

Assembling the genome of ExPEC MT78

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Escherichia coli are gram negative bacteria that lives commensally in our microbiota. Still, due to the incredible genome plasticity of this species, lots of lineages diverged from the commensal strains, acquiring the ability to cause disease not only in humans but also in other warm-blood animals, often impairing the poultry, cow and pig farming industry. The APEC (Avian Pathogenic *Escherichia coli*) pathotype causes extraintestinal infections in avian species, known as colibacillosis; the infection usually starts at the respiratory tract, and may evolve to colisepticemia resulting in bird's death. Matter et al. (2011. Vet. Microbiol. 148:51) tested the capacity of adhesion and invasion of a nine avian *E. coli* strains, among which APEC MT78 (O2:H⁺) strain showed high levels of those traits, evidencing the need of further genomic analysis. The goal of this work was to clarify some of the new findings about this lineage. The MT78 sequenced genome was obtained through Illumina sequencing and was assembled in 118 contigs. Furthermore, we have downloaded from the NCBI genome bank the DNAs of 33 *E. coli* strains for BLASTn and BRIG comparative analysis. Evaluation of the results showed the presence of an apparent ≈140 kbp plasmid with high Bit score with the pMDR56 plasmid, followed by pAPEC-ColBM and p1ColV5155 plasmids. MDR (Multi Drug Resistant) and Colicin encoding plasmids are commonly known for its high fitness and virulence expression. Colicin production plasmids have long been associated with virulence in APEC and has also been found it frequently in serogroups O78, O1, O7 and O18. These results converged with the ones found by BLAST comparisons that indicated a great level of similarity between the MT78 and O18 strains (e. g. PMV-1, APEC O18, NMEC O18, RS218, NU14 among others). Still, the highest similarity was with the IMT5155 genome, which belongs to the O2 serogroup. Our results are in agreement with the ones obtained by Ge et al. (2014. PLoS One 9: e112048) which showed a close genomic relationship between IMT5155 and O18 strains. Further phylogenetic analysis could reveal more about the MT78 relation to other strains and possibly unraveling more of its virulence mechanisms.

