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Viral Interference During Flavivirus Coinfections

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Superinfection exclusion describes the phenomenon of closely related viruses being unable to simultaneously coinfect the same cells. Despite being reported across a wide range of virus families, no general mechanism responsible has been identified. To study how closely related viruses interact, it's often necessary to use tagged or otherwise genetically modified viruses, since classic detection methods like antibodies or RNA/DNA probes are usually not specific enough to differentiate between them. This, however, comes with potential caveats: depending on the virus used, tagging it can lead to reduced replication rates, which could influence viral interactions. Additionally, any genetic modifications to a virus's genome, even if not influencing its replication rate, could influence its interaction with the host or other viruses.

In this study, we describe an antibody-based staining method capable of differentiating the two closely related mosquito-borne Orthoflaviviruses WNV and USUV without any genetic modifications. We use it to characterize their interference with one another during simultaneous and sequential coinfections, finding evidence for superinfection exclusion occurring between them. We supplement our findings with qRT-PCR showing that reduced viral infection rates translate to reduced genome replication.

Keywords

Flaviviruses, Coinfection, Superinfection Exclusion, Detection Methods, Viral Interference

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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