OLB03
2-hour Oral Session
Late breaker session: Colistin resistance

Human as a source of colistin resistance: presence of the mcr-1 gene in the gut microbiome

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Background: Colistin is our last line of defense in the treatment of infections caused by multidrug-resistant pathogens. However, resistance against colistin has been observed around the world. In a recent study, a plasmid mediated colistin resistance gene (*mcr-1*) was identified for the first time. While this is an evidence that the dissemination of colistin resistance via horizontal gene transfer is possible, and the emergence of pandrug resistant pathogens might be faced in a very near future, a natural question that "*what is the current span of mcr-I in the resistome ecosystem?*" immediately raises. It is well known that, one of the main reservoirs of resistome in its ecosystem is the human microbiome. Taking this fact into consideration, here we conducted *in silico* search of *mcr-1* and its mediator pHNSHP45 plasmid on large metagenomics datasets of human gut microbiome, deposited to the public metagenome databases in different geographies.

Material/methods: The gut metagenome of 344 Chinese and 145 European individuals were investigated. These two cohorts were among the datasets with largest amount of indiviuals from different geographies, and this is the underlying reason for employing them in the search. The basic methodology for mining metagenome data for *mcr-1* gene and pHNSHP45 plasmid was using BLASTn program. A nucletotide identity threshold of 95% identity was set and the reads aligning under that similarity scores were filtered out. According to the gene annotation of pHNSHP45 plasmid each open reading frame is determined and the metagenomic fragments mapped on each gene were

recorded. Also the percentage coverage of the plasmid for each metagenome after alignment were calculated by reference-based assembly of the plasmid fragments.

Results: According to our investigation, 6 out of 344 individuals harbor *mcr-1* gene and close homologues of pHNSHP45 plasmid in their gut microbiata in the Chinese cohort whereas no related genetic elements were in the European cohort. Collectively, around 78% of the entire plasmid (>50,000bp, >96% identity) was covered by the metagenome reads, and that included reads from all 82 open reading frames annotated on the plasmid.

Conclusions: As human gut microbiome is one of the important reservoirs of resistome, the presence of *mcr-1* gene in human microbiata is alarming. From an anthropocentric point of view, this dissemination means a key element for the emergence of the superpathogens has made its way to our bodies, and it is a matter of time that the dissemination of *mcr-1* gene will be prevalent in the clinic, bringing the world closer to an antibiotic crisis. Further investigation in the countries where colistin resistance has become a serious problem, such as Turkey, should be considered as the surveillance of related dissemination.