

Sequencing Analysis of *Mycoplasma gallisepticum* Wild Strains in Vaccinated Chicken Breeder Flocks

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Abstract

Mycoplasma gallisepticum (MG) infection is still of continuing economic concern in commercial broiler breeder chicken flocks in Egypt. MG infection continues to emerge despite the application of vaccination programs in breeder flocks. This prompted flock surveillance including MG isolation and molecular characterization of the circulating MG strains. The present study was concerned with 15 broiler breeder flocks of different ages (5-51 weeks). Three flocks were apparently healthy and 12 flocks were diseased. The aim of the study was to characterize the MG strains recovered from tracheal swabs. Four positive MG DNA extracts identified by rt-PCR and confirmed by isolation were subjected to sequencing of the *mgc2* gene and intergenic spacer region (IGSR). The current molecular study demonstrated the presence of 3 different wild-type MG strains (RabE1-08, RabE2-09 and RabE3-09) in vaccinated diseased flocks, while the fourth strain (RabE4-08), which was isolated from a nonvaccinated apparently healthy breeder flock, scored 100% of homology and similarity to the F-strain vaccine by the sequence analysis of *mgc2* and IGSR. It can be assumed that the vaccine F strain, which is supposed to replace field strains not only failed to do that, but also infected nonvaccinated flocks. Accordingly, there is a need to revise the control program including vaccine strategy in parallel with biosecurity measures. © 2014 S. Karger AG, Basel