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ABSTRACT

Several viruses have been reported to infect lettuce. The most important is *Lettuce mosaic virus* (LMV), a potyvirus found worldwide transmitted by seeds and aphids, in a non-persistent manner. LMV causes quite variable symptoms, including mosaic, dwarfing, failure to form proper heads, and sometimes necrotic reactions. Cultivars carrying the *mo1*[1] and *mo1*[2] genes have resistance to the common strains, although *m*ost (*mo* breaking seed transmitted) strains can overcome this resistance. At least three species of tospovirus, including *Tomato spotted wilt virus* (TSWV), *Tomato chlorotic spot virus* (TCSV) and *Groundnut ringspot virus* (GRSV) causes significant losses, especially during summer, in which high populations of thrips vectors can be found in the field. Tospoviruses causes systemic necrosis and plant death. During the cooler season (May to September), two viruses have been found associated with big-vein disease, *Mirafiori lettuce big-vein virus* (MLBVV) which belongs to the genus *Ophiovirus* and *Lettuce big-vein associated virus* (LBVaV; genus *Varicosavirus*). LBVaV and MLBVV are both transmitted by the soil-borne fungus *Olpidium brassicae*. Lettuce mottle virus (LeMoV, genus *Sequivirus*); *Cucumber mosaic virus* (CMV, genus *Cucumovirus*), and Bidens mosaic virus (BiMV, genus *Potyvirus*) are also found to cause mosaic symptoms on lettuce, although their incidence in lettuce fields is low throughout the year. Epidemiological aspects, variability of viruses, methods of control, genetic variability for lettuce resistance and breeding programs will be discussed.

Keywords: *Bidens mosaic virus*, *Cucumber mosaic virus*, *Lettuce big-vein associated virus*, *Lettuce mosaic virus*, *Lettuce mottle virus*, *Mirafiori lettuce big-vein virus*, tospovirus

CONTENTS

INTRODUCTION

Lettuce (*Lactuca sativa* L) was domesticated in the Mediterranean area of Europe and was introduced in Brazil by the Portuguese by 1650. Lettuce is cultivated worldwide and is one of the most important vegetables consumed in the world (FAOSTAT, http:www.fao.org).

Nowadays it is the most consumed leaf plant in Brazil and cultivated over about 30,000 hectares, the largest producer being the state of São Paulo (Agrianual 2004). In Brazil lettuce is cultivated in open fields, in hydroponic systems, in greenhouses or as organic cultures, typically on small family-owned periurban areas in green belts.

Brazilian lettuce cultivation occurs all year long and plants are therefore permanently exposed to phytopathogen attack. Of these the viruses are of particular importance because they are difficult to control and their vectors are present year around. Furthermore, viruses directly affect the quality of the leaves, preventing sale of affected plants. Depending on the environmental conditions and on the degree of care given to the culture, viruses can be responsible for the loss of up to 100% of lettuce crops (Resende and Cupertino 1995). Even under hydroponic cultivation viruses have been identified in different producing regions. In this article the main types of virus occurring in Brazil, as well as issues related to diagnosis, control and strain variability are described.

LETTUCE VIRUSES

Lettuce mosaic virus – LMV

Lettuce mosaic virus (LMV) is one of the most important pathogens of lettuce (*Lactuca sativa*) worldwide (Dinant and Lot 1992). LMV belongs to the genus *Potyvirus* within the family *Potyviridae*. The genomic organization of LMV is typical of potyviruses, with a single positive-sense genomic RNA of 10,080 nucleotides (nt) encapsidated as flexuous rods (Revers *et al*. 1997). The genome organization of LMV is typical of potyviruses, with a single positive-sense, single-stranded genomic RNA of 10,080 nucleotides (nt) encapsidated by coat protein subunits as flexuous rods (Revers *et al*. 1997). The viral genomic RNA has a virus encoded protein linked covalently at its 5′ end, a poly-A tail at its 3′ end, and contains a single open reading frame (ORF) which encodes a large polyprotein with 3255 amino acids

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Fig. 1 Elisa lettuce cultivar infected by *Lettuce mosaic virus* (right). Healthy plant (left).

(Revers *et al*. 1997).

Disease symptoms are quite variable and depend on the particular isolate–host plant combination but frequently include dwarfing, failure to form proper heads, leaf distortion, leaf mosaic or mottling, vein clearing and sometimes necrosis (Candresse *et al*. 2007). Lettuce plants may fail to 'heart' and inner leaves remain dwarfed and rosetted (**Fig. 1**). Infected plants like *Chenopodium amaranticolor* develop pale green or chlorotic local lesions (usually with reddish margins) after 8-10 days and systemic yellow veinal flecks or yellow netting of the younger leaves especially in winter. *C. quinoa* is more sensitive than *C. amaranticolor* and local lesions more numerous but without reddish margins followed by systemic yellow vein-net symptoms with twisting and stunting of apical leaves can be observed. *Gomphrena globosa* develop whitish, local necrotic dots (4-7 days) enlarging into red-rimmed lesions (http://www.dpvweb.net/dpv/showdpv.php?dpvno=399).

As with other potyviruses, LMV is transmitted efficiently by aphids in a nonpersistent manner (Tomlinson 1970), notably by *Myzus persicae*, *Macrosiphum euphorbiae* and *Acyrthosiphon scariolae barri*. Non-vectors include *Nasonovia ribisnigri*. All instars of *M. persicae* transmit but alates are less efficient than apterae. Transmission efficiency increases with increasing periods of fasting (5-240 min), but decreases with increasing acquisition access time from 5 to 120 min (Sylvester 1955).

Rapid epidemics can develop in susceptible lettuce cultivars, leading to losses of up to 80-100% (Dinant and Lot 1992). In addition, a number of LMV isolates can also be transmitted through infected seeds (Grogan *et al*. 1952; Tomlinson 1970). Seed transmission is probably the major factor in the spread of the disease (Broadbent *et al*. 1951; Grogan *et al*. 1952; Tomlinson 1962). Spread occurs (a) from seedlings infected through the seed and (b) from neighboring infected lettuce. The disease can be controlled by ensuring that the crop is isolated from external sources of virus and that less than 0.1% of the seed carries the virus (Zink *et al*. 1956; Tomlinson 1962; Grogan 1980). Even where adjacent crops are infected, use of mosaic-free seed provides some control (Tomlinson 1962). LMV transmission rate varies among genotypes as a function of LMV variability. This rate depends on the time the receptor plant has been infected as well as on the genotype and on environmental conditions. The highest levels are observed when the plant grows in mild temperatures. Studies related to the seed transmission of LMV showed transmission rates of 1.9 and 16.5%, respectively in tolerant and susceptible lettuce cultivars (Jadão *et al*. 2002).

LMV-susceptible species occur in 20 genera (9 genera of Compositae) in 10 families. The virus is transmissible by inoculation with sap from young infected plants, but transmission with sap from old leaves may be difficult. Weeds and ornamental plants can serve as reservoirs of LMV (Costa and Duffus 1958; McLean and Kinsey 1963; Zerbini *et al*. 1995, 1997).

Detection of LMV in infected plants or in seed lots is routinely carried out using immunological techniques such as ELISA (Clark and Adams 1977; Falk and Purcifull 1983) or radioimmunosorbent assay (Ghabrial and Sheperd 1982). More recently, efforts have been made to develop more sensitive techniques for the detection of LMV based on the polymerase chain reaction (PCR) (Revers *et al*. 1999; Peypelut *et al*. 2004). Degenerate primer pair 08894p (5′-CCG TACATAGCIGARTGTGCT-3′) and 09171m (5′-GCGTTG ATGTCGTCATCYTT-3′) that amplifies a fragment of 278 nucleotide size covering part of the CP region of LMV can be used for general detection of LMV isolates (Revers *et al*. 1997a; Krause-Sakate *et al*. 2002; Peypelut *et al*. 2004) and primer pair Most5930p (5′-GATGGGGGTATTTTCGAT-3′) and Most6544m (5′-GACAAGATAAGCTCTAATTCCAC-3′) can be used for the specific detection of Most isolates (Peypelut *et al*. 2004).

The control of lettuce mosaic relies on prophylactic measures such as the elimination of contaminated commercial seed lots and on genetic resistance (Dinand and Lot 1992; Ryder 1970). Two alleles of the recessive gene *mo1* (*mo1*^{1}, formerly named *g*, and *mo1*^{2}, formerly named *mo*) were introgressed into different lettuce cultivars, conferring either tolerance (systemic virus accumulation but no symptoms) or resistance (no systemic virus accumulation), depending on the virus isolate considered. The *mo1* alleles from resistant and susceptible lettuce cultivars were isolated recently and shown to encode the cap-binding protein, eIF4E (Nicaise *et al*. 2003).

LMV isolates capable of overcoming the resistance afforded by *mo1* have been described in various parts of the world, including Europe (Dinant and Lot 1992; Pink *et al*. 1992a, 1992b; Revers *et al*. 1997a; Varveri *et al*. 2002), South America (Stangarlin *et al*. 2000) and North Africa (Fakhfakh *et al*. 2001). While generally resistance-breaking isolates generally are not seed-borne, limiting their economic significance to local outbreaks, these newly observed LMV isolates combine resistance breaking and efficient seed transmission in resistant hosts. In a study of the genetic diversity within LMV isolates collected on a worldwide scale, such isolates clustered separately, suggesting a monophyletic origin of this group of isolates for which the name LMV-Most (for *mo1*-breaking, seed transmitted) was proposed (Krause-Sakate *et al*. 2002). Similarly, the name LMV-Common was proposed for another monophyletic group corresponding to the seed-borne isolates that are unable to causes symptoms on *mo1* plants. The *mo1* alleles also provide control of seed transmission for the LMV-Common isolates because, even in the tolerance cases, these isolates accumulate in the mother plants containing *mo1*^{1} or *mo1*^{2}, but do not access the embryo.

Most-type isolates should be considered an increasing threat to lettuce production worldwide, because of their ability to spread in seed lots even in the presence of the two available LMV resistance genes. To evaluate the occurrence of these two types of LMV isolates, a survey was carried out during 2002-2005 in three lettuce production areas of São Paulo State, on susceptible cultivars, LMV-Common isolates were prevalent (77.3% of the plants evaluated) and LMV-Most isolates were found frequently associated with tolerant (*mo1*^{1}) lettuce cultivars. Susceptible cultivars are grown today in most of the lettuce production areas in São Paulo State. So, despite the ability of LMV-Most isolates to overcome the resistance provided by the recessive *mo1*^{1} gene, they are not prevalent in our conditions (Firmino *et al.* 2008). The comparison of LMV-AF-199 (Most) and LMV-AF198 (Common) on susceptible cultivars reveals that the Most strain reduces drastically the fresh weight, leaf area and chlorophyll content, on the White Boston (susceptible) and Elisa (*mo1*^{1}) cultivars (Jadão *et al*. 2003). At least one naturally recombinant isolate between LMV-Most and LMV-Common was identified in Tunisia (Krause-Sakate *et al*. 2004).

Among the many control measures that should be adopted one may mention the use of virus-free seeds, vector aphid control in order to keep insect population low in the fields and elimination of alternative hosts. Also, should the virus incidence be low, it is recommended to remove and burn infected plants as well as to use quality shoots produced under screen-surrounded by aphid-free environments.

Big-vein disease

Lettuce big vein disease was first described in California (Jagger and Chandler 1934), and is a soil-borne disease found worldwide (Roggero *et al*. 2003). In Brazil the disease was reported in 2003 and observed during the cooler season (Colariccio *et al*. 2003; Lima Neto *et al*. 2004). The name of the disease refers to the appearance of chlorotic areas surrounding the vascular tissue that confers the aspect of an anomalous vein enlargement (**Fig. 2**), commonly accompanied by severe leaf deformations and growth reductions. The economic importance of the disease is a result of the unsightliness of the lettuce foliage, which reduces market value, due to delayed head formation, decreased head size and a reduced proportion of harvestable plants (Zink and Grogan 1954). The symptom expression of big-vein disease is dependent on local factors such as low temperature, luminosity and soil condition (Walsh 1994). This disease is more common when temperatures remain below 20°C. In Brazil symptoms are observed mainly in winter when daylight temperatures range from 18 to 22°C and night temperatures from 10 to 16°C (Colariccio *et al*. 2003).

The big vein symptoms were historically attributed to *Lettuce big-vein associated virus* (LBVaV; genus *Varicosavirus*), formerly known as *Lettuce big-vein virus* (LBVV), but a causative relationship was never confirmed (Kuwata *et al*. 1983; Vetten *et al*. 1987). According to Roggero *et al*. (2000), the *Mirafiori lettuce big-vein virus* (MLBVV), formerly known as Mirafiori lettuce virus (MiLV), which belongs to the genus *Ophiovirus*, was reported to be the causal agent of big-vein disease. Symptoms occur in plants after they have been inoculated mechanically with MLBVV or by the vector (Lot *et al*. 2002). LBVaV and MLBVV have a segmented genome of ssRNA and virus particles contain RNA molecules of both polarities. Negative-sense RNAs predominate for LBVaV while MLBVV contain nearly equimolar amounts of RNA molecules of both polarities (Sasaya *et al*. 2001, 2002; van der Wilk *et al*. 2002; Sasaya *et al*. 2004)

LBVaV and MLBVV are both transmitted by the soil-borne fungus *Olpidium brassicae* (Lot *et al*. 2002). The resting spores of the fungus can persist for over 20 years in soil and can retain the ability to transmit the virus for over 15 years (Campbell 1996). Both LBVaV and MLBVV are sap transmitted, but with low efficiency (Lot *et al*. 2002; Sanches *et al*. 2008). LBVaV are transmitted to *C. quinoa*, *C. amaranthicolor*, *Nicotiana benthamiana*, *N. clevel*and*ii* and *N. occidentalis* (Hujberts 1990). MLBVV is transmitted to *C. quinoa*, *N. benthamiana*, *N. tabacum* White Burley, *N. occidentalis* (Roggero *et al*. 2000), *N. clevel*and*ii* (Lot *et al*. 2002) and *N. hesperis* (van der Wilk *et al*. 2002). The natural infection of *Sonchus oleraceus* by both viruses was also observed by Navarro *et al*. (2005) indicating that this weed acts as a reservoir for the viruses and for *O. brassicae*.

Fig. 2 Symptoms exhibited by *Lettuce big-vein associated virus* and *Mirafiori lettuce big-vein virus*.

LBVaV and MLBVV detection can be carried out with virus-specific antiserum (Lot *et al*. 2002; Colariccio *et al*. 2003; Roggero *et al*. 2003; Colariccio *et al*. 2005), as well as by RT-PCR, where the primers described by Rosales *et al*. (2004) or Navarro *et al*. (2004) can be used. Navarro *et al*. (2004) observed that both LBVaV and MLBVV show greatest concentration on the older roots and leaves of lettuce plants and that symptoms begin 40-50 days after transplanting, coinciding with the peak of spore production of vector *Olpidium brassicae*.

Previous studies have found that plants exhibiting big vein symptoms were frequently co infected with both viruses, suggesting that LBVaV may also contribute to the disease symptoms (Roggero *et al*. 2003; Navarro *et al*. 2004, 2005b). The presence of symptomatic lettuce plants, MLBVV-negative, but LBVaV-positive by ELISA, also has been observed in a field survey (Roggero *et al*. 2003).

LBVaV and MLBVV are widespread in the important lettuce-producing areas of São Paulo State and most plants are co-infected with LBVaV and MLBVV (Sanches *et al*. 2008). Similar results were reported by Roggero *et al*. (2003), Navarro *et al*. (2004) and Hayes *et al*. (2006), showing a strong correlation between big vein symptom expression and MLBVV presence, and indicating that coinfection with both MLBVV and LBVaV could be due to the shared vector (Lot *et al*. 2002). In Brazil during summer plants were found infected alone or in combination by both MLBVV and LBVaV, but the plants did not show any symptoms of the disease (Sanches *et al*. 2007).

The amino acid identities in the coat protein (CP) gene between brazilian LBVaV isolates and other sequences deposited in the Genbank is higher than 93% and no correlation of the geographic origin can be made. For the MLBVV isolates, the aminoacid identities is higher tham 91%, and MLBVaV brazilian isolates belong to the Subgroup A (Sanches *et al*. 2008) according to Navarro *et al*. (2005) classification, that implies the presence of an *Rsa*I restriction site in the CP gene. The subgroup B consists only of Spanish isolates (ALM1, ALM4, ALM5 and SON3) previously described by Navarro *et al*. (2005). These results supports the suggestion of Hayes *et al*. (2006) that research on big vein disease in the United States, Europe and Japan will likely be relevant for lettuce production in others areas as well, due to nucleotide sequence conservation among lettuce isolates of these pathogens, including countries in South America.

For an effective disease control several cultural measures like irrigation, to avoid fungal zoospore dissemination, the use of healthy shoots, elimination of alternative hosts, soil solarization to reduce fungal population and sowing with plastic films to reduce soil humidity and increase temperature therefore reducing zoospore activity, are recommended (Jones 2003; Lathan and Jones 2004). Fletcher *et al*. (2005) recommends the use of products like carbendazim, propamocarb or thiabendazole to improve lettuce production in high incidence areas. Culture rotation is indicated specially during winter, the season when the disease is most prevalent in lettuce. No tolerant or resistant varieties exist in Brazil.

Lettuce-infecting *Tospovirus* species

Tospovirus is the only plant-infecting genus in the family

Fig. 3 Tospovirus disease observed on Elisa lettuce cultivar.

Bunyaviridae, a large group of enveloped, mostly arthropod-transmitted, animal-infecting viruses with tripartite negative-stranded ssRNA genomes (Nichol *et al*. 2005). TSWV is the type species and has a genome consisting of three negative or ambisense ssRNAs designated S (2.9 kb), M (4.8 kb), and L (8.9 kb) (Nichol *et al*. 2005). The RNAs may form a panhandle conformation created by base pairing of about 60 complementary nucleotides at the 3′ and 5′ ends of each strand (De Haan 1989). The core of the virion contains ribonucleoproteins (RNPs) composed of the ssRNA components encapsidated by the nucleoprotein (N) and a few copies of the viral RNA-dependent RNA polymerase (RdRp or L protein). The 80-120 nm pleiomorphic virus particles are formed by enclosure of the RNPs in a host derived lipid membrane studded with surface projections composed of two viral glycoproteins, GN and GC (Nichol *et al*. 2005).

At least 10 species of insects in the order *Thysanoptera* (commonly known as thrips) transmit viruses in the genus *Tospovirus* (Whitfield *et al*. 2005). Tospoviruses are transmitted in a persistent propagative fashion and are transstadially passed on their insect vector. Thrips eggs are oviposited into plant tissue and within a few days the first instar larvae emerge. Virus acquisition occurs solely during the larval stages after which the virus is passed transstadially to the adult. The pupal stages are non-feeding and do not move, although they do maintain virus infection. In nature, *Frankliniella occidentalis* pupates in the soil. Many other vector species, e.g., *Thrips tabaci*, pupate in the foliage. Adults emerge and have a tendency to disperse widely. Only adult thrips (male and female) that acquired the virus during their larval stages can transmit tospoviruses (Whitfield *et al*. 2005). *F. occidentalis*, *F. schultzei*, *T.s tabaci* and *T. palmi* are the main vetors species of tospovirus in Brazil (Nagata and Inoue-Nagata 2003).

In Brazil the first report of a disease caused by a virus of the genus *Tospovirus* was made by Costa and Forster (1938). The lettuce is a natural host of tospoviruses in the field (Costa and Forster 1942). Since 1986 severe losses are related to tospoviruses in lettuce. In the summer, (December to March) losses may occur from 30 to 100% in field conditions (Moraes *et al*. 1986) or 40% under hydroponic cultivation (Colariccio *et al*. 2004).

Symptoms observed in lettuce are circular necrotic stains and browning of the leaves. With systemic infection the plant usually falls to one side. Eventually it becomes completely necrotic and death of the plant occurs (**Fig. 3**).

The identification of species in the genus *Tospovirus* is made by examining host range, serology, and according to the divergence of amino acids in the nucleoprotein (N Protein) (de Ávila *et al*. 1993a, 1993b; Pozzer *et al*. 1999). Such species infect plants in 92 botanical families (van Regenmortel *et al*. 2000), causing significant losses in several vegetable crops. Assay plants like *Nicotiana glutinosa*, *N. rustica*, *Gomphrena globosa* and *Tropaeolum majus* can be used to propagate the virus. Local lesions in *Petunia hybrida*, chlorotic and necrotics lesion in *N. glutinosa* and necrotic lesions in *Datura stramonium* can indicate the presence of tospoviruses (Costa and Forster 1942). TSWV can infect 550 species of plants, including monocots and dicots (de Ávila 1992).

The following tospovirus species have been reported in Brazil: *Tomato spotted wilt virus* (TSWV), *Tomato chlorotic spot virus* (TCSV), *Groundnut ringspot virus* (GRSV), *Chrysanthemum stem necrosis virus* (CSNV), *Zucchini lethal chlorotic virus* (ZLCV), and *Iris yellow spot virus* (IYSV) (Pozzer *et al*. 1999). In lettuce, only TSWV, TCSV and GRSV were observed (Chaves *et al*. 2001). TCSV is the main tospovirus in the state of São Paulo where it is harmful to different crops, but especially to vegetables, while GRSV is prevalent in lettuce in the São Francisco River Valley, in the state of Pernambuco (Colariccio *et al*. 2001). TCSV is also found in hydroponically-grown lettuce in São Paulo State (Colariccio *et al*. 2004). Both TCSV and GRSV are efficiently transmitted by the thrips species *F. occidentalis* Pergande and *F. schultzei* (Wijkamp *et al*. 1995; Borbon and Garcia 1996), which are prevalent in tropical and subtropical regions (Wijkamp *et al*. 1995).

Breeding cultivars for high resistance levels seems to be the best control strategy, since thrips control has not been efficient. In this context, cultures susceptible to tospoviruses, including vegetables and ornamentals, represent important sources for spreading these viruses. Eradication of weeds and volunteer growth close to lettuce fields, in association with other cultural practices, could minimize and prevent infection by tospoviruses. Before sowing the following measures should be adopted: culture rotation with non-susceptible plants, sowing in sites without adjacent susceptible crops and alternate vector and virus host control. During sowing, virus-free shoots should be used, insecticide should be regularly applied (both in the field and in shoot storage areas), trap-plants like broccoli, cauliflower and tolerant wild tomato species, which blossom intensely attracting thrips, be set up and corn barriers around the crop area to hinder vector insect migration and reduce cultivation operations that avoid the motion of thrips from infected to healthy plants, be erected. After harvesting, it is recommended to let the areas with high disease incidence rest for 3 to 4 weeks, and to treat soil (fumigation) to eliminate thrips associated with harvest left-overs. Soil handling is not totally effective if virus and vector have high incidence all over the area. In those conditions sowing should be avoided. Community cooperation is important for thrips control. TSWV resistance has been observed in Tinto and PI 342517 ("Ancora") cultivars and such resistance is of partial dominance. Research towards resistance transfer and selection of plants more adequate to the local conditions are being carried out by Norberto da Silva (unpublished).

Lettuce viruses of minor importance in Brazil

Bidens mosaic virus (BiMV) is a tentative species of the genus *Potyvirus*. It has flexuous rod shaped particles around 720 nm length by 12-13 nm diameter (Kitajima *et al*. 1961). It was verified naturally infecting lettuce in Brazil by Costa and Kitajima (1966). So far this virus has been described only in Brazil.

Besides lettuce, some BiMV isolates also infect tobacco (*Nicotiana tabacum* Turkish), sunflower (*Helianthus annus*), *Physalis floridana*, *Chenopodium amaranticolor*, *C. ambrosioides*, broom stick (*Bidens pilosa*), *Cassia occidentalis*, *Leonotis nepaetifolia* (Kitajima *et al*. 1961), *Pisum sativum* (Nagata *et al*. 1995), *Zinia elegans*, *N. tabacum* TNN (Hasegawa 2004), *Emilia sonchifolia*, *Acanthospermum hispidum*, *Amaranthus* sp., *Solanum nigrum* (Kuhn *et al*. 1980) and Coreopsis *lanceolata* (Rodrigues *et al*. 1991). Hasegawa 2006 observed that a BiMV isolate from lettuce was not able to infect sunflowers, *B. pilosa* or *N. tabacum* TNN,

Fig. 4 Symptoms exhibited by Bidens mosaic virus.

hosts therefore considered susceptible for the virus.

Symptoms observed in lettuce include mosaic and foliar deformation very similar to those caused by LMV (**Fig. 4**). The diagnosis of the virus is hindered by the absence of good antisera and of RT-PCR-specific oligonucleotides.

The virus is sap transmitted and also by the aphids *Myzus persicae*, *Aphis coreopsidis* and *Dactynotus* sp. In lettuce, transmission tests with *Myzus persicae* showed results from 20 to 80% depending on the cultivar. The virus is not transmitted by the seed (Kuhn *et al*. 1980).

There is no study in Brazil in the incidence of this virus in field conditions. Economic losses have been observed in sunflowers and peas (Nagata *et al*. 1995). However the lettuce cultivars in São Paulo appear to be susceptible to at least one BiMV isolate naturally collected from lettuce. Of the tested cultivars only 'Gizele' has proved tolerant to the virus (Krause-Sakate, pers. comm.). Control measures for this virus include handling to keep vector insect population low, elimination of infected plants and alternative hosts as well as the use of tolerant varieties.

Lettuce mottle virus (LeMoV) is a possible member of the genus *Sequivirus*, family *Sequiviridae* (Jadão *et al*. 2007) infecting lettuce in Brazil (Marinho *et al*. 1982) and Chile (Krause-Sakate *et al*. 2005). It is closely related to *Dandelion yellow mosaic virus* (DaYMV) a sequivirus that infects lettuce in Europe. LeMoV possesses isometric particles 30 nm in diameter, occurs at low concentration in plants and is sap-transmitted but has a narrow host range (Marinho *et al*. 1982; Jadão *et al*. 2007). *C. quinoa* is systemically infected by the virus and some lettuce cultivars like 'Vanguard-75' and 'Elisa' are tolerant (Jadão *et al*. 2007). LeMoV is not seed-borne in lettuce and causes mosaic symptoms very similar to LMV (**Fig. 5**) (Jadão *et al*. 2007). Transmission is in a semi-persistent manner by *Hyperomyzus lactucae* (Marinho *et al*. 1982). Specifics primers for LeMoV (Lmo3 5′-ACATGAGCACTAGTGAGG-3′ and Lmo4 5′-AGATAGAGCCGTCTGGCG-3′) can be used for diagnosis by RT-PCR. The incidence of LeMoV in the field is low. A survey was carried out in São Paulo State and in 1,362 samples of lettuce showing mosaic symptoms tested, only 137 (10.05%) were positive for LeMoV. LeMoV can also be found in mixed infections with LMV (Krause-Sakate *et al*. 2008).

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Fig. 5 Symptoms exhibited by Lettuce mottle virus.

Turnip mosaic virus (TuMV, genus *Potyvirus*) was first reported infecting lettuce in California. In susceptible lettuce cultivars the initial symptoms include abundant, small, light-green lesions, circular to irregular lesions distributed randomly on the leaves (Duffus 1997). Non-persistent transmission can be performed by aphids *Myzus persicae* and

Brevicoryne brassicae (Brunt *et al*. 1996). No data on its incidence in the field exist in Brazil.

Cucumber mosaic virus (CMV, genus *Cucumovirus*) also cause symptoms similar to LMV but is not seed borne like LMV so distribution within the field is usually along margins. The virus is transmitted by several species of aphids including in a non-persistent manner. There is no data of incidence of CMV on lettuce in Brazil, and the disease can be prevented by controlling the vector sources. There is no information of resistance cultivars to CMV.

CONCLUSIONS

Lettuce viruses are one of the great current challenges to its culture since no tolerant or resistant varieties are available commercially for most viruses herein described in this review. Improvement programs towards multiple viral resistance cultivars are in progress at FCA/UNESP/Botucatu, using sources tolerant to tospoviruses, Lettuce mosaic virus, LMV common and most strains, LeMoVLettuce mottle virus and Bidens mosaic virusBiMV in different lettuce groups. This genetic research has made it possible in 2007 the introduction of the cultivar 'Cuesta' with that carries multiple resistances resistance genes to tospoviruses, LMV and LeMoV.

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