E. coli-producing ESBL harbouring mcr-1 from Ecuador

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Background: After the identification of transferable colistin resistance in *Enterobacteriaceae* (ColRE) mediated by the phosphoethanolamine transferases MCR-1 and MCR-2, these resistance traits have been increasingly reported worldwide. Furthermore, ColRE have been identified not only in clinical settings but also have been recovered from environmental sources (including foods of animal origin) suggesting complex dynamics of transmission, highlighting the importance of the *One Health* approach. However, the epidemiology of ColRE remains underestimated, particularly in developing countries where limited surveillance data are available. In Ecuador there are scarce data about ColRE and the genetic determinants involved in multi-resistant isolates. We present the microbiological and genomic characterization of 3 E. coli strains from Ecuador.

Materials/Methods: We screened a collection of 111 isolates recovered from poultry houses in Ecuador. We identified two ESBL-producing *E. coli* isolates (designated 109B and 160A, respectively) harboring *mcr-1*. Using whole genome sequencing we performed phylogenetic comparisons of these two isolates plus an additional colistin-resistant *E. coli* (isolate 1409) recovered in 2015 from a human patient in Quito. Resistance profiles were carried out using Vitek2® system. Genetic analysis included PCR, Sanger sequencing and WGS on Illumina platform. The tools from the Center for Genomic Epidemiology were used to characterize the strain genomes and analyzed using standard methodology.

Results: The poultry isolates 109B and 160A belonged to ST602 and ST665 respectively, while the human isolate 1409 belonged to ST609. Of note, these STs have been previously related to environmental origin. All strains harbored genes encoding ESBLs that included $bla_{\text{CTX-M-14}}$, $bla_{\text{CTX-M-65}}$ and $bla_{\text{CTX-M-55}}$ in 109B, 160A and 1409, respectively. All strains harbored resistance determinants to aminoglycosides, trimethoprim/sulfamethoxazole, tetracycline and chloramphenicol. Additionally, 160A (animal isolate) carried the *aac(6')Ib-cr* gene and was also resistant to fluoroquinolones, while 1409 (human isolate) exhibited resistance to tigecycline. All strains were enriched in genes coding siderophores which are considered important virulence determinants in *E. coli* with poultry isolates harboring more putative virulence determinants than the human clinical isolate. The contigs carrying *mcr-1* gene (12-14 Kb) were highly similar between all isolates and showed high nucleotide identity (99%) with previously reported *mcr-1* carrying plasmids.

Conclusion: Poultry isolates in Ecuador seem to harbor important number of resistance determinants including transferable colistin resistance. Of note, the strains seem to be highly equipped to cause disease in human harboring a cadre of virulence determinants. Overall, our results highlight the importance of resistance in the animal industry as a source of potential dissemination into humans in developing countries.