of Pharmacology and Biomedical Centre Martin, Jessenius Faculty of Medicine in Martin, Comenius University, Martin, SLOVAKIA, <sup>2</sup> National Institute of Tuberculosis, Lung Diseases and Thoracic Surgery, Vyšné Hágy, SLOVAKIA, <sup>3</sup> Department |

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|                               |     |                          |                          |     |  | of Molecular Medicine and Biomedical Centre Martin, Jessenius Faculty of Medicine in Martin, Martin, SLOVAKIA, <sup>4</sup> Department of Pharmacology, Jessenius Faculty of Medicine in Martin, Comenius University, Martin, SLOVAKIA.   |
| <a href="#">2022-A-28-NGS</a> | 142 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Surveillance of SARS CoV-2 genomic variants in wastewater  | <b>s. sherchan;</b><br>Morgan State University, Baltimore, MD.  |
| <a href="#">2022-A-17-NGS</a> | 143 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | A flexible Galaxy-based platform for the analysis of microbial WGS data in public health   | <b>B. Bogaerts,</b> J. Van Braekel, R. Winand, N. H. Roosens, S. C. De Keersmaecker, K. Vanneste;<br>Sciensano, Brussels, BELGIUM.  |
| <a href="#">2022-A-19-NGS</a> | 144 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | NGS-Based Agnostic Diagnostics: BARDA's Vision for Pandemic Preparedness   | <b>D. Mittar,</b> K. Caravelli, S. Selimovic, S. Patel;<br>BARDA\DRIVE, Washington DC, DC.  |
| <a href="#">2022-A-33-NGS</a> | 146 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Detecting within-host diversity of <i>Staphylococcus aureus</i> during colonization: "Pool" genomes vs. Individual genomes         | <b>V. Raghuram</b> <sup>1</sup> , J. J. Gunoskey <sup>2</sup> , N. F. Jacko <sup>2</sup> , K. S. Hofstetter <sup>1</sup> , T. D. Read <sup>1</sup> , M. Z. David <sup>2</sup> ;<br><sup>1</sup> Emory University, Atlanta, GA, <sup>2</sup> University of Pennsylvania, Philadelphia, PA. |
| <a href="#">2022-A-4-NGS</a>  | 147 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | Impact of COVID-19 multi-lineage co-infections on consensus genomes & repository errors, and evidence of within-host recombination | <b>M. Shakya;</b><br>Los Alamos National Laboratory, Los Alamos, NM.  |
| <a href="#">2022-A-10-NGS</a> | 148 | 10/17/2022<br>5:00:00 PM | 10/17/2022<br>7:00:00 PM | 120 | <b>Insights to Pathogenic Potential: Genomic</b>   | <b>G. H. Morales;</b><br>Vanderbilt, Nashville, TN.   |

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|  |  |  |  |  | <b><u>Analysis<br/>of Escherichia<br/>coli from<br/>Asymptomatic and<br/>Symptomatic<br/>Patients</u></b> |  |
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Late Breakers:

**Poster board no. 149**

***Andrew Beck***

Molecular Epidemiology of a Complex, Post-Elimination Measles Outbreak Incorporating Validation of Whole-Genome Phylogenetics by Case Linkage

**Poster board no. 150**

***Clement Tsui***

Genome surveillance revealed *Candida auris* outbreak among COVID-19 pandemic patients and the emergence of echinocandin resistant isolates

**Poster board no. 151**

***Sara Zufan***

Rapid Identification and Antimicrobial Susceptibility Prediction for *Mycobacterium abscessus* Using Nanopore Sequencing