Abstract
In this study, a total of 24 Listeria spp. strains were analyzed. Twenty-two isolates were obtained in San Luis (Argentina) from human, animal, and food samples. Two types of strains, Listeria monocytogenes CLIP 22762 and Listeria innocua CLIP 74915, were included as reference strains. All isolates were biochemically identified and characterized by serotyping, phage typing, and amplification of the flaA gene by polymerase chain reaction (PCR). Repetitive intergenic consensus (ERIC) sequence-based PCR was used to generate DNA fingerprints. On the basis of ERIC-PCR fingerprints, Listeria spp. strains were divided into three major clusters matching origin of isolation. ERIC-PCR fingerprints of human and animal isolates were different from those of food isolates. In addition, groups I and II included ten L. monocytogenes strains, and only one Listeria seeligeri strain. Group III included nine L. innocua strains and four L. monocytogenes strains. Computer evaluation of ERIC-PCR fingerprints allowed discrimination between the tested serotypes 1/2b, 4b, 6a, and 6b within each major cluster. The index of discrimination calculated was 0.94. This study suggests that the ERIC-PCR technique provides an alternative method for the identification of Listeria species and the discrimination of strains within one species.

Keywords
Listeria spp., ERIC-PCR, fingerprints DNA.