The Connection between Persistent, Disinfectant-Resistant Listeria monocytogenes Strains from Two Geographically Separate Iberian Pork Processing Plants: Evidence from Comparative Genome Analysis

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Abstract

The aim of this study was to investigate the basis of the putative persistence of *Listeria* monocytogenes in a new industrial facility dedicated to the processing of ready-to-eat (RTE) Iberian pork products. Quaternary ammonium compounds, which included benzalkonium chloride (BAC), were repeatedly used as surface disinfectants in the processing plant. Clean and disinfected surfaces were sampled to evaluate if resistance to disinfectants was associated with persistence. Of the 14 isolates obtained from product contact and nonproduct contact surfaces, only five different pulsed-field gel electrophoresis (PFGE) types were identified during the 27-month study period. Two of these PFGE types (S1 and S10-1) were previously identified to be persistent and BAC-resistant (BAC^r) strains in a geographically separate slaughterhouse belonging to the same company. The remaining three PFGE types, which were first identified in this study, were also BAC^r. Whole-genome sequencing and *in silico* multilocus sequence typing (MLST) analysis of five BAC^r isolates of the different PFGE types identified in this study showed that the isolate of the S1 PFGE type belonged to MLST sequence type 31 (ST31), a low-virulence type characterized by mutations in the inlA and prfA genes. The isolates of the remaining four PFGE types were found to belong to MLST ST121, a persistent type that has been isolated in several countries. The ST121 strains contained the BAC resistance transposon Tn6188. The disinfectionresistant L. monocytogenes population in this RTE pork product plant comprised two distinct genotypes with different multidrug resistance phenotypes. This work offers insight into the L. monocytogenes subtypes associated with persistence in food processing environments.

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