The purpose of this study was to evaluate fluorescent amplified fragment length polymorphism (AFLP) analysis for the inter- and intraspecies differentiation of a collection of 96 strains of Listeria monocytogenes and 10 non- L. monocytogenes strains representing six other Listeria species of different origin. The AFLP technique was compared with three other molecular typing methods - ribotyping, random amplified polymorphic DNA analysis (RAPD), and pulsed-field gel electrophoresis (PFGE) - in terms of discriminatory ability. PCR-restriction fragment length polymorphism was included for virulence gene allele characterization. The 96 L. monocytogenes strains were divided into two major clusters by AFLP fingerprinting at a similarity level of 82% in concordance with the results of PFGE, RAPD, and ribotyping. One main cluster consisted of all of the 24 L. monocytogenes hly allele 1 strains, while another main cluster consisted of all of the 72 L. monocytogenes hly allele 2 strains. This indicates the existence of two distinct phylogenetic divisions. Isolates of the remaining Listeria species were not included in the clusters. AFLP, PFGE, and RAPD typing were highly discriminatory methods, with discrimination (D) indices of 0.974, 0.969, and 0.954, respectively, whereas ribotyping had a lower D index of 0.874. AFLP, PFGE, and RAPD typing showed some level of agreement in terms of strain grouping and differentiation. However, all three methods subdivided types of strains grouped by the other methods. Isolates with identical DNA profiles were distributed across the spectrum of origin. It was not possible to associate certain types with specific food sectors or clinical cases, which is indicative of the spread of L. monocytogenes clones across species. Overall, AFLP fingerprinting was suitable for the high-resolution genotyping of L. monocytogenes and had an equally high or higher differentiation power compared to PFGE or RAPD typing.
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