

**S3-01****UPDATE ON THE MOLECULAR EPIDEMIOLOGY OF INFECTIOUS BURSAL DISEASE VIRUS IN WESTERN EUROPE IN 2021-2022**

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Infectious bursal disease (IBD) is an immunosuppressive disease of chickens of global relevance caused by infectious bursal disease virus (IBDV), a double-stranded, bi-segmented RNA virus belonging to the family Birnaviridae, genus Avibirnavirus. The intense viral evolution of IBDV, mostly ascribable to mutation and reassortment, resulted in a remarkable heterogeneity in terms of genetic features, pathogenicity and antigenicity, with profound impacts on the clinical manifestation, diagnosis and control of the disease. In recent years, a shift towards subclinical IBD forms has been observed in different parts of the world, posing new challenges and demanding an attentive monitoring of the epidemiological situation. The present study focused on Western Europe, aiming to characterize the field IBDV strains circulating in this region based on the results of molecular diagnostic activities conducted throughout 2021-2022 at the Laboratory of Infectious Diseases of the MAPS Department of the University of Padova. A total of 958 samples, each consisting in a pool of bursae collected from a single flock, were first tested using a RT-PCR targeting a portion of the VP2 followed by sequencing, allowing a preliminary distinction between vaccine and field strains. Then, partial VP1 sequencing was conducted on field strains only, to classify them based on phylogenetic analyses considering both genome segments. Samples were collected from 9 Western European countries, mostly for routine monitoring. According to the available anamnestic information, 462 flocks were immunized with live vaccines (48.2%), 301 with immune complex ones (31.5%) and 95 with vector vaccines (9.9%). Out of the remaining, 9 received no IBD vaccination (0.9%), while no information was available for 91 flocks (9.5%). The molecular assays revealed 254 samples to be positive for field strains (26.5%) and 453 for vaccines (47.3%), while 14 were positive but unsequenceable (1.5%) and 237 tested negative (24.7%). Field strains were detected in all investigated countries but Spain. The majority of these strains (n. 219), found in samples from Belgium, Denmark, France, Germany, the Netherlands, Portugal and the UK, were classified as reassortants (genotype A3B1) having a very virulent-like VP2 and a classical-like VP1. Their genetic features were consistent with viruses recently reported in other parts of North-Western Europe and associated to subclinical infections. All strains detected in Italy (n. 16) also belonged to genotype A3B1, but clustered with viruses signaled only in Russia, Kazakhstan and Middle Eastern countries. Other IBDVs found in Portugal (n. 17) fell within genotype A9B1, which is suspected to have been circulating in the Iberian Peninsula for more than a decade despite its recent characterization. A single French strain showed a high homology with an atypical strain described in the same country in 2019 and tentatively classified as genotype AxB1. Lastly, a serotype 2 strain (genotype AOB1) was detected in another sample from France. The obtained results confirmed the rapid spread of A3B1 reassortants, which currently represent the main field type in most of the region, and allowed the characterization of other IBDV types which seemingly circulate on a more local scale. Adding to the understanding of IBDV evolution and population dynamics, the collected data highlight the importance of maintaining awareness of IBD persistence even in countries where routine vaccination is consistently adopted, along with the need for tailored and coordinated diagnostic and control approaches.

**Keywords**

infectious bursal disease virus, Gumboro disease, reassortment, Europe, molecular epidemiology