Abstract:

Carbapenemase producing Enterobacterales (CPE) has become a global health burden, they are mostly associated with hospital acquired infections, thus limiting treatment options given that they confer resistance to multiple antibiotics. In many situations, resistance is manifested by enzymes spreading between species and clones, facilitated by plasmids and other mobile genetic elements. Thus, the aim is to characterize the mechanism of the carbapenem resistance as well as the mechanisms of dissemination.

Methodology involves the identification of the bacterial species, identification of the genes encoding for the carbapenemase enzymes, Short-reads sequencing. This is followed up by Long-reads sequencing to obtain a complete genome with circular plasmids facilitating the analysis of the plasmids and mobile genetic elements behind the possible dissemination of the resistance genes. And finally further analysis on the detected outbreak such as SNPs analysis, phylogenetic tree with genomes available from the database.

Results have shown that the dissemination of some genes, for example bla_{KPC} was linked to plasmid dissemination and this was due to the conjugative nature of the plasmids in question. Furthermore, For the detected bla_{VIM} in Czech Republic it was found that the dissemination was in majority linked with the integron In110, and also it was found that plasmids helped this dissemination. On the other hand, the detected bla_{GES} isolates were different, they highlighted a persistence of plasmids in silent reservoirs and their ongoing evolution and also found that the bacterial isolate was also able to assemble plasmids from environmental sources. Finally, bla_{NDM} isolates detected in Lebanon, were found to be spreading with multiple clones and plasmids.

In conclusion, this emphasizes the need for implementing infection control measures to prevent transmission, as well as performing in-depth analysis to discover new patterns in plasmid evolution and other mobile genetic element.