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**Mechanisms of virus assembly on membranes**[1] GUILLERMO LAZARO, MICHAEL HAGAN, Brandeis Univ — We present a computational model motivated by icosahedral enveloped viruses, which consist of nucleocapsid (a protein shell encasing the genome) and an outer envelope composed of a lipid membrane and transmembrane glycoproteins. Viruses acquire their envelope by budding through a host cell membrane. Despite extensive experimental efforts, it remains an open question whetherthe nucleocapsid is necessary for budding (nucleocapsid-driven assembly), or whether interactions between glycoproteins are sufficient to simultaneously drive membrane deformation and assembly of an icosahedral structure (glycoprotein-driven assembly).To study this question, we use a coarse-grained computational model for the nucleocapsid, glycoproteins, and the membrane. Our simulations demonstrate that glycoproteins alone are sufficient to drive budding; however, barriers due to membrane elasticity can lead to malformed capsids lacking icosahedral symmetry. In contrast, with a nucleocapsid present, icosahedral structures form over a broad range of parameter values. Our simulations also identify a key role for glycoprotein geometry in reshaping the membrane and avoiding membrane deformations that frustrate assembly.

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