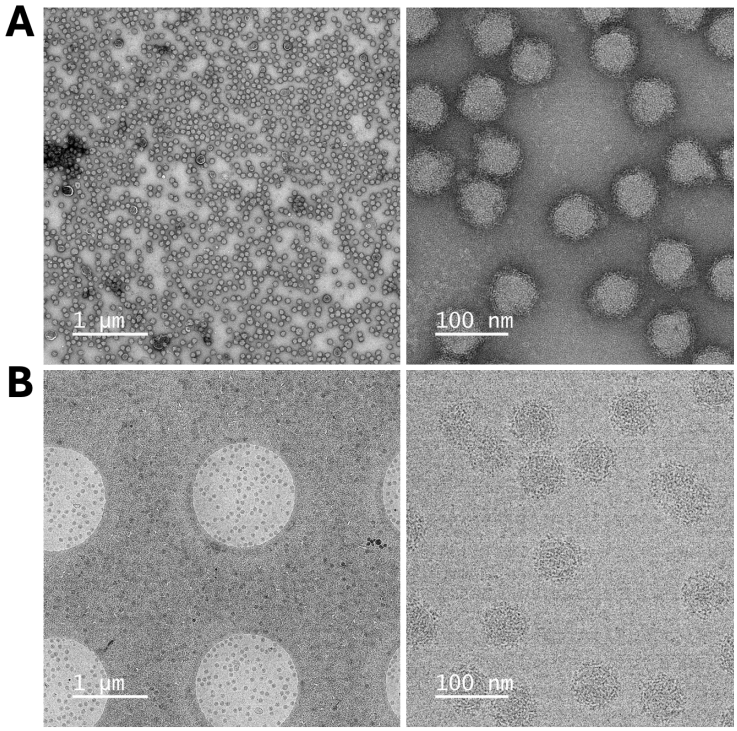

Figure 1. mages of wild type Sindbis virus (SINV) TE12 strain. (A) Images of negatively stained virus sample at low and high magnifications. (B) cryo-EM images of frozen hydrated virus sample.

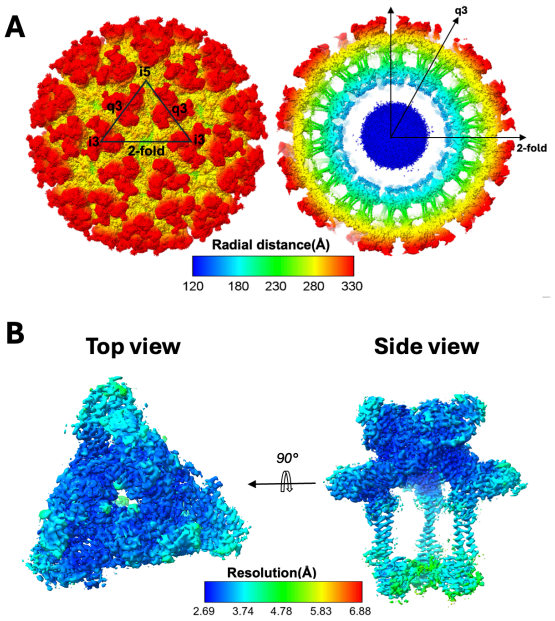

Figure 2. Structural Analysis of SINV. (A) Radial depth-colored surface representation of SINV particles, highlighting icosahedral symmetry axes (black arrows indicating two-, three-, and fivefold axes). (B) Density maps of the SINV trimer at 3.1 Å resolution. The map is color-coded based on the calculated local resolution.

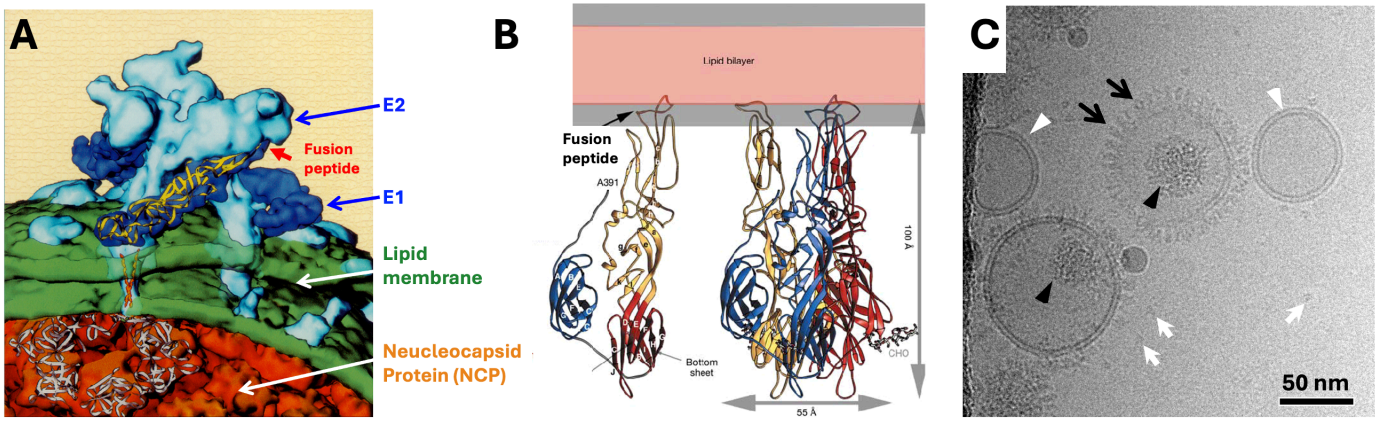

Figure 3. Composition of SINV structural proteins and post-fusion complex. (A) Illustration of a SINV protein trimer and its interaction with the nucleocapsid protein core. E1 is the viral fusion protein. E2 is the receptor binding protein. Both are transmembrane proteins that traverse through the viral membrane. The E1 fusion peptide is sequestered underneath the E2 protein. (B) Crystal structure of post-fusion E1 trimer of Semliki Forest virus (another alphavirus, PMID: 14737160). (C) Cryo-EM image of SINV and liposome fusion. White arrow heads show unfused liposomes. Black arrow heads show SINV nucleocapsid cores fused into liposomes. Black arrows are post-fusion protein densities on the fused membrane. White arrows show protein densities distributed in the solution.