Introduction:
We study the population structure and resistome of MDR Enterobacterales and Pseudomonas aeruginosa isolates, C/T-susceptible or -resistant, recovered from low respiratory, intraabdominal and urinary tract infections of ICU patients of 11 Portuguese Hospitals (STEP study, 2016-2017).

Methods:
MICs were determined (ISO-broth microdilution, EUCAST) and 30 Escherichia coli, 79 Klebsiella spp. and 42 P. aeruginosa isolates were selected for Whole Genome Sequencing (Illumina-NovaSeq 6000, OGC, UK). Assembly (SPAdes), annotation (Prokka) and in silico MLST were performed. Resistance genes were identified (Abricate). E. coli phylogroup (ClermonTyping), serotypes (SerotypeFinder) and fimH-types (FimTyper) were determined. Klebsiella spp. capsule (K) and LPS (O) serotype were predicted (Kleborate). P. aeruginosa O-specific antigen was identified (Blastn).

Results:
In E. coli, two VIM-2 producers were found (ST131-B2-H30-O25:H4-CTX-M-15 and ST88-C-H39-O22:H4) (C/T-MIC=0.5/4-1/4 mg/L). A KPC-3-ST5463-clade-V-H160-O164:H56 (16/4 mg/L) was also detected. The most frequent ESBL-E. coli clone was ST131-B2-H30-O25:H4 (n=14) (0.25/4-1/4 mg/L), related to CTX-M-15 (10/14) or CTX-M-27 (4/14). Ninety-five percent of carbapenemase-Klebsiella isolates (n=21) were C/T resistant (2/4->64/4 mg/L). KPC-3-ST13-KL3-O1v2 (n=5), KPC-3-ST5-KL112-O1v1 (n=2), KPC-3-ST231-KL51-O1v2 (n=2), OXA-181-ST17-KL25-O5 (n=2) and OXA-48-ST215-KL16-O1v1 (n=2) were the most frequent clones. A high diversity was found in ESBL (n=41) and non-ESBL (n=17) strains (0.5/4->64/4 mg/L). In P. aeruginosa, the most frequent clone was GES-13-ST235-O11 (n=13) (32/4->64/4 mg/L). VIM-2 was found in ST244-O5 and ST179-O6 (>64/4 mg/L) and KPC-3 in ST499-O1 and ST253-O12 (1/4 mg/L). A high clonal diversity was found in non-carbapenemase producers (0.5/4-4/4 mg/L).

Conclusion:
Carbapenemase genes are not always associated with C/T resistance in Enterobacterales and P. aeruginosa, but other mechanisms might be involved.