was separated from those associated with human infections by 14 (n=1), 17 (n=1) and ≥20 (n=7).

Conclusion. WGS analysis revealed clinically relevant ESCs genes in closely related S. Berta isolates from human and animal sources. Presence of these genes in NTS highlights the need for enhanced One-Health surveillance and judicious use of antibiotics in humans and food-animal production.

Disclosures. All Authors: No reported disclosures

1437. Biochemical characterization of L1 and L2 β-lactamases from clinical isolates of Stenotrophomonas maltophilia
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Session: P-66. Resistance Mechanisms

Background. Stenotrophomonas maltophilia is a Gram-negative, non-fermenting opportunistic pathogen. Two β-lactamases provide intrinsic resistance to β-lactams: a class B Metallo-β-lactamase L1, and a class A serine β-lactamase (SβL) L2. Recently, we described novel variants of the L1 and L2 in a collection of clinical S. maltophilia isolates collected in the US, and showed through analyses of the amino acid sequences that L1 and L2 grouped into 4 (A-D, B, C, and E) and 2 (A and D) clades, respectively. We aimed to characterize the new L1 and L2 clinical variants biochemically.

Methods. Representative blaL1 and blaL2 genes from each of the identified clades were cloned into pBSC-K and pET24 vectors and transformed into E. coli DH10B and BL21 (DE3) cells, respectively. Minimal inhibitory concentrations (MICs) were determined using CLSI approved methods. Cell-based assays and biochemical characterization was performed on purified enzymes, including circular dichroism (CD), thermal stability, and steady-state kinetics assays, were performed.

Results. Susceptibility testing results using DH10 B E. coli strains expressing the L1 and L2 variants are shown in Table 1. Remarkably, while all L1 variants confer the same level of resistance to carbapenems, L2B conferred higher MICs to 3rd gen cephalosporins and aztreonam than L2D. Kinetics assays confirmed differences in the kcat of both enzymes to cefazolin (32 s-1 for L2B vs. 7 s-1 for L2D) and avibactam inhibition constant Ki (1.7 μM for L2B vs. 4.5 μM for L2D). Structurally, L2B and L2D present distinctive CD spectra and thermal stabilities (∆Tm 5°C).

Table 1

1438. Dissecting the Multifaceted Nature of Antibiotic Resistance in Clinical Isolates of Neisseria gonorrhoeae by Natural Transformation
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Session: P-66. Resistance Mechanisms

Background. Neisseria gonorrhoeae (NG) causes the sexually transmitted disease gonorrhea. It has developed resistance to every antibiotic introduced for gonorrhea treatment such that NG clinical isolates with multidrug resistance (MDR) are increasingly common. We hypothesize that natural transformation could be used to transfer genetic determinants of antibiotic resistance to NG clinical isolates without pre-knowledge of the genetic determinants to a new background under antibiotic selection to generate isogenic transformants for further characterization.

Methods. Natural transformation, PCR amplification and DNA sequencing, and antibiotic susceptibility testing were used in the study.

Results. We have validated the hypothesis using genomic DNA from an MDR including cipirofloxacin-resistant NG clinical isolate as a donor and a ciprofloxacin-susceptible NG isolate as a recipient under the selective pressure of ciprofloxacin. This led to a series of transformants that contain single or multiple genetic resistance determinants. Experiments are on the way to determine the structural basis of these observations and implications of these for the design of novel β-lactamase inhibitors.

Disclosures. Kristzina M. Papp-Walace, PhD (Grant/Research Support); Merck (Grant/Research Support); Venator (Grant/Research Support); Robert A. Bonomo, MD, Entasis, Merck, Venator (Research Grant or Support)

Conclusion. As opposed to the L2 variants, our results suggest that the L1 variants may not be functionally nor structurally different. Differences between L2B and L2D might have arisen due to the use of cephalosporins and SβL inhibitors. Further experiments are on the way to determine the structural basis of these observations and the implication of these for the design of novel β-lactamase inhibitors.

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1439. High Rates of Drug Resistance in Escherichia coli from a Pilot Antimicrobial Resistance Surveillance System in Cambodia
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Session: P-66. Resistance Mechanisms

Background. Antimicrobial resistance (AMR) is a major and growing global public health problem. The Cambodian Ministry of Health established a pilot laboratory-based AMR surveillance system for blood specimens in 2017. The objective of this study is to characterize AMR among pathogenic isolates from blood samples.

Methods. A retrospective analysis was performed using one year of data from a pilot AMR Surveillance system in Cambodia. Four blood culture isolate pathogens were included: Escherichia coli, Klebsiella pneumoniae, Salmonella Typhi /Salmonella Paratyphi A and Staphylococcus aureus. Blood culture isolates were analyzed at the National Public Health Laboratory for Antimicrobial Resistance Surveillance System in Cambodia. Four blood culture isolate pathogens were included: Escherichia coli, Klebsiella pneumoniae, Salmonella Typhi /Salmonella Paratyphi A and Staphylococcus aureus. Blood culture isolates were analyzed at the National Public Health Laboratory for Antimicrobial Resistance Surveillance System in Cambodia. Four blood culture isolate pathogens were included: Escherichia coli, Klebsiella pneumoniae, Salmonella Typhi /Salmonella Paratyphi A and Staphylococcus aureus. Blood culture isolates were analyzed at the National Public Health Laboratory for Antimicrobial Resistance Surveillance System in Cambodia.

Conclusion. We demonstrated the utility of natural transformation in dissecting the multifaceted nature of antibiotic resistance in NG clinical isolates.

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