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Host Reaction of *Watermelon mosaic virus* Isolates Infecting Melon from Different Geographical Origins in Xinjiang of China

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A B S T R A C T

Watermelon mosaic virus (WMV) is one of the major viruses infecting cucurbit crops worldwide. Although WMV is very common worldwide, little is known about the biological traits of WMV isolates from China. Hence, this study aimed to characterize 11 WMV isolates infecting melon from different geographical origins in Xinjiang based on experimental hosts. Sap inoculation of the 11 WMV isolates onto a range of 13 plant species revealed some differences compared to the WMV isolates collected from other countries. Our results showed that, overall, there were no obvious correlations of host responses to inoculation with WMV isolates from different geographical origins. However, isolate JS-1 caused mild mosaic on *Cucurbita moschata*, whereas the remaining 10 isolates were asymptomatic on this plant species. Moreover, in *Datura stramonium*, isolate TYG-1 induced mosaic, whereas the remaining 10 isolates did not infect this species. All isolates infected systemically *Cucurbita pepo* and *Cucumis melo* plants, causing severe symptoms. All isolates did not induce any symptoms on *Cucumis sativus*, but the virus could be detected using RT-PCR. Additionally, all isolates infected systemically *Nicotiana tabacum* plants, causing mild mosaics. *Chenopodium amaranticolor* and *Chenopodium quinoa* reacted to all isolates by chlorotic local lesions in the inoculated leaves, and the virus was detected in the inoculated leaves using RT-PCR. In addition, the attempts to transmit the isolates to *Luffa cylindrica*, *Vicia faba*, *Phaseolus vulgaris*, *Vigna unguiculata* or *Pisum sativum* failed as confirmed by negative RT-PCR. Our results would be useful for understanding the biological variability of WMV.

Keywords: melon; *Watermelon mosaic virus*; host range; biological traits; mechanical inoculation

1. Introduction

Watermelon mosaic virus (WMV) which belongs to the genus *Potyvirus* in the family *Potyviridae* is one of the major viruses infecting cucurbit crops, mostly in temperate and Mediterranean climatic regions of the world (Desbiez et al., 2009; Lecoq et al., 2011). WMV causes economically important diseases on several horticultural crops, mostly cucurbits (Sharifi et al., 2008). The virus can also cause severe diseases in legumes and orchids and it infects many weeds that can be alternative hosts (Gara et al., 1997; Desbiez et al., 2009; Lecoq et al., 2011). WMV has a wide host range and it infects more than 170 plant species experimentally (Sharifi et al., 2008).

Melon (*Cucumis melo* L.), which belongs to the Cucurbitaceae family, is one of the most important horticultural crops worldwide (Mascarell-Creus et al., 2009). China is the largest melon-producing country in the world (FAOSTAT, 2014). The Xinjiang Uygur autonomous region which covers an area of 1.66 million km^2 is located in the northwest region of China (Rui et al., 2002). Melon is one of the most economically important crops in Xinjiang and the region is currently the largest area for melon production in China (Xinjiang Statistical Yearbook, 2015). Although WMV is very common worldwide and is associated with significant economic and yield losses of cucurbit crops, little is known about the biological traits of WMV isolates from China. Hence, this study aimed to characterize 11 WMV isolates infecting melon from multiple

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Table 1 Comparison of the percent nucleotide (top and right) and amino acid (bottom and left) identities among the complete coat protein sequences of *Watermelon mosaic virus* isolates %

	JS-1	HY-1	LKQ-1	PZ-1	TYG-1	TP-1	TKS-1	SHZ-1	CJ-1	FK-1	WQ102-1	AJ579524	AJ579483	AF322376	JX028594	JX028595	EF122501	DQ399708	AJ579481	D13913
JS-1	*	95.1	95.5	98.2	96.3	94.6	94.9	98.0	95.2	98.2	98.2	94.6	94.7	94.2	94.5	94.8	94.5	94.2	94.3	93.8
HY-1	99.3	*	96.0	94.9	95.6	97.6	94.8	94.9	98.9	94.9	95.2	93.2	93.5	92.6	98.2	98.4	98.0	97.4	92.7	92.1
LKQ-1	98.9	98.9	*	96.3	98.2	96.5	93.8	96.1	95.9	96.3	96.3	93.5	93.9	92.8	95.2	95.5	95.4	94.8	93.5	92.9
PZ-1	100.0	99.3	98.9	*	97.2	95.2	94.3	99.5	95.1	99.5	99.8	94.2	94.3	93.6	94.3	94.7	94.3	94.1	94.5	93.9
TYG-1	99.3	99.3	98.9	99.3	*	96.1	93.4	96.9	95.5	97.4	97.2	93.8	93.9	93.1	94.8	95.4	95.1	94.5	93.3	92.9
TP-1	99.3	100.0	98.9	99.3	99.3	*	94.6	94.7	97.8	94.9	94.9	93.2	93.8	92.7	97.1	97.2	96.8	96.2	92.1	91.5
TKS-1	97.2	97.2	96.1	97.2	96.5	97.2	*	94.1	95.4	94.3	94.3	92.6	92.9	92.2	94.9	95.1	94.2	94.2	91.6	91.0
SHZ-1	100.0	99.3	98.9	100.0	99.3	99.3	97.2	*	94.8	99.3	99.8	94.0	94.1	93.4	94.1	94.5	94.1	93.9	94.2	93.6
CJ-1	99.3	100.0	98.9	99.3	99.3	100.0	97.2	99.3	*	95.1	95.1	93.3	93.9	92.9	98.4	98.7	98.4	98.0	92.7	92.1
FK-1	99.6	98.9	98.6	99.6	99.6	98.9	96.8	99.6	98.9	*	99.5	94.5	94.6	93.9	94.3	94.7	94.3	94.1	94.8	94.2
WQ102-1	100.0	99.3	98.9	100.0	99.3	99.3	97.2	100.0	99.3	99.6	*	94.2	94.3	93.6	94.3	94.7	94.3	94.1	94.5	93.9
AJ579524	98.6	97.9	97.5	98.6	98.6	97.9	95.8	98.6	97.9	98.9	98.6	*	98.8	97.2	92.8	93.2	92.6	94.8	94.3	93.5
AJ579483	98.6	97.9	97.5	98.6	98.6	97.9	95.8	98.6	97.9	98.9	98.6	100.0	*	97.2	93.4	93.8	93.2	95.4	94.1	93.3
AF322376	97.5	96.8	96.5	97.5	97.5	96.8	94.7	97.5	96.8	97.9	97.5	98.2	98.2	*	92.5	92.8	92.2	94.5	94.2	93.4
JX028594	98.6	98.9	98.2	98.6	98.6	98.9	96.1	98.6	98.9	98.2	98.6	97.2	97.2	96.1	*	98.9	98.1	97.3	92.0	91.4
JX028595	99.3	100.0	98.9	99.3	99.3	100.0	97.2	99.3	100.0	98.9	99.3	97.9	97.9	96.8	98.9	*	98.5	97.6	92.3	91.8
EF122501	97.9	98.6	97.5	97.9	97.9	98.6	95.8	97.9	98.6	97.5	97.9	96.5	96.5	95.4	97.5	98.6	*	97.3	92.0	91.4
DQ399708	98.6	99.3	98.2	98.6	98.6	99.3	96.5	98.6	99.3	98.2	98.6	98.6	98.6	97.5	98.2	99.3	97.9	*	93.9	93.3
AJ579481	97.2	97.2	96.5	97.2	96.8	97.2	95.1	97.2	97.2	97.2	97.2	97.5	97.5	96.5	96.1	97.2	95.8	97.9	*	98.4
D13913	95.8	95.8	95.1	95.8	95.8	95.8	93.6	95.8	95.8	96.1	95.8	96.5	96.5	95.4	94.7	95.8	94.3	96.5	98.2	*

* represents the comparison between itself and itself.

Table 2 Reaction of host plants to *Watermelon mosaic virus* (WMV) isolates from Xinjiang and confirmation of infection by RT-PCR

Family	Plant species	WMV isolate										
		JS-1	HY-1	LKQ-1	PZ-1	TYG-1	TP-1	TKS-1	SHZ-1	CJ-1	FK-1	WQ102-1
Cucurbitaceae	*Cucurbita pepo*	B, LD (+)	M (+)	M, LD (+)	M (+)	M, LD (+)	B, LD (+)	M (+)	M (+)	M (+)	M (+)	M (+)
	Cucumis sativus	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)
	Cucumis melo	M, LD (+)	VC (+)	M, LD (+)	M (+)	M, B, LD (+)	M (+)	B, M (+)	M (+)	M (+)	M (+)	M (+)
	Luffa cylindrica	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)
	Cucurbita moschata	M (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)	0 (+)
Chenopodiaceae	*Chenopodium amaranticolor*	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)
	Chenopodium quinoa	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)	CLL (il+)
Solanaceae	*Datura stramonium*	0 (−)	0 (−)	0 (−)	0 (−)	M (+)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)
	Nicotiana tabacum	M (+)	M (+)	M (+)	M (+)	M (+)	M (+)	M (+)	M (+)	M (+)	M (+)	M (+)
Fabaceae	*Pisum sativum*	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)
	Phaseolus vulgaris	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)
	Vigna unguiculata	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)
	Vicia faba	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)	0 (−)

Note: WMV isolates JS-1, HY-1, LKQ-1, PZ-1, TYG-1, TP-1, TKS-1, SHZ-1, CJ-1, FK-1, and WQ102-1 were obtained from Jiashi County (JS), Huayuan township in Hami City (HY), Lukeqin township in Shanshan County (LKQ), Pizhan township in Shanshan County (PZ), Tuyugou township in Shanshan County (TYG), Turpan City (TP), Toksun County (TKS), Shihezi City (SHZ), Changji City (CJ), Fukang City (FK), and Wujiaqu 102-regiment (WQ102), respectively. M, B, VC, LD, CLL, and 0 indicate mosaic, blistering, vein clearing, leaf deformation, chlorotic local lesion, and symptomless, respectively. In addition, +, –, and il+ represent RT-PCR positive, RT-PCR negative, and inoculated leaf, respectively.

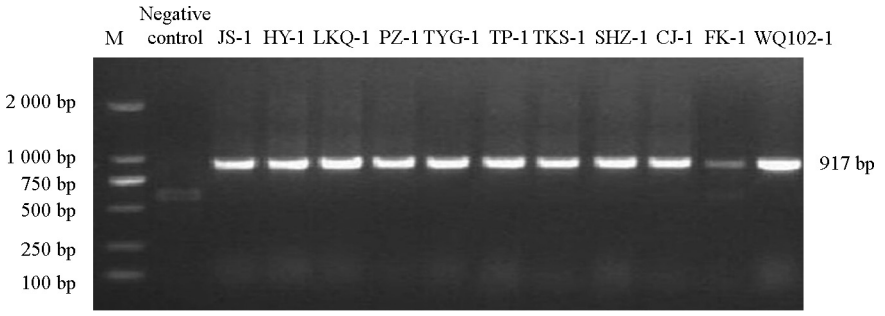

Fig. 1 Electrophoresis pattern of DNA fragments amplified by RT-PCR

WMV isolates JS-1, HY-1, LKQ-1, PZ-1, TYG-1, TP-1, TKS-1, SHZ-1, CJ-1, FK-1, and WQ102-1 were obtained from Jiashi County (JS), Huayuan township in Hami City (HY), Lukeqin township in Shanshan County (LKQ), Pizhan township in Shanshan County (PZ), Tuyugou township in Shanshan County (TYG), Turpan City (TP), Toksun County (TKS), Shihezi City (SHZ), Changji City (CJ), Fukang City (FK), and Wujiaqu 102-regiment (WQ102), respectively.

locations in Xinjiang region of China based on experimental hosts. Our observation that some of WMV isolates tested in this study appeared to induce different symptoms prompted us to generate information on the biological variability of WMV.

2. Materials and methods

2.1. *Virus isolates and biological cloning*

WMV isolates were collected from melon plants growing in 11 major melon-growing locations in Xinjiang during the 2013 and 2014 growing seasons. The eleven locations are Jiashi County (JS), Toksun County (TKS), Turpan City (TP), Shihezi City (SHZ), Changji City (CJ), Fukang City (FK), Wujiaqu 102-regiment (WQ102), Lukeqin township in Shanshan County (LKQ), Tuyugou township in Shanshan County (TYG), Pizhan township in Shanshan County (PZ), and Huayuan township in Hami City (HY).

Melon samples were randomly selected among plants showing virus-like symptoms in every location and WMV positive samples were identified by reverse transcription-polymerase chain reaction (RT-PCR) as described by Coutts et al. (2011). Specific PCR primer pairs WMV-F (5′-GGTTGCTGY GARTCAGTGTC-3′) and WMV-R (5′-CGACCCGAAATGCTAACT-3′) were adopted from a previous publication by Liu and Xiang (2008) for amplification of WMV coat protein (CP) gene. The identities of obtained amplicons were confirmed by sequencing. Sequence identity was calculated using MegAlign program by the DNASTAR Lasergene package (Madison, WI, USA). Multiple sequence alignment was carried out using Clustal X 2.0 (Larkin et al., 2007). Phylogenetic tree was constructed by Neighbor-joining (NJ) method using MEGA 5 (Tamura et al., 2011) and bootstrapped 1000 times to determine the robustness of the groupings.

From melon samples infected with WMV by RT-PCR, 11 specimens were chosen according to geographical origins, and WMV isolates infecting these 11 specimens were biologically cloned by 3 local lesion passages in quinoa (*Chenopodium quinoa*). Such biologically cloned viruses are hereafter called isolates, and after multiplication in zucchini (*Cucurbita pepo*) plants they were used for biological characterization. After multiplication in zucchini plants, the isolates were confirmed by RT-PCR as described above. The isolates were named according to their geographical origins (Table 1).

2.2. *Bioassay and host range test*

The eleven isolates were characterized biologically by reaction to inoculation of a variety of hosts. Thirteen different plant species including *C. melo* 'Queen', *Cucumis sativus* 'Xintai Mici', *Cucurbita moschata* 'Wuman-I', *C. pepo* 'Changqi-I', *Luffa cylindrica* 'Changxiang Sigua', *Datura stramonium*, *Chenopodium amaranticolor*, *C. quinoa*, *Vigna unguiculata* 'Techang Lütiao Jiangdou', *Phaseolus vulgaris* 'Fengshou-I', *Vicia faba* 'Liangfeng Candou', *Pisum sativum* 'Xianshi Wandou', and *Nicotiana tabacum* were selected for host range test by mechanical inoculation.

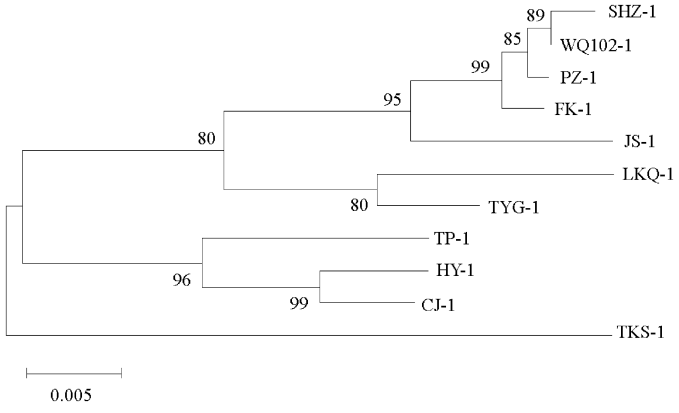

Fig. 2 Neighbor-joining tree

WMV isolates JS-1, HY-1, LKQ-1, PZ-1, TYG-1, TP-1, TKS-1, SHZ-1, CJ-1, FK-1, and WQ102-1 were obtained from Jiashi County (JS), Huayuan township in Hami City (HY), Lukeqin township in Shanshan County (LKQ), Pizhan township in Shanshan County (PZ), Tuyugou township in Shanshan County (TYG), Turpan City (TP), Toksun County (TKS), Shihezi City (SHZ), Changji City (CJ), Fukang City (FK), and Wujiaqu 102-regiment (WQ102), respectively. Tree branches were bootstrapped with 1000 replications. Numbers at nodes indicate bootstrap scores. The scale bar represents a genetic distance of 0.005 for horizontal branch lengths.

For mechanical inoculation, infected zucchini leaves were ground in 10 mmol·L^{-1} sodium phosphate buffer (pH 7.0) containing 10 mmol·L^{-1} sodium sulfite at a ratio of 1:10 (w/v), and the saps were rubbed on the tested plant leaf surfaces that were dusted with carborundum. Healthy control plants were inoculated with buffer only. Bioassay and host range tests were repeated twice with at least 3 plants for each inoculation. Inoculated plants were maintained in an insect-proof, air-conditioned glasshouse at 18–25 °C and observed over 21 days. Infections were confirmed at 3 weeks post-inoculation (wpi) by RT-PCR as described above. Furthermore, a principal component analysis (PCA) was carried out to estimate relationships among variables based on biological responses to WMV isolates of each plant species using SPSS software.

3. Results

3.1. *Virus isolates*

In this study, 11 WMV isolates infecting melon from Xinjiang were obtained (Table 1). After multiplication in zucchini plants, the isolates were confirmed by RT-PCR as described above. As expected, a DNA fragment of approximately 917 bp was amplified from the analyzed isolates (Fig. 1). The identities of obtained amplicons were confirmed by sequencing. Sequence analysis showed that the sequenced region contain the complete CP nucleotide sequences of WMV. Thus, the complete CP nucleotide sequences of the 11 WMV isolates were obtained in this study.

Sequence analysis demonstrated that the complete CP nucleotide sequences of the 11 WMV isolates obtained in this study shared nucleotide identities of 93.4% to 99.8% (96.1% to 100.0% amino acid identities). The full-length CP sequences of the 11 WMV isolates and 9 WMV isolates previously reported from GenBank were 91.0%–98.9% identical at the nucleotide level (93.6%–100.0% identity at the amino acid level) (Table 1). Additionally, phylogenetic tree was constructed using the full-length CP nucleotide sequences of the 11 WMV isolates obtained in this study (Fig. 2).

3.2. *Bioassay and host range test*

Reaction of host plants to WMV isolates obtained in this study is summarized in Table 2. All isolates infected systemically *C. pepo* and *C. melo* plants, causing severe symptoms. The symptoms included mosaic, blistering, vein clearing, and leaf

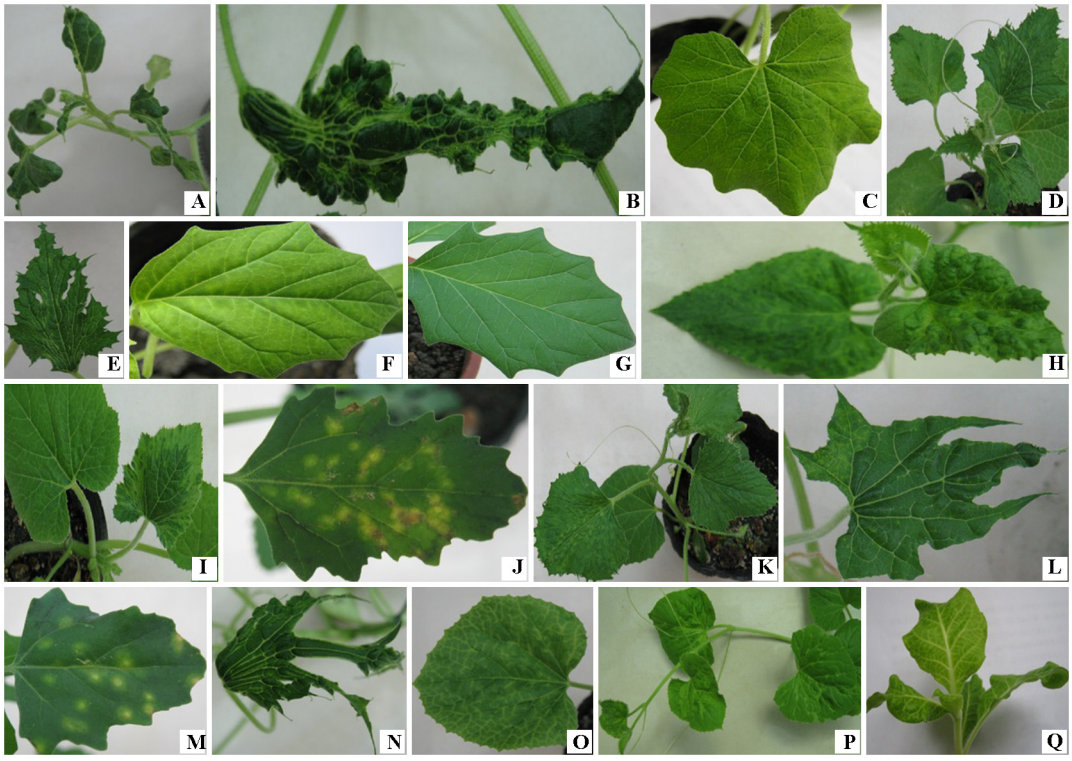

Fig. 3 Symptoms of different hosts inoculated with *Watermelon mosaic virus* isolates from Xinjiang

A: Mosaic and leaf deformation caused by isolate JS-1 in *Cucumis melo*; B: Blistering and leaf deformation caused by isolate JS-1 in *Cucurbita pepo*; C: Mild mosaic in *Cucurbita moschata* infected with isolate JS-1; D: Blistering, mosaic and leaf deformation induced by isolate TYG-1 in *Cucumis melo*; E: Mosaic and leaf deformation induced by isolate TYG-1 in *Cucurbita pepo*; F: Mosaic caused by isolate TYG-1 in *Datura stramonium*; G: Healthy control plant of *Datura stramonium*; H: Blistering and mosaic induced by isolate TKS-1 in *Cucumis melo*; I: Mosaic in *Cucurbita pepo* infected with isolate TKS-1; J: Chlorotic local lesions induced by isolate TKS-1 in *Chenopodium quinoa*; K: Mosaic and leaf deformation induced by isolate LKQ-1 in *Cucumis melo*; L: Mosaic and leaf deformation induced by isolate LKQ-1 in *Cucurbita pepo*; M: Chlorotic local lesions induced by isolate PZ-1 in *Chenopodium quinoa*; N: Blistering and leaf deformation caused by isolate TP-1 in *Cucurbita pepo*; O: Vein clearing caused by isolate HY-1 in *Cucumis melo*; P: Mosaic induced by isolate FK-1 in *Cucumis melo*; Q: Mosaic in *Nicotiana tabacum* infected with isolate CJ-1.

deformation (Table 2). In *C. pepo*, isolates JS-1 and TP-1 caused blistering and leaf deformation (Fig. 3, B,N). Isolates TYG-1 and LKQ-1 caused mosaic and leaf deformation (Fig. 3, E,L). Isolate TKS-1 (Fig. 3, I), HY-1, PZ-1, SHZ-1, CJ-1, FK-1, and WQ102-1 caused mosaic on this plant species. Moreover, in *C. melo*, isolates JS-1 and LKQ-1 caused mosaic and leaf deformation (Fig. 3, A,K). Isolate TYG-1 caused blistering, mosaic and leaf deformation (Fig. 3, D). Isolate TKS-1 caused blistering and mosaic (Fig. 3, H). Isolate HY-1 caused vein clearing (Fig. 3, O). Isolate FK-1 (Fig. 3, P), PZ-1, TP-1, SHZ-1, CJ-1, and WQ102-1 caused mosaic on this plant species.

All isolates did not induce any symptoms on *C. sativus*, but the virus could be detected using RT-PCR. In *D. stramonium*, isolate TYG-1 induced mosaic (Fig. 3, F,G), whereas the remaining 10 isolates did not infect this species. Additionally, all isolates infected systemically *N. tabacum* plants, causing mild mosaics (Fig. 3, Q). *C. quinoa* reacted to all isolates by chlorotic local lesions in the inoculated leaves (Fig. 3, J,M), and the virus was detected in the inoculated leaves using RT-PCR. Moreover, all isolates induced chlorotic local lesions on the inoculated leaves of *C. amaranticolor* and the virus could be detected using RT-PCR. The attempts to transmit the isolates to *L. cylindrica*, *V. faba*, *P. vulgaris*, *V. unguiculata* or *P. sativum* failed as confirmed by negative RT-PCR.

Overall, there were no obvious correlations of host responses to inoculation with WMV isolates from different geographical origins (Table 2). However, isolate JS-1 from the southern region of Xinjiang caused mild mosaic on *C. moschata* (Fig. 3, C), whereas the remaining 10 isolates were asymptomatic on *C. moschata*, but the virus could be detected using RT-PCR. In addition, PCA based on biological responses of plant species to each WMV isolate did not reveal evidence of clustering among isolates from different geographical origins in Xinjiang.

4. Discussion

Biological properties such as host range have been used for the differentiation of strains of viruses (Xiao et al., 1993). In this study, we attempted to determine if there were differences in host responses to inoculation with WMV isolates from different geographical locations in Xinjiang. Sap inoculation of 11 WMV isolates onto a range of 13 plant species revealed differences in symptoms and host range. Overall, there were no obvious correlations of host responses to inoculation with WMV isolates from different geographical locations. However, isolate JS-1 caused mild mosaic on *C. moschata*, whereas the remaining 10 isolates were asymptomatic on this plant species. This may be because location JS is located in the southern region of Xinjiang and it is far away from other locations. Interestingly, *C. sativus* was also a Cucurbitaceae crop which is seriously affected by WMV, but in these results all isolates did not induce any symptoms on this plant species. This may be a consequence of the use of a specific cucumber cultivar in this study. The different reactions of host plants could be due to the resistant or susceptible variety used for disease test (Romay et al., 2014).

Sequence analysis based on the NIb-CP region revealed the existence of 3 distinct WMV molecular groups (Desbiez et al., 2007). From those, isolates of group 1 is predominant and considered to contain the 'classical' isolates (CL isolates). Group 2 isolates represent distinct molecular lineage and originate from different parts of the world. Group 3 isolates were frequently associated with severe symptoms (thus called 'emerging') (EM isolates) and were found in the southeastern part of France (Desbiez et al., 2007, 2009). In addition, the three groups correlated well with one motif at the N-terminal extremity of the CP (Desbiez et al., 2007). Group 1 usually had a 'KEA' motif at positions 3–5 in the CP, while group 2 displayed a 'KET', and group 3 had a 'KEKET' motif at positions 3–7 in the CP (Desbiez et al., 2007). The previous study by Lecoq et al. (2011) showed that *C. quinoa* was systemically infected by CL isolates but not by EM isolates. All CL isolates induced systemic chlorotic spots or mosaic on *C. quinoa* and the virus was detected by ELISA in the young non-inoculated leaves. In contrast, EM isolates produced only chlorotic local lesion in inoculated leaves in this host and the virus was not detected by ELISA in the young non-inoculated leaves which showed no symptoms (Lecoq et al., 2011). Our results showed that all WMV isolates from different geographical origins in Xinjiang induced only chlorotic local lesion in inoculated leaves in *C. quinoa* and the virus was not detected by RT-PCR in the young non-inoculated leaves which showed no symptoms. This indicates that the isolates obtained in this study may possibly belong to group 3. The evidence that the eleven WMV isolates obtained in this study belong to molecular group 3 is also supported by the fact that they code for the amino acid motif KEKET at positions 3–7 in the CP. The KEKET motif has been described by Desbiez et al. (2007) as a characteristic of molecular group 3 isolates. In any case, further phylogenetic analysis based on the NIb-CP region of WMV is needed to confirm this.

Although the host range of 11 isolates tested in this study was similar, biological properties on different hosts revealed some differences compared to the WMV isolates collected from other countries such as France (Lecoq et al., 2011), Iran (Sharifi et al., 2008), Spain (Moreno et al., 2004), Italy (Finetti-Sialer et al., 2012), and Turkey (Kamberoglu et al., 2015). For example, isolate WMV-Le from Italy can induce symptoms (severe mosaic and leaf deformation) on *C. sativus* (Finetti-Sialer et al., 2012). In contrast, all isolates tested in this study did not induce any symptoms on this plant species. Previous studies have shown that severe symptoms were generally observed in cucurbits, especially in *C. pepo* and *C. melo* (Moreno et al., 2004; Sharifi et al., 2008; Lecoq et al., 2011; Finetti-Sialer et al., 2012; Kamberoglu et al., 2015). In support of this we found that all isolates tested in this study induced severe symptoms in *C. melo* and *C. pepo*. In addition, our results showed that all isolates tested in this study did not infect 4 plant species belonging to *Fabaceae*. No infection in *P. sativum* and *P. vulgaris* also has been described for WMV isolates from Iran and Spain (Moreno et al., 2004; Sharifi et al., 2008). These results suggested that in the field, cucurbits, especially *C. pepo* and *C. melo*, are the most important virus source. The comparison made in the present work only reflects reaction of 13 plant species to WMV isolates from Xinjiang; presumably, there are differences in other host plant species. Comparisons involving more host plant species are needed to clarify this. Therefore, further research is needed to understand the reaction of more host plant species to WMV isolates from Xinjiang.

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REFERENCES

Coutts, B.A., Kehoe, M.A., Webster, C.G., Wylie, S.J., Jones, R.A.C., 2011. Indigenous and introduced potyviruses of legumes and *Passiflora* spp. from Australia: biological properties and comparison of coat protein nucleotide sequences. Arch Virol, 156: 1757–1774.

Desbiez, C., Costa, C., Wipf-Scheibel, C., Girard, M., Lecoq, H., 2007. Serological and molecular variability of *Watermelon mosaic virus* (genus *Potyvirus*). Arch Virol, 152: 775–781.

Desbiez, C., Joannon, B., Wipf-Scheibel, C., Chandeysson, C., Lecoq, H., 2009. Emergence of new strains of *Watermelon mosaic virus* in South-eastern France: evidence for limited spread but rapid local population shift. Virus Res, 141: 201–208.

FAOSTAT, 2014. The FAO Statistical Database (FAOSTAT). Food and Agriculture Organization of the United Nations. http://faostat3.fao.org. (Accessed 15 July 2016).

Finetti-Sialer, M.M., Mascia, T., Cillo, F., Vovlas, C., Gallitelli, D., 2012. Biological and molecular characterization of a recombinant isolate of *Watermelon mosaic virus* associated with a watermelon necrotic disease in Italy. Eur J Plant Pathol, 132: 317–322.

Gara, I.W., Kondo, H., Maeda, T., Inouye, N., Tamada, T., 1997. Stunt disease of *Habenaria radiata* caused by a strain of *Watermelon mosaic virus* 2. Ann Phytopathol Soc Jpn, 63: 113–117.

Kamberoglu, M.A., Desbiez, C., Caliskan, A.F., 2015. Characterization of an emerging isolate of *Watermelon mosaic virus* in Turkey. Int J Agric Biol, 17: 211–215.

Larkin, M.A., Blackshields, G., Brown, N.P., Chenna, R., McGettigan, P.A., McWilliam, H., 2007. Clustal W and Clustal X version 2.0. Bioinformatics, 23: 2947–2948.

Lecoq, H., Fabre, F., Joannon, B., Wipf-Scheibel, C., Chandeysson, C., Schoeny, A., Desbiez, C., 2011. Search for factors involved in the rapid shift in *Watermelon mosaic virus* (WMV) populations in South-eastern France. Virus Res, 159: 115–123.

Liu, W.R., Xiang, B.C., 2008. Nucleotide sequence analysis of coat protein gene of *Watermelon mosaic virus 2* Xinjiang Changji isolates. Acta Phytopathol Sin, 38: 576–581. (in Chinese)

Mascarell-Creus, A., Cañizares, J., Vilarrasa-Blasi, J., Mora-García, S., Blanca, J., Gonzalez-Ibeas, D., Saladié, M., Roig, C., Deleu, W., Picó-Silvent, B., López-Bigas, N., Aranda, M.A., Garcia-Mas, J., Nuez, F., Puigdomènech, P., Caño-Delgado, A.I., 2009. An oligo-based microarray offers novel transcriptomic approaches for the analysis of pathogen resistance and fruit quality traits in melon (*Cucumis melo* L.). BMC Genomics, 10: 467.

Moreno, I.M., Malpica, J.M., Díaz-Pendćn, J.A., Moriones, E., Fraile, A., García-Arenala, F., 2004. Variability and genetic structure of the population of *Watermelon mosaic virus* infecting melon in Spain. Virology, 318: 451–460.

Romay, G., Lecoq, H., Geraud-Pouey, F., Chirinos, D.T., Desbiez, C., 2014. Current status of cucurbit viruses in Venezuela and characterization of Venezuelan isolates of *Zucchini yellow mosaic virus*. Plant Pathol, 63: 78–87.

Rui, Z.Y., Goldfarb, R.J., Qiu, Y.M., Zhou, T.H., Chen, R.Y., Pirajno, F., Yun, G., 2002. Paleozoic–early Mesozoic gold deposits of the Xinjiang Autonomous Region, northwestern China. Mineral Deposita, 37: 393–418.

Sharifi, M., Massumi, H., Heydarnejad, J., Hosseini Pour, A., Shaabanian, M., Rahimian, H., 2008. Analysis of the biological and molecular variability of *Watermelon mosaic virus* isolates from Iran. Virus Genes, 37: 304–313.

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S., 2011. MEGA 5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol Biol Evol, 28: 2731–2739.

Xiao, X.W., Frenkel, M.J., Teakle, D.S., Ward, C.W., Shukla, D.D., 1993. Sequence diversity in the surface-exposed amino-terminal region of the coat proteins of seven strains of *Sugarcane mosaic virus* correlates with their host range. Arch Virol, 132: 399–408.

Xinjiang Statistical Yearbook, 2015. Statistic Bureau of Xinjiang Uygur Autonomous Region. http://www.xjtj.gov.cn/sjcx/tjnj_3415/.