Mycoplasma hyorhinis in Taiwan diagnosis and isolation of swine pneumoniae pathogen

葉光勝

Lin JH;Chen SP;Yeh KS;Weng CN

摘要

Abstract

This study attempted to determine whether one multiplex polymerase chain reaction (PCR) is an effective adjunct method for diagnosing Mycoplasma hyopneumoniae and Mycoplasma hyorhinis infection, and whether M. hyorhinis should be considered as an enzootic pneumonia or porcine respiratory disease complex pathogen in Taiwan. To our knowledge, this study is the first to isolate and identify M. hyorhinis as a porcine pathogen in Taiwan. A novel isolation method and a multiplex PCR test were applied to detect and isolate M. hyorhinis. The correlation of M. hyorhinis with swine pneumonia was also examined using a challenge test. Based on weight, 18 pigs were assigned to three groups and housed throughout the study in a specific-pathogen-free (SPF) facility and provided with aseptic feed and water. Groups 1 (n=6) and 2 (n=6) were challenged with 5mL M. hyorhinis culture via tracheal intubation on day 1. The M. hyorhinis strains ATIT-1, -3, and-7 were used to infect group 1 and the strain ATCC 27717 was used for group 2. Culture medium was replaced by phosphate-buffered saline in group 3 (n=6). All pigs were slaughtered on day 28, and their lungs were removed for examination of lesions. Of the six pigs in group 1 challenged with wild-type strains, two had typical mycoplasma pneumonia lesions. No gross lung lesions were observed in groups 2 and 3. Although further examination is necessary to confirm that wild-type strains can cause pneumonia, it appears that M. hyopneumoniae is no longer the only mycoplasma pathogen implicated in the diagnosis of swine enzootic pneumonia (SEP).