Comprehensive typing and genetic analysis of *L. monocytogenes* isolates: implication for food safety and antibiotic resistance surveillance

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Abstract: Listeria species are commonly found in various environments and contaminated food, with livestock serving as a significant source of foodborne pathogens. Among these species, *Listeria monocytogenes (L. monocytogenes)* is particularly noteworthy as it can affect both livestock and humans. Antibiotics are frequently used in food animals for disease treatment and prevention on a large scale. This practice can lead to the selection of antibiotic-resistant bacterial strains, which can then spread to humans through the food chain. Consequently, *L. monocytogenes,* a ubiquitous foodborne pathogen, has been associated with global outbreaks of foodborne illnesses. To address this concern, the aim of the study was to conduct comprehensive typing and genetic analysis of 13 *L. monocytogenes* isolates obtained from food and food-processing environments. Among the 13 *L. monocytogenes* isolates, eight sequence types (ST) were identified: two isolates were identified as belonging to ST9; one as ST155; four as ST3, two as ST121, one as ST8; one as ST87; one as ST1; and one new ST belonging to CC121. Core-genome clustering analysis of *L. monocytogenes* was made to assess the genetic relatedness among the isolates. The core genome Multilocus Sequence Typing (cgMLST) analysis revealed three genetic clusters of high closely related isolates (£7 allelic differences (ADs)): cluster 1. Regarding *L. monocytogenes* typing, ST3 was the most prevalent among the isolates, found in 4 isolates, followed by ST9 and ST121. Some of these isolates, like ST1, ST9 and ST87, were previously associated with human clinical cases. We used Whole Genome Sequencing (WGS) alongside epidemiological data to link strains to human illnesses and potential food sources. Through cgMLST analysis, we identified genetic clusters of closely related isolates, all linked to the same producers. This approach helped us pinpoint common sources of contamination and gain insights into the transmission dynamics of *L. monocytogenes* in the context of food safety and public health. The escalating antibiotic resistance in *Listeria* species, particularly *in L. monocytogenes*, emphasizes the need for heightened surveillance and improved hygiene practices in the food industry to curb the spread of antibiotic resistance and ensure food safety.