

Flying viruses –mass spectrometry meets X-rays

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Viruses affect basically all organisms on earth. Some are detrimental to human development as we experienced during the COVID-19 pandemic, whereas those targeting pathogenic bacteria or crop pathogens can be beneficial for us. An integral part of icosahedral viruses is the capsid protein shell protecting the genome. Many copies of the capsid protein often self-assemble into shells of defined size. Low binding affinity of individual subunits allows efficient assembly and gives rise to highly stable particles. However, modifications can alter their size. Proteoforms also matter in viral replication, e.g. in polyprotein processing, or antigenicity of the glycoproteins.

Capsids and viral proteoforms can be studied by native mass spectrometry (MS), a single molecule like approach, in terms of stoichiometry, dynamics, assembly pathways and stability revealing coexisting states. However, the structural resolution provided is limited. Therefore, we built a prototype native mass spectrometer in the MS SPIDOC project to deliver select species to X-ray sources for gas phase SAXS and single particle imaging. First experiments reveal good performance of the MS setup.

User consent

yes

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