MCR bearing Salmonella enterica phylogeny and the evolution of antibiotic resistance

Maria Luiza Andreani, Juliana José, Marcelo Brocchi

University of Campinas

The emergence of new antibiotic resistance mechanisms is a major public health concern. Colistin is a last resort antibiotic to which resistance genes have increasingly been reported, with at least 10 different variations registered to date. Although colistin is not a preference for clinical treatment, it is widely used in animal production, creating an environment where resistance can rise, spread, and be undetected. Salmonella enterica is a gram-negative bacterium that can infect both humans and livestock and has been shown to carry mobilized colistin resistance (mcr) genes, posing as a potential threat to public health. In order to control mcr spread and antibiotic resistance rise on Salmonella enterica a better understanding of evolutionary context is necessary. Here, we analyze the phylogenetic relationship among Salmonella enterica isolates coming from environmental and clinical context and harboring at least one plasmid with mcr genes (mcr-1 to mcr-9) as well as their pangenome. Moreover, we also analyze the phylogenetic relationship of the plasmids present on those isolates, unraveling the relationship among different mcr variants in Salmonella. This data provide a better understanding of colistin resistance spread and status on Salmonella and can be useful to prevent it by public health measures.

1. What is your pathogen? Multiple options possible (e.g. if working on coinfections)
   Bacteria: Salmonella enterica

2. On a scale of 1-5 is your work mostly eco/epidemiological or evolutionary? 4

3. On a scale of 1-5 is your work mostly theoretical or experimental/empirical? 3