Abstract

The present study was conducted to characterize the infectious bursal disease virus (IBDV) circulating in clinically diseased broiler chicken flocks with previous vaccination history during 2015-2016 in Egypt. IBDVs were isolated from 48 out of 63 of the investigated bursae from 10 flocks onto embryonated chicken eggs (ECEs) and verified by reverse transcriptase-polymerase chain reaction (RT-PCR). Histopathologically, bursae lesions revealed some lymphocytes depletion as well as the presence of vesicles in the lining epithelium. The hyper variable region (HVR) of VP2 and VP1 genes of the 10 isolates (1 isolate/flock) were partially sequenced and subjected to comparative alignment and phylogenetic analysis. Phylogenetically, IBDV isolates were clustered into two distinct genetic lineages: variants of classical virulent (cv) and very virulent (vv) IBDV strains based on VP1 and VP2 amino acid (aa) sequences. Alignment analysis of HVR-VP2 aa sequences has demonstrated that the vvIBDV isolates have the conserved residues of the vvIBDV pathotype (A222, I242, and I256), while, the cvIBDV isolates have the same aa sequences of the classical attenuated vaccine strain (D78). Expected single point mutation occurred at position 253 (H253N). All previously characterized isolates were re-subjected to molecular analysis with VP1 protein due to its correlation with virulence and pathogenicity of IBDVs. vvIBDV isolates have the conserved tripeptide (TDN), while, the cvIBDV isolates have aa substitutions at conserved tripeptide including NEG at 145-147 amino acid. The present study has demonstrated that variants of classical virulent and very virulent IBDV circulated among vaccinated flocks in Egypt during 2015-2016.

Key words: IBDV, broiler, very virulent, variant, RT-PCR