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Proteomic Profiling Reveals Distinct Molecular Response to West Nile Virus Infection Across Host Species

Inhalt

West Nile virus (WNV) is a mosquito-borne Orthoflavivirus, naturally circulating between its vector mosquitoes and its reservoir, birds. Mammals, like horses and humans, can be infected but are considered as dead-end hosts. Avian WNV symptoms can differ from asymptomatic to multiple organ failure. Most infected mammals show no symptoms, but in rare cases neurological diseases can occur, which can be fatal. This project aims to identify the molecular mechanisms for these diverse host responses during WNV infection. Kidney cell lines (Vero, human HEK-293, horse PFN, goose GN-R) were analyzed as possible targets of WNV infection. At 24 hours post infection, WNV titers were high in Vero, HEK-293 and GN-R, while PFN cells showed a tenfold lower titer, suggesting less efficient virus replication in equine cells. These observations were supported by immunofluorescence and transmission electron microscopy where virus particles were detected in endoplasmic reticulum, Golgi apparatus and transport vesicles. In proteome analyses, genes related to viral immune response were upregulated only in Vero cells while response in the other cells was weak. However, HEK-293 and PFN showed markers for viral infection which were absent in GN-R. In this study, we examined the replication of and host response to WNV in kidney cell lines from four different host organisms of WNV for the first time, providing insights into potentially distinct regulatory mechanisms against the virus.

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West Nile virus, kidney cell lines, immunometabolism, proteome

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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