

Identification of a novel infectious bursal disease virus genotype circulating in Portugal**Matteo Legnardi¹, Giovanni Franzo¹, Claudia Maria Tucciarone¹, Konstantinos Koutoulis², Isabel Duarte³, Marco Silva³, Bertrand Le Tallec⁴, Mattia Cecchinato¹**

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Infectious bursal disease virus (IBDV) is among the most impactful pathogens affecting the global poultry industry. It causes an immunosuppressive disease that could either result in overt clinical outbreaks or remain subclinical, though leading to secondary infections and vaccine failures. IBDV is a non-enveloped virus of the family Birnaviridae, featuring a bisegmented, double stranded RNA genome. Two serotypes, 1 and 2, are recognized, with only the former being pathogenic. Historically, serotype 1 has been further divided based on antigenicity and pathogenicity into classical, variant and very virulent strains. Nowadays, however, strains are more frequently classified according to genetic features by sequencing portions of viral protein 1 (VP1) and 2 (VP2) genes, allowing for a cost-effective, easily standardized IBDV classification, which is also best suited to describe the growing number of new IBDV subtypes and reassortant strains identified in recent years. This work reports the results of an epidemiological survey performed in Portuguese broiler farms between December 2020 and December 2021. A hundred bursal samples were collected as part of routine diagnostic activities and analyzed by RT-PCR targeting a portion of the VP2 gene, resulting in 70 positive samples. Fifty-three strains were characterized as vaccine strains by Sanger sequencing and phylogenetic analysis. The other 17 field strains were further investigated by sequencing a portion of the VP1 gene. Three of these strains showed features consistent with the reassortant strains that are increasingly detected in several other European countries. Based on all the available classification criteria, the remaining fourteen strains form a novel IBDV genotype, which features multiple amino acid changes in key positions within the VP2, and clusters with classical strains at VP1 level. The newly described genotype seems to have been circulating extensively in Portugal in recent years, prompting an attentive monitoring of the local epidemiological scenario. Nonetheless, further *in vivo* studies are still required to shed light on the pathogenicity of this genotype, and therefore its actual clinical relevance, as well as on the protection conferred by available vaccines.

Keywords: infectious bursal disease virus; molecular epidemiology; broiler; Portugal