

## Genomic Diversity of Clostridium perfringens Strains in Food and Human Sources

**Authors :** Asma Afshari, Abdollah Jamshidi, Jamshid Razmyar, Mehrnaz Rad

**Abstract :** Clostridium perfringens is a serious pathogen which causes enteric diseases in domestic animals and food poisoning in humans. Spores can survive cooking processes and play an important role in the possible onset of disease. In this study RAPD-PCR and REP-PCR were used to examine the genetic diversity of 49 isolates of C. Perfringens type A from 3 different sources. The results of RAPD-PCR revealed the most genetic diversity among poultry isolates, while human isolates showed the least genetic diversity. Cluster analysis obtained from RAPD-PCR and based on the genetic distances split the 49 strains into five distinct major clusters (A, B, C, D, and E). Cluster A and C were composed of isolates from poultry meat, cluster B was composed of isolates from human feces, cluster D was composed of isolates from minced meat, poultry meat and human feces and cluster E was composed of isolates from minced meat. Further characterization of these strains by using (GTG) 5 fingerprint repetitive sequence-based PCR analysis did not show further differentiation between various types of strains. To our knowledge, this is the first study in which the genetic diversity of C. perfringens isolates from different types of meats and human feces has been investigated.

**Keywords :** C. perfringens, genetic diversity, RAPD-PCR, REP-PCR

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