EVALUATION OF THE PHYLOGENETIC RELATEDNESS OF 106 GENOGROUP 2 IBDV FROM SEVEN DIFFERENT COUNTRIES IN SOUTH AMERICA, EUROPE AND ASIA

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INTRODUCTION

Infectious bursal disease (IBD, also known as Gumboro disease) is one of the most important immunosuppressive infections of chickens which causes high economic losses to the poultry industry worldwide. The Gumboro virus (IBDV) was generally divided into three main groups according to antigenic and virulence properties: classical virulent (cvIBDV), very virulent (vvIBDV) and antigenic variants (avIBDV). In 2018, a new nomenclature that includes a genotyping system was established and viruses belonging to this last group were classified into Genogroups G2, G4, G5, G6, and G7[1]. In recent years, several publications have described the huge impact the subclinical form of Gumboro has had on large farms in America and Asia, especially due to the circulation of novel G2 IBDV viruses that might not be controlled with current commercial Del-E Variant type vaccines[2]. A broad analysis of the characterization and circulation of G2 type viruses in different countries is necessary for a better understanding of the virus evolution and implementation of proper measures to improve the control of the disease worldwide.

MATERIALS AND METHODS

A total of 106 G2 IBDV nucleotide sequences containing the hypervariable region of the capsid protein VP2 were analysed with the objective of evaluating their phylogenetic relatedness. The 106 strains were obtained from Peru (U), Spain (A), Philippines (P), Mexico (M), France (A), Poland (A), Portugal (A), Malaysia (A) and South Africa (A) from 2020 to 2021. For the analyses, the 106 nucleotide sequences were translated into their predicted amino acid sequences and were then aligned with seven known IBDV standards including those from Variant G2, USA Classic G1, European Classic G1, USA Lukert Classic G1 and European vvIBDV G3. The Geneious software program and Neighbour Joining phylogenetic analysis were used to compare the sequences.

RESULTS & DISCUSSION

The Neighbor Joining phylogenetic analysis data are shown in Figure 1.

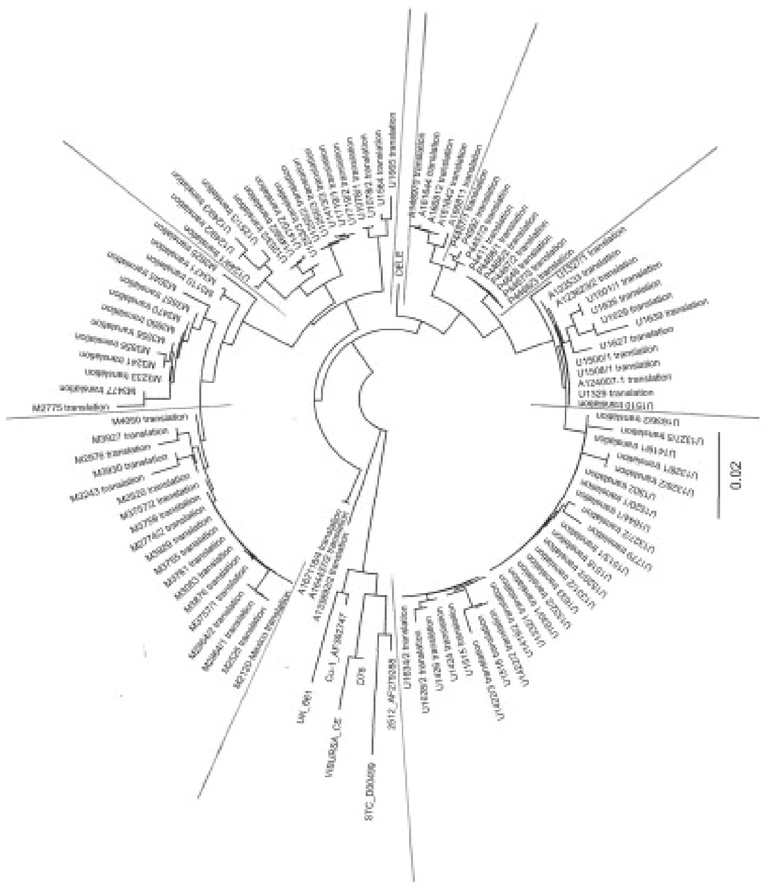

Fig. 1. Neighbor Joining phylogenetic analysis data for the 106 G2 IBDV nucleotide sequences.

The data indicated that all the 106 sequences analyzed were located in Genogroup 2 on 7 different sub-branches. Two viruses (A167118/4 and A164437/2) were located on a sub-branch in Genogroup 2 but were closely related to the Del-E Variant. The other viruses were located on one of 6 sub-branches identified as Genogroup 2, but unlike the Del-E type strain. The M3110 and M3471 grouped together but were on a separate branch from the other “M” viruses. Likewise, the M3925 virus was alone on a separate branch but within the “M” virus group. These three viruses were more distantly related to the other viruses in this group.
The rest of the viruses located on each of the sub-branches had the same country of origin.

DISCUSSION & CONCLUSIONS

The results obtained in this evaluation show the extensive and distinct evolution of the Genogrup 2 virus around the world. However, the virus seems to have a similar evolution within a specific region, which may respond to similar production managements.

Many studies have shown that Genogroup 2 viruses on sub-branches may be antigenically distinct from the Del-E Variant type strain and might not be neutralized by the antibodies of the current commercial Del-E Variant type vaccines[3]. In such a scenario, the use of live vaccines with good competitive exclusion capacity might be a good solution for the control of these emergent variant strains.

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