

# Phenotypic and Genetic Characterization of Avian Influenza H5N2 Viruses in Taiwan

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## Background/Objective

Emerging novel avian influenza viruses (AIVs) usually pose the potential of cross-species transmission and pandemic threat. Two duck influenza H5N2 viruses isolated from virological surveillance at a live-poultry market in Taiwan, showed phylogenetic closeness but exhibited different replication capabilities in cell lines. This study aims to characterise the replication properties of the two H5N2 viruses and the determinants involved.

## Method

Growth kinetics were evaluated in both a mammalian cell line MDCK and an avian cell line DF1. To further investigate potential intra-host variation, plaque-purification was conducted to isolate different viral strains, and their growth properties were also characterised. Distinct genetic differences were found among the studied viral strains by full-genome sequencing. In addition, a binding assay on cells and a minigenome assay were utilised to elucidate the potential mechanisms.

## Result

One duck H5N2 virus, DV518, had higher replication efficiencies than another virus, DV413, in both MDCK and DF1 cell lines. Two viral strains plaque-purified from DV518 (p518-S and p518-L) exhibited distinguishable replication kinetics in MDCK cells. And both two strains, p518-S and p518-L, showed greater binding to MDCK cells than the virus purified from DV413. Additionally, polymerase activity assays suggested the role of vRNP in replication advantages of p518-L in mammalian cell lines.

## Conclusion

These results demonstrate the differences in replication of two low pathogenic AIVs from different hosts and the phenotypic variation within an avian individual. In view of the emerging viruses, this study provides further information in pathogenicity and viral evolution.