PRN12-282

Pestivirus Glycoprotein Erns: Specificities of lipid binding

Aberle Daniel, Meyers Gregor

Friedrich-Loeffler Institut, Tübingen, Germany

Glycoprotein E^{rns} represents one of the four structural proteins of pestiviruses. The polypeptide consists of 227 amino acids and forms homodimers via a cysteine at position 171. It is heavily glycosylated and has an intrinsic RNase activity. E^{rns} is essential for the production of infectious virus particles but low amounts of the protein are secreted from infected cells. The E^{rns} RNase function represents an important virulence factor in the natural host.

E^{rns} lacks a typical hydrophobic membrane anchor sequence but was nevertheless shown to represent a membrane bound protein that is attached to the virion and intracellular membranes by a so far unknown mechanism. Previous studies had shown that E^{rns} is not bound as strong as an integral membrane protein. Membrane anchoring is conferred by its carboxyterminal end. Instead of a hydrophobic sequence the carboxyterminal region of E^{rns} has an amphipathic character when folded as an α-helix. The amphipathic character is important for membrane binding.

In our studies we analyzed the binding of the E^{rns} carboxyterminal sequence to liposomes containing different amounts of typical membrane lipids. To this end the E^{rns} carboxyterminal anchor was expressed in Bacteria, purified and incubated with different liposome compositions. The solution was centrifuged and the amount of protein in the solution was compared with the amount of protein in the lipid pellet. The E^{rns} anchor showed a high affinity to negatively charged lipids like dimyristoylphosphatidylglycerol (DMPG) and a low affinity to zwitterions like dimyristoylphosphatidylcholin (DMPC).