Characterization of Evolutionary Potential of the Viruses Analyzed

ACMV (*African cassava mosaic virus*)

Host range. Narrow; cassava is the main source of inoculum for infection of cassava crops

Transmission. Persistent nonpropagative, by the whitefly *Bemisia tabaci*

Seed transmission. None, but transmission occurs through plant cuttings

Survival at site. Medium to high, depending on cropping systems (overlapping crops)

Population size. Host frequent, vector active, survival high, population large: risk category 3

Gene flow. Medium, in tens of kilometers: risk category 2

Genetic exchange. Reassortment and recombination are frequent: risk category 3

Risk. 8

BCMV (*Bean common mosaic virus*)

Host range. Narrow, species in the Fabaceae; main inoculum source is contaminated seed; except in East Africa, weeds are not a source of inoculum

Transmission. Nonpersistent, by several species of aphids

Seed transmission. About 30%

Survival at site. Low

Population size. Host range narrow, vectors periodical, survival low: risk category 1

Gene flow. High, with long-distance dispersal through seed: risk category 3

Genetic exchange. Recombinants are frequent: risk category 3

Risk. 7

BCTV (*Beet curly top virus*)

Host range. Very large, more than 300 species in 44 dicot families

Transmission. Persistent nonpropagative, by the leafhopper *Circulifer tenellus*

Seed transmission. None

Survival at site. High, different strains favored in weeds and in crops

Population size. Risk category 3

Gene flow. Medium, dispersal over tens of kilometers: risk category 2

Genetic exchange. Recombinants occur but are not frequent: risk category 2

Risk. 7

BLRV (*Bean leafroll virus*)

Host range. Narrow, species in the Fabaceae only

Transmission. Persistent nonpropagative, by 12 aphid species

Seed transmission. None

Survival at site. High in perennial legumes; alfalfa and clovers are sources of inoculum for infection of pea

Population size. Narrow host range, high survival: risk category 2

Gene flow. Unknown, but only one strain has been found worldwide: risk category 3

Genetic exchange. Not analyzed, but only one strain has been reported worldwide: risk category 1

Risk. 6

BNYVV (*Beet necrotic yellow vein virus*)

Host range. Narrow, species in the Chenopodiaceae

Transmission. In cystosori of the soil fungus *Polymyxa betae*

Seed transmission. None, but transmission occurs through soil contaminating roots, water, or fruits

Survival at site. High

Population size. Narrow host range, high survival: risk category 2

Gene flow. Low naturally, but with a high potential through human-mediated movement on contaminated machinery; regulations in Europe limit movement: risk category 1

Genetic exchange. Acquisition of genomic segments is rare; no recombination reported: risk category 1

Risk. 4

BYDV (*Barley yellow dwarf virus*)

Host range. Moderate, many species in the Poaceae

Transmission. Persistent nonpropagative, by several aphid species

Seed transmission. None

Survival at site. High in perennial grasses and volunteer barley

Population size. Moderate: risk category 2

Gene flow. High; barley-adapted strains are similar around the world: risk category 3

Genetic exchange. No recombination reported: risk category 1

Risk. 6

CLCuV (*Cotton leaf curl virus*)

Host range. Broad, species in several dicot families

Transmission. Persistent nonpropagative, by *B. tabaci*

Seed transmission. None

Survival at site. High, frequently in weeds and volunteer cotton

Population size. Host frequent all year round, vector active, survival high: risk category 3

Gene flow. Medium, 10–100 km: risk category 2

Genetic exchange. Recombinants are frequent: risk category 3

Risk. 8

CMV (*Cucumber mosaic virus*)

Host range. Very broad, species in more than 80 mono- and dicot families

Transmission. Nonpersistent, by more than 70 aphid species

Seed transmission. In some hosts, but not in cucumber cultivars

Survival at site. Low, severe bottlenecks in winter

Population size. Large host range, low survival at site: risk category 2

Gene flow. Long-range; Asian strains invaded Europe in the 1980s: risk category 3

Genetic exchange. Recombinants and reassortants described: risk category 3

Risk. 8

GRV (*Groundnut rosette virus*)

Host range. Narrow, *Arachis* spp. only

Transmission. More or less circulative, by a few aphid species

Seed transmission. None

Survival at site. Low

Population size. Low: risk category 1
Gene flow. At regional level: risk category 2
Genetic exchange. Recombinants not reported: risk category 1
Risk. 4

LMV (*Lettuce mosaic virus*)
Host range. Moderate, species in 10 dicot families
Transmission. Nonpersistent, by several aphid species
Seed transmission. 3–10%
Survival at site. Moderate
Population size. Moderate host range and survival: risk category 2
Gene flow. High dispersal through seed: risk category 3
Genetic exchange. Recombinants not found: risk category 1
Risk. 6

MNSV (*Melon necrotic spot virus*)
Host range. Narrow, a few cucurbit species
Transmission. In resting spores of soil fungi, *Olpidium* spp.
Seed transmission. Yes
Survival at site. High
Population size. Moderate, with narrow host range and high survival: risk category 2
Gene flow. High dispersal through seed: risk category 3
Genetic exchange. Recombination reported in a resistance-breaking (RB) strain: risk category 2
Risk. 7

MSV (*Maize streak virus*)
Host range. Moderate, species in the Poaceae; weeds can be inoculum sources
Transmission. Persistent (for weeks), by leafhoppers, *Cicadulina* spp.
Seed transmission. None
Survival at site. High in riverine weeds or maize, depending on cropping systems
Population size. Large: risk category 3
Gene flow. Dispersal not long-range: risk category 2
Genetic exchange. Recombinants are frequent: risk category 3
Risk. 8

PEMV (*Pea enation mosaic virus*)
Host range. Narrow, primarily species in the Fabaceae
Transmission. Persistent nonpropagative, by a few aphid species
Seed transmission. Low, 1.5%
Survival at site. High, in perennial legumes; clovers are the main source of inoculum for infection of pea
Population size. Narrow host range, high survival: risk category 2
Gene flow. Different geographical isolates exist: risk category 2
Genetic exchange. Recombinants not described: risk category 1
Risk. 5

PMMoV (*Pepper mild mottle virus*)
Host range. Narrow, pepper only
Transmission. Plant-to-plant contact
Seed transmission. Yes
Survival at site. Moderate; crop debris can maintain infective virus for months
Population size. Moderate; population structure does not change with time: risk category 2
Gene flow. Long-range dispersal through seed: risk category 3
Genetic exchange. None: risk category 1
Risk. 6

PSbMV (*Pea seed-borne mosaic virus*)
Host range. Narrow, a few pulse crops; weeds are not important sources of inoculum
Transmission. Nonpersistent, by several aphid species
Seed transmission. 30–50%
Survival at site. Low
Population size. Narrow host range, low survival: risk category 1
Gene flow. Long-range dispersal through seed: risk category 3
Genetic exchange. Not analyzed, but generally high in potyviruses: risk category 3
Risk. 7

PVX (*Potato virus X*)
Host range. Moderate, solanaceous crops and weeds
Transmission. Primarily plant-to-plant contact
Seed transmission. Through tubers
Survival at site. Moderate
Population size. Low (with good sanitation): risk category 1
Gene flow. High in tubers, but regulated in Europe for many years: risk category 2
Genetic exchange. None: risk category 1
Risk. 4

PVY (*Potato virus Y*)
Host range. Moderate, solanaceous crops and weeds
Transmission. Nonpersistent, by many aphid species
Seed transmission. In potato tubers, but not in pepper or tobacco
Survival at site. Moderate
Population size. In potato, risk category 2; in tobacco and pepper, risk category 1
Gene flow. Effective dispersal through tubers, movement regulated in Europe: risk category 2
Genetic exchange. Recombinants are frequent: risk category 3
Risk. 7 (potato), 6 (pepper and tobacco)

RpRSV (*Raspberry ring spot virus*)
Host range. Very large, hosts in many mono- and dicot families
Transmission. By nematodes, *Longidorus* spp., in which the virus persists for up to 9 months
Seed transmission. In many hosts; transmission also occurs in vegetative propagation of raspberry
Survival at site. High
Population size. Large: risk category 3
Gene flow. Low dispersal: risk category 1
Genetic exchange. Recombinants not described, reassortants selected against: risk category 1
Risk. 5

RGSV (*Rice grassy stunt virus*)
Host range. Narrow, rice only
Transmission. Propagative, not transovarial, by the planthopper *Nilaparvata lugens*
Seed transmission. None
Survival at site. Low to high, according to cropping systems
Population size. Large in southern and southeastern Asia: risk category 3
Gene flow. Long-range dispersal of viruliferous vectors by monsoons: risk category 3
Genetic exchange. Reassortants reported: risk category 2
Risk. 8

RSV (*Rice stripe virus*)
Host range. Moderate, about 40 species in the Poaceae
Transmission. Propagative transovarial, by the planthopper *Laodelphax striatellus*
Seed transmission. None
Survival at site. Moderate to high, depending on cropping systems
Population size. Moderate, in Japan: risk category 2

Gene flow. High, long-range dispersal: risk category 3
Genetic exchange. Probably: risk category 2
Risk. 7

RTSV (*Rice tungro spherical virus*)
Host range. Narrow, species in the Poaceae; weeds are not inoculum sources
Transmission. Semipersistent (for 5 days), by the leafhopper *Nephotettix virescens*
Seed transmission. None
Survival at site. High in continuous rice crops
Population size. Large in southeast Asia (mainland and archipelagos): risk category 3
Gene flow. Not long-distance, in the range of 100 km: risk category 2
Genetic exchange. Recombinants reported: risk category 3
Risk. 8

SBWMV (*Soil-borne wheat mosaic virus*)
Host range. Narrow, very few graminaceous crops and weeds
Transmission. By the soil fungus *Polymyxa graminis,* with long-term survival in cystosori
Seed transmission. None
Survival at site. High
Population size. High survival, narrow host range, but large host populations: risk category 2
Gene flow. Short-range dispersal: risk category 1
Genetic exchange. Recombinants not reported, but defective RNAs of RNA2 occur, and reassortants can be formed: risk category 2
Risk. 5

SMV (*Soybean mosaic virus*)
Host range. Narrow; soybean is the only inoculum source
Transmission. Nonpersistent, by a few aphid species
Seed transmission. About 30%
Survival at site. Low
Population size. Small: risk category 1
Gene flow. High dispersal through seed: risk category 3
Genetic exchange. Not analyzed, but exchange is frequent in potyviruses: risk category 3
Risk. 7

TBRV (*Tomato black ring virus*)
Host range. Very large, species in many mono- and dicot families and in the Coniferae
Transmission. By nematodes, *Longidorus* spp.
Seed transmission. Very efficient in many species
Survival at site. High
Population size. Large: risk category 3
Gene flow. Low: risk category 1
Genetic exchange. Not reported: risk category 1
Risk. 5

TMV (*Tobacco mosaic virus*)
Host range. Narrow, mostly tobacco
Transmission. Plant-to-plant contact
Seed transmission. None
Survival at site. High, in plant debris (2–3 years)
Population size. Moderate: risk category 2
Gene flow. High dispersal in processed tobacco: risk category 3
Genetic exchange. None: risk category 1
Risk. 6

ToMV (*Tomato mosaic virus*)
Host range. Narrow, including tomato, pepper, and eggplant
Transmission. Plant-to-plant contact
Seed transmission. Yes
Survival at site. Moderate, in plant debris
Population size. Moderate: risk category 2
Gene flow. Long-range dispersal through seed: risk category 3
Genetic exchange. None: risk category 1
Risk. 6

TSWV (*Tomato spotted wilt virus*)
Host range. Very broad, species in many mono- and dicot families
Transmission. Persistent propagative, by thrips
Seed transmission. Not important (less than 1%)
Survival at site. High
Population size. Large: risk category 3
Gene flow. Moderate-range dispersal by thrips; populations differ in different areas of the United States: risk category 2
Genetic exchange. Reassortants described: risk category 2
Risk. 7

TuMV (*Turnip mosaic virus*)
Host range. Very broad, species in 43 dicot families
Transmission. Nonpersistent, by many aphid species
Seed transmission. None
Survival at site. High in wild *Brassica oleracea*
Population size. Broad host range, high survival: risk category 3
Gene flow. World population structured at continental level: risk category 3
Genetic exchange. Recombinants are frequent: risk category 3
Risk. 9

TYLCV (*Tomato yellow leaf curl virus*)
Host range. Moderate, a few crops and weeds
Transmission. Persistent propagative, by *B. tabaci*
Seed transmission. None
Survival at site. High, because of overlapping crops and weeds
Population size. Large: risk category 3
Gene flow. Long-range dispersal by the vector: risk category 3
Genetic exchange. Recombinants are frequent: risk category 3
Risk. 9

Characterization of Resistance in Hosts

ACMV-cassava
Resistance from Java varieties
Genetics. Polygenic recessive
Expression. Decreased infection
Deployed. Uganda, 1940s
Overcome. Pandemic started in 1988
Overcoming strains. Reassortants and recombinants of *East African cassava mosaic virus* (EACMV) and ACMV (UgV isolates)
Resistance from *Manihot glaziovii*
Genetics. Polygenic recessive
Expression. Decreased virus accumulation and systemicity
Deployed. Madagascar, 1940; East Africa, 1993; 25% of surface in Uganda in 1998

Overcome. Never overcome in Madagascar; in East Africa, resistance is effective against ACMV, EACMV, and UgV

BCMV-bean

Resistance from *bc* genes

Genetics. Monogenic recessive

Expression. Immunity

Deployed. United States, 1930

Overcome. Shortly after deployment; strain US2 reported in 1938; US3 and US4, 1961; US5, 1962; US6, 1964; resistance is durable in dry beans

Overcoming strains. US2 to US6 plus necrotic strains

Properties. Variants of BCMV with a gene-for-gene relationship with *bc* alleles

Resistance from *I* gene

Genetics. Monogenic incompletely dominant

Expression. Immunity in homozygotes, hypersensitive response (HR) in heterozygotes

Deployed. 1935

Overcome. Not overcome

Overcoming strains. So-called necrotic strains, first reported in 1963; outbreaks in the United States, 1984–90, but RB strains are not prevalent

Properties. A different potyvirus (with about 10% sequence divergence) now called *Bean common mosaic necrotic virus* (BCMNV)

BCTV-bean

Resistance from bean

Genetics. Two dominant epistatic genes

Expression. Diminished infection (escape)

Deployed. Washington State, 1930s

Overcome. Not overcome

Overcoming strains. Yes

Properties. Infection can occur under glasshouse conditions very favorable for disease

BCTV-beet

Resistance from beet

Genetics. Polygenic, inheritance not clear

Expression. Lower accumulation and systemicity

Deployed. California, 1933

Overcome. Late 1960s

Overcoming strains. Differ by up to 20% in nucleotide sequence from milder strains

Properties. Different pathogenicity in different hosts; poor competitors in weeds

BLRV-pea

Resistance from pea

Genetics. Monogenic recessive, *lr* gene

Expression. Resistance to infection

Deployed. Before 1980 (mid-1970s?)

Overcome. Not overcome

Overcoming strains. Not reported

BNYVV-beet

Resistance from *Beta vulgaris* subsp. *maritima*

Genetics. Monogenic dominant, *Rz* gene

Expression. Lower accumulation and systemicity

Deployed. Europe, 1982, with large-scale deployment in 1985

Overcome. Not overcome

Overcoming strains. Strain P

Properties. Additional satellite-like RNA (RNA5)

BYDV-barley

Resistance from Ethiopian varieties

Genetics. Incompletely dominant, *Yd2* gene

Expression. Lower titer, not expressed in protoplasts; interference with movement

Deployed. Since late 1970s

Overcome. Not overcome

Overcoming strains. Resistance is effective against strains PAV and MAV, but not strain RPV

Properties. RPV, formerly considered a strain of BYDV, is a different virus species in a different genus

CLCuV-cotton

Resistance from Indian cotton accessions

Genetics. Monogenic dominant

Expression. Immunity

Deployed. Punjab, Pakistan, 1994; 75% of the crop in 2001

Overcome. 2001

Overcoming strains. Present in a few localized areas, but spreading

Properties. Unknown

CMV-cucumber

Resistance from Asian accessions of *Cucumis sativus*

Genetics. Three recessive genes

Expression. Lower accumulation

Deployed. Early 1970s

Overcome. Not overcome

Overcoming strains. Not overcome, but the degree of protection depends on the strain

GRV-groundnut

Resistance from Virginia-type groundnut (*Arachis hypogaea* subsp. *hypogaea*)

Genetics. Two independent recessive genes

Expression. Resistance to GRV only, not to *Groundnut rosette assistor virus* (GRAV); no infection causing either chlorotic rosette or green rosette

Deployed. 1970s, mostly since 1980 in West Africa

Overcome. Not overcome

Overcoming strains. Not reported

LMV-lettuce

Resistance from lettuce cultivars from Argentina and Egypt

Genetics. Monogenic recessive, two alleles at *mo1*

Expression. Decreased accumulation and systemicity; no seed transmission

Deployed. Since 1975, largely used in Europe (more than 70% surface), much less in the United States

Overcome. Not overcome

Overcoming strains. Reported since the 1980s, but not seed-transmitted; overcoming seed-transmitted strains (LMV-Most) reported 1989

Properties. Very different strains (about 5% nucleotide sequence divergence)

MNSV-melon

Resistance from melon

Genetics. Monogenic recessive, *nsv* gene

Expression. HR-like

Deployed. Southeast Spain, 1994

Overcome. Not overcome

Overcoming strains. Reported in 1999, but not found in later surveys

Properties. Nucleotide sequence 93% similar to that of the common strain; recombinant at 3′ noncoding region

MSV-maize

Resistance from TZ yellow

Genetics. Polygenic, two or three genes involved

Expression. Decreased accumulation and systemicity

Deployed. 1982

Overcome. Not overcome

Overcoming strains. Not reported in Africa, but resistance is not effective in La Réunion

Properties. Nucleotide sequence of isolates from La Réunion are about 98% similar to those of strains prevalent in Africa

Resistance from Vaalhart composite

Similar to resistance from TZ yellow

Deployed. South Africa, 1978

Resistance from cultivar Revolution

Genetics. Polygenic

Expression. Decreased accumulation and systemicity

Deployed. La Réunion, 1960s

Overcome. Not overcome

Overcoming strains. Not reported; resistance is also effective against African strains

PEMV-pea

Resistance from pea

Genetics. Monogenic dominant, *En* gene

Expression. Decreased accumulation

Deployed. Since the late 1960s

Overcome. Not overcome

Overcoming strains. Not reported; only one strain of PEMV has been reported worldwide

PMMoV-pepper

Resistance from *Capsicum* spp.

Genetics. Monogenic dominant, *L* locus, alleles *L2* and *L3*

Expression. HR

Deployed. *L2* and *L3* in Holland, since 1979, and in Spain, since 1985

Overcome. In about 5 years

Overcoming strains. Pathotype P1,2 overcomes *L2* and P1,2,3 overcomes *L3* in a gene-for-gene manner

Properties. P1,2 and P1,2,3 differ in a single amino acid in the coat protein

Resistance from *Capsicum chacoense*

Genetics. Monogenic partially dominant, *L* locus, allele *L4*

Expression. HR

Deployed. Holland and Spain, since 1990

Overcome. Not overcome

Overcoming strains. Not reported

PSbMV-pea

Resistance from pea

Genetics. Monogenic recessive, *sbm1* gene

Expression. Immunity

Deployed. United States, 1978

Overcome. Not overcome

Overcoming strains. Resistance is effective against strains P1 and P2; the overcoming strain P4 was reported in 1989

Properties. P4 is 81% homologous to P1 in nucleotide sequence; avirulent gene is central region of VPg; P4 is very poorly seed-transmitted and does not compete with P1 in mixed infections

PVX-potato

Resistance from *Nb* gene

Genetics. Monogenic dominant

Expression. HR to strains 1 and 2, elicited by the 25K movement protein

Deployed. Since 1920–1930

Overcome. By strain 3, but cultivars with this gene are still widely grown in Europe with good protection

Overcoming strains. Strain 3 is the most frequent in Europe; strain 4 is not present in the field

Properties. One amino acid change determines the RB phenotype

Resistance from *Nx* gene

Genetics. Monogenic dominant

Expression. HR to strains in groups 1 and 3, elicited by the coat protein

Deployed. 1920–1930

Overcome. Not overcome

Overcoming strains. Strain 2 is uncommon in Europe; strain 4 is not present in the field

Properties. One or two amino acid changes determine the RB phenotype

Resistance from *Rx* gene

Genetics. Monogenic dominant

Expression. Immunity to strains in groups 1–4, elicited by the coat protein

Deployed. Since 1950s

Overcome. Not overcome

Overcoming strains. Strain HB, frequent in Bolivia, not in Europe

Properties. A single amino acid change determines the HB phenotype

PVY-pepper

Resistance from *pvr2* gene

Genetics. Monogenic recessive

Expression. Impairment of cell-to-cell movement resulting in lower virus accumulation

Deployed. Allele *pvr2*^{1}, effective against pathotype P(0), deployed in Europe, 1960–1970

Overcome. Not overcome

Overcoming strains. Pathotypes P(1) and P(2); P(1) is infrequent in the field, and P(2) is not found in the field

Properties. All three pathotypes belong to the same genetic strain, and a few amino acid changes determine the phenotype

Resistance from *Pvr4* gene

Genetics. Monogenic dominant

Expression. HR

Deployed. Europe, about 1990

Overcome. Not overcome

Overcoming strains. Not reported; resistance is effective against pathotypes P(0), P(1), and P(2)

PVY-potato

Resistance from *Nc* gene

Genetics. Monogenic dominant

Expression. HR

Deployed. Early 20th century

Overcome. Dates not known, but overcoming strain PVY$^{\mathrm{O}}$ was present in Europe before World War II

Overcoming strains. *Nc* gene is effective against PVY$^{\mathrm{C}}$ but overcome by PVY$^{\mathrm{O}}$ and PVY$^{\mathrm{N}}$

Properties. Strains C, O, and N are genetically very different (about 10% divergence in nucleotide sequence)

Resistance from *Ny* gene

Genetics. Monogenic dominant

Expression. HR to PVY$^{\mathrm{O}}$

Deployed. Early 20th century

Overcome. 1960s

Overcoming strains. Strain PVY$^{\mathrm{N}}$, prevalent in potato in Europe since 1960s, causes a mild infection in potato; the severe overcoming strain PVY$^{\mathrm{NTN}}$ spread in the late 1980s

Properties. PVY$^{\mathrm{N}}$ is a different genetic strain from PVY$^{\mathrm{O}}$, about 90% similar in nucleotide sequence; PVY$^{\mathrm{NTN}}$ is a recombinant between PVY$^{\mathrm{N}}$ and PVY$^{\mathrm{O}}$

Resistance from *Ry* gene

Genetics. Monogenic dominant

Expression. Immunity

Deployed. Europe, 1980
Overcome. Not overcome
Overcoming strains. Not reported

PVY-tobacco
Resistance from *va* gene
Genetics. Monogenic recessive
Expression. Decreased accumulation and systemicity
Deployed. In Europe since the early 20th century in Burley and dark air-cured varieties, and since the 1980s in Virginia types
Overcome. Not overcome
Overcoming strains. Resistance is effective against pathotype P(0) of PVY^{N}; PVY^{N} has been present in tobacco in Europe since 1952, and the overcoming pathotypes P(1) and P(1,2) have been present since 1990, but P(0) is still prevalent over most of Europe
Properties. All pathotypes belong to PVY^{N} and are more than 95% similar in nucleotide sequence

RpRSV–red raspberry
Resistance from *Rubus idaeus*
Genetics. Monogenic dominant, *Irr* gene
Expression. Immunity
Deployed. Scotland, 1940s
Overcome. Not overcome
Overcoming strains. Lloyd George strain, reported in 1963
Properties. Resistance breaking is determined by RNA1, linked to determinants for low virulence, low seed transmission, and poor competitive ability

RGSV-rice
Resistance from *Oryza nivara*
Genetics. Monogenic dominant, *Gs* gene
Expression. Resistance to infection
Deployed. Southeast Asia (continent and archipelagos), 1970s
Overcome. Yes
Overcoming strains. Strain 2, reported in the Philippines in the early 1980s, and similar strains reported in Indonesia, Thailand, and India
Properties. Strains of RGSV differ by up to 10% in nucleotide sequence

RSV-rice
Resistance from *Oryza sativa indica*
Genetics. Monogenic, incompletely dominant, $St2^1$ gene
Expression. Resistance to infection
Deployed. 1972
Overcome. Not overcome
Overcoming strains. Not reported

RTSV-rice
Resistance from line TKM6
Genetics. Monogenic recessive
Expression. Resistance to infection
Deployed. Philippines, since 1972
Overcome. Not overcome
Overcoming strains. Strain Vt6 or III, reported 1992, did not become prevalent
Properties. RTSV strains differ by 5–18% in nucleotide sequence
Resistance from cultivar Utri Merah
Genetics. Two recessive genes
Expression. Resistance to infection
Deployed. Philippines, 1998; Utri Merah was in use before the etiology of rice tungro was known
Overcome. Not overcome
Overcoming strains. Not reported; resistance is also effective against Vt6

SBWMV-wheat
Resistance from wheat
Genetics. Monogenic dominant, three alleles at a locus, $R^{mv} > r^{m} > r^{mv}$
Expression. R^{mv} confers resistance to mosaic and rosette, r^{m} to rosette only, and r^{mv} to neither; resistance is expressed as decreased accumulation and systemic movement of the virus
Deployed. U.S. Midwest, since the 1920s
Overcome. Not overcome
Overcoming strains. Not reported

SMV-soybean
Resistance from *Rsv1* gene
Genetics. Monogenic incompletely dominant
Expression. Immunity in homozygotes, HR in heterozygotes
Deployed. United States and Korea, since 1960
Overcome. Different alleles of this gene have been overcome by different SMV pathotypes, since 1974 in Korea and since the late 1970s in the United States
Overcoming strains. Strains G1 to G7 according to alleles in a gene-for-gene-like relationship
Properties. HC-Pro-P3 cistrons elicit the gene; a few nucleotide changes determine new phenotype
Resistance from *Rsv2* gene
Genetics. Monogenic dominant
Expression. Immunity
Deployed. United States, since 1980
Overcome. Not overcome
Overcoming strains. Not reported

TBRV–red raspberry
Resistance from *Rubus idaeus*
Genetics. Monogenic resistant, *Itb* gene
Expression. Immunity
Deployed. Scotland, 1940s
Overcome. Not overcome
Overcoming strains. Not reported until the 1970s, when production was discontinued

TMV-tobacco
Resistance from *Nicotiana glutinosa*
Genetics. Monogenic dominant, *N* gene
Expression. HR
Deployed. Worldwide since 1940 in dark air-cured and Burley varieties
Overcome. Not overcome
Overcoming strains. Only the pepper-infecting tobamovirus *Obuda pepper virus,* which is not found in tobacco
Properties. The helicase domain of the viral 183K protein is the elicitor

ToMV-pepper
Resistance from *Capsicum annuum*
Genetics. Monogenic dominant, *L1* allele at *L* locus
Expression. HR
Deployed. Holland, mid-1960s; Spain, late 1970s
Overcome. P1 in Holland, 1974; P1,2 in France, 1978, and Spain, 1983
Overcoming strains. Strains P1, P1,2, and P1,2,3
Properties. P1 is a different tobamovirus*, Paprika mosaic virus;* P1,2 and P1,2,3 are PMMoV; the coat protein is the elicitor

ToMV-tomato
Resistance from *Tm1* gene
Genetics. Monogenic incompletely dominant
Expression. Decreased virus replication and decreased accumulation

Deployed. United Kingdom, 1966

Overcome. 1968

Overcoming strains. P1

Properties. 183K protein is the elicitor; a change at nucleotide 979 determines the new phenotype

Resistance from *Tm2* gene

Genetics. Monogenic dominant

Expression. HR

Deployed. Europe, about 1970

Overcome. In 2–3 years

Overcoming strains. Pathotype P2

Properties. MP is the elicitor of the gene; two amino acid changes determine the new phenotype

Resistance from *Tm2*^{2} gene

Genetics. Monogenic dominant, allelic with *Tm2*

Expression. HR

Deployed. Europe, about 1975

Overcome. Not overcome

Overcoming strains. Pathotype P2^2

Properties. MP is the elicitor; two amino acid changes determine the new phenotype; RB isolates are outcompeted by non-RB isolates

TSWV-pepper

Resistance from *Tsw* gene from *Capsicum chinense*

Genetics. Monogenic dominant

Expression. HR

Deployed. Italy and Spain, 1999

Overcome. 2000

Overcoming strains. Yes

Properties. RB strains are biologically similar to the wild type, and both are transmitted by thrips

TSWV-tomato

Resistance from *Lycopersicon pimpinellifolium*

Genetics. Polygenic?

Expression. Resistance to infection

Deployed. Hawaii, 1946

Overcome. Within 10 years

Overcoming strains. Many

Resistance from *L. peruvianum*

Genetics. Monogenic dominant, *Sw-5* gene

Expression. HR

Deployed. Mid-1990s (1996 in Spain)

Overcome. 2002

Overcoming strains. An overcoming strain was spreading in northeast Spain in 2002

TuMV-lettuce

Resistance from *Lactuca sativa*

Genetics. Monogenic dominant, *Tu* gene

Expression. Extreme resistance

Deployed. Before 1970

Overcome. Not overcome

Overcoming strains. Resistance is effective against all tested pathotypes of TuMV

TuMV-rape

Resistance from *Brassica napus*

Genetics. Monogenic dominant, *TuRB01* gene

Expression. Extreme resistance

Deployed. Early 1980s

Overcome. Not overcome

Overcoming strains. *TuRB01* is effective against pathotype 1, the commonest in Europe, but is overcome by P4, the second most common, and by P3, which is infrequent

Properties. A single nucleotide change in the CI cistron determines the RB phenotype; however, RB isolates are less fit than P1 in competition experiments

TYLCV-tomato

Resistance from *Lycopersicon chilense*

Genetics. Monogenic dominant, *Ty* gene

Expression. Decreased accumulation and systemicity, also tolerance

Deployed. Spain, since 1996

Overcome. Partially; more infectious strains have been reported since 1999, but tolerance still operates

Overcoming strains. Recombinant TYLCV and *Tomato yellow leaf curl Sardinia virus*

Properties. More infectious to tomato, and with a broader host range