



Molecular Characterization of *Listeria monocytogenes* Based on the PFGE and RAPD in Korea

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ABSTRACT

This study was performed to characterize 35 *L. monocytogenes* isolates from animals, foods, environmental samples collected between 1997 and 2007 with no apparent epidemiological relations, and five reference isolates using serotypic, genotypic and molecular typing methods to understand the pattern of strain distribution in Korea. For this study, we used serotyping and detected 6 different virulence-associated genes (*inlA*, *inlB*, *plcA*, *plcB*, *hlyA*, and *actA*) and 16s rRNA using multiplex-PCR. We also compared RAPD and PFGE to determine genetic characterization of *L. monocytogenes* strains to define the genetic diversity. Serotype patterns of the 30 *L. monocytogenes* strains was as follows: 9 isolates (30.0%) belonged to serotype, 7 isolates (23.3%) belonged to serotype 4b, 4 isolates (13.3%) belonged to serotype 1/2b, 3 isolates (10.0%) belonged to serotype 1/2c, 2 (6.7%) isolates belonged to 4c, 2 (6.7%) isolates belonged to NT (Non Type), one isolate (3.2%) belonged to 3a and 3b, and 4a, respectively. Although, a limited number of isolates were analyzed in this study, molecular typing with RAPD and PFGE indicated that PFGE is more discriminatory for the subtyping *L. monocytogenes* than RAPD. Some *L. monocytogenes* isolates by RAPD and PFGE types are associated with specific sources. And, combining data obtained by these methods will increase the likelihood of strain discrimination.

KEYWORDS

Listeria monocytogenes; PFGE; RAPD

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