patterns to separate plant rhabdoviruses into two major taxonomic groups: the *Cytorhabdovirus* genus and the *Nucleorhabdovirus* genus.

Presently, eight viruses (barley yellow striate mosaic virus, broccoli necrotic yellows virus, Festuca leaf streak virus, lettuce necrotic yellows virus, northern cereal mosaic virus, Sonchus virus, strawberry crinkle virus, and wheat American striate mosaic virus) are assigned to the *Cytorhabdovirus* genus. The *Nucleorhabdovirus* genus has six members (Datura yellow vein virus, eggplant mottled dwarf virus, maize mosaic virus, potato yellow dwarf virus, Sonchus yellow net virus, and sowthistle yellow vein virus). Of these, Sonchus yellow net virus (SYNV) and lettuce necrotic yellows virus (LNYV) have been the most extensively characterized. Less extensive cytopathological and physicochemical information is available about other rhabdoviruses within the *Cytorhabdovirus* and *Nucleorhabdovirus* genera. Only preliminary and less reliable descriptions are available for other plant rhabdoviruses; consequently, more than 60 members and possible members have yet to be assigned to a genus ***(3)***.

The bacilliform or bullet-shaped rhabdovirus virions are complex, with three distinct layers varying in electron density observed in high resolution electron micrographs (**Fig. 1A**). These layers appear to represent glycoprotein surface projections, an outer membrane, and a helical striated inner nuclear core with a central canal (**Fig. 1B**). The membrane contains host-derived lipids and glycoprotein spikes that probably associate as trimers and protrude 5–10 nm through the membrane. The nucleocapsid contains three proteins, designated N (nucleocapsid), P (phosphoprotein), and L (polymerase), that encapsidate the negative-strand genomic RNA. This RNA ranges in size from 11 to 14 kb, depending on the virus. A matrix (M) protein is thought to mediate coiling of the nucleocapsid and its association with the membrane. Analogs of these five proteins have been found in all rhabdoviruses that have been carefully analyzed. A sixth protein is encoded by the genomes of some rhabdoviruses. In SYNV, this gene, which we have provisionally designated sc4, is virion-associated and has no obvious sequence relatedness to the sixth accessory proteins of other rhabdoviruses ***(4)***. The entire genome of SYNV has been sequenced; consequently, we have available a detailed genetic map (**Fig. 1C**), and have considerable information about the nature of the viral proteins (*see* **ref. *4*** and references therein). A genome map ***(5)*** and limited sequence analysis of LNYV is also available ***(6)***.

The methods that have the broadest spectrum of applicability for purification of rhabdoviruses have arisen from studies of SYNV and LNYV. We have described the method developed for SYNV in this review because it has been successfully used for a large number of rhabdoviruses. An earlier procedure was developed for LNYV, which used chromatography over calcium phosphate gels, and the last iteration of the protocol has been described in some