

Molecular identification of two genetic markers that distinguish between pathogenic and nonpathogenic strains of *Mycoplasma gallisepticum*.

ABSTRACT

A total of 571 *Mycoplasma gallisepticum* (MG) field isolates originated from progenies and commercial poultry farms in Malaysia and 7 reference and vaccine strains were characterized by amplification of selected gene target specific sequences to MG pMGA and pvpA genes using conventional PCR of sequence specific primers. A total of 281 MG positive field isolates out of 571 MG samples were detected with the primer targeted pMGA gene and a total of 188 MG positive field isolates out of 571 MG samples were detected with the primer targeted pvpA gene. Similar and identical banding pattern among MG isolates obtained from progenies samples however, there was a variable on the banding pattern among MG isolates obtained from commercial chickens using the agarose gel electrophoresis. The sequencing analysis results of MG based on selected genes targeted specific sequences were obtained. The genetic diversity of the pMGA and pvpA genes of MG field isolates detected in progenies and commercial chickens were investigated. The gene size variation patterns of the pMGA and pvpA genes among MG field isolates shared identical variations with the pathogenic reference and vaccine strains that is an insertion bp fragments by using the pMGA gene primer set and a deletion bp fragments by using the pvpA gene primer set. However, the gene size variation patterns are quite different from the variation pattern of the less pathogenic vaccine strain that can't be transmitted vertically. The polymorphism pattern of the primer for pMGA gene might be considered as a pathogenic vertical marker and the polymorphisms patterns of the two primers sets for both pMGA and pvpA genes might be useful for determining the two genetic potential pathogenic marker for MG infection that can differentiate between the highly and the less pathogenic MG isolates.

Keyword: *Mycoplasma gallisepticum*; PMGA gene; PvpA gene; Polymorphisms patterns; Pathogenic marker; Malaysia.