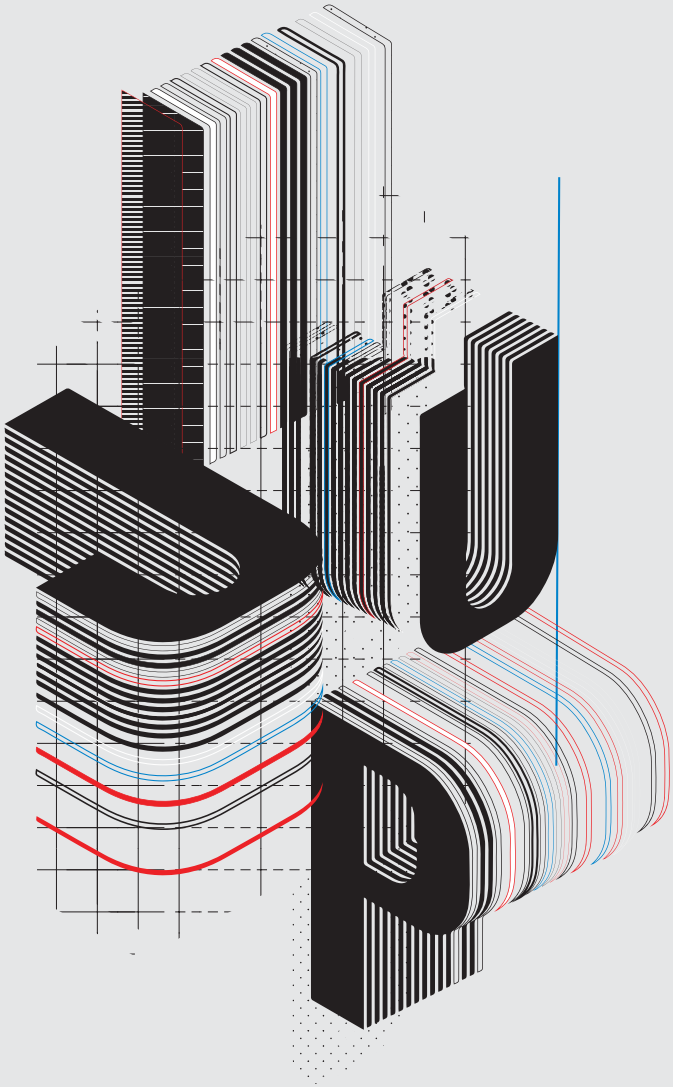
BOOK OF ABSTRACTS

12TH MEETING
OF YOUNG RESEARCHERS
OF **UNIVERSITY OF PORTO**



- ## 15065 | Widespread of ampicillin-multidrug-resistant Enterococcus faecium in raw chicken meat, Portugal

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Ampicillin resistance-AmpR often occurs in Enterococcus faecium-Efm from hospitalized-humans (clade-A1) and less in community isolates (clade-A2: human/animal; clade-B:human-commensal). AmpR plus specific virulence factors were proposed as molecular markers of Efm linked to human infections, which can have an impact in Efm strains risk assessment in different public health contexts (PMID:29519512). We studied the occurrence of AmpR-Efm with potential public health impact in raw chicken-meat samples.
Samples (n=53; neck skin of 10 carcasses; 29 producers) obtained at processing level were pre-enriched (Buffered-Peptone-Water; 37ºC/16-18h), enriched (BHI-broth+Amp-16µg/mL) and plated [Slanetz-Bartley-(SB) and SB+Amp-16mg/L]. Susceptibility was studied for 11 antibiotics (disk-diffusion; EUCAST/CLSI). Identification (ddl), virulence (esp/sgrA/ecbA/complete-acm/hyl/ptsD/orf1481/IS16), copper-tolerance (tcrB/cueO) and linezolid resistance (optrA/poxtA; DNA extracted from the pre-enrichment) genes (PCR) and clonality (SmaI-PFGE/MLST) were studied.
AmpR-Efm (49 isolates) occurred in 83% of samples. They were co-resistant to tetracycline, erythromycin-both 100%, quinupristin-dalfopristin-94%, ciprofloxacin-73%, streptomycin-31%, gentamicin-12% or chloramphenicol-2%. Ten clones were identified (PFGE), some persisting for long periods and from diverse producers (PFGE-A:7-isolates/6-producers/5-months; C:10-isolates/10-producers/5-months; B:2-isolates/2-producers/2-months; G:3-isolates/3-producers/2-months). The most widespread A (ST462) and C (ST1091) belonged to clade-A2. The ptsD occurred in clone G and acm in C/G/I/J. The tcrB, cueO, optrA, poxtA were negative.
A high rate of AmpR-Efm was detected in chicken-meat-samples, suggesting a selective pressure by beta-lactams in the poultry production. The evaluation of the pathogenic potential of AmpR-Efm widespread clones is required, as they do not carry virulence genes combinations often linked to human infection´s strains.