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P2547 High rates of ampicillin multidrug-resistant *Enterococcus faecium* in chicken meat from Portugal

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Background: Resistance to ampicillin-AmpR is associated with *Enterococcus faecium-Efm* from hospitalized-humans (clade-A1) and at lesser extent with community-based isolates (clade-A2: human and animal strains; clade-B: human-commensal strains). Recently, AmpR combined with specific putative virulence factors were proposed as molecular markers of Efm linked to human infections, which can have an impact in Efm risk assessment in different public health contexts (PMID:29519512). Here we evaluated the occurrence of AmpR-Efm with potential public health impact in chicken-meat samples.

Materials/methods: Pooled chicken-meat samples (n=53; neck skin of 10 carcasses of the same batch each; 29 producers) obtained after slaughter and chilling at processing level were collected during 6 months of 2018. Samples (25g) were pre-enriched in Buffered-Peptone-Water (37ºC/16-18h), enriched in BHI-broth+Amp-16µg/mL (37ºC/24h) and plated in Slanetz-Bartley-(SB) and SB+Amp-16mg/L (37ºC/48h). Susceptibility was studied for 11 antibiotics (disk-diffusion; EUCAST/CLSI) in one Efm per sample/plate. Species identification (*ddl*), search of virulence factors (surface-proteins:*esp/sgrA/ecbA*/complete-*acm*; enhanced colonization:*hyl/ptsD/orf1481;* genomic plasticity:*IS16*) and copper-tolerance (*tcrB/cueO*) genes were searched by PCR. Linezolid resistant genes (*optrA*, *poxtA*) were directly searched in DNA extracted from the pre-enrichment by PCR. Clonality was evaluated in representative isolates by *Sma*I-PFGE and MLST.

Results: AmpR-Efm were present in 83% (n=44/53) of samples. Isolates (n=49) were mostly recovered from SB+Amp plates (n=45/49-92%). AmpR-Efm were co-resistant to tetracycline, erythromycin (both 100%-n=49/49), quinupristin-dalfopristin (94%-n=46/49), ciprofloxacin (73%-n=36/49), streptomycin (31%-n=15/49), gentamicin (12%-n=6/49) or chloramphenicol (2%-n=1/49), all multidrug-resistant (MDR). Glycopeptides or linezolid (including the presence of *optrA/poxtA* in samples) resistance was not observed. By PFGE, 10 clones were identified, some persisting for long periods and from diverse producers (PFGE-A:7-isolates/7-samples/6-producers/5-months; C:10-isolates/10-samples/10-producers/5-months; B:2-isolates/2-samples/2-producers/2-months; G:3-isolates/3-samples/3-producers/2-months). The most widespread ones, A and C, were identified as ST462 and ST1091, respectively (both clade-A2). The *ptsD* was detected in clone G (n=1) and *acm* in clones C, G, L, I and J (n=5). The *tcrB/cueO* were not detected.

Conclusions: A high rate of AmpR-MDR-Efm was recovered from recent chicken-meat-samples, suggesting a high selective pressure by beta-lactams in the poultry production setting. The evaluation of the pathogenic potential of the AmpR-Efm widespread clones is required, as they do not carry virulence genes combinations (PMID:29519512) often associated with human infection's strains.