



BACTERIAL DISEASES

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MYCOPLASMA HYOPNEUMONIAE GENOTYPE COMPARISON OF FIELD STRAINS DETECTED IN VACCINATED ANIMALS AT SLAUGHTERHOUSES AND THE STRAIN OF THE VACCINE USED

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Introduction

Mycoplasma hyopneumoniae (*Mhyo*) strains circulate in most vaccinated farms. Nevertheless, there is few information regarding the similarity among field and vaccine strains. The purpose of this study was to compare the *Mhyo* genotype of the strains detected in slaughtered animals from vaccinated farms with the strain of the vaccines used.

Material and Methods

Lungs showing *Mhyo*-like lesions from 3 animals from 10 vaccinated farms were collected at Spanish slaughterhouses. To confirm *Mhyo* as the cause of the lesions, these samples were tested by qPCR. Within each farm, those qPCR positive samples with Ct value lower than 30 were genotyped by sequencing different loci (p97, p146, H1 and H5). Characterization was based on counting the variable number of tandem repeats (VNTR) for each locus. Five commercial vaccines against *Mhyo* used (A, B, C, D and Hyogen®) and two reference strains (ATCC 25095 and ATCC 25934) were also genotyped. Sequences of nucleotides and VNTR were aligned with MUSCLE v3.8.31 to compare the similarity among *Mhyo* field and vaccine strains.

Results

From the 30 analyzed samples, 21 were qPCR positive whereas samples from three farms (two vaccinated with Hyogen® and another with vaccine B) were negative. Among these positive samples, 12 *Mhyo* typing profiles were found according to the VNTR for each locus. Each vaccine strain and reference strains displayed different genotypes. *Mhyo* typing profile detected on each farm was different from the vaccine profiles.

Discussion and conclusion

Mhyo was detected in all vaccinated farms, but those that received Hyogen® and vaccine B. In positive cases, field strains were different from the strain of the corresponding vaccine applied. Further analyses are needed to elucidate the influence of vaccination on *Mhyo* circulating strains.

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