

Observation of risk factors, clinical manifestations and genetic characterization of recent Newcastle disease virus outbreak in West Malaysia

ABSTRACT

Background: Newcastle disease virus remains a constant threat in commercial poultry farms despite intensive vaccination programs. Outbreaks attributed to ND can escalate and spread across farms and states contributing to major economic loss in poultry farms.

Results: Phylogenetic analysis in our study showed that eleven of the samples belonged to genotype VIIId. All farms were concurrently positive with two immunosuppressive viruses; Infectious Bursal Disease Virus (IBDV) and Marek's Disease Virus (MDV). Amino acid sequence analysis confirmed that eleven of the samples had sequence motifs for velogenic/mesogenic strains; three were lentogenic.

Conclusion: In conclusion, no new NDV genotype was isolated from the 2011 NDV outbreak. This study suggests that the presence of other immunosuppressive agents such as IBD and MDV could have contributed to the dysfunction of the immune system of the chickens, causing severe NDV outbreaks in 2011. Risk factors related to biosecurity and farm practices appear to have a significant role in the severity of the disease observed in affected farms.

Keyword: Newcastle disease virus; Infectious bursal disease; Marek's disease; Immunosuppressive agents; Recent outbreak; Risk factors; Phylogenetic study; Genetic characterization