

Research Article

Prevalence, Genetic Heterogeneity, and Antibiotic Resistance Profile of *Listeria* spp. and *Listeria monocytogenes* at Farm Level: A Highlight of ERIC- and BOX-PCR to Reveal Genetic Diversity

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This study aimed to identify *Listeria* spp. and *L. monocytogenes*, characterize the isolates, and determine the antibiotic resistance profiles of the isolates *Listeria* spp. and *L. monocytogenes* in fresh produce, fertilizer, and environmental samples from vegetable farms (organic and conventional farms). A total of 386 samples (vegetables, soil, water, and fertilizer with manure) were examined. The identification of bacterial isolates was performed using PCR and characterized using ERIC-PCR and BOX-PCR. The discriminating power of the typing method was analyzed using Simpson's Index of Diversity. Thirty-four (n=34) *Listeria* spp. were subjected to antimicrobial susceptibility test using the disc-diffusion technique. The PCR analysis revealed that *Listeria* spp. were present in 7.51% (29/386) of all the samples (vegetable, soil, fertilizer, and water). None of the samples examined were positive for the presence of *L. monocytogenes*. Percentages of 100% (15/15) and 73.30% (11/15) of the *Listeria* spp. isolated from vegetables, fertilizer, and soil from organic farm B had indistinguishable DNA fingerprints by using ERIC-PCR and BOX-PCR, respectively. *Listeria* spp. isolated from 86 samples of vegetable, fertilizer, and environment of organic farm A and conventional farm C had distinct DNA fingerprints. Simpson's Index of Diversity, D, of ERIC-PCR and BOX-PCR is 0.604 and 0.888, respectively. Antibiotic susceptibility test revealed that most of the *Listeria* spp. in this study were found to be resistant to ampicillin, rifampin, penicillin G, tetracycline, clindamycin, cephalothin, and ceftriaxone. The isolates had MAR index ranging between 0.31 and 0.85. In conclusion, hygienic measures at farm level are crucial to the reduction of *Listeria* transmission along the food chain.

1. Introduction

Listeria is a gram-positive, rod-shaped, and non-spore-forming bacterium [1]. Genus of *Listeria* is classified into 17 species including *Listeria monocytogenes* that is a common causative agent of human foodborne infection, listeriosis [2]. Listeriosis is usually treated with antibiotic therapy involving the use of penicillin, ampicillin, rifampin, gentamicin, tetracycline, erythromycin, chloramphenicol, or trimethoprim with sulfamethoxazole alone or in combination [3, 4]. Previous researches have shown that *Listeria* spp. may be resistant to several antibiotics such as clindamycin, daptomycin,

oxacillin, tetracycline, and nalidixic acid [5, 6]. Therefore, it is important to monitor the antibiotic susceptibility of *Listeria* spp. and *L. monocytogenes* to ensure the effectiveness of listeriosis treatment.

Repetitive sequence-based PCR (Rep-PCR) is a DNA amplification technique for bacterial genomic fingerprinting by using repetitive DNA elements present within bacterial genome. There are four main types of repetitive sequences used for molecular typing which include enterobacterial repetitive intergenic consensus (ERIC) sequence, BOX elements, repetitive extragenic palindromic sequences (REP elements), and (GTG)₅ [7]. Utilization interspersed repetitive