PSTA-264

Functional domains of Pseudorabies Virus pUL34

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The conserved herpesviral pUL34 and pUL31 form a complex that is required for nuclear egress and sufficient for the formation of primary envelopes from the inner nuclear membrane (INM). pUL34 is a type II membrane protein of 262 amino acids (aa) and its transmembrane region (TM) is predicted between aa 245 and 261 leaving only one amino acid in the C-terminus probably reaching the perinuclear space. The INM lamina associated protein (Lap) 2ß of 452 aa specifies a TM predicted between aa 413 and 430, a C-terminal domain of 31 aa, a lamin B binding domain (aa 299-373) and a LEM motif (aa 111-152). To analyze function of pUL34, we constructed chimeras between PrV pUL34 and Lap2ß by (i) substituting the pUL34TM against the Lap2ß TM including the C-terminal domain, (ii) the C-terminal 100 aa of pUL34 by respective Lap2ß sequences including the lamin B binding domain, or (iii) 100 aa of the pUL34 N-terminus by Lap2ß sequences including the LEM motif. pUL34-Lap2ßTM and pUL34-Lap2ßCT showed typical nuclear rim localization and interaction with pUL31, while pUL34-Lap2ßNT no longer colocalized with pUL31. pUL34-Lap2ßTM expression complemented the replication defect of PrV-ΔUL34, but did not restore wild-type plaque size. Preliminary experiments suggest that pUL34-Lap2ßCT shows a similar complementation. Our data suggest that substitution of the transmembrane domain or of 100aa of the C-terminus of pUL34 by LAP2ß sequences have no significant impact on localization or function.