

Genotypic comparison of *Ornithobacterium rhinotracheale* isolates from commercial chickens of Iran

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Abstract

Ornithobacterium rhinotracheale (ORT) is a newly emerging respiratory bacterial pathogen that causes significant economic losses to the poultry industry. Previous studies in Iran have shown high molecular and genetic similarity among ORT isolates by SDS-PAGE, ERIC-PCR and 16SrRNA gene sequencing during 1999-2009. The aim of this study was the genotyping of ORT isolates recovered from commercial chickens by using RAPD-PCR with OPG11 primer and multilocus sequence typing (MLST). In total, 30 ORT isolates recovered from commercial chickens of Iran during 2000-2017 and confirmed by bacteriological, biochemical and PCR tests were used in this study. All 30 ORT isolates were subjected to RAPD-PCR with OPG11 primer. For MLST, 5 isolates were selected based on their RAPD patterns. Seven primer pairs were synthesized for amplification and sequencing of seven housekeeping genes of *adk*, *aroE*, *fumC*, *gdhA*, *mdh*, *pgi* and *pmi* in MLST assay. In RAPD-PCR with OPG11 primer, 9 different genotypes were found. The DNA sequences of the distinct alleles of these seven loci of 5 ORT strains were compared with other alleles deposited in GenBank. Four out of 5 strains belonged to sequence type 9 (ST9) and one strain was found to be a new ST. Based on the results of the present study, a new sequence type among ORT isolates of Iran was found that has not been previously reported from elsewhere in the world. Further studies on more ORT isolates may help in identification of different sequence types and dominant ST in the country.

Key words: Genotyping, MLST, *Ornithobacterium rhinotracheale*, Poultry, RAPD-PCR

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