Grapevine is an economically important fruit crop and is widely cultivated worldwide. Although grapevine is susceptible to many viral diseases, grapevine leafroll disease is the most devastating with losses up to 40,000 USD/hectare of vineyards. *Grapevine leafroll-associated virus 3* (GLRaV-3) is the chief causal agent of the disease. GLRaV-3 is the prototype of the genus *Ampelovirus* (family *Closteroviridae*) and contains one of the largest RNA genomes. However, little is known about the molecular biology of GLRaV-3 or how it interacts with the grapevine host. Positive sense, single-stranded RNA viruses compartmentalize their genome replication within membrane-bound viral replication complexes (VRCs). To form VRCs, viral-encoded proteins target host intracellular membranes and induce invaginations. Viruses encode “replicase” proteins to replicate and transcribe their genomes, these replicase proteins often contain the organelle targeting and membrane association signals required for VRC formation. Previous electron microscopy suggests that GLRaV-3 forms VRCs from the outer mitochondrial membrane of host cells. We hypothesize that the ORF1a replicase protein encoded by GLRaV-3 targets the outer mitochondrial membrane to form VRCs. To test this, we will use bioinformatic tools to identify putative sequences responsible for membrane association and mitochondrial targeting. We will next tag ORF1a with *GFP* and express it within experimental plants to observe its localization through confocal microscopy. Further, we will create a series of mutations targeting key candidate residues to probe their potential role in targeting. Lastly, we will engineer a mini-replicon containing both ORF1a and ORF1b replicase sequences flanked by the untranslated regions to test if they are sufficient to induce VRCs in plant cells.