

Occurrence of cucumber mosaic virus and turnip mosaic virus in *Alliaria petiolata* in Ukraine

Angelina Kyrychenko¹, Halyna Snihur^{1,2}, Tetiana Shevchenko²,
Ivan Shcherbatenko¹

¹*Institute of Microbiology and Virology. D.K. Zabolotnogo National Academy of Sciences of Ukraine, Acad. Zabolotnogo str., 154, Kyiv 03143, Ukraine*

²*Virology Department, ESC “Institute of Biology and Medicine”, Taras Shevchenko National University, 64/13 Volodymyrska Str., Kyiv, 01601, Ukraine*



What do we know about the Garlic mustard?

Invasive, Destructive, Edible

In addition to becoming a serious invader, garlic mustard can serve as **a host to several viruses**, which may affect agricultural crops

First-year plants



Second-year plants



Infected plants



To date, the following viruses have been found to infect plants:

- ✓ Cucumber Mosaic Virus (*Bromoviridae*)
- ✓ Turnip Mosaic Virus (*Potyviridae*)
- ✓ White Clover Mosaic Virus (*Alphaflexiviridae*)
- ✓ Turnip Vein-clearing Virus (*Virgaviridae*)
- ✓ Turnip Crinkle Virus (*Tombusviridae*)
- ✓ Turnip Yellow Mosaic Virus (*Tymoviridae*)

Garlic mustard (***Alliaria petiolata*** M.Bieb., Cavara & Grande, *Alliaria officinalis* Andr. Ex. Bieb)

What was the purpose of the study ?

to identify the virome of garlic mustard growing in Ukraine

SAMPLES: plants showing **vein banding, mosaic and leaf deformation** were collected in May-June of 2020-2021 growing seasons from ruderal sites of five Kyiv regions

METHODS:

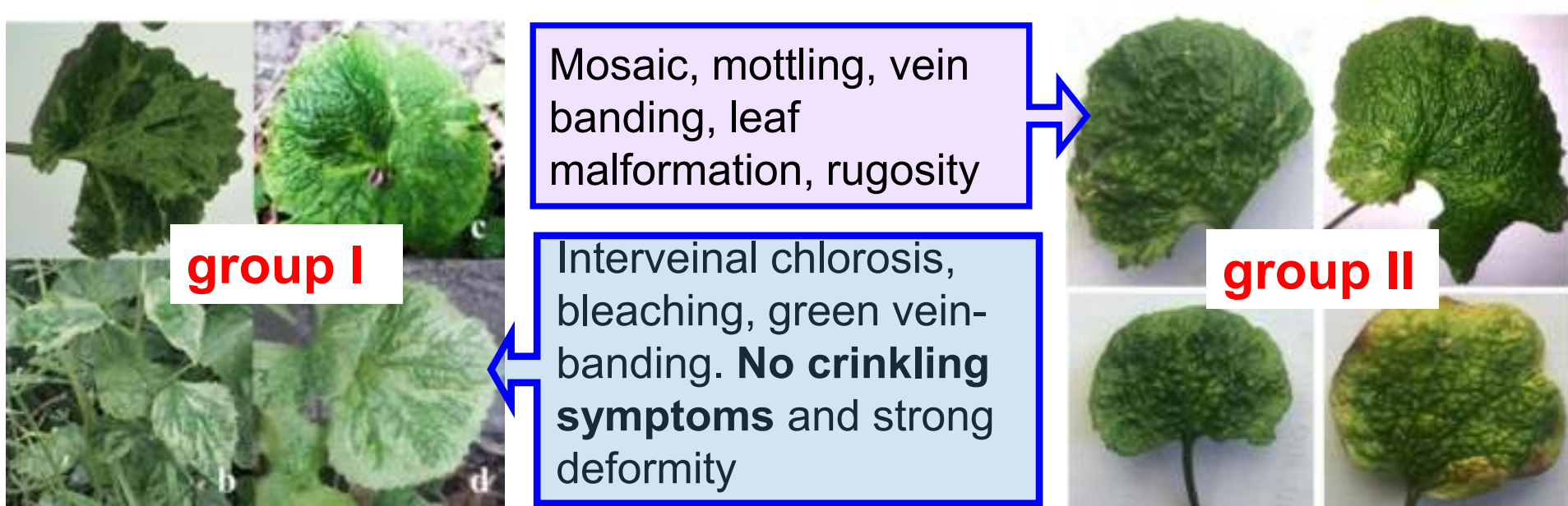
- ❖ Transmission electron microscopy (TEM)
- ❖ Experimental host range assays
- ❖ Enzyme-linked immunosorbent assays (ELISA) - ACP-ELISA for detection of potyviruses (73 species) and DAS-ELISA for detection of CMV, TYMV, TuMV and WMV II
- ❖ Reverse transcription polymerase chain reaction (RT-PCR) and sequencing
- ❖ Phylogenetic analysis of CMV and TuMV

Primer pairs:

CMV-F/R 5'-TATGATAAGAAGCTTGTTTCGCGCA-3'; 5'-TTTTAGCCGTAAGCTGGATGGACAACCC-3'
TCV (HZ632/HZ633 5'-AAAGGCAAAAFCTGGGTGGGA-3'; 5'-TAAAGTTTGCGGCTAGGGG -3'
TuMV CP-F/R5'-TATACACGCCGGAGCAGACG-3'; 5'-CGCAGTGCTGCTGCTTTTCAT-3

RESULTS

The collected first-year plants differed in the symptoms of the disease and therefore were divided into two groups:



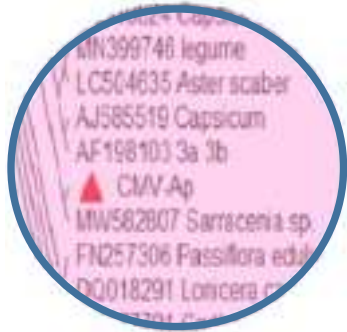
Using the methods listed above, we found that plants of **group I** were mostly infected by CMV or, most unexpectedly, had mixed infection with CMV and TuMV viruses. In the plants of **group II**, we identified the only virus – TuMV:

60% – positive for CMV, 20% – infected with TuMV, and 20% – co-infected with CMV + TuMV

What are the main phylogenetic analysis results?

✓ Our study is the **first report of TuMV (TuMV-Ap)** naturally infecting garlic mustard in Ukraine

✓ **TuMV-Ap** represent the highest identity (98.6%) to **Iranian** isolate from *Rapistrum rugosum* and **Turkish** isolate from *Raphanus raphanistrum*



✓ CMV from garlic mustard (**CMV-Ap**) has the greatest similarity to the isolates from **Germany** (MW582807), **Slovakia** (MN792886), and **Japan** (AB006813)

✓ Despite the fact that previous reports showed the prevalence in Ukraine CMV of subgroup I, the present study showed that the CMV-Ap belongs to subgroup II. Thus, the CMV isolates distributed in Ukraine belong **to both subgroups** - that have a worldwide distribution (IA or II) as well as to subgroup restricted mainly to Asia (IB).

The results obtained indicate the important role of infected garlic mustard as alternative host and natural reservoir of CMV and TuMV from which these economically important viruses can spread to other wild and cultivated plants

