



ID der Kurzfassung : 238

Deciphering Lineage-Specific Determinants of Usutu Virus through Targeted prM/E Substitutions

Inhalt

Usutu virus (USUV) is an emerging mosquito-borne flavivirus that primarily affects birds but can also cause neuroinvasive disease in humans. Despite the growing number of outbreaks and increasing concern, many aspects of its biology remain poorly understood. Several viral lineages have been identified, but a systematic comparison of mutations within the pre-membrane (prM) and envelope (E) proteins has not yet been conducted. To investigate the functional impact of prM/E protein variations, we engineered a panel of six recombinant USUV strains using a common genetic backbone derived from aEU2 lineage strain. Within this conserved scaffold, the prM/E coding regions were replaced by reverse genetics with those from representative lineages, allowing for an in-depth evaluation of lineage-specific differences in these critical structural proteins. The resulting viruses are being extensively characterized in vitro in mammalian and mosquito cell lines, and in vivo experiments have been planned. Additional characterization is being conducted in ovo to explore infection dynamics in a vertebrate model. Embryonated chicken eggs are sampled over 5 days, and tissues are harvested for downstream analyses. Altogether, this comprehensive dataset is expected to provide valuable insights into the effects of prM/E mutations on key viral traits, contributing to a better understanding of USUV pathogenesis, host interaction, and lineage-specific phenotypes.

Keywords

reverse genetics, Usutu virus

Registration ID

OHS25-76

Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

Track Klassifizierung: Emerging Pathogens

Typ des Beitrags: Both options possible