EMMERGENCE OF A NOVEL IBV PATHOTYPE IN A BREEDER FARM IN IBADAN, NIGERIA

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ABSTRACT

Infectious bronchitis virus (IBV) is a prototype member of the genus *Gammacoronavirus* in the subfamily *Coronavirinae* and family *Coronaviridae* which is found in the order *Nidovirales*. IBV genome is made up of a single molecule of a positive sense, single-stranded RNA of 27.6 kb in size encoding four structural proteins, polyproteins 1a and 1ab, and many accessory proteins. The structural proteins are spike (S), envelope (E), membrane (M) and nucleocapsid (N). The S protein of IBV especially the S1 subunit, which is formed by post-translational cleavage of S protein, has been well studied because of its importance. S protein has been reported to be crucial for antigenic neutralization, haemagglutination, cell tropism determination and in the molecular detection and analysis of IBV. The continuous emergence of new IBV genotypes and lack of cross protection among different IBV genotype have been the important challenges in poultry farms. Vaccination has been considered to be the most cost effective approach to controlling IBV infection. However, with the continual emergence of new variants, there will be an unending labour of developing a new vaccine as the variants to which the currently available vaccines are effective disappear. This challenge is essentially with the use of live attenuated IB vaccines which although they remarkably induce a potent immune response, the potential risk of reversion to virulence, neutralization by the maternal antibodies, recombination and mutation capabilities are of serious concern in poultry industry. There is a risk in using genotype to determine the pathotype of IBV as there may not be correlation and a few amino acid substitutions which may result in 2% nucleotide sequence divergence can alter IBV serotype. Therefore, this study is carried out to present the suspected emergence of a novel IBV pathotype in a layer breeder farm in Nigeria among vaccinated birds; to reinforce the possibility of IBV infection in a vaccinated flock and to query the effectiveness of the usage of different IBV strain vaccines to protect against IBV infection. The breeder farm studied had flock of more than 50,000 birds with rapid spread of a novel IBV pathotype that has an ardent affinity for active ovarian follicles. The finding of this study shows that IBV is mutating in spite of the comprehensive vaccination

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programmes involving the use of variant vaccine strains in this country with the evidence of an emergent new strain of the virus peculiar to Nigeria which may lead to further outbreaks of novel IBV in other countries. There is therefore the need for continuous surveillance, disease reporting and/or production of vaccines with the indigenous strains of the virus and its sustainable control in Nigeria. In addition, with the virus breakthrough to affecting other organs and animal species, the risk of adapting in human who are in frequent contact with birds, like severe acute respiratory syndrome coronavirus (SARS-CoV) – that is in the same family with studied virus, should be considered in order to develop more effective preventive measure to abate the potential mutation of the virus or plan an eradication strategy for it.

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