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DETECTION OF CUCUMBER MOSAIC VIRUS IN NOVEL HOST PLANTS IN UKRAINE

Background. Cucumber mosaic virus (CMV; species *Cucumovirus* CMV, genus *Cucumovirus*, family *Bromoviridae*) has the widest host range among plant viruses, infecting over 1,000 species across diverse genera and families. Various CMV strains and isolates are constantly evolving, adapting to new hosts, and may pose significant threats to the cultivation of economically important crops.

Methods. This study aimed to detect CMV in atypical host plants in Ukraine. Double antibody sandwich (DAS) enzyme-linked immunosorbent assay (ELISA) was employed to identify CMV and to exclude mixed infections with other viruses, including alfalfa mosaic virus (AMV), arabis mosaic virus (ArMV), impatiens necrotic spot virus (INSV), potato virus X (PVX), potato virus Y (PVY), soybean mosaic virus (SMV), tobacco mosaic virus (TMV), tobacco rattle virus (TRV), tobacco ringspot virus (TRSV), tomato mosaic virus (ToMV), tomato spotted wilt virus (TSWV), turnip mosaic virus (TuMV), and turnip yellow mosaic virus (TYMV), using commercial ELISA kits (Loewe Biochemica GmbH, Germany).

Results. Screening of agroecosystems and ornamental plantings in several regions of Ukraine revealed CMV-infected plants. CMV monoinfections were detected in *Hosta longissima* (Asparagaceae), *Echinacea purpurea*, *Erigeron annuus*, and *Heliopsis helianthoides* (Asteraceae), *Alliaria petiolata* (Brassicaceae), *Silene latifolia* (Caryophyllaceae), and *Euphorbia epithymoides* (Euphorbiaceae).

Conclusions. These findings demonstrate the circulation of CMV in different regions of Ukraine across host plants from diverse families, including Asparagaceae, Asteraceae, Brassicaceae, Caryophyllaceae, and Euphorbiaceae. Notably, CMV was detected for the first time in *E. annuus*, *H. helianthoides*, and *E. epithymoides*, expanding the known host range of this economically significant virus in the *Bromoviridae* family.

Keywords: CMV, *Bromoviridae*, host range, identification, enzyme-linked immunosorbent assay.

Background

Cucumber mosaic virus (CMV; species *Cucumovirus* CMV, genus *Cucumovirus*, family *Bromoviridae*) has the broadest host range among all plant viruses, infecting over 1,000 species across diverse genera and families. Each year, new host plant species are reported for CMV, including economically important crops, ornamentals, and weeds (Palukaitis, & García-Arenal, 2019). CMV has a worldwide distribution and exists in numerous strains, some of which harbor satellite RNAs. The viral genome is tripartite, consisting of three molecules of single-stranded positive-sense RNA, with a total length of 8,621 nucleotides (Ding, 1994). Satellite RNAs can be encapsidated within CMV virions, facilitating their spread by vectors from plant to plant. The severity and nature of disease symptoms depend on interactions among the satellite RNA, CMV strain, and host plant species or cultivar (García-Arenal et al., 2000). CMV virions are icosahedral, approximately 29 nm in diameter, and are detectable in the cytoplasm of all infected plant tissues, often forming inclusions of variable morphology (Jacquemond, 2012).

CMV is transmitted in a non-persistent manner by more than 75 aphid species, with the most efficient vectors including *Aphis craccivora*, *A. fabae*, *A. pisum*,

Rhopalosiphum padi, *Myzus persicae*, *M. euphorbiae*, and *A. solani*. Vector transmission efficiency depends on the viral strain, vector species, host plant species, season, and environmental conditions (Edwardson, & Christie, 1986; Mauck et al., 2014). CMV can also be transmitted via seeds, mechanically, and through parasitic plants such as dodder (*Cuscuta* sp.) (Ali, & Kobayashi, 2010). Seed transmission has been documented in *Stellaria media* (Caryophyllaceae), with up to 40 % of seedlings from infected seeds carrying the virus. Seed transmission was also observed in infected *Lamium purpureum* (4 %), *Cerastium holosteoides* (2 %), and *Spergula arvensis* (2 %) (Tomlinson, & Carter, 1970). CMV seed transmission occurs across multiple plant families, including economically important crops such as members of *Amaranthaceae* (syn. *Chenopodiaceae*; e.g., spinach), *Brassicaceae*, *Fabaceae* (syn. *Leguminosae*; e.g., bean, chickpea, cowpea, lentil, lupin, subterranean clover), and *Lamiaceae*. This mode of transmission contributes to the annual emergence of CMV-infected legumes in commercial fields and increases the likelihood of viral persistence in nature.

According to the literature, CMV infects a wide range of host plants from various families (Table 1).

Table 1

Natural host plants of cucumber mosaic virus

Family	Genus	Species	Reference
Adoxaceae	<i>Viburnum</i>	<i>Viburnum lentago</i>	Kwon et al., 2025
Amaranthaceae	<i>Amaranthus</i>	<i>Amaranthus spinosus</i>	Asala et al., 2014
	<i>Spinacia</i>	<i>Spinacia oleracea</i>	Ahsan et al., 2021
Amaryllidaceae	<i>Allium</i>	<i>Allium cepa</i>	Santosa, & Ertunc, 2021
		<i>Allium sativum</i>	Taher et al., 2024
	<i>Hippeastrum</i>	<i>Hippeastrum hybridum</i>	Prajapati et al., 2024

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Ending table 1

Family	Genus	Species	Reference
Apiaceae	<i>Daucus</i>	<i>Daucus carota</i>	Afreen et al., 2009
	<i>Petroselinum</i>	<i>Petroselinum crispum</i>	Sevik, & Akcura, 2011
Apocynaceae	<i>Calotropis</i>	<i>Calotropis gigantea</i>	Hu et al., 2022
Araceae	<i>Arum</i>	<i>Arum italicum</i>	Gaudin, et al., 2025
Asparagaceae	<i>Hosta</i>	<i>Hosta spp.</i>	Fisher, 2013
	<i>Hyacinthoides</i>	<i>Hyacinthoides sp</i>	Gaudin et al., 2025
Asteraceae	<i>Arctium</i>	<i>Arctium lappa</i>	Dunich et al., 2022
	<i>Aster</i>	<i>Aster scaber</i>	Ko et al., 2020
	<i>Calendula</i>	<i>Calendula officinalis</i>	Milošević et al., 2015
	<i>Crepis</i>	<i>Crepis biennis</i>	Mrkvová et al., 2024
	<i>Dahlia</i>	<i>Dahlia sp</i>	Yeşil, 2022
	<i>Echinacea</i>	<i>Echinacea purpurea</i>	Mishchenko et al., 2021
	<i>Helianthus</i>	<i>Helianthus annuus</i>	Salamon, 2003
	<i>Lactuca</i>	<i>Lactuca serriola</i>	Mrkvová et al., 2024
	<i>Melanpodium</i>	<i>Melanpodium divaricatum</i>	Asala et al., 2014
	<i>Sonchus</i>	<i>Sonchus arvensis</i>	Mrkvová et al., 2024
	<i>Tridax</i>	<i>Tridax procumbens</i>	Asala et al., 2014
Basellaceae	<i>Basella</i>	<i>Basella alba</i>	Adediji, 2019
Brassicaceae	<i>Alliaria</i>	<i>Alliaria petiolata</i>	Kyrychenko et al., 2022
	<i>Capsella</i>	<i>Capsella bursa-pastoris</i>	Gaudin et al., 2025
Campanulaceae	<i>Campanula</i>	<i>Campanula punctata</i>	Wei, 2025
Caprifoliaceae	<i>Valeriana</i>	<i>Valeriana qfficinalis</i>	Faan, & Johnson, 1951
Caryophyllaceae	<i>Cerastium</i>	<i>Cerastium glomeratum</i>	Gaudin et al., 2025
		<i>Cerastium holosteoides</i>	Tomlinson, & Carter, 1970
		<i>Gypsophila</i>	<i>Gypsophila paniculata</i>
	<i>Pseudostellaria</i>	<i>Pseudostellaria heterophylla</i>	Lee et al., 2020
	<i>Silene</i>	<i>Silene armeria</i>	Okuno et al., 2002
		<i>Silene latifolia</i>	Mueller et al., 2012
		<i>Silene pratensis</i>	Faan, & Johnson, 1951
	<i>Spergula</i>	<i>Spergula arvensis</i>	Tomlinson, & Carter, 1970
	<i>Stellaria</i>	<i>Stellaria aquatica</i>	Choi et al., 2004
<i>Stellaria media</i>		Tomlinson, & Carter, 1970	
Cleomaceae	<i>Cleome</i>	<i>Cleome spinosa</i>	Faan, & Johnson, 1951
Commelinaceae	<i>Commelina</i>	<i>Commelina diffusa</i>	Nouri et al., 2014
Cucurbitaceae	<i>Citrullus</i>	<i>Citrullus lanatus</i>	Apalowo et al., 2022
	<i>Cucumis</i>	<i>Cucumis melo</i>	Biltekin, & Akdura, 2024
		<i>Cucumis sativus</i>	Shevchenko et al., 2018
	<i>Cucurbita</i>	<i>Cucurbita pepo</i>	Shevchenko et al., 2015
	<i>Telfairia</i>	<i>Telfairia occidentalis</i>	Adediji, 2019
Euphorbiaceae	<i>Euphorbia</i>	<i>Euphorbia heterophylla</i>	Asala et al., 2014
		<i>Euphorbia hirta</i>	CABI/EPPO 2022
Fabaceae	<i>Cicer</i>	<i>Cicer arietinum</i>	Latham et al., 2001
	<i>Crotalaria</i>	<i>Crotalaria retusa</i>	Asala et al., 2014
	<i>Lens</i>	<i>Lens culinaris</i>	Makkouk, & Attar, 2003
	<i>Medicago</i>	<i>Medicago lupulina</i>	Mrkvová et al., 2024
	<i>Pisum</i>	<i>Pisum sativum</i>	Ahsan et al., 2021
	<i>Trifolium</i>	<i>Trifolium incarnatum</i>	Gaudin et al., 2025
		<i>Trifolium repens</i>	Mrkvová et al., 2024
	<i>Vigna</i>	<i>Vigna angularis var</i>	Kim et al., 2014
		<i>Vigna radiata</i>	Purivirojkul et al., 1978
	<i>Vicia</i>	<i>Vicia ervilia</i>	Latham et al., 2001
		<i>Vicia faba</i>	
<i>Vicia narbonensis</i>			
Iridaceae	<i>Gladiolus</i>	<i>Gladiolus sp</i>	Sovinska et al., 2021
Lamiaceae	<i>Lamium</i>	<i>Lamium maculatum</i>	Bešta-Gajević et al., 2013
		<i>Lamium purpureum</i>	Tomlinson et al., 1970
		<i>Salvia</i>	<i>Salvia patens</i>
	<i>Salvia</i>	<i>Salvia sclarea</i>	Sinha, & Samad, 2021
		<i>Salvia splendens</i>	Ali et al., 2014
	<i>Stachys</i>	<i>Stachys arvensis</i>	Gaudin et al., 2025
Liliaceae	<i>Lilium</i>	<i>Lilium davidii var. unicolor</i>	Su et al., 2024
		<i>Lilium orientalis</i>	Zhang et al., 2019
		<i>Lilium sp.</i>	Niimi et al., 2003
Malvaceae	<i>Hibiscus</i>	<i>Hibiscus esculentus</i>	Asala et al., 2014
Molluginaceae	<i>Mollugo</i>	<i>Mollugo verti-cillata</i>	Faan, & Johnson, 1951
Musaceae	<i>Musa</i>	<i>Musa acuminata</i>	Kebede, & Majumder, 2021
Papaveraceae	<i>Chelidonium</i>	<i>Chelidonium majus</i>	Mrkvová et al., 2022
	<i>Papaver</i>	<i>Papaver rhoeas</i>	
		<i>Papaver somniferum</i>	

Ending table 1

Family	Genus	Species	Reference
Passifloraceae	<i>Passiflora</i>	<i>Passiflora edulis</i>	Gioria et al., 2002
Plantaginaceae	<i>Penstemon</i>	<i>Penstemon acuminatus</i>	Sampangi et al., 2009
Poaceae	<i>Zea</i>	<i>Zea mays</i>	Kim et al., 2011
Polemoniaceae	<i>Phlox</i>	<i>Phlox drummondii</i>	Habili, & Elahinia, 1979
		<i>Phlox paniculata</i>	Cardin et al., 2007
		<i>Phlox subulata</i>	Hammond, & Reinsel, 2011
	<i>Polemonium</i>	<i>Polemonium caeruleum</i>	Faan, & Johnson, 1951
Polygonaceae	<i>Rumex</i>	<i>Rumex obtusifolius</i>	Mrkvová et al., 2024
Primulaceae	<i>Anagallis</i>	<i>Anagallis arvensis</i>	Gaudin et al., 2025
Ranunculaceae	<i>Aconitum</i>	<i>Aconitum spp.</i>	Fukumoto et al., 2008
	<i>Delphinium</i>	<i>Delphinium spp.</i>	Ahmed, & Bailiss, 1975
Rosaceae	<i>Fragaria</i>	<i>Fragaria ananassa</i>	Chen et al., 2014
	<i>Geum</i>	<i>Geum urbanum</i>	Mrkvová et al., 2024
Solanaceae	<i>Capsicum</i>	<i>Capsicum annum</i>	Kim et al., 2002
	<i>Physalis</i>	<i>Physalis angulata</i>	Asala et al., 2014
		<i>Physalis heterophylla</i>	Hobbs et al., 2000
	<i>Solanum</i>	<i>Solanum lycopersicum</i>	Shevchenko et al., 2015
		<i>Solanum ptycanthum</i>	Hobbs et al., 2000
Talinaceae	<i>Talinum</i>	<i>Talinum fruticosum</i>	Adediji, 2019
Violaceae	<i>Viola</i>	<i>Viola alba Besser</i>	Mrkvová et al., 2024
		<i>Viola cornuta</i>	Arneoda et al., 2005

As shown in Table 1, cucumber mosaic virus (CMV) infects representatives of at least 74 genera from 36 plant families. Natural hosts of this pathogen comprise both eudicots (formerly dicotyledons) and monocots, including members of the Poaceae family. The broad host range of CMV reflects its high variability and highlights its potential threat as a pathogen to the cultivation of economically important crops, especially considering its non-persistent transmission by a large number of aphid species relevant to Ukraine.

In Ukraine, CMV has been detected in agronomic crops (Shevchenko et al., 2015; Shevchenko et al., 2018; Taher et al., 2024), ornamental plants (Sovinska et al., 2021), medicinal crops (Mishchenko et al., 2021), as well as in certain weeds (Kyrychenko et al., 2022; Dunich et al., 2022). Different CMV strains and isolates are continuously evolving, adapting to new hosts, and may pose a risk to the production of valuable crops. Studies of Ukrainian CMV isolates will facilitate the development of effective control strategies and help prevent disease outbreaks. The aim of the present study was to detect CMV in atypical host plants in Ukraine.

Methods

Sample Collection

Between 2022 and 2024, plants were surveyed in agroecosystems and green plantings across various regions of Ukraine for the presence of symptoms typical of CMV infection. Symptomatic plants representing different families, including Amaranthaceae, Apiaceae, Asparagaceae, Asteraceae, Brassicaceae, Boraginaceae, Caryophyllaceae, Euphorbiaceae, Fabaceae, Lamiaceae, Solanaceae, and Urticaceae, were collected for further analysis.

Double Antibody Sandwich Enzyme-Linked Immunosorbent Assay (DAS-ELISA)

Collected symptomatic samples were tested for the presence of cucumber mosaic virus (CMV). To exclude mixed infections, samples were also screened for other viruses, including alfalfa mosaic virus (AMV), arabis mosaic virus (ArMV), impatiens necrotic spot virus (INSV), potato virus X (PVX), potato virus Y (PVY), soybean mosaic virus (SMV), tobacco mosaic virus (TMV), tobacco rattle virus (TRV), tobacco ringspot virus (TRSV), tomato mosaic virus (ToMV), tomato spotted wilt virus (TSWV), turnip mosaic

virus (TuMV), and turnip yellow mosaic virus (TYMV) using commercial ELISA kits (Loewe Biochemica GmbH, Sauerlach, Germany).

For each sample, 500 mg of plant tissue was homogenized in sample buffer (pH 7.4) at a 1:10 (w/v) ratio using a mortar and pestle. The homogenate was centrifuged at 5,000 rpm for 20 minutes at 4°C to remove cellular debris. The resulting supernatant was used for subsequent viral diagnostics.

The assay was performed according to standard guidelines (Ward et al., 2004) and following the manufacturer's instructions. Antibodies conjugated to alkaline phosphatase and p-nitrophenyl phosphate substrate (Loewe Biochemica GmbH, Sauerlach, Germany) were employed. Absorbance values were measured at 405 nm using a µQuant™ microplate spectrophotometer (BioTek Instruments, Inc., USA). Samples were considered positive only if the absorbance value exceeded three times that of the negative control.

Results

Between 2022 and 2024, surveys of agroecosystems and green plantings in various regions of Ukraine were conducted to identify plants from different families exhibiting symptoms typical of cucumber mosaic virus (CMV) infection. Symptomatic plants showing mosaic patterns, leaf spotting, leaf deformation, and stunted growth were tested using solid-phase enzyme-linked immunosorbent assay (ELISA) with a commercial kit for CMV identification. In addition, the plants were screened for the presence of other viruses, including AMV, ArMV, INSV, PVX, PVY, SMV, TMV, TRV, TRSV, ToMV, TSWV, TuMV, and TYMV, to exclude mixed infections. None of these additional viruses were detected, indicating that the symptomatic plants were infected solely with CMV.

CMV was identified in *Hosta longissima* (Asparagaceae); *Echinacea purpurea*, *Erigeron annuus*, and *Heliopsis helianthoides* (Asteraceae); *Alliaria petiolata* (Brassicaceae); *Silene latifolia* (Caryophyllaceae); and *Euphorbia epithymoides* (Euphorbiaceae) (Table 2).

On CMV-infected Asteraceae plants, mosaic symptoms and leaf deformation were observed, while *Heliopsis helianthoides* did not produce flowers (Fig. 1).

Table 2

Detection of CMV in different host plants in Ukraine

Family	Plant species	OD 405/630 nm
Amaranthaceae	<i>Chenopodium album</i>	0,072±0,002
Apiaceae	<i>Apium graveolens</i>	0,045±0,001
Asparagaceae	<i>Hosta longissima</i>	0,649±0,003
Asteraceae	<i>Echinacea purpurea</i>	2,627±0,008
	<i>Erigeron annuus</i>	2,064±0,003
	<i>Heliopsis helianthoides</i>	1,487±0,007
	<i>Taraxacum officinale</i>	0,044±0,001
Brassicaceae	<i>Alliaria petiolata</i>	1,511±0,005
Boraginaceae	<i>Cynoglossum officinale</i>	0,087±0,001
Caryophyllaceae	<i>Silene latifolia</i>	1,725±0,006
Euphorbiaceae	<i>Euphorbia epithymoides</i>	0,719±0,003
Fabaceae	<i>Glycine max</i>	0,063±0,002
	<i>Phaseolus vulgaris</i>	0,049±0,001
	<i>Pisum sativum</i>	0,058±0,002
	<i>Vicia faba</i>	0,081±0,003
Lamiaceae	<i>Lamium purpureum</i>	0,039±0,001
Solanaceae	<i>Capsicum annuum</i>	0,067±0,002
	<i>Petunia Juss</i>	0,059±0,001
	<i>Physalis alkekengi</i>	0,048±0,001
	<i>Solanum lycopersicum</i>	0,082±0,002
	<i>Solanum tuberosum</i>	0,079±0,001
Urticaceae	<i>Urtica urens</i>	0,063±0,001
k + – positive control		2,598±0,004
k- 1 – negative control, healthy sap		0,073±0,002
k- 2 – negative control, buffer		0,023±0,001



Fig. 1. Symptoms on naturally CMV-infected plants of the family Asteraceae: (a) *Erigeron annuus* (Kyiv region), (b) *Heliopsis helianthoides* (Kyiv region), (c) *Echinacea purpurea* (Kharkiv region), (k) healthy control

On CMV-infected *Alliaria* plants (garlic mustard, *Brassicaceae*), clear mosaic patterns were observed, with occasional leaf deformation. In CMV-infected *Silene*

plants (*Silene latifolia*, *Caryophyllaceae*), symptoms included mild interveinal mosaic, with all leaves showing deformation (Fig. 2).



Fig. 2. Symptoms on naturally CMV-infected plants: (a) *Alliaria petiolata* (*Brassicaceae*, Kyiv region), (b) *Silene latifolia* (*Caryophyllaceae*, Vinnytsia region), (k) healthy control

In Fig. 3, (a) shows clear mosaic patterns and leaf deformation in *Hosta longissima* (*Hosta*, *Asparagaceae*) infected with CMV compared to healthy plants, while (b) shows CMV-infected *Euphorbia epithymoides* (*Euphorbia*, *Euphorbiaceae*) exhibiting ring-spot symptoms.



Fig. 3. Symptoms on naturally CMV-infected plants: (a) *Hosta longissima* (*Asparagaceae*, Kyiv region), (b) *Euphorbia epithymoides* (*Euphorbiaceae*, Kyiv region), (k) healthy control

Discussion and conclusions

The detection of CMV in *Asteraceae* aligns with previous reports of CMV infection in composite plants in Ukraine (Dunich et al., 2022). However, this study represents the first worldwide report of CMV infection in *Erigeron annuus* and *Heliopsis helianthoides*. CMV infection in *Alliaria petiolata* has also been reported in Ukraine (Kyrychenko et al., 2022), while infections in *Hosta longissima* and *Silene latifolia* have been documented in international publications (Fisher, 2013; Mueller et al., 2012). Notably, this study is the first worldwide report of natural CMV infection in *Euphorbia epithymoides*.

It should be noted that CMV-infected plants were collected from different regions of Ukraine: *Silene latifolia* from central Ukraine (Vinnytsia region), *Echinacea purpurea* from eastern Ukraine (Kharkiv region), and all other CMV-positive plants from northern Ukraine (Kyiv region).

Cucumber mosaic virus (CMV) is the most widespread plant virus with the broadest host range. It poses a potential threat to the commercial cultivation of numerous crops, as it continues to evolve into diverse strains and adapt to different geographic regions and host species. Isolates from atypical host plants are of particular concern, as they may possess new properties and high pathogenicity.

This study demonstrates the circulation of CMV isolates across different regions of Ukraine in host plants from various families, including *Asparagaceae*, *Asteraceae*, *Brassicaceae*, *Caryophyllaceae*, and *Euphorbiaceae*. The findings are consistent with previous literature; however, this study reports for the first time worldwide the detection of CMV in *Erigeron annuus* and *Heliopsis helianthoides* (*Asteraceae*) and *Euphorbia epithymoides* (*Euphorbiaceae*). These results expand the known host range of this economically important virus in the *Bromoviridae* family.

Authors' contribution: Halyna Snihur – designed the study; Pavlo Burba and Halyna Snihur – prepared material for the experiments and collected data.

Since none of the other tested viruses were detected in these plants, the infections can be considered CMV mono-infections.

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ВИЯВЛЕННЯ CUCUMBER MOSAIC VIRUS НА НОВИХ РОСЛИНАХ-ХАЗЯЯХ В УКРАЇНІ

Вступ. *Cucumber mosaic virus* (*Cuscutovirus*, *Bromoviridae*) має найширший спектр рослин-хазяїв серед усіх вірусів, він уражує понад 1000 видів рослин із різних родів і родин. Існують різні штами та ізоляти зазначеного збудника, які постійно еволюціонують, адаптуються до нових хазяїв і можуть становити потенційну небезпеку для виробництва цінних культур. Метою цього дослідження було виявити *cucumber mosaic virus* на нетипових рослинах-хазяях в Україні.

Методи. Імуноферментний аналіз у модифікації "сендвіч" (DAS-ELISA) використовували для ідентифікації *cucumber mosaic virus* (CMV) і для спростування змішаної інфекції з іншими вірусами, зокрема *alfalfa mosaic virus* (AMV), *arabis mosaic virus* (ArMV), *impatiens necrotic spot virus* (INSV), *potato virus X* (PVX), *potato virus Y* (PVY), *soybean mosaic virus* (SMV), *tobacco mosaic virus* (TMV), *tobacco rattle virus* (TRV), *tobacco ringspot virus* (TRSV), *tomato mosaic virus* (ToMV), *tomato spotted wilt virus* (TSWV), *turnip mosaic virus* (TuMV) та *turnip yellow mosaic virus* (TYMV) із застосуванням комерційних тест-систем (Loewe Biochemica GmbH, Germany).

Результати. Проведено скринінг агробіоценозів і зелених насаджень у населених пунктах різних областей України на наявність рослин, уражених *cucumber mosaic virus*. Виявлено моноінфекцію CMV у рослинах хости доогої (*Hosta longissima*) родини *Asparagaceae*; ехінацеї пурпурної (*Echinacea purpurea*), злинок однорічної (*Erigeron annuus*) і соняшника садового (*Helianthus annuus*) родини *Asteraceae*; часникової трави (*Alliaria petiolata*) родини *Brassicaceae*; смілки широколистої (*Silene latifolia*) родини *Caryophyllaceae*; молочаю різнобарвного *Euphorbia epithymoides* родини *Euphorbiaceae*.

Висновки. Показано циркуляцію CMV у різних регіонах України на рослинах-хазяях із різних родин, зокрема *Asparagaceae*, *Asteraceae*, *Brassicaceae*, *Caryophyllaceae* та *Euphorbiaceae*. Уперше виявлено зазначеного збудника на нових хазяях: *E. annuus*, *H. helianthoides* і *E. epithymoides*. Отримані дані розширюють знання про коло рослин-хазяїв найбільш небезпечного вірусу родини *Bromoviridae*.

Ключові слова: CMV, *Bromoviridae*, спектр хазяїв, ідентифікація, імуноферментний аналіз.

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