Reproduction/Replication

As in other organisms, the information for virus reproduction is contained within its genome (Figure 6).

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| http://www.apsnet.org/edcenter/intropp/PathogenGroups/PublishingImages/PlantViruses06_sm.jpgFigure 6 |

Although the genetic material for most organisms is double-stranded (ds) DNA, only a minority of plant viruses possess dsDNA genomes. Some of the plant viruses have genomes that are composed of single-stranded (ss) DNA. However, the majority of plant viruses do not use DNA at all. Instead, the genomes of nearly all plant viruses are made of RNA. Most of these genomes are composed of ssRNA that is the same (positive-sense) polarity as the messenger RNAs of the cell. Some of the RNA viruses use ssRNAs of negative polarity, and yet others have genomes made of dsRNA. Due to this enormous variation in the very nature of the genetic material of viruses, the reproductive cycles/replication cycles and life styles of different viruses are often very distinct from each other.

Since plant viruses are obligate, biotrophic parasites, their life cycles start by penetration of the virion into the cell. Plant viruses are unable to penetrate the plant cuticle and cell wall. It is believed that the virion enters the cytoplasm of the cell passively through wounds caused by mechanical damage to the cuticle and cell wall. The next phase of virus infection is the partial or complete removal of the coat protein shell of the virion in the cytoplasm. Next the cell mediates expression of the viral genome by providing a transcription apparatus (for DNA viruses) and a translation apparatus (for all viruses). The DNA viruses must be transported to the nucleus for transcription in order to gain access to the cell proteins required for the production of messenger RNA from viral DNA. Translation of viral RNA in the cytoplasm produces viral proteins that are required for completion of the virus life cycle.

All viruses must direct the formation of at least three types of proteins: replication proteins that are essential for nucleic acid production, structural proteins that form the protein shell and other components contained in the virions, and movement proteins that mediate virus transport between plant cells (Figure 6). The viral replication proteins combine with cellular proteins to produce a complex of proteins that manufactures multiple copies of the virus genome. These newly made genomes interact with the structural proteins to form new virions. The diagram below (Figure 7) illustrates the steps that occur within the cell during the replication of *Tobacco mosaic virus*.

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| http://www.apsnet.org/edcenter/intropp/PathogenGroups/PublishingImages/PlantViruses07_sm.jpgFigure 7 |

The next step in the virus reproduction cycle is movement of the virus into neighboring cells. Depending on the virus, the viral genomes or the virions are transported into neighboring cells through small channels called plasmodesmata that form connections between cells. Many viruses produce movement proteins that modify the plasmodesmata channels and facilitate viral movement into neighboring cells. The following diagram (Figure 8) illustrates the movement of *Tobacco mosaic virus* from an infected cell to a neighboring cell.

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| http://www.apsnet.org/edcenter/intropp/PathogenGroups/PublishingImages/PlantViruses08_sm.jpgFigure 8 |

The process of cell-to-cell movement is relatively slow: it takes from one to a few hours for a virus to multiply in a cell and move to the next cell. To successfully colonize an entire plant, a virus needs to enter the vascular system of the plant. The process of systemic, or long-distance transport normally proceeds through the phloem sieve elements where viruses move passively with the flow of photosynthates. After quite rapid systemic spread of the virus (centimeters per hour) in the phloem, the virus moves from the phloem into surrounding cells where it reproduces and spreads by cell-to-cell movement. The time between initial infection of one or a few cells and systemic infection of the plant varies from a few days to a few weeks depending on the virus, host plant, and environmental conditions. Transmission of the virus from one plant to another (see section on survival and dissemination) completes the virus life cycle.

Systematics

Ideally, systematics (the study of the kinds of organisms and the relationships between them) should reflect the evolutionary history of a biological species. This history can be constructed by analysis of fossilized predecessors and by comparison of the genes of existing organisms (phylogenetic analysis). Since viruses left no fossils, their evolution can be reconstructed with some confidence only by phylogenetic analysis. This analysis works reasonably well at the intermediate taxonomic levels, such as virus genus and family. However, due to the nature of the viral form of life, it gets more complicated or even unfeasible at the lower (species) level or higher levels. Because the viruses exhibit very high rates of reproduction and mutation, each reproduction cycle results in a number of genetically similar, but not identical variants. Further selection and evolution of slightly different genomes results in a continuum of variants that range from point mutants to virus strains. Unlike cellular organisms, which are believed to originate from a common ancestor, the viruses most likely originated more than once. The diverse origins of different virus groups permit their evolutionary classification only within particular virus types, such as viruses that have positive-sense RNA genomes, or small ssDNA genomes.

When we consider plant virus classification, we should remember that it was the mid 1930s before the first plant virus was purified and characterized. Prior to this time, most plant virologists named a virus based on the host plant in which it was found and the type of symptom that the virus caused in the plant. For example, *Tobacco mosaic virus* was first described in tobacco in which it induces a mosaic pattern in the leaves (Figure 9). Virus names are usually shortened to an acronym, for example, *Tobacco mosaic virus* is shortened to TMV, and *Tomato spotted wilt virus* is shortened to TSWV. The names of many virus genera and families are derived from an important virus within the family. For example, the family name *Bromoviridae* is derived from *Brome mosaic virus* which is in this family.

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| http://www.apsnet.org/edcenter/intropp/PathogenGroups/PublishingImages/PlantViruses09_sm.jpgFigure 9 |

The largest subdivisions of plant viruses are defined by the chemical form of their genomes (Plant Viruses Online <http://image.fs.uidaho.edu/vide/refs.htm> ). By far, the largest number of plant viruses possess single-stranded (ss), positive-sense RNA genomes, and these viruses are called positive-strand RNA viruses. Examples of the most economically important families of the positive-strand RNA viruses are *Bromoviridae, Closteroviridae, Luteoviridae*, and *Potyviridae*. Relatively few plant viruses, exemplified by the families *Bunyaviridae* and *Rhabdoviridae,* possess negative-sense RNA genomes. *Reoviridae* is the largest family of the double-stranded (ds) RNA viruses. There is only one family of the plant viruses with dsDNA genomes, the *Caulimoviridae*family or so-called pararetroviruses, and replication of these viruses involves an RNA intermediate. The true plant DNA viruses are represented by the large and economically important family *Geminiviridae*. These viruses possess ssDNA genomes, and they have a dsDNA intermediate in their life cycle (Hull 2002). The evolutionary relationships among the positive-strand, negative-strand, and dsRNA viruses, as well as the pararetroviruses and ssDNA viruses appear to be extremely distant if not absent.