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Molecular survey of infectious bronchitis virus in commercial flocks in Macedonia reveals presence of different genotypes

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Abstract

Introduction: Preliminary testing of commercial flocks using molecular and phylogenetic analysis revealed presence of genotypes QX and 4/91 in poultry farms with clinical signs and in poultry farms without clinical signs. Poultry farms are performing different vaccination programs without the knowledge of the genotype of the circulating strains. The purpose of this study was to detect presence of IBV in commercial flocks in Macedonia by molecular methods and to genotype the detected strains thus to establish a map of circulating genotypes in the country.

Methods: Molecular survey was performed in 35 poultry farms representative for the whole territory of the country without clinical signs at different production age as part of active surveillance for avian influenza. From each farm 30 cloacal swabs were taken totalling 1050 samples. Samples were pooled by five in the laboratory. Additionally, samples (oropharyngeal swabs, affected organs) were taken from 15 farms with clinically signs (respiratory signs, drop in egg production, altered egg quality) and post-mortem (respiratory, ovary and kidney lesions) findings associated to IBV. A real-time RT-PCR was performed targeting UTR region on all samples. A two-step nested RT-PCR was performed on all positive samples with primers targeting the S1 gene. Genotyping and subsequent phylogenetic analysis was performed by partial sequencing of the S1 gene region.

Results: Results of the present study revealed presence of following genotypes of IBV's circulating in commercial poultry in Macedonia: 4/91, Italy-02, QX, Mass, D274. This is first report of detection of Italy-02 in Macedonia.

Conclusions: Establishing a map of circulating IBV genotypes will help towards better optimisation of vaccination protocol of poultry farms and will contribute towards better understanding of epidemiological situation on a country and regional level.