A structural analysis of M protein in coronavirus assembly and morphology

The M protein of coronavirus plays a central role in virus assembly, turning cellular membranes into workshops where virus and host factors come together to make new virus particles. We investigated how M structure and organization is related to virus shape and size using cryo-electron microscopy, tomography and statistical analysis. We present evidence that suggests M can adopt two conformations and that membrane curvature is regulated by one M conformer. Elongated M protein is associated with rigidity, clusters of spikes and a relatively narrow range of membrane curvature. In contrast, compact M protein is associated with flexibility and low spike density. Analysis of several types of virus-like particles and virions revealed that S protein, N protein and genomic RNA each help to regulate virion size and variation, presumably through interactions with M. These findings provide insight into how M protein functions to promote virus assembly.

Keyword: Cryo-electron microscopy, Viral matrix protein, Coronavirus, Pleomorphic virus structure, Cryo-electron tomography

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