Structural Features of the Seneca Valley Virus Internal Ribosome Entry Site (IRES) Element: a Picornavirus with a Pestivirus-Like IRES - DTU Orbit (26/01/2019)

The RNA genome of Seneca Valley virus (SVV), a recently identified picornavirus, contains an internal ribosome entry site (IRES) element which has structural and functional similarity to that from classical swine fey virus (CSFV) and hepatitis C virus, members of the FLAVIVIRIDAE: The SVV IRES has an absolute requirement for the presence of a short region of virus-coding sequence to allow it to function either in cells or in rabbit reticulocyte lysate. The IRES activity does not require the translation initiation factor eIF4A or intact eIF4G. The predicted secondary structure indicates that the SVV IRES is more closely related to the CSFV IRES, including the presence of a bipartite IIId domain. Mutagenesis of the SVV IRES, coupled to functional assays, support the core elements of the IRES structure model, but surprisingly, deletion of the conserved IIId2 domain had no effect on IRES activity, including 40S and eIF3 binding. This is the first example of a picornavirus IRES that is most closely related to the CSFV IRES and suggests the possibility of multiple, independent recombination events between the genomes of the Picorniviridae and Flaviviridae to give rise to similar IRES elements.

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