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Brief Report

Molecular characterization of infectious bursal disease virus (IBDV): Diversity of very virulent IBDV in Tanzania

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Summary

Nucleotide sequences of the VP2 hypervariable region (VP2-HVR) of 14 infectious bursal disease viruses (IBDVs) isolated in Tanzania from 2001 to 2004 were determined. Phylogenetic analysis showed that the isolates diverged into two genotypes and belonged to the very virulent (VV) type. In the phylogenetic tree, strains in one genotype clustered in a distinct group and were closely related to some strains isolated in western Africa, with nucleotide similarities of 96.1–96.8%, while strains in another genotype were clustered within the European/Asian VV type with nucleotide similarities ranging from 97.5 to 99.3%. Both genotypes were widely distributed throughout Tanzania, and had conserved putative virulence marker amino acids (aa) at positions 222(A), 242(I), 256(I), 294(I) and 299(S). Our findings demonstrate for the first time the existence of both African and European/Asian VV-IBDV variants in Tanzania.

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Infectious bursal disease virus (IBDV) is a causative agent of infectious bursal disease (IBD) of young chickens [5]. IBDV is a member of the genus *Avibirnavirus* of the family *Birnaviridae* [3]. The virus infects the surface of IgM-bearing B-lymphocytes in the bursa of Fabricius [16], leading to immunosuppression. There are two distinct serotypes of IBDV, 1 and 2. Serotype 1 viruses are pathogenic to chickens and are classified as classical virulent, antigenic variant and very virulent (VV) IBDVs based on their difference in virulence. Serotype 2 viruses are non-pathogenic to chickens [6].

The IBDV genome consists of 2 segments of double-stranded RNA (dsRNA), segments A (~3.4 kb) and B (~2.8 kb). The large segment A encodes 4 viral proteins, the two capsid proteins VP2 (48 kDa) and VP3 (32–35 kDa), the viral protease VP4 (24 kDa) and a non-structural protein VP5

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(17–21 kDa), while the smaller segment B encodes VP1 (90 kDa), an RNA-dependent RNA polymerase. The hypervariable region (HVR) within VP2, between amino acid residues 206 and 350, has the highest amino acid sequence variation among serotype 1 strains, and the nucleotide and deduced amino acid sequences of this region are widely used for molecular diagnosis and genotyping of IBDVs [7].

IBDV is an important virus worldwide in the poultry industry as it causes immunosuppression and mortalities of infected chickens. The emergence of a pathotypic variant with enhanced virulence, termed very virulent IBDV (VV-IBDV), in 1987 from an unknown origin in Europe, led to difficulties in control of IBD using classical vaccines [2]. In Tanzania, the first outbreaks occurred in 1988 in broiler flocks from the states of Dar-es-Salaam and Kibaha in the eastern, coastal zone within the coastal rim of the Indian Ocean [8]. Since then, the molecular characteristics of the field IBDVs from this country have not yet been studied. Currently, many IBD outbreaks are increasingly being reported from different parts of Tanzania, both in vaccinated and non-vaccinated flocks, causing significant economical losses [9].

In the current study, we characterized the Tanzanian field IBDV strains. The IBDV isolates were obtained from 14 IBD outbreaks in five geographical regions in Tanzania, namely Morogoro (east-coastal), Dar-es-Salaam (east), Mwanza (north-lake), Tabora (west) and Arusha (north), from 2001 to 2004 (Table 1). The bursae were directly smeared on separate filter papers and fixed with 99% ethanol for molecular characterization as described previously (Maw et al., Avian Dis. 2006, a manuscript in press). The samples were transported to Japan under the Tanzanian government exports

Table 1. Description of IBDV strains investigated in this study

Strain/ isolate	Region[a]	Geographical location/zone	Isolation year	Host of origin	Age (wks)	Vaccinated	Mortality rate	Accession number
KMRG-00	Morogoro	eastern, coastal	2001	layer	5	Yes	88/158 (55.7%)	AB200975
KMRG-38	Morogoro	eastern, coastal	2001	broiler	4	No	21/210 (10.0%)	AB200981
KMRG-26	Morogoro	eastern, coastal	2001	broiler	6	No	4/37 (10.8%)	AB200978
KMRG-46	Morogoro	eastern, coastal	2002	broiler	5	Yes	132/213 (62.0%)	AB201125
KMRG-48	Morogoro	eastern, coastal	2002	broiler	5	Yes	86/150 (57.3%)	AB200983
KMRG-40	Morogoro	eastern, coastal	2002	indigenous	6	No	2/19 (10.5%)	AB200982
KMRG-79	Morogoro	eastern, coastal	2004	broiler	6	Yes	76/201 (37.8%)	AB200986
KDSM-32	Dar-es-Salaam	eastern	2003	layer	Y	Yes	ND	AB201124
KDSM-02	Dar-es-Salaam	eastern	2004	broiler	6	Yes	34/123 (27.6%)	AB200976
KDSM-35	Dar-es-Salaam	eastern	2004	broiler	Y	Yes	ND	AB200980
KMZA-28	Mwanza	northern, lake	2004	layer	Y	Yes	26/92 (28.3%)	AB200979
KMZA-78	Mwanza	northern, lake	2004	layer	5	Yes	28/127 (22.0%)	AB200985
KTBR-18	Tabora	western	2004	broiler	Y	Yes	ND	AB200977
KARS-53	Arusha	northern	2004	broiler	6	Yes	18/97 (18.6%)	AB200984

ND No data.
Y Young ($\leq$6 weeks).
[a] Region in Tanzania where the viruses were isolated.

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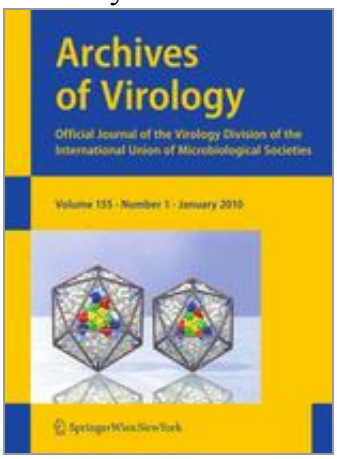

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