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Distribution of Viruses and Their Nematode Vectors

Giovanni P. Martelli and Charles E. Taylor

Introduction

There are several landmarks on the pathway of our expanding knowledge of nematode transmission of plant viruses. The initial discovery of *Xiphinema index* as vector of grapevine fanleaf virus (GFLV) (51) stimulated the search for nematode vectors of other soil-borne viruses, and this was accompanied by research on many aspects of the biology, ecology, and taxonomy of both nematodes and viruses. Early investigations established that plant viruses specifically associate with their nematode vectors, and the mechanism of this association began to emerge when it was discovered that the virus coat protein was a key factor in the adsorption of particles at virus retention sites within the nematodes. The importance of wild hosts for both viruses and vectors, the perennation of viruses in weed seeds, and the insight into the feeding behavior of vector nematodes improved our understanding of how viruses survive and spread in nature, and a basis for their control in commercial crops.

In recent years, improved technology has provided detailed information on the characteristics of viruses of the Nepovirus and Tobravirus groups. Members of both groups have a bipartite genome made up of two functional and separately encapsidated RNA species, which may recombine under both experimental and natural conditions to give rise to pseudo-recombinant strains (48, 108).

Now that the physicochemical composition of nepoviruses and their hydrodynamic and serological properties are known, subgroups that are broadly consistent with the geographical distribution and presumed origin of the different viruses have been established. Interest in the taxonomy of the virus vectors longidorids and trichodorids continues, as the number of

Giovanni P. Martelli, Dipartimento di Patologia vegetale, University of Bari and Centro di Studio del CNR sui Virus e le Virosi delle Colture Mediterranee, 70126 Bari, Italy.

Charles E. Taylor, Honorary Research Associate, Scottish Crops Research Institute, Invergowrie, Dundee, DD2 5DA Scotland.

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species known increases and the role of nematodes as vectors is better understood (63, 139).

There have been numerous reviews on many aspects of nematode transmission of viruses (47, 63, 68, 69, 83, 86, 122, 124, 125, 127, 128, 132, 133). In this most recent review, here, we consider the geographical distribution of the nepoviruses and tobnaviruses as an approach to understanding the ecological and biological association between these viruses and their vectors.

Nematode-Transmitted Viruses as Plant Pathogens

Diseases Induced by Nepoviruses

Nepoviruses are reported to infect wild plants, annual crops, and perennial crops. The natural host range varies greatly with individual viruses, as does the severity of the diseases they induce. Some nepoviruses are pathogens of primary economic importance, since they affect and damage major crops. Other nepoviruses are restricted to a single or a few hosts; thus, they are, for the most part, only of scientific interest. Grasses and cultivated cereals do not appear to be hosts to nepoviruses, and the only gymnosperm host so far reported is *Cycas revoluta* in Japan (39, 61).

The diseases caused by nepoviruses have been reviewed repeatedly, and most recently by Murrant et al. (89) and Stace-Smith and Ramsdell (122). Thus, they will only be summarized here, with a few selected examples in the following plant categories.

VEGETABLES

The artichoke (*Cynara scolymus*) seems to be one of the vegetables most frequently attacked by nepovirus. Three different viruses, viz., artichoke Italian latent (AILV), artichoke yellow ringspot (AYRV), and artichoke vein banding (AVBV) viruses, are named after this host (36, 73, 95). Two additional members of the group, strains of raspberry ringspot (RRV) and of tomato black ring (TBRV) viruses, have been recovered from artichoke plants in the eastern Mediterranean area (96) and in France (80), respectively.

Depending upon the cultivar and, perhaps, growing conditions, nepovirus-infected artichokes may either be symptomless (AILV, RRV) or exhibit symptoms ranging from mild chlorotic discolorations (AVBV, RRV, TBRV) to generalized yellowing and stunting (AILV), scattered yellow blotches (RRV), and intense chrome yellow rings and line patterns accompanied by necrosis and stunting (AYRV). The yield is variously affected, but no estimates of crop loss have been made (94).

Potato (*Solanum tuberosum*) is one of the most important potato black ringspot virus B (AVB) (55), syndrome characterize the leaves (112). In E "bouquet" and "pseudonecrotic spots, rings and losses of up to 30% have been reported.

Cucurbits (melon, watermelon) are affected by tobacco ring virus (TRV). Infected plants have mottled leaves and poor fruit set (122). Symptoms include mottling, ringspotting, and necrosis.

Five different nepoviruses have been reported to infect grapevine: grapevine chrome mosaic virus (GCMV), grapevine fanleaf virus (GLV), and TBRV have been reported to cause grapevine fanleaf (GLV), or chlorotic mottling, and necrosis (ArMV, SLRV).

Interestingly, of the nepoviruses, none seems to be transmitted by nematodes.

SMALL FRUITS

The consensus is that strawberries are the most important small fruit crops affected by nepoviruses more than any other.

No less than twelve different viruses have been reported to affect strawberries with two major grapevine viruses, viz., grapevine fanleaf virus (GLV) and "grapevine decline virus" (BBLMV), grape peach rosette mosaic virus (TomRSV).

Grapevine degeneration is a major problem in the Pannonic basin and all other regions of the Balkans where several nepoviruses (GLV, SLRV, and TBRV), either alone or in combination, induce a comparable syndrome, characterized by distinct syndromes, chlorotic leaves, and canes; chlorotic leaves (fanleaf); or by bright yellow or chrome yellow flecks into the interveinal tissue. The leaves are typically affected, with a

natodes as vectors is better

many aspects of nematode 122, 124, 125, 127, 128, 132, consider the geographical viruses as an approach to association between these

Plant Pathogens

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Potato (*Solanum tuberosum*) has its own nepoviruses in Peru, such as potato black ringspot (PBRV), potato virus U (PVU), and arracacha virus B (AVB) (55, 56, 112), of which only PBRV induces a field syndrome characterized by necrotic spotting or generalized yellowing of the leaves (112). In Europe, potato is affected by TBRV, the cause of "bouquet" and "pseudo- aucuba" diseases, the symptoms of which are necrotic spots, rings and malformations of the leaves, and stunting. Crop losses of up to 30% have been estimated in secondarily infected plants (5).

Cucurbits (melon, watermelon, squash, cucumber) are seriously affected by tobacco ringspot virus (TobRSV) in the United States. Infected plants have mottled and malformed leaves, ringspotting, stunting and poor fruit set (122). In Europe, arabis mosaic virus (ArMV) induces mottling, ringspotting and stunting of field-grown cucumbers (84).

Five different nepoviruses, ArMV, chicory yellow mottle (CYMV), grapevine chrome mosaic (GCMV), strawberry latent ringspot (SLRV), and TBRV have been associated in Europe with diseases of celery (*Apium graveolens*), in which they cause bright yellow mottling (GCMV, CYMV) or chlorotic mottling, distortion and crinkling of the leaves, stunting, and necrosis (ArMV, SLRV, TBRV) (72, 84, 85, 93).

Interestingly, of the three nepoviruses named after tomato, that is, TBRV, tomato ringspot (TomRSV), and tomato top necrosis (TTNV) viruses, none seems to be of economic importance to this crop.

SMALL FRUITS

The consensus is that grapevine (*Vitis vinifera*), raspberry (*Rubus idaeus*), and strawberry (*Fragaria × ananassa*) are affected by nepoviruses more than any other small fruit species.

No less than twelve different nepoviruses have been found associated with two major grapevine disorders known as "grapevine degeneration" and "grapevine decline." These viruses are ArMV, AILV, blueberry leaf mottle (BBLMV), grapevine Bulgarian latent (GBLV), GCMV, GFLV, peach rosette mosaic (PRMV), RRV, SLRV, TobRSV, TBRV, and TomRSV.

Grapevine degeneration is typically caused by GFLV in the Mediterranean basin and all other viticultural areas, except for Central Europe and the Balkans where several other nepoviruses (ArMV, GCMV, RRV, SLRV, and TBRV), either alone or in association with GFLV, are able to induce a comparable disease. Grapevine degeneration consists of three distinct syndromes, characterized either by deformations of the leaves, shoots, and canes; chlorotic mottling; reduced vigor and poor fruit setting (fanleaf); or by bright yellow discolorations of the foliage (yellow mosaic) or chrome yellow flecks along the main veins, which sometimes spread into the interveinal tissues (vein banding) (10). The crop may be drastically affected, with average losses up to or above 60% (110).

Grapevine decline typically occurs in *V. vinifera* and *Vitis labrusca* grown in the northern United States and Canada. It shows leaf and cane symptoms comparable to those of fanleaf, but affected vines die more frequently, especially when they are European cultivars. Tomato ringspot virus is the main cause of grapevine decline, together with three additional American nepoviruses [BBLMV, PRMV, and TobRSV (71)].

Raspberry has been reported to be a host to seven different nepoviruses: ArMV, cherry leafroll (CLRV), cherry rasp-leaf (CRLV), RRV, SLRV, TBRV, and TomRSV, all of which are pathogenic, except for CRLV whose infections are latent (122).

The field syndromes induced in raspberry by nepoviruses vary with the agent, or association of agents, and the cultivar. There are cultivars that are resistant or immune to individual viruses (ArMV, RRV, SLRV, TBRV) or some of their isolates (ArMV). Susceptible cultivars react to viral infections with a variety of foliage changes (chlorotic mottling, vein yellowing, yellow speckling, yellow or chlorotic ringspotting, curling), reduced vigor, stunting, and reduction and deformation of fruit (89).

Although, compared with raspberry, fewer nepoviruses (ArMV, RRV, SLRV, TBRV, and TomRSV) have been found to infect strawberry plants, their effects on this crop are equally destructive. Except for TomRSV, which rarely causes a natural infection in strawberry (26), all other viruses are major pathogens, especially in Great Britain and Central Europe, where mixed infections (e.g., ArMV and SLRV; RRV and TBRV) are common.

Symptoms consist of chlorotic spots, rings, and/or yellow blotches of the leaves, which may also be twisted, cupped, or crinkled. With mixed infections, the symptoms are usually more severe; the plants are stunted and often die (89).

FRUIT TREES

Nepovirus-induced diseases of pome fruit trees are rare, apple (*Malus sylvestris*) being the only species known to be affected. Two disorders of apple have been described, both in North America: "flat apple" and "union necrosis and decline," which are induced by CLRV and TomRSV, respectively (123).

Flat apple derives its name from the flattened appearance of the fruit borne by diseased plants. The affected plants become progressively weaker, stunted, and densely bushy.

In apple decline, the infected trees develop a necrosis of the woody cylinder at the graft union, possibly due to the hypersensitive reaction of the scion to the virus, which leads to a progressive decline.

Several nepoviruses cause diseases of economic importance in stone fruits.

Cherry (*Prunus avi* nepoviruses two of v typical, nepovirus-indi terized by enations or are reported from we agents differ. Rasp-le America (121), where: nepoviruses (ArMV or type (29).

Stem pitting and dec TomRSV. Affected tr pitting of the vascular agent (TomRSV), affe this disease, known as different patterns of : leaves (119).

Other economically are peach rosette mos peach willow leaf ros disorders, there are v leaves and a progressi

A high incidence of (*Juglans regia*) in Eur differs dramatically, de is grafted to rootstock (e.g., Paradox = *J. reg* are tolerant of infectio chlorotic ringspots an blotching (117). Graft condition known as "l limiting factor to waln hypersensitivity of wal by the virus, necrotize union (89).

Finally, the olive (C natural host of nepovi olive was affected by detection of virus parti different viruses have trees, by sap inoculatio olive latent ringspot vi them, however, causes been found to be asso fruits of cv. Ascolana 1

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omic importance in stone

Cherry (*Prunus avium*) is reported to be susceptible to six different nepoviruses two of which (CLRV and CRLV) are named after it. A typical, nepovirus-induced disease of cherry is rasp-leaf, which is characterized by enations on the underside of the leaves. Rasp-leaf syndromes are reported from western North America and Europe, but the causal agents differ. Rasp-leaf is caused by a single virus (CRLV) in North America (121), whereas in Europe it originates from mixed infections of nepoviruses (ArMV or RRV) and viruses of the prunus necrotic ringspot type (29).

Stem pitting and decline is another serious disease of cherry caused by TomRSV. Affected trees have reduced vigor and yield, with extensive pitting of the vascular cylinder. A similar disease, induced by the same agent (TomRSV), affects peach (*Prunus persica*) in North America. With this disease, known as yellow bud mosaic, stem pitting is accompanied by different patterns of yellow discoloration and severe distortion of the leaves (119).

Other economically important diseases of peach caused by nepoviruses are peach rosette mosaic, caused by PRMV in North America (58), and peach willow leaf rosette, caused by SLRV in Europe (28). In both disorders, there are various degrees of mottling and distortion of the leaves and a progressive decline of the tree.

A high incidence of CLRV infections has been found in English walnut (*Juglans regia*) in Europe and North America. The effect of the virus differs dramatically, depending on whether the host is on its own roots or is grafted to rootstocks of species other than *J. regia*, or their hybrids (e.g., Paradox = *J. regia* × *Juglans hindisii*). Self-rooted English walnuts are tolerant of infection; most plants are symptomless or, at most, show chlorotic ringspots and line patterns, or an occasional bright yellow blotching (117). Grafted walnuts, however, go into a severe decline, a condition known as "black line," which, in several areas, constitutes a limiting factor to walnut production. This disease depends upon CLRV hypersensitivity of walnut rootstocks, the tissues of which, when invaded by the virus, necrotize to give rise to a black line of dead cells at the graft union (89).

Finally, the olive (*Olea europaea*) should be briefly mentioned as a natural host of nepoviruses. A long debate, started in 1938 on whether olive was affected by virus diseases, ended some 10 years ago with the detection of virus particles in developing pollen grains (91). So far, seven different viruses have been recovered, mostly from symptomless olive trees, by sap inoculation (70). Of these viruses, four are nepoviruses, viz., olive latent ringspot virus (OLRV), ArMV, CLRV, and SLRV. None of them, however, causes a specific disease, except for SLRV, which has been found to be associated with striking malformations of leaves and fruits of cv. Ascolana tenera (67).

Diseases Induced by Tobraviruses

Among the tobnaviruses, tobacco rattle virus (TRV) has the widest natural host range. This range includes herbaceous weeds and wild, woody perennials, as well as annual and perennial crops (44–46).

In naturally infected plants, TRV tends to remain localized in the roots—the initial site of infection. In certain hosts, however, the virus moves to the above-ground parts, as in the case of pepper (*Capsicum annuum*), in which TRV induces bright yellow ring and line patterns in the leaves and yellow blotching, puckering, and malformation of the fruit (25).

Limited TRV systemic infection also occurs in potato plants originating from tubers affected by spraing disease—a severe disorder characterized by areas of corky tissues in the tuber flesh and mottled foliage (21).

Pea early-browning virus (PEBV) has a natural host range restricted to Leguminosae. Pea (*Pisum sativum*), French bean (*Phaseolus vulgaris*), broad bean (*Vicia faba*), and alfalfa (*Medicago sativa*) are the only plants from which the virus has been recovered. The infection is usually systemic and the symptoms shown by the foliage range from mild mottling and deformation to yellow chevrons and bands to extended necrosis (46).

Pepper ringspot virus (PRV) has been reported only from Brazil, where it systemically invades crops like tomato, pepper, and artichoke, to produce various patterns of bright yellow rings, lines, and bands on the foliage (46).

Causal Agents

Nepoviruses

The nepovirus group is one of the most rapidly expanding taxonomic groups of plant viruses. Its initial membership of eight, inclusive of definitive and possible members (47), had already grown to twenty-six in 1982 (79), and currently numbers thirty-four (Table 6.1). Of these, only eleven have a recognized nematode vector (see also Table 6.4). The rest owe their present taxonomic assignment to the possession of specific biological characteristics (i.e., host range responses, transmission through seeds) and physicochemical and other properties such as the type of intracellular behavior that conform those typical of the group.

Although all nepoviruses have isometric particles ~30 nm in diameter and a bipartite genome with two functional RNA species (42), wide differences exist in the physicochemical and hydrodynamic properties of individual members. Their serological properties, geographical distribution, vectors, and means of natural spread also differ. Such differences may be used to subdivide the group into smaller coherent clusters.

GROUPING ON A MOLE

Nepoviruses differ with hydrodynamic behavior of particles, corresponding to shells; M, nucleoprotein RNA (RNA-2); and B, larger RNA (RNA-1). A different type of particle determines whether the (heterogeneity) buoyant

Nepoviruses with a large differences in the molecular sedimentation behavior of M particles.

Finally, the protein having a single polypeptide made up of two or three different molecular weights daltons, respectively).

Taking these differences and coworkers (68, 74) clusters; Murant and T. clusters. These subdivisions the properties of some many of the published viral weight may not be based on whether RNA

These two ways of shown in Table 6.1 delineates definitive from not fully characterized; that related viruses fall serological cross-reactivity

The presence of two major single criterion with tentative members of the symptomless virus (LAS in which nucleoproteins 99), all other tentative nucleoprotein centrifugation the group.

The importance of the separation of definitive a Francki et al. (33). The

GROUPING ON A MOLECULAR BASIS

Nepoviruses differ with respect to their physicochemical properties and hydrodynamic behavior. Normally, these viruses contain three types of particles, corresponding to centrifugal component T, empty protein shells; M, nucleoproteins containing one molecule of the smaller genomic RNA (RNA-2); and B, nucleoproteins containing one molecule of the larger RNA (RNA-1). However, a few members (six in all), contain a different type of particle that encapsidates two molecules of RNA-2. This determines whether the B component yields one (homogeneity) or two (heterogeneity) buoyant density classes when centrifuged at equilibrium.

Nepoviruses with a homogeneous B component also exhibit clear-cut differences in the molecular weight of RNA-2, which influences the sedimentation behavior and, hence, the sedimentation coefficient of the M particles.

Finally, the protein coat of eight members of the group, rather than having a single polypeptide with a molecular weight of ~55,000 daltons, is made up of two or three smaller polypeptides (e.g., AVBV) with a different molecular weight (21,000–29,000 daltons and 42,000 to 47,000 daltons, respectively).

Taking these differences in physical properties into account, Martelli and coworkers (68, 74) divided the Nepovirus group into four distinct clusters; Murant and Taylor (87) however, divided the group into three clusters. These subdivisions were questioned by Francki et al. (33), since the properties of some nepoviruses are incompletely known and since many of the published values of particle sedimentation and RNA molecular weight may not be correct. They (33) proposed instead two subgroups, based on whether RNA-1 and RNA-2 differed significantly in size.

These two ways of subgrouping both have their merits. The scheme shown in Table 6.1 delineates the complexity of the group as a whole; it separates definitive from tentative members, except for TTNV, which is not fully characterized; and it is consistent with serological clustering, in that related viruses fall into the same subgroup. In no case is there serological cross-reactivity between members of different clusters.

The presence of two kinds of coat proteins seems to constitute the major single criterion whereby some nepoviruses are still regarded as tentative members of the group. In fact, except for lucerne Australian symptomless virus (LASV) and rubus Chinese seed-borne virus (RCSV), in which nucleoproteins apparently sediment as a single component (4, 99), all other tentative nepoviruses, including SLRV (35), have two nucleoprotein centrifugal components, as do the definitive members of the group.

The importance of the difference in protein coat composition in the separation of definitive and tentative nepoviruses has been questioned by Francki et al. (33). They pointed out that the smaller polypeptides

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TABLE 6.1. Grouping of nepoviruses according to their physicochemical properties.

Protein coat with one polypeptide		Protein coat with two polypeptides
B component homogeneous (one molecule of RNA-1)	B component heterogeneous (one molecule of RNA-1 or two molecules of RNA-2)	Arracacha virus B (AVB) Artichoke vein banding virus (AVBV) Cherry raspleaf virus (CRLV) Lucerne Australian symptomless virus (LASV) Lucerne Australian latent virus (LALV) Rubus Chinese seed-borne virus (RCSBV) Satsuma dwarf virus (SDV) Strawberry latent ringspot virus (SLRV)
M component with $S_{20,w}$ up to 100; MW of RNA-2, $\sim 1.5 \times 10^6$	M component with $S_{20,w}$ above 110; MW of RNA-2, above 2×10^6	
Arracacha virus A (AVA) Artichoke Italian latent virus (AILV) Cocoa necrosis virus (CNV) Crimson clover latent virus (CCLV) Cycas necrotic stunt virus (CNSV) Grapevine chrome mosaic	Artichoke yellow ringspot virus (AYRV) Blueberry leaf mottle virus (BBLMV) Cassava green mottle virus (CGMV) Cherry leafroll virus (CLRV) Chicory yellow mottle virus (CYMV)	
	Arabis mosaic virus (ArMV) Grapevine fanleaf virus (GFLV) Olive latent ringspot virus (OLRV) Potato black ringspot virus (PBRV) Raspberry ringspot virus (RRV) Tobacco ringspot virus (TobRSV)	

M component with $S_{20,w}$ up to
100; MW of RNA-2,
 $\sim 1.5 \times 10^6$

M component with $S_{20,w}$
above 110; MW of RNA-2,
above 2×10^6

Arabis mosaic virus (ArMV)
Grapevine fanleaf virus
(GFLV)
Olive latent ringspot virus
(OLRV)
Potato black ringspot virus
(PBRV)
Raspberry ringspot virus
(RRV)
Tobacco ringspot virus
(TobRSV)

Rubus Chinese seed-borne
virus (RCSBV)
Satsuma dwarf virus (SDV)
Strawberry latent ringspot
virus (SLRV)

Arracacha virus A (AVA)
Artichoke Italian latent virus
(AILV)
Cocoa necrosis virus (CNV)
Crimson clover latent virus
(CCLV)
Cycas necrotic stunt virus
(CNSV)
Grapevine chrome mosaic
virus (GCMV)
Mulberry ringspot virus
(MRV)
Tomato black ring virus
(TBRV)
Tomato top necrosis virus
(TTNV)

Artichoke yellow ringspot
virus (AYRV)
Blueberry leaf mottle virus
(BBLMV)
Cassava green mottle virus
(CGMV)
Cherry leafroll virus (CLRV)
Chicory yellow mottle virus
(CYMV)
Grapevine Bulgarian latent
virus (GBLV)
Hibiscus latent ringspot virus
(HLRV)
Lucerne Australian latent
virus (LALV)
Myrobalan latent ringspot
virus (MyLRV)
Peach rosette mosaic virus
(PRMV)
Potato virus U (PVU)
Tomato ringspot virus
(TomRSV)

detected in protein coat preparations of viruses like satsuma dwarf (SDV) may just be dimers and trimers of the true coat protein subunit, which is estimated to have a molecular weight of 14,500 daltons, that is, a value comparable to that calculated for the smallest polypeptides observed in dissociated virus protein preparations of TomRSV, TobRSV, and OLRV. This polypeptide is thought to be the basic unit of the tetrameric coat protein (55,000–60,000 daltons) typical of the group (23, 24, 115).

Different views are held by other workers (99), who consider some of the tentative nepoviruses with more than one coat polypeptide to be sufficiently distinct from the rest to warrant classification either as a true taxonomic subgroup of nepoviruses or as a new group with SLRV as the type member; they propose the name Slaterivirus for this new group.

This controversy results from the fact that it is not known whether the two polypeptides originate from (a) a *Comovirus*-like translational strategy of RNA-2, whereby a single large polyprotein precursor, produced in vivo, cleaves by internal proteolysis to form two smaller capsid proteins (for a review, see ref. 38) or (b) the originally single, large subunit, simply cleaves during chemical dissociation of the protein coat for electrophoretic analysis.

Serological Grouping

The taxonomy of nepoviruses, that is, the establishment of individual "species" within the group, is largely based on serology, which, as indicated in the preceding section, is in turn linked with their physico-chemical properties.

Most of the nepoviruses (22 out of 34 definitive and possible members) are serologically distinct and are apparently not related to any other member of the group. Their identification as separate entities is, therefore, unambiguous.

Serological stability seems to be highest with viruses infecting a single host or a narrow range of hosts. A primary example of this is GFLV, the populations of which, regardless of their geographical origin, their host (species or cultivars of *Vitis*), and the type of symptomatological responses they induce in host plants, exhibit a remarkable serological uniformity (69). A naturally occurring serological variant of GFLV was only recently discovered in Tunisia (116) after a long search.

A possible explanation offered for the striking serological uniformity of GFLV—which may be applicable to comparable cases with other viruses—is the low selection pressure to which the virus has been subjected in nature because of its strict adaptation to a single host (*V. vinifera* in particular) (69).

Nepoviruses with a wide natural host range apparently vary much more serologically and often give rise to distinct "species." Here, the distinction between close and distant relationship is arbitrary, and, therefore, it

may be hard to decide viruses or different strains.

A conservative approach serologically distinguishes type virus, rather than European strains form mottle isolate of TobRS variant of the type virus (120, 122).

A comparable situation in the eastern serological variants from Scottish and English strains index of 3 to 6 (96), the GFLV from ArMV, or When the geographical infects is a typical Mexican appropriate to regard this. This possibility appears indicating that although homology with the English with the Turkish isolate.

An intriguing aspect largely consistent with 6.2 and 6.3) and hence,

TABLE 6.2. Grouping of r
Serolog

1. Arabis mosaic virus (ArMV)
Grapevine fanleaf virus (GFLV)
2. Tomato black ring virus (TBRV)
ringspot strain)
Grapevine chrome mosaic
Cocoa necrosis virus (CNV)
3. Raspberry ringspot virus (RRSV)
grapevine, and cherry strain
Artichoke strain
4. Strawberry latent ringspot virus (SLRV)
Rubus Chinese seed-borne
5. Blueberry leaf mottle virus (BLMV)
(blueberry and grapevine)
Grapevine Bulgarian latent
6. Tobacco ringspot virus (TRSV)
Eucharis mottle strain
Potato black ringspot virus

es like satsuma dwarf (SDV) coat protein subunit, which is 500 daltons, that is, a value just polypeptides observed in IRSV, TobRSV, and OLRV. unit of the tetrameric coat e group (23, 24, 115).

(99), who consider some of one coat polypeptide to be classification either as a true ew group with SLRV as the ivirus for this new group.

it is not known whether the omovirus-like translational polyprotein precursor, pros to form two smaller capsid the originally single, large sociation of the protein coat

establishment of individual sed on serology, which, as n linked with their physico-

itive and possible members) y not related to any other s separate entities is, there-

ith viruses infecting a single xample of this is GFLV, the ographical origin, their host e of symptomatological re- it a remarkable serological ological variant of GFLV was er a long search.

ing serological uniformity of aparable cases with other which the virus has been adaptation to a single host

apparently vary much more species." Here, the distinc- arbitrary, and, therefore, it

may be hard to decide whether virus isolates are best considered different viruses or different strains of the same virus.

A conservative approach has been used with CLRV, for which many serologically distinguishable variants have been regarded as strains of the type virus, rather than as different viruses, even though American and European strains form two distinct clusters (54). However, the eucharis mottle isolate of TobRSV has been considered either a distant serological variant of the type virus (86) or a separate entity worthy of its own name (120, 122).

A comparable situation exists with the RRV "strain" recovered from artichoke in the eastern Mediterranean area. This virus, of which minor serological variants from Greece and Turkey are known, differs from Scottish and English serotypes of RRV by a serological differentiation index of 3 to 6 (96), that is, a value equal to or above that separating GFLV from ArMV, or TBRV from GCMV or cocoa necrosis virus (CNV). When the geographical origin of the virus and the fact that the host it infects is a typical Mediterranean species are considered, it would seem appropriate to regard the artichoke strain of RRV as a distinct nepovirus. This possibility appears to be strongly supported by recent information indicating that although the Greek isolate has only a 9% sequence homology with the English serotype of RRV, it shares 73% of its sequence with the Turkish isolate (105).

An intriguing aspect of serological clustering of nepoviruses is that it is largely consistent with the geographical distribution of the viruses (Table 6.2 and 6.3) and hence, with their possible centers of origin. For instance,

TABLE 6.2. Grouping of nepoviruses according to serological relatedness.

Serological clusters	Geographical origin
1. Arabis mosaic virus (ArMV) (type and hop strain) Grapevine fanleaf virus (GFLV)	Europe Mediterranean-Near East
2. Tomato black ring virus (TBRV) (type and beet ringspot strain) Grapevine chrome mosaic virus (GCMV) Cocoa necrosis virus (CNV)	Europe Europe Africa
3. Raspberry ringspot virus (RRV) (Scottish, English, grapevine, and cherry strains) Artichoke strain	Europe Mediterranean-Near East
4. Strawberry latent ringspot virus (SLRV) Rubus Chinese seed-borne virus (RCSBV)	Europe Far East
5. Blueberry leaf mottle virus (BBLMV) (blueberry and grapevine strain) Grapevine Bulgarian latent virus (GBLV)	North America Europe
6. Tobacco ringspot virus (TobRSV) (type strain) Eucharis mottle strain Potato black ringspot virus (PBRV)	North America South America South America

TABLE 6.3. Grouping of nepoviruses according to presumed geographical origin.

Presumed origin and viruses	Natural host range ^a	Present distribution ^a
<i>1. Europe</i>		
Arabid mosaic virus (ArMV)	Very wide (fruits, vegetables, ornamentals)	Very wide
Cherry leafroll virus (CLRV)	Very wide (fruits, shrubs)	Very wide
Crimson clover latent virus (CCLV)	Crimson clover	Wide
Grapevine Bulgarian latent virus (GBLV)	Grapevine	Wide
Grapevine chrome mosaic virus (GCMV)	Grapevine, celery	Wide
Raspberry ringspot virus (RRV)	Very wide (especially small fruits)	Wide
Strawberry latent ringspot virus (SLRV)	Very wide (fruits, vegetables, ornamentals)	Wide
Tomato black ring virus (TBRV)	Very wide (fruits, vegetables, ornamentals)	Wide
<i>2. Mediterranean—Near East</i>		
Artichoke Italian latent virus (AILV)	Narrow (vegetables, grapevine)	Wide
Artichoke vein banding virus (AVBV)	Artichoke	Restricted
Artichoke yellow ringspot virus (AYRV)	Narrow (vegetables)	Restricted
Chicory yellow mottle virus (CYMV)	Narrow (vegetables)	Restricted
Grapevine fanleaf virus (GFLV)	Grapevine	Ubiquitous
Myrobalan latent ringspot virus (MyLRV)	Narrow (fruits)	Restricted
Olive latent ringspot virus (OLRV)	Olive	Restricted
Raspberry ringspot virus, artichoke strain	Artichoke	Restricted
<i>3. North America</i>		
Blueberry leaf mottle virus (BBLMV)	Blueberry, grapevine	Restricted
Cherry rasp leaf virus (CRLV)	Narrow (fruits)	Restricted
Peach rosette mosaic virus (PRMV)	Narrow (fruits)	Restricted
Tobacco ringspot virus (TobRSV)	Very wide (fruits, vegetables, ornamentals)	Wide
Tomato ringspot virus (TomRSV)	Very wide, (fruits, vegetables, ornamentals)	Very wide
Tomato top necrosis virus (TTNV)	Tomato	Restricted
<i>4. South America</i>		
Arracacha virus A (AVA)	Arracacha	Restricted
Arracacha virus B (AVB)	Arracacha, ocra, potato	Restricted
Potato black ringspot virus (PBRV)	Potato	Restricted

TABLE 6.3. Continued

Presumed origin and	
Potato virus U (PVU)	
Tobacco ringspot virus, e strain	
<i>5. Africa</i>	
Cocoa necrosis virus (CNV)	
Hibiscus latent ringspot virus (HLRV)	
<i>6. Australia</i>	
Cassava green mottle virus (CGMV)	
Lucerne Australian latent virus (LALV)	
Lucerne Australian symptom virus (LASV)	
<i>7. Far East</i>	
Cycas necrotic stunt virus	
Mulberry ringspot virus (MRSV)	
Rubus Chinese seed-borne virus (RCSBV)	
Satsuma dwarf virus (SDV)	

^a Ubiquitous, occurring in all countries in two or more countries; restricted, recorded from a single country.

North American Tobacco ringspot virus is part of the continent. European ArMV, RRV, further south: RRV, area, and CNV in Africa; serologically interrelated ancestor. The fact that though separated regions have developed in the

GEOGRAPHICAL ORIGIN

There is a consensus among plant and thus dependent (as opposed to nematode) reviews, refs. 40 and

ng to presumed geographical

host range ^a	Present distribution ^a
s, vegetables,	Very wide
s, shrubs)	Very wide
	Wide
	Wide
y	Wide
cially small fruits)	Wide
s, vegetables,	Wide
s, vegetables,	Wide
les, grapevine)	Wide
	Restricted
les)	Restricted
les)	Restricted
	Ubiquitous
	Restricted
	Restricted
	Restricted
vine	Restricted
	Restricted
	Restricted
i, vegetables,	Wide
s, vegetables,	Very wide
	Restricted
potato	Restricted
	Restricted
	Restricted

TABLE 6.3. Continued

Presumed origin and viruses	Natural host range ^a	Present distribution ^a
Potato virus U (PVU)	Potato	Restricted
Tobacco ringspot virus, eucharis strain	Eucharis	Restricted
5. Africa		
Cocoa necrosis virus (CNV)	Cocoa	Restricted
Hibiscus latent ringspot virus (HLRV)	Hibiscus	Restricted
6. Australia		
Cassava green mottle virus (CGMV)	Cassava	Restricted
Lucerne Australian latent virus (LALV)	Alfalfa, white clover	Restricted
Lucerne Australian symptomless virus (LASV)	Alfalfa	Restricted
7. Far East		
Cycas necrotic stunt virus (CNSV)	Cycas	Restricted
Mulberry ringspot virus (MRSV)	Mulberry	Restricted
Rubus Chinese seed-borne virus (RCSBV)	Rubus	Restricted
Satsuma dwarf virus (SDV)	Satsuma mandarin	Restricted

^a Ubiquitous, occurring in all major areas of cultivation of the host plant; very wide, recorded from many countries in two or more continents; wide, recorded from many countries in the same continent; restricted, recorded from a single or two adjacent countries.

North American TobRSV has serological counterparts in the southern part of the continent (TobRSV eucharis strain and PBRV), and, similarly, European ArMV, RRV, and TBRV have serologically related "species" further south: RRV artichoke strain and GFLV in the Mediterranean area, and CNV in Africa. The viruses within each of these clusters are serologically interrelated, which indicates evolution from a common ancestor. The fact that these viruses occur in physically contiguous, though separated regions, is therefore in line with the likelihood that they have developed in these regions.

GEOGRAPHICAL ORIGIN AND DISTRIBUTION

There is a consensus that nepoviruses are primarily pathogens of wild plants and thus depend for their survival and spread in natural environments (as opposed to man-made agricultural environments) on dissemination by nematode vectors and host plant seeds that they may infect (see reviews, refs. 40 and 86). It follows that these viruses have little natural

mobility, so they tend to be localized in specific territorial enclaves in which they become firmly established.

It is therefore conceivable that the geographical distribution of nepoviruses broadly corresponds to their areas of origin or differentiation, in which their hosts, primary and alternative (usually crop plants), and vectors are readily available.

The notion that nepoviruses may have differential geographical origins, first put forward with reference to viruses infecting grapevines in Europe and North America (68, 69) and recently extended to other nematode-borne viruses of the American continent (122), seems tenable and is consistent with the distribution of vectors. Therefore it seems reasonable to hypothesize a presumed geographical origin of currently recognized nepoviruses, as shown in Table 6.3. From this table, it is evident that nepoviruses that generally infect a wide range of hosts have a much wider distribution, especially if the hosts are vegetatively propagated perennial crops, than have viruses with a few or a single host. Such viruses, as would be expected, have a restricted distribution.

A remarkable exception to the latter is GFLV, which although a highly specialized pathogen has the widest geographical distribution of the nepoviruses. Uncontrolled marketing of infected budwood and rooted cuttings have greatly facilitated the spread of GFLV and its major vector, *X. index*, to virtually all the viticultural areas of the world. This also applies to records of European nepoviruses such as SLRV, TBRV and ArMV, from grapevines in eastern Mediterranean regions (Turkey and Israel) and Japan (9); from grapevines, cherry, rhubarb and parsley in North America (122), as well as the American TomRSV, from a shrub in Australia (24). No plausible explanation is presently available for the records of ArMV from a native shrub in the United States (122) and of TobRSV from soybean in the People's Republic of China (144).

Another widely distributed virus, CLRV, is recorded from cultivated and native plant species in Europe and North America. Simple dissemination through infected propagative material may not account for the widespread occurrence of CLRV outside Europe, its presumed area of origin, since there is serological evidence that strains of CLRV may have independently arisen in Europe and North America. This is compatible with the notion that, in nature, CLRV spreads by air-borne pollen rather than by nematodes (54, 122) (Table 6.4).

Tobraviruses

Tobraviruses constitute the other recognized taxonomic group of plant viruses transmitted by nematodes (*Trichodorus* and *Paratrichodorus*). These viruses have rigid, rod-shaped particles that vary in length: very short, ~45 nm.; short (S), 50 to 110 nm; and long (L), 185 to 200 nm. Their

TABLE 6.4. Grouping of

Virus
1. Transmitted by nematodes
Arabis mosaic virus (ArMV), All strains
Artichoke Italian latent virus (AILV)
Italian strain
Greek strain
Cherry rasp leaf virus (CRLV)
Grapevine fanleaf virus (GFLV)
Mulberry ringspot virus (MRSV)
Peach rosette mosaic virus (PRMV)
Raspberry ringspot virus (RRV)
Scottish strain
English strain
Strawberry latent ringspot virus (SLRV)
All strains
Tobacco ringspot virus (TobRSV)
All strains
Tomato black ring virus (TBRV)
Type strain
Beet ringspot strain
Tomato ringspot virus (TomRSV)
Type strain
Grapevine yellow vein strain
2. Transmitted by pollen to mother plants, no vector found
Cherry leafroll virus (CLRV)
Blueberry leaf mottle virus (BBLMV)
Artichoke yellow ringspot virus (AYRV)
3. Vector unknown
Arracacha virus A (AVA)
Arracacha virus B (AVB)

TABLE 6.4. Grouping of nepoviruses according to means of natural spread.

Virus	Seed transmission in naturally and/or artificially infected hosts	Vector
1. <i>Transmitted by nematodes</i>		
Arabid mosaic virus (ArMV) All strains	Yes	<i>Xiphinema diversicaudatum</i>
Artichoke Italian latent virus (AILV) Italian strain	Not detected	<i>Longidorus apulus</i>
Greek strain		<i>Longidorus fasciatus</i>
Cherry rasp leaf virus (CRLV)	Yes	<i>Xiphinema americanum</i>
Grapevine fanleaf virus (GFLV)	Yes	<i>Xiphinema index</i> , <i>Xiphinema italiae</i>
Mulberry ringspot virus (MRSV)	Yes	<i>Longidorus martini</i>
Peach rosette mosaic virus (PRMV)	Yes	<i>Xiphinema americanum</i> , <i>Longidorus diadecturus</i> , <i>Longidorus elongatus</i>
Raspberry ringspot virus (RRV) Scottish strain	Yes	<i>Longidorus elongatus</i>
English strain		<i>Longidorus macrosoma</i>
Strawberry latent ringspot virus (SLRV) All strains	Yes	<i>Xiphinema diversicaudatum</i>
Tobacco ringspot virus (TobRSV) All strains	Yes	<i>Xiphinema americanum</i>
Tomato black ring virus (TBRV) Type strain	Yes	<i>Longidorus attenuatus</i>
Beet ringspot strain		<i>Longidorus elongatus</i>
Tomato ringspot virus (TomRSV) Type strain	Yes	<i>Xiphinema americanum</i> , <i>Xiphinema rivesi</i>
Grapevine yellow vein strain		<i>Xiphinema californicum</i>
2. <i>Transmitted by pollen to mother plants, no vector found</i>		
Cherry leafroll virus (CLRV)	Yes	
Blueberry leaf mottle virus (BBLMV)	Yes	
Artichoke yellow ringspot virus (AYRV)	Yes	
3. <i>Vector unknown</i>		
Arracacha virus A (AVA)	Yes	
Arracacha virus B (AVB)	Yes	

or
specific territorial enclaves in

hical distribution of nepovi-
origin or differentiation, in
(usually crop plants). and

erential geographical origins,
ecting grapevines in Europe
xtended to other nematode-
(122), seems tenable and is
erefore it seems reasonable
gin of currently recognized
this table, it is evident that
of hosts have a much wider
atively propagated perennial
ngle host. Such viruses, as
ution.

LV, which although a highly
raphical distribution of the
ected budwood and rooted
GFLV and its major vector,
eas of the world. This also
such as SLRV, TBRV and
anean regions (Turkey and
rry, rhubarb and parsley in
n TomRSV, from a shrub in
presently available for the
e United States (122) and of
blic of China (144).

is recorded from cultivated
h America. Simple dissemi-
al may not account for the
urope, its presumed area of
t strains of CLRV may have
America. This is compatible
ds by air-borne pollen rather

d taxonomic group of plant
lorus and *Paratrichodorus*).
les that vary in length: very
ong (L), 185 to 200 nm. Their

TABLE 6.4. *Continued*

Virus	Seed transmission in naturally and/or artificially infected hosts	Vector
Artichoke vein banding virus (AVBV)	Not tested	
Cassava green mottle virus (CGMV)	Not tested	
Chicory yellow mottle virus (CYMV)	Yes	
Cocoa necrosis virus (CNV)	Yes	
Crimson clover latent virus (CCLV)	Yes	
Cycas necrotic stunt virus (CNSV)	Yes	
Grapevine Bugarian latent virus (GBLV)	Not tested	
Grapevine chrome mosaic virus (GCMV)	Not tested	
Hibiscus latent ringspot virus (HLRV)	Not detected	
Lucerne Australian latent virus (LALV)	Yes	
Lucerne Australian symptomless virus (LASV)	Yes	
Myrobalan latent ringspot virus (MyLRV)	Not tested	
Olive latent ringspot virus (OLRV)	Not tested	
Potato black ringspot virus (PBRV)	Not detected	
Potato virus U (PVU)	Yes	
<i>Rubus</i> Chinese seed-borne virus (RCSBV)	Yes	
Satsuma dwarf virus (SDV)	Yes	
Tomato top necrosis virus (TTNV)	Not tested	

bipartite genome has two functional RNA species, their S particles encapsidate one molecule of the smaller RNA (RNA-2), and their L particles contain one molecule of the larger RNA (RNA-1). Coat protein subunits are of a single type and have a molecular weight of 21,000-23,000 daltons.

In contrast with nepoviruses, tobnaviruses have increased very little in number: The two members constituting the group when it was first established (47) are now three (46) (Table 6.5).

The classification of tobnaviruses is based on molecular hybridization, that is, the extent of sequence homology between RNA-1 species, rather

TABLE 6.5. Tobnavirus group: Members, host range, vectors, and geographical distribution.

Geographical distribution

Vectors

Seed transmission

TABLE 6.5. Tobravirus group: Members, host range, vectors, and geographical distribution.

Virus	Natural Host Range	Seed transmission	Vectors	Geographical distribution
Tobacco rattle virus (TRV)	Very wide (vegetables, ornamentals, woody perennials, shrubs)	Yes	<i>Trichodorus cylindricus</i> , <i>T. hooperi</i> , <i>T. primitivus</i> , <i>T. similis</i> , <i>T. viruliferus</i> ; <i>Paratrichodorus allius</i> , <i>P. anemones</i> , <i>P. christiei</i> , <i>P. minor</i> , <i>P. nanus</i> , <i>P. pachydermus</i> , <i>P. porosus</i> , <i>P. teres</i> , <i>P. tunisiensis</i>	Very wide (Europe, Mediterranean, North America, Japan, New Zealand)
Pea early-browning virus (PEBV)	Narrow (legumes only)	Yes	<i>Trichodorus primitivus</i> , <i>T. viruliferus</i> ; <i>Paratrichodorus anemones</i> , <i>P. pachydermus</i> , <i>P. teres</i>	Wide (Europe, Mediterranean)
Pepper ringspot virus (PRV)	Narrow (vegetables)	Yes	<i>Paratrichodorus christiei</i>	Restricted (Brazil)

species, their S particles RNA (RNA-2), and their L RNA (RNA-1). Coat proteinular weight of 21,000-23,000 have increased very little in the group when it was first described (5).
on molecular hybridization, between RNA-1 species, rather

than on serology. This led to the recognition of three distinct viruses, each with its own separate gene pool: TRV, PEBV, and PRV (106).

Isolates belonging to any given virus or "species" have strongly conserved RNA-1 genes, whereas their RNA-2 genes vary. Therefore, serology is, at most, only useful for separating strains within each "species." For example, broad bean yellow band virus (BBYBV) was originally considered to be a possible new member of the group because it is not apparently related serologically to the English or Dutch strains of PEBV (111). However, it was later demonstrated that its RNA-1 has substantial sequence homology with PEBV RNA-1, and, therefore, despite its lack of serological relatedness, it was synonymized with PEBV as a new serotype (107).

The use of serology to identify certain tobnaviruses can be misleading. In fact, since sequences of a gene pool of a tobnavirus "species" may be captured in nature by a gene pool of a different "species", new pseudo-recombinants arise in which the RNA-2 (i.e., the part of the genome responsible for serological specificity as it codes for the coat protein) of a given virus becomes dependent for its replication on the RNA-1 of another virus, conferring upon it the serological characteristics of the former virus (108).

The geographical distribution of tobnaviruses seems to differentiate, to a certain extent, individual members of the group from one another, thus justifying the concept of the existence of gene pools.

Vectors

Many species of nematodes ingest viruses when they feed on the roots of virus-infected plants, but it is now well established that the natural transmission of nepoviruses is only by longidorid nematodes, and of tobnaviruses by trichodorid nematodes. However, of the 157 species of *Xiphinema* and 82 species of *Longidorus* described to date (early 1989), relatively few have been implicated as vectors and, indeed, not all nepoviruses require nematode vectors for their survival and dissemination (Table 6.4). So far, at least 14 of about 50 described species of *Trichodorus* and *Paratrichodorus* are vectors of the tobnaviruses TRV and PEBV, but each species may only transmit a particular strain. A third tobnavirus, PRV, has been described from Brazil and *P. christiei* has been implicated as a vector (22, 113) (Table 6.5).

Distribution of *Xiphinema* and *Longidorus*

Xiphinema and *Longidorus* have been reported from most parts of the world where nematode surveys have been undertaken. Individual species mostly occur as discrete populations in a particular region, and analyses

of their distribution and phylogenetic relationships have characteristics of different origins. For example, that *Xiphinema* originates from Pangaea, the genus *sp* from Africa, from where the South American region

Longidorus, with *Pa* have originated in South America, united, and a later spread a main speciation of Europe.

In their analysis of the (135) relate the relative to Quaternary glacial activity in eastern Mediterranean plate tectonic activity in the Americas also present on species richness and

Much of the present terms, be related to present times, many species have been disseminated. Examples include *X.* distributed throughout vines are grown from *Xiphinema rivesi*, a vector probably been exported particularly in western virus. Among *Longidorus* *L. vineacola* have been garden planting material in Apulia (southern Italy) propagation (109).

Species that have because of their genetically separated populations characteristics to be evidence of morphological *Xiphinema* and *Longidorus* terms of taxonomy by transmission.

Brown and Tophan *sicaudatum* from differentially, as well as by cycle

of three distinct viruses, each with a unique RNA-1, and PRV (106). The "species" have strongly divergent A-2 genes. Therefore, separating strains within each virus band (BBYBV) was a major factor of the group because it was found that its RNA-1 has a unique RNA-1, and, therefore, it was synonymized with PEBV.

aviruses can be misleading. The tobamovirus "species" may be different "species", new A-2 (i.e., the part of the genome as it codes for the coat protein for its replication on the basis of serological characteristics

as seems to differentiate, to group from one another, thus the pools.

When they feed on the roots of plants, it is established that the natural hosts of longidorid nematodes, and of course, of the 157 species of longidorids described to date (early 1989), are plants and, indeed, not all of them. Their survival and dissemination of 50 described species of longidorids of the tobamoviruses TRV and TSWV is a particular strain. A third species, *P. christiei* has been

is

derived from most parts of the world. Individual species are found in a particular region, and analyses

of their distribution have been made in an attempt to deduce their phylogenetic relationships. From a comparison of several morphological characteristics of different longidorid genera, Coomans (27) concluded that *Xiphinema* originated in Gondwanaland and, before the break-up of Pangaea, the genus spread to Laurasia. The main speciation occurred in Africa, from where the majority of species have been described, with South America regarded as another important speciation area.

Longidorus, with *Paralongidorus* and *Longidoroides*, is considered to have originated in Southeast Africa and India when these areas were still united, and a later spread to Laurasia was accompanied, and followed, by a main speciation of Longidorus in the holarctic region, especially Europe.

In their analysis of the European longidorid fauna, Topham and Alpey (135) relate the relative impoverishment of species in the northern regions to Quaternary glaciation and attribute the highly diverse fauna of the eastern Mediterranean countries of Israel, Italy, and Malta to Miocene plate tectonic activity in that area. The distribution of longidorid species in the Americas also provides evidence of the effect of changing latitude on species richness and diversity.

Much of the present distribution of longidorid species can, in broad terms, be related to paleoecology (16, 30, 78, 98, 135), but in relatively recent times, many species, especially those associated with crop plants, have been disseminated from their centers of origin by man's activities. Examples include *X. index*, the vector of GFLV, which has been distributed throughout Europe and the areas of the world where grapevines are grown from its center of origin in ancient Persia (50, 82). *Xiphinema rivesi*, a vector of TomRSV in the eastern United States, has probably been exported to Europe where it occurs in scattered localities particularly in western France, but so far without association with the virus. Among *Longidorus* species, there is evidence that *L. elongatus* and *L. vineicola* have been introduced into the Scottish Western Islands with garden planting material (7, 16) and that *L. apulus* has been distributed in Apulia (southern Italy) on soil adhering to artichoke sprouts used for propagation (109).

Species that have been widely dispersed survive in new biotopes because of their genetic adaptability. With time, many of the geographically separated populations may change sufficiently in their taxonomic characteristics to be considered new species. Certainly there is much evidence of morphometric variation within widely dispersed species of *Xiphinema* and *Longidorus*, and this has caused problems not only in terms of taxonomy but also in the identification of their role in virus transmission.

Brown and Topham (17) found that populations of *Xiphinema diversicaudatum* from different countries were distinguishable morphometrically, as well as by certain aspects of their biological behavior, including

their reproductive ability and their ability to transmit virus. However, although populations could be grouped morphometrically, the differences were not considered to be sufficient to establish new species. Morphometric differences between dispersed populations have also been noted in *Xiphinema coxi*, *L. elongatus*, *L. profundorum*, and *L. vineacola*, and these species, together with *X. diversicaudatum*, may be regarded as species complexes in which the biological characteristics of the populations also differ to some degree. *Xiphinema americanum* was recognized as a species complex by Lima (62), who concluded that it comprised seven parthenogenetic species, four of which he described as new. Other workers (52, 123) supported this view, although they thought the demarcation of these species were problematical and unsatisfactory. However, Lamberti and Bleve-Zacheo (62) divided *X. americanum sensu lato* into six groups of species, totaling 25 in all, with 15 of them new. They thought that *X. americanum sensu stricto* is restricted in its geographical distribution to the eastern part of North America, and they designated *Xiphinema californicum* a new species to define the morphologically distinct group of the western seaboard of the United States. Apart from some outstanding queries, records of *X. americanum* in European countries have been assigned to *Xiphinema pachtaicum* or *Xiphinema brevicolle*, neither of which species has been shown to be a vector in field situations (16).

Because of the taxonomic reconstruction of *X. americanum* (62) many of the records of its association with TomRSV or TobRSV in North America need to be reconsidered. *Xiphinema americanum sensu stricto* remains as the vector of some strains of TomRSV, and so far it is the only recognized vector of TobRSV, although the geographical distribution of the virus is not entirely coincident with that of the vector; however, *X. californicum* is established as the vector of California-type strains of TomRSV (53) and is presumed to be the vector of CRLV (62, 90). Similarly, *X. rivesi* is the vector of strains of TomRSV in eastern Canada and Pennsylvania (USA) (34), and *X. utahense* and *X. occidum* are also considered to be potential vectors of some strains of TomRSV (62, 144).

Records of virus transmission of *X. americanum* or derived species outside North America may be authentic but at most are associated with outlier populations of the nematode that have been dispersed, through man's agency, from the center of origin of both the vector and the virus in North America.

The other species in North America that have been associated with the transmission of nepoviruses in field situations are *X. index*, which was introduced from Europe, and which is unique in its association with GFLV, and *Longidorus diadecturus*, which is a vector of PRMV in Ontario (Canada), with *X. americanum* also being recorded as a less efficient vector of the virus (1, 2). In a recent paper (2a), an Ontario population of *L. elongatus* was also recorded as a vector of PRMV but only at a low transmission level.

Longidorus diadecturus in Japan (143), are unknown. *Longidorus* species in ce

Distribution of *Tricho.*

Trichodorid nematodes have been recorded from relatively isolated islands; that different species are a geographical region so. In a survey of trichodorid and *Trichodorus primitivus* countries, whereas *Paratrichodorus* in Italy, and *Trichodorus* Trichodorid species described to be localized, but surely establish the extent of t.

Although groupings of (65), their taxonomy does of origin. However, the occurrence of several species active speciation is occurring.

Some species are common. *Paratrichodorus minor* been distributed by mechanical injury as occurs are unlikely to survive. However, they may be (6, 114), and their ability exploit new environments.

Most of the records are from Europe and North America. research interest in these associations may be expected. Currently, there are isolates from New Zealand, and

Isolates of TRV from are transmitted by different geographical separation vector. So far, PEBV have been identified implicated as vectors.

o transmit virus. However, ometrically, the differences blish new species. Morpho- ions have also been noted in um, and *L. vineacola*, and atum, may be regarded as aracteristics of the popula- umericanum was recognized oncluded that it comprised he described as new. Other gh they thought the demar- id unsatisfactory. However, umericanum sensu lato into of them new. They thought in its geographical distribu- they designated *Xiphinema* hologically distinct group of part from some outstanding opean countries have been nema brevicolle, neither of in field situations(16).

f *X. americanum* (62) many RSV or TobRSV in North i *americanum sensu stricto* RSV, and so far it is the only geographical distribution of at of the vector; however, of California-type strains vector of CRLV (62, 90). omRSV in eastern Canada se and *X. occidum* are also ains of TomRSV (62, 144). icanum or derived species at most are associated with ve been dispersed, through n the vector and the virus in

ve been associated with the s are *X. index*, which was ue in its association with is a vector of PRMV in being recorded as a less ent paper (2a), an Ontario l as a vector of PRMV but

Longidorus diadecturus and *Longidorus martini*, the vector of MRSV in Japan (143), are unknown in Europe; they are distinct from other *Longidorus* species in certain morphological details (11).

Distribution of *Trichodorus* and *Paratrichodorus*

Trichodorid nematodes are widespread in North America and Europe and have been recorded from many parts of the world, including some relatively isolated islands. Most species appear to be locally distributed so that different species are present in different landmasses, although within a geographical region some species may be more widespread than others. In a survey of trichodorids in Europe (3), *Paratrichodorus pachydermus* and *Trichodorus primitivus* were found to occur in most of the northern countries, whereas *Paratrichodorus tunisiensis* has so far been found only in Italy, and *Trichodorus hooperi* only in the southwest of England. Trichodorid species described from Africa, India, and Japan also appear to be localized, but surveys in those regions have been insufficient to establish the extent of their geographical distribution.

Although groupings of trichodorids species have been recognized (31, 65), their taxonomy does not indicate evolutionary directions and centers of origin. However, the abundance of species in Europe, and the usual occurrence of several species in a single soil sample (64, 90), suggests that active speciation is occurring and new biotopes are being invaded.

Some species are cosmopolitan in their distribution, for example, *Paratrichodorus minor* and *Paratrichodorus porosus* (66), and may have been distributed by man, although trichodorids are susceptible to such mechanical injury as occurs in the rough handling of soil samples (8), and are unlikely to survive casual transportation from one region to another. However, they may be successfully dispersed in flood or irrigation waters (6, 114), and their ability to reproduce rapidly allows them to invade and exploit new environments quickly (59).

Most of the records of tobnavirus transmission by trichodorid species are from Europe and North America (63, 127, 140), but this reflects the research interest in these regions, and, in due course, more virus-vector associations may be expected to be identified in other parts of the world. Currently, there are isolated records of TRV transmissions from Japan and New Zealand, and of PRV from Brazil.

Isolates of TRV from North America differ from those from Europe and are transmitted by different species, which supports the view that geographical separation is associated with differentiation of virus and vector. So far, PEBV has been found only in Europe, but several strains have been indentified and at least five trichodorid species have been implicated as vectors.

Virus-Vector Associations

Much of the accumulated experimental evidence of nematode transmission of plant viruses indicates that there is a high degree of specificity in the association between virus and vector. Thus, although serologically unrelated nepoviruses may share a common vector species (e.g., *X. diversicaudatum* transmits ArMV and SLRV), strains of a virus that are serologically distinct are transmitted by different, although closely related species of the same nematode genus. For example, the Scottish strains of RRV and the unrelated TBRV are transmitted by *L. elongatus*, but the English strains of these viruses have *Longidorus macrosoma* and *Longidorus attenuatus*, respectively, as vectors. Further, the division of *X. americanum* species complex into several discrete species (62) now supposes the association of serologically distinct strains of TomRSV with different vector species (63).

Evidence of the specific association between tobnaviruses and trichoroid vectors is less clear. American and European isolates of TRV are serologically distinguishable (see earlier section) and, in nature, are associated with different species of *Trichodorus* and *Paratrichodorus*; indeed, only species of the latter genus have been recorded as vectors in North America.

In comparing the transmission of TRV by nine species of *Trichodorus* and *Paratrichodorus* from the Netherlands, van Hoof (141) found that transmission occurred only when the nematode and virus came from the same locality. A high level of specificity is also apparent with the transmission of PEBV, different isolates of which are transmitted by several trichodorid species (37, 142). Other evidence suggests that specificity of transmission is not well developed. In Britain, the spinach yellow mottle strain of TRV was transmitted by a mixed population of *Trichodorus* and *Paratrichodorus* species (60); in Belgium, five trichoroid species transmitted TRV, infecting a potato crop (92), although in this case it was not recorded whether a single virus strain was involved.

A recent study in eastern Scotland (19) showed that a close relationship may be established between different species of trichodorid nematodes and serologically distinct isolates of TRV. At two field sites, *P. pachydermus* transmitted the majority of the several isolates of TRV (PRN serotype) that were present, but *Trichodorus cylindricus* transmitted isolates of a previously uncharacterized serotype.

For some years, it has been recognized that if the vector status of a nematode is to be established with any certainty, several criteria must be met in experimental work (75, 127, 136). These include (a) the virus must be available to the nematode; (b) test conditions must be suitable for transmission to occur; (c) the possibility of virus contamination of the bait plants must be avoided. To these criteria, Trudgill et al. (139) added (d) the virus and nematode must be correctly identified; (e) bait plant

tissues must be shown to be free of virus; (f) the nematode being tested must meet these criteria, and differences in efficiency of transmission between longidorids and trichodorids must be related into the procedure. Anomalous results previously reported, unsupported by field evidence, and vector associations are in doubt.

Efficient extraction of virus from nematodes for transmission tests, virus-vector associations, and sorting and sieving techniques are satisfactory procedures for

Variation in Transmission

Although the authenticity of the virus has been established, the different results suggest that transmission is not uniform; but because it has been difficult to substitute one vector for another, it was demonstrated that vectors of ArMV, whereas vectors of RRV (Scottish isolates) (134, 138).

Recent experiments have widely separated geographical regions of the virus with widely separated populations of *X. diversicaudatum* and SLRV, Brown (12, 14) rarely transmitted the virus, but all efficient vectors (14) to the British strains of TBRV exposed to an Italian strain did not improve. In another experiment, Italy was exposed to two strains of SLRV. The Scottish population of virus, but did not transmit all three viruses sorbent electron microscopy they had ingested the virus electron microscopy of

tissues must be shown to be infected with the virus being tested; and (f) the nematode being tested must be shown to be the only possible vector in that experiment. Test procedures have now been developed to meet these criteria, and they are sufficiently sensitive to detect small differences in efficiency of transmission between different species of longidorids and trichodorids (19, 138). Further, the refinements incorporated into the procedures have led to the conclusion that some of the anomalous results previously obtained in laboratory experiments and unsupported by field evidence (127, 132) might have been due to contamination (77) and that two-thirds of the published results of virus-vector associations are invalid (139).

Efficient extraction of nematodes from the soil is a prerequisite for virus transmission tests. In a comparison of methods used to extract virus-vector nematodes, Brown and Boag (18a) concluded that a decanting and sieving technique, with 200-g soil samples, is the most satisfactory procedure for longidorid and trichodorid nematodes.

Variation in Transmission

Although the authenticity of many of the virus-vector associations is well established, the different results of transmission tests obtained by different workers suggest that vector species differ in their efficiency of transmission; but because of the different experimental conditions, this has been difficult to substantiate. However, when precise test procedures were used, it was demonstrated that *X. diversicaudatum* is an efficient vector of ArMV, whereas *L. elongatus* and *L. macrosoma* are inefficient vectors of RRV (Scottish strain) and RRV (English strain), respectively (134, 138).

Recent experiments have also shown that vector populations that are widely separated geographically may differ in their efficiency of transmission of the virus with which they are normally associated. Comparing populations of *X. diversicaudatum* from 10 countries as vectors of ArMV and SLRV, Brown (12, 14) found that those from France, Italy, and Spain rarely transmitted the viruses, whereas populations from other countries were all efficient vectors (Table 6.6). These populations had been exposed to the British strains of the viruses, but when the Italian population was exposed to an Italian strain of SLRV, the efficiency of transmission did not improve. In another test (18), *X. diversicaudatum* from Scotland and Italy was exposed to two Italian strains and the type (British) strain of SLRV. The Scottish population readily transmitted the type strain of the virus, but did not transmit the Italian strains; the Italian population transmitted all three virus strains but at a very low frequency. Immunosorbent electron microscopy (100) of the nematodes demonstrated that they had ingested the viruses to which they had been exposed, but electron microscopy of sections of the odontophore, the site of virus

TABLE 6.6. Transmission of the type strains of arabis mosaic (ArMV) and strawberry latent ringspot (SLRV) viruses by 10 populations of *Xiphinema diversicaudatum*.^a

Nematode Population	Percentage number of transmissions ^b	
	ArMV	SLRV
Bulgaria	100	48
England	96	60
New Zealand	96	60
Norway	96	40
Scotland	92	68
Switzerland	96	56
United States	48	36
France	10	10
Italy	4	2
Spain	0	15

^a Compiled from Brown (12, 14) and Brown and Trudgill (18).

^b Using groups of two nematodes per test pot; 25 replicates of each test.

retention in *Xiphinema* vectors, revealed that few or no virus particles were present in those populations that failed to transmit. Although no significant morphometric differences were apparent between the populations of *X. diversicaudatum* from the 10 countries (17), the marked difference in transmission efficiency of the Italian, and possibly also the French and Spanish, populations could be considered to indicate putative new species. However, it is interesting to note that the Scottish and Italian *X. diversicaudatum* were capable of cross-breeding and that the resulting progeny were intermediate between the parents in efficiency of transmission (13).

Differences in efficiency of transmission have also been shown to occur among *Longidorus* vectors. A Scottish population of *L. elongatus* transmitted the type strains of TBRV and RRV more frequently than the English population, and neither population transmitted the German potato bouquet strain of TBRV, which is a distinct serotype and is considered to have as a vector *L. attenuatus* (15).

In laboratory tests, potato bouquet and two other isolates of TBRV were transmitted less frequently by an English population of *L. attenuatus* than were several English isolates of the virus, including an isolate associated with celery yellow vein disease (20). This, and similar evidence for other vectors, supports the contention that local populations of a vector species are most efficient at transmitting local virus isolates, and, thus, geographical separation tends to lead to high levels of specificity between virus and vector.

Nematode-Virus Interactions

Electron microscopy of thin sections of nematode vectors has identified the virus retention sites within each of the vector genera. In *Longidorus*



FIGURE 6.1. Transverse section of *Longidorus elongatus* reared on virus (V) are present and between the odontophore. W.M. Robertson.

species, virus particles (129, 132, 138), may also be located between the odontophore (Figure 6.1). In *X. americanum* carry (130), virus particles are located at the odontophore, the maximum concentration of the odontophore.

of arabis mosaic (ArMV) and 10 populations of *Xiphinema*

centage number of transmissions ^b	
V	SLRV
	48
	60
	60
	40
	68
	56
	36
	10
	2
	15

^beach test.

at few or no virus particles ed to transmit. Although no pparent between the popula- countries (17), the marked Italian, and possibly also the nsidered to indicate putative note that the Scottish and cross-breeding and that the n the parents in efficiency of

ave also been shown to occur lation of *L. elongatus* trans- V more frequently than the on transmitted the German a distinct serotype and is s (15).

two other isolates of TBRV sh population of *L. attenua-* e virus, including an isolate). This, and similar evidence that local populations of a ing local virus isolates, and, to high levels of specificity

atode vectors has identified ector genera. In *Longidorus*

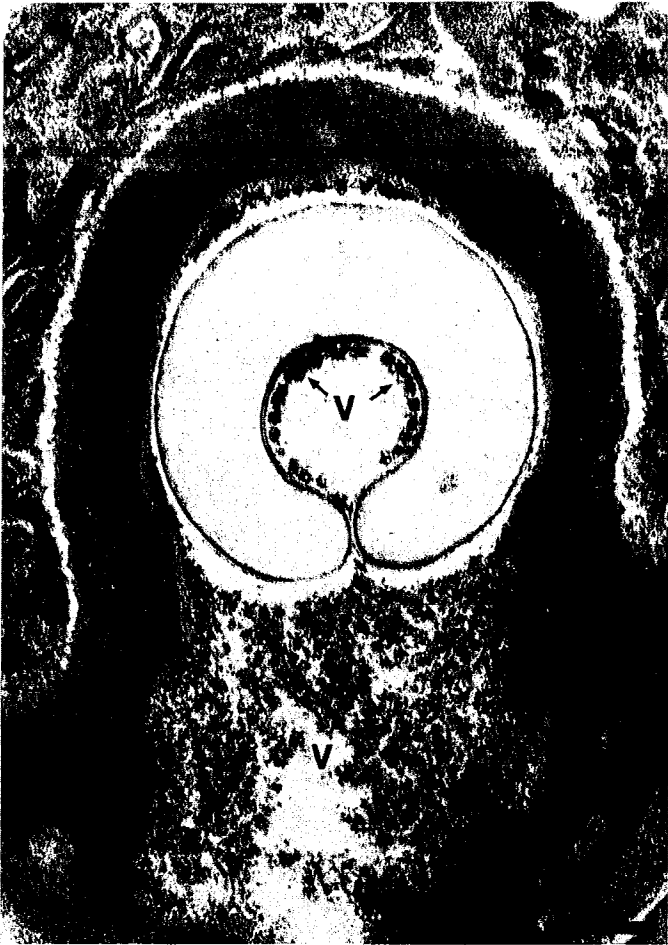


FIGURE 6.1. Transverse section of the odontostyle and guiding sheath of *Longidorus elongatus* reared on a plant infected with raspberry ringspot virus. Particles of the virus (V) are present in association with the inner surface of the odontostyle and between the odontostyle and the guiding sheath (bar, 200 nm). Courtesy of W.M. Robertson.

species, virus particles are adsorbed to the inner surface of the onto- style (129, 132, 138), and in *L. elongatus*, particles of RRV and TBRV may also be located between the odontostyle and the guiding sheath (129) (Figure 6.1). In *X. diversicaudatum* carrying ArMV or SLRV (130), *X. americanum* carrying TomRSV (76), or *X. index* carrying GFLV (97, 130), virus particles are specifically associated with the cuticular lining of the odontophore, the slender esophagus, and the esophageal pump; the maximum concentration of particles usually occurs in the anterior region of the odontophore.

In trichodorid vectors, TRV particles have been found to be retained in association with the lining of the food canal from the anterior region of the esophastome to the esophagointestinal valve (131) but not attached to the onchiostyle. The tubular particles may be attached by their sides or their ends: the long particles tend to line up parallel to the long axis of the food canal, whereas the short particles tend to adhere by their ends (104, 132).

Experiments with pseudo-recombinant isolates of RRV and TBRV have indicated that the specific association of a nepovirus with its vector is determined by the RNA-2 of the virus genome, which carries the coat protein cistron (41, 43, 49). Thus, association between virus and vector appears to depend on some feature of the protein coat that interacts specifically with the retention site within the nematode.

The tobnaviruses also have RNA genomes in two pieces. Pseudo-recombinants of TRV strains have been produced (46), and although they have not been used in transmission experiments with trichodorid vectors, it seems likely that the mechanism of specific association between virus and vector is similar to that of nepoviruses.

The mechanism whereby virus particles are adsorbed specifically at the retention site within the nematode vector has been a subject for speculation for some time (127, 133). Recent investigations indicate that specific recognition between virus and vector may involve the interaction of complementary molecules at their point of contact, as occurs in a variety of host-pathogen systems (118). In *X. diversicaudatum*, a discontinuous layer of carbohydrates lines the odontophore and esophagus, and ArMV and SLRV particles attach only to the carbohydrate zones (101, 102, 103) (Figure 6.2). In *P. pachydermus*, a vector of TRV, the total lining of the wall of the esophagus also stains for carbohydrates (102). Thus, virus retention in *Xiphinema* and trichodorid vectors may involve an interaction between carbohydrate moieties on the food canal wall and complementary lectin-like molecules on the protein coat of the virus.

Carbohydrates have not been detected on the guiding sheath or the odontostyle in *L. elongatus* (101). However, by labeling the odontostyle with cationized ferritin, a strong negative charge was shown to be present on the exterior surface of the odontostyle and on the wall of the lumen, and this may account for the retention of positively charged virus particles (101).

Dissociation of virus particles from the retention site is thought to occur when the pH of the lumen is changed by the passage of secretions from the esophageal glands during the initial stages of feeding (127, 133). In Longidorus vectors, specificity and efficiency of transmission may be determined in some cases, if not in all, by the mechanism of dissociation of the virus particles from the retention site (127). For example, when *L. macrosoma* was exposed to the English and Scottish strains of RRV, the former was transmitted, but not the latter, as expected, although virus particles were found to be adsorbed to the inner surface of the onto-



FIGURE 6.2. (A) Transverse section of *Xiphinema diversicaudatum* showing association with cloud-like structure within the cloud-like arthropore of *X. diversicaudatum* and stained with uranyl acetate (200nm). Courtesy of W. Taylor.

style in both sets of vectors. This was corroborated by the esophageal particles of the English strain but that it did not occur in the Scottish strain (127).

The assumed difference between the two vectors, compared to other observed differences, reflects other observed differences. Viruses are retained in the retention site and transmission is efficient, however, associated with the retention site, transmission is efficient.

Discussion

The survival and dissociation of transmission and the retention. Tobnaviruses and their nematode vectors in their local population, but distribution of infect

been found to be retained in from the anterior region of the (131) but not attached to the attached by their sides or their el to the long axis of the food here by their ends (104, 132). isolates of RRV and TBRV of a nepovirus with its vector nome, which carries the coat on between virus and vector e protein coat that interacts e nematode.

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tention site is thought to occur ne passage of secretions from ages of feeding (127, 133). In ency of transmission may be he mechanism of dissociation (127). For example, when *L.* d Scottish strains of RRV, the , as expected, although virus inner surface of the onto-

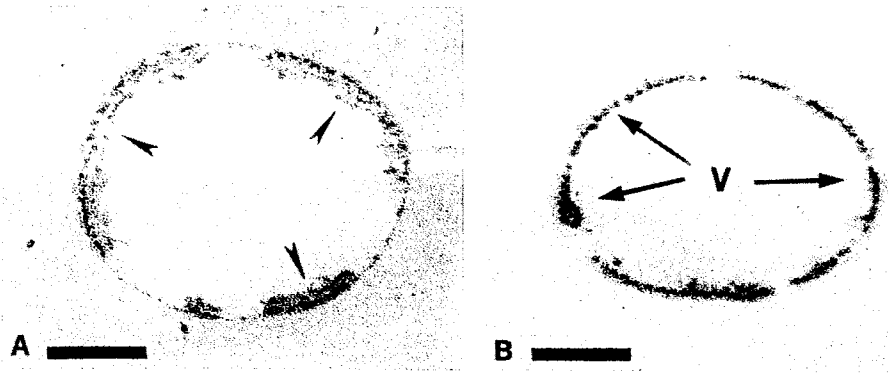


FIGURE 6.2. (A) Transverse section of the lumen of the odontophore of *Xiphinema diversicaudatum* reared on a plant infected with arabis mosaic virus. The section is stained to show the thin discontinuous carbohydrate layer in association with cloud-like areas (arrows). The unstained virus particles are within the cloud-like areas. (B) Transverse section of the lumen of the odontophore of *X. diversicaudatum* reared on a plant infected with arabis mosaic virus and stained with uranyl acetate and lead citrate to show virus particles (V) (bars, 200nm). Courtesy of W.M. Robertson.

style in both sets of nematodes (132, 137). In terms of surface charge density, this was considered to indicate that the change in pH brought about by the esophageal gland secretions altered the surface charge of the particles of the English strain and resulted in detachment and transmission but that it did not have a similar effect on the virus particles of the Scottish strain (127).

The assumed difference in the mechanism of transmission in *Longidorus* vectors, compared with *Xiphinema* and trichodorid vectors, also reflects other observed differences between the two groups of nematodes. Viruses are retained for only a few weeks, at most, in *Longidorus* vectors and transmission is inefficient; in *Xiphinema* and trichodorid vectors, however, associated viruses may be retained for several months and transmission is efficient.

Discussion

The survival and dissemination of plant viruses depends on their effective transmission and their access to suitable host plants for their multiplication. Tobraviruses and nepoviruses are dispersed over short distances by their nematode vectors, that is, to the extent of the area occupied by the local population, but dissemination to new sites may occur through the distribution of infected weed seeds or pollen. Thus, nematodes may not

appear to be essential for the maintenance and spread of tobnaviruses and nepoviruses, and, indeed, some of the nepoviruses are not associated with nematode vectors (Table 6.4). However, the interaction between virus, nematode, and host plant is a dynamic process, which, at various stages, offers opportunities for genetic selection to the advantage of the virus.

The nematode-transmitted viruses are essentially parasites of wild plants and usually infect them without causing obvious symptoms of infection. However, when crop plants are infected, symptoms are almost invariably severe and, in some cases, may cause the death of the plants, as RRV in some raspberry cultivars and ToBRSV and CLRV in union necrosis in apple and walnut, respectively. Similarly, most of the longidorid and trichodorid vectors have wide host ranges among wild plants with which they are compatible enough as not to cause excessive injury by their feeding; but when the roots of crop plants are attacked, they are often severely galled and the growth of the plant is affected (127).

The feeding apparatus of *Longidorus* and *Xiphinema* nematodes is a long tubular odontostyle with which they pierce the young roots and feed on the cell contents. Feeding commences with the penetration of a column of cells near the root apex, and each cell may be fed on progressively until the tip of the odontostyle is located at the feeding site some five to seven cells distant from the rhizodermis. Secretions from the esophageal glands induce a hypertrophic reaction in the root cells around the feeding site, and the coenocyte or cisternum that is formed, depending on the species, provides a rich and readily accessible food source for the nematode. The high metabolic activity of the cells presumably is also conducive to the multiplication and translocation of viruses within the root tissues.

In trichodorid nematodes, the feeding apparatus is in the form of a solid tooth, or onchiostyle, which is used to penetrate the rhizodermal cells of the root tip. Secretions from the esophageal glands are injected into the cell soon after the wall has been penetrated and the contents of the cell are usually ingested within a few seconds, after which the nematode moves to another rhizodermal cell. It is thought that virus particles are also injected into the cell with the secretions of the esophageal glands, and that the virus quickly passes to adjacent cells, or possibly that virus transmission occurs on those occasions when the nematode fails to ingest the total contents of the cell on which it is feeding.

Seemingly, nematodes are passive carriers of the viruses with which they are associated, in the sense that the viruses do not invade the nematode tissues or have any obvious effect on their biological behavior. Nevertheless, the vectors may affect the transmission of the viruses. For instance, vector species vary from being efficient to highly inefficient in their ability to transmit virus. Populations of *X. diversicaudatum* from Britain are efficient vectors of ArMV and SLRV, whereas Italian popula-

tions only infrequently may be disseminated. Adsorption of virus particles involves the interaction of the cuticular lining and may have a selective effect.

Because of the requirement to ensure the survival of the virus, the coat protein would be a relevant factor; however, increasing the number of antigenic variants of a virus has often been revealed with particular virus are possible.

Variants of RRV are found in some raspberry cultivars in Scotland. Recently, further investigations on raspberry cultivars that are resistant to graft-inoculation tests have shown that they can apply a selection pressure. These variants have characteristics that are different from those outside of the crop. Stability and lack of virulence are not believed to be the only factors.

In the above example, the transmission of wild herbaceous species by nematodes contrasts with that of viruses, which so far have been found only in crop plants.

The genome of nematodes is located in separate particles. The coat protein, it is assumed, is encoded by the nematode vector. There is evidence for linking the coat protein to the virus, and hence linking the virus to the nematode vector. There remains the possibility that the virus is important for the attachment of the nematode vector to the plant. Further, some proper selection by the vector, as a pseudorecombinant source of its RNA-2 (128).

The RNA-1 and RNA-2 have different lengths, and the thickness of thin sections of the virus particles so far made, are distributed at the site of infection.

and spread of tobnaviruses and epoviruses are not associated. However, the interaction between the virus and the nematode is a complex process, which, at various stages, is to the advantage of the

essentially parasites of wild plants. When obvious symptoms of infection are present, symptoms are almost always caused by the death of the plants, as in the case of PmRSV and CLRV in onion. Similarly, most of the longi- and short-range viruses among wild plants do not cause excessive injury to plants. When plants are attacked, they are usually not affected (127).

and *Xiphinema* nematodes is a disease of the young roots and feeders. With the penetration of a nematode, each cell may be fed on. The virus is located at the feeding site in the rhizodermis. Secretions from the nematode in the root cells around the feeding site form a mass that is formed, depending on the accessibility of food source for the nematode. The virus in the cells presumably is also located in the feeding site.

The apparatus is in the form of a solid structure that penetrates the rhizodermal cells of the plant. Glands are injected into the cells, and the contents of the cell are ingested. When the nematode moves to the next cell, virus particles are also injected into the new cell. The pharyngeal glands, and that the virus transmission by the nematode fails to ingest the total

of the viruses with which the nematode does not invade the cell on their biological behavior. The transmission of the viruses. For the transmission to be highly inefficient in the case of *X. diversicaudatum* from Italy, whereas Italian popula-

tions only infrequently transmit these viruses. Thus, the same viruses may be disseminated at different rates in different regions. Also, the adsorption of virus particles at the site of retention within the vectors involves the interaction of the virus coat protein with particular features of the cuticular lining of the nematode food canal, and this in itself may have a selective effect on the virus.

Because of the requirement of compatibility between virus and vector to ensure the survival of the virus, it might be expected that the coat protein would be a relatively invariant property of each virus. There is, however, increasing evidence that, in field situations, several minor antigenic variants of a virus may be present together. Such variants have often been revealed when cultivars that are considered to be immune to a particular virus are planted and become infected.

Variants of RRV and ArMV that broke the resistance of raspberry cultivars in Scotland were revealed in this way (88, 134), and, more recently, further isolates of both viruses were found to infect raspberry cultivars that had been shown to be immune to the viruses in graft-inoculation tests (57). Crops constitute a large monoculture area that can apply a selection pressure to the viruses, but the new isolates may have characteristics that are unfavorable in an ecological environment outside of the crop. Such characteristics include poor seed transmissibility and lack of virulence (40), which are conferred by RNA-1, and thus are not believed to be influenced by nematode transmission.

In the above examples, the viruses have wide host ranges that include wild herbaceous species, and the genetic variation displayed by these viruses contrasts with the lack of variation of GFLV, which in nature has so far been found only in association with *Vitis* spp.

The genome of nepoviruses is bipartite, with RNA-1 and RNA-2 located in separate particles, but because these viruses have a similar coat protein, it is assumed that each type is equally ingested and transported by the nematode vector. However, although there is good circumstantial evidence for linking transmission with the properties of the virus coat protein, and hence linking it with the antigenic characteristics of the virus, there remains the possibility that the regions in the coat protein that are important for the attachment and release of particles at retention sites in the nematode vector are not involved in the immunological reaction (20). Further, some properties determined by RNA-1 may affect transmissibility by the vector, as suggested to explain the poorer transmissibility of a pseudorecombinant isolate of TBRV compared to that of the parental source of its RNA-2 (43).

The RNA-1 and RNA-2 of tobnaviruses are located in particles of different lengths, and these are readily visualized by electron microscopy of thin sections of the vector species. In the limited number of observations so far made, short and long particles of TRV are randomly distributed at the site of retention in the nematode. Different isolates of

the virus, however, cannot be identified in thin sections of the nematodes and the experimental evidence is inconclusive about specific transmission by trichodorid vectors.

The RNA-1 of tobnaviruses is strongly conserved, and the RNA-2 is variable; in nepoviruses, however, both parts of the genome diverge more or less in parallel (32). The RNA-2 nucleotide sequence seems to differ markedly between isolates. Harrison and Robinson (46) suggest that the variation in the tobnavirus particle protein indicates that there is no selection pressure for its conservation, and hence it does not play a key role in determining vector transmissibility and specificity. A wide range of naturally occurring strains of both tobnaviruses and nepoviruses has been found, but the processes by which these variants are produced remain a matter of speculation.

Nepoviruses and tobnaviruses have two complementary methods of dispersion that ensure their survival in a particular location and their distribution to new areas. The nematode vectors are usually static populations, and the spread of virus is slow, but this slow spread is compensated for by the long period of retention of the viruses in the vectors, which, in the case of *Xiphinema* and trichodorid nematodes, may ensure survival between plantings of susceptible crops or through periods when plants are absent in natural situations. Infection of the seeds of weed hosts provides a means of perennation of the viruses over long periods of time and a means of spread to new sites. Weed seed infection is more prevalent among *Longidorus* vectors, which retain viruses for only a few weeks, compared with retention for several months in *Xiphinema* and trichodorid nematodes.

In the past, dispersal of viruses to new areas was probably attained solely through infected weed seeds, and continued existence of viruses would depend on their coming into contact with suitable vector species. In more recent times, man has been responsible for the distribution of virus and vector with commercial vegetative material, examples of which are *X. diversicaudatum* and ArMV and *X. index* and GFLV. However, only the less vulnerable of the nematode vector species have been widely distributed, and most species remain in relatively limited areas. Thus, it is not surprising that surveys continue to record more and more species in the genera associated with virus transmission. If nematode vectors apply some selection pressure on the viruses they carry, then it seems likely that there will be a continuing genetic drift of both viruses and vectors to establish new associations.

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