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BOOK OF ABSTRACTS

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Ready-to-eat salads a vehicle of bacteria and clinically relevant antibiotic resistance genes

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Background. The increase demand for fresh vegetables is causing an expansion of the market for minimally processed vegetables along with new recognized food safety problems. The aim of this study was to analyse the microbiological quality of Portuguese ready-to-eat salads (RTS) and their role in the spread of bacteria carrying antibiotic resistance (ABR) genes.

Methods. RTS (n=50; 7 brands; split or mixed leaves, carrot, cornmeal) were collected in 5 supermarkets in Porto (2010). We screened for *Salmonella*, *Listeria monocytogenes* and aerobic mesophilic counts, coliforms and *Escherichia coli* (standard methods). Samples were also plated in different selective media with/without antibiotics before and after enrichment. ABR was studied by agar diffusion/E-test (CLSI/EUCAST) and detection of extended-spectrum β-lactamase (ESBL) by double disk synergy test and sequencing. Species were identified by PCR (Gram positive), API ID32GN/16S PCR (Gram negative). ABR genes, integron types and *E. coli* phylogenetic groups (PHG) by PCR, clonality by MLST/PFGE in *E. coli* and conjugation assays in specific isolates were performed.

Results. A high number of RTS presented poor microbiological quality (86% for aerobic mesophilic, 74%-coliforms, 4%-*E.coli*), despite the absence of pathogens. *E. coli* was detected in 13 samples (n=78; all types and 4 brands; PHG A, B1, B2, D) with resistance to tetracycline (72%; *tetA* and/or *tetB*), streptomycin (56%; *aadA* and/or *strA-strB*), sulfametoxazole (50%; *sul1* and/or *sul2*), trimethoprim (50%; *dfrA1* or *dfrA12*), ampicillin (47%; bla_{TEM}), nalidixic acid (36%), ciprofloxacin (5%) or chloramphenicol (3%; *catA*). Two integron types (*dfrA1-aadA*, *dfrA12-aadA*) were detected in 12 multidrug resistant isolates (MDR), which includes *E. coli* (n=2; D) belonged to the widespread clonal lineage ST69. Among coliforms, were detected 2 *Raoutella* sp (2 samples) carrying an ESBL SHV-2 and 1 *Citrobacter freundii* with a *qnrB* gene. Among *Enterococcus* (n=108; 35 samples; *E.casseliflavus*-40, *E.faecalis*-20, *E.faecium*-18, *E.hirae*-9, *E.gallinarum*-5, and *Enterococcus spp*-16) ABR was detected for tetracyclines (6%; *tet*M and/or *tet*L), erythromycin (3%; *erm*B), nitrofurantoin (1%) or ciprofloxacin (1%).

Conclusions. The present study positions RTS within the spectrum of ecological niches that may be reservoirs/vehicles for antibiotic resistance bacteria/genes with clinical interest (e.g. *E. coli*-D-ST69; bla_{SHV-2}; *qnrB*) being these findings worthy of attention as their spread to humans by ingestion cannot be dismissed.

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