ID der Kurzfassung : **154**

Granger-causality analysis reveals defective viral genomes with antiviral potential

Inhalt

During viral infection, replication errors can generate defective viral genomes (DVGs) that may interfere with virus replication and reduce infectious virus concentration. Identifying DVGs responsible for these effects is important because of their potential as antiviral candidates. However, experimentally screening all candidates is time- and resource-intensive, creating a need for computational prioritization. We therefore applied Granger-causality analysis to time-series data from continuous influenza A virus (IAV) infection to prioritise DVGs whose abundance predicts changes in infectious virus concentration.

We analysed next-generation sequencing counts of 1,968 IAV DVGs alongside infectious virus concentrations in infected cell cultures. For each DVG, we compared two ordinary least squares models: a restricted model using infectious virus concentration alone and a full model additionally including DVG counts. We also tested the reverse relationship, enabling classification as Granger-causing, Granger-caused, bidirectional, or unrelated.

After Benjamini-Hochberg correction, 255 DVGs showed Granger-causing or bidirectional relationships with infectious virus concentration. Previously validated defective interfering particle candidates also received plausible Granger labels. These findings suggest that Granger-based classification reflects antiviral activity and can help prioritise DVGs for experimental validation.

Keywords

Registration ID

INF26-104

Professional status of the speaker

PhD student

Junior scientist status

Yes, I am a junior scientist.

Track Klassifizierung: Antivirals and Vaccines

Typ des Beitrags: Oral presentation