

# MOLECULAR CHARACTERIZATION OF FIELD INFECTIOUS BURSAL DISEASE VIRUSES (vIBDV) IN NORTHEAST OF ALGERIA

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**T**he low efficiency of weakly attenuated vaccines in controlling Algerian field infectious bursal disease viruses (IBDV) suggests an increase of virulence in circulating viruses. To confirm this hypothesis, five IBDV-positive samples, originating from the Northeast of Algeria, were genetically characterized. Using a pair of primers selected from a well-conserved region in a viral genome encoding the VP2 variable region, one cDNA fragment of 743 bp was reverse-transcribed and amplified in one-step reverse transcription-polymerase chain reaction (RT-PCR). The five fragments were subjected to sequence and phylogenetic analysis including some reference strains available in GenBank. The five studied isolates showed a little antigenic drift as attested by a low nonsynonymous to synonymous ratio of nucleotide substitution when they were compared with classic IBDV (no more than 0.18). All conserved putative virulence marker amino acids at positions 222A, 256I, 294I, and 299S were present in all Algerian strains except the 20ALG isolate which kept the asparagine (N) at position 299. The studied strains also contained the BspMI and SspI restriction sites, reported as indicative of hypervirulent phenotype. The SspI cleavage site was nevertheless displayed at different position compared to the one observed in very virulent (vv) IBDV. The Algerian strains clustered with the vIBDV in the phylogenetic consensus tree and showed between themselves no more than 0.4% of amino acid divergence. This was the first report of vIBDV in Algeria, based on genetic characterization. Further investigations are needed in the future to track the evolution of these viruses.

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