

# A comprehensive view of the infectious bursal disease virus epidemiological landscape in Africa

Legnardi Matteo<sup>(1,\*)</sup>, DVM PhD; Franzo Giovanni<sup>(1)</sup>, DVM MSc PhD Dipl. ECVM; Tucciarone Claudia Maria<sup>(1)</sup>, DVM PhD; Cecchinato Mattia<sup>(1)</sup>, DVM PhD Dipl. ECPVS

(1)Department of Animal Medicine, Production and Health, University of Padua, Viale dell'Università 16, 35020 Legnaro (PD), Italy

**Corresponding author:** email: [matteo.legnardi@unipd.it](mailto:matteo.legnardi@unipd.it), Tel: +39 0498272968

Infectious bursal disease (IBD) is an immunosuppressive disease of chickens causing severe damage to the worldwide poultry industry. Its etiological agent is a double-stranded, bi-segmented RNA virus known as infectious bursal disease virus (IBDV). IBDV displays a remarkable antigenic, pathogenic and genetic heterogeneity, which has significant repercussions on its clinical manifestation, diagnosis and control. To provide an overview of IBDV epidemiological situation in Africa, a comprehensive phylogenetic study has been conducted considering all publicly available sequences ever reported in the continent.

A total of 1095 sequences, collected between 1979-2021 in 13 countries, were retrieved from GenBank. In line with the current phylogenetic classification system, two subsets were prepared, including respectively 197 VP1 and 489 VP2 sequences of field strains with known collection date and location. Four field genotypes were identified, with all VP2 sequences being characterized as very virulent whereas the VP1 ones belonged to four different genogroups. The most frequent genotype showed very virulent-like features in both segments and was detected all over Africa. Nonetheless, several subclades were discerned, allowing to infer separate spreading networks among different countries. Two other genotypes, circulating in Zambia and Nigeria, included strains forming distinct VP1 genogroups. Puzzlingly, the only strains closely related to Zambian ones were reported in Europe. The Nigerian cluster also included Senegalese VP2 sequences, but the absence of the respective VP1 sequences prevented a full characterization. Lastly, two types of reassortant strains with a very virulent-like VP2 and a classical-like VP1 were found in Zambia in 2004 and in Algeria in 2015. Phylodynamic analyses were subsequently performed on clades of local or transboundary relevance



to shed light on their emergence and spread. The collected data will help addressing current knowledge gaps in IBDV epidemiology and the planning of IBD control strategies.

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