

Electronic Supplementary Material

Re-isolation of Wuxiang Virus from Wild Sandflies Collected from Yangquan County, China

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Table S1 Primers used for the sequencing of WUXV genes

Primers	Amplified fragment	Sequence information 5'-3'	Amplified fragment (bp)
L1-9F	L	GCGCCTGTACATCATGAATTC	315
L1-323R		CTCCTTTTCCCGAAGACACTG	
※W2L2-172F	L	GAGCACTTTGACGTGGGCTC	833
※W2L2-1004R		GCAGGGACTTGTACTGTGCT	
※W2L3-857F	L	TCGCTGGAGCTATGGAGGAT	834
※W2L3-1690R		TTGAGCAGGTGGGCTTGATT	
※W2L4-1473F	L	CCACCAGCCCCTCTAATCAA	923
※W2L4-2395R		ACTCGTCACTTTCTGGCCTC	
※W1L5-2057F	L	TGTCACAGCCAGAAGTACCA	600
※W1L5-2656R		GCCTGTCCCTGGAATACGAC	
※W1L6-2369F	L	AGGACCAGAGGCCAGAAAGT	703
※W1L6-3071R		GGGTGCCATCTAGGATGTGT	
※W1L7-2855F	L	CCAGATCTGTGGGTCGGTTC	809
※W1L7-3633R		CACCTCAGGCAAACCTGCAAC	
※W1L8-3259F	L	ACCACTGGGATGATGCAAGG	796
※W1L8-4054R		TCAGTACTATCGCCCCACCA	
※W1L9-3837F	L	GAGATGGAGGGATCCAGGAC	885
※W1L9-4721R		AACGGGCTCCTTTGAAGAGT	
※W1L10-4521F	L	AGAGGCCACACAGACTAGGA	625
※W1L10-5145R		AAACCCACCCACTATGCCAG	
※W1L11-5002F	L	TTCGACACTCCTGCAATAGACA	715
※W1L11-5716R		CCTTGCACTAGACCCAGCAA	
※W1L12-5519F	L	AGCTCCTTGTCAACAGATCCA	857
※W1L12-6375R		ACATTTGTGCTGCAAAGGGG	
L9-6134F	L	GAGATGTCAGGAACTTATTGG	265
L9-6398R		TAGCCCATGGGACTAAGCTATACA	
M1-9F	M	CTGGTGCATTAATGTTTGA	185
M1-193R		GGCATCTTAGCCATCTCGTA	
※w1M2(1)-60F	M	TGACGTTCGTCTGGACTCATC	306
※w1M2(1)-366R		GAGTGCTCCAGCCATCATGT	
※w1M2(2)-217F	M	AAGTTCATGACAGCAGAGAACG	442
※w1M2(2)-659R		TGCTTTTCAACCTCCTGCTTCT	
M3-523F	M	GTAGCCGTCAGTTAGAAGAG	938
M3-1460R		CATCGGTCCATTATAGTCAG	
※w2M4-1246F	M	CCCAGAGGAGTGCCCTCAAT	525
※w2M4-1770R		TTCACTGTGCAAGCGTACT	
※w1M5-1431F	M	TGGGCCGATGGAGATTCCCTA	566
※w1M5-1996R		TGGCAGCTGATATCTTGAATCC	
M6-1865F	M	ACCCAGTGTGTGGGATTTG	958
M6-2822R		CACTCCGTATTGGGTGGTCC	

※w2M7-2643F	M	GGTGTGGTCAACGTGAAAGC	994
※w2M7-3636R		TTCTAGCACCCCTCGTTGCAG	
M8-3507F	M	ACAGTGCAAGCCCTAACCTC	574
M8-4080R		TGACCATCCCCTGACTCTA	
M9-3920F	M	CAAGGCTGGAGACTGGAGTTTATGGA	403
M9-4322R		TTGAGTTGCGAATGACACAAAGACCG	
S1-1F	S	ACACAAAGTCCCCCTAGTAAAG	458
S1-458R		GAGACATCCTCTCTTGCATCTT	
※w3S2-356F	S	GGCCTTTTGGATTCCCTGACT	652
※w3S2-1007R		CTGCTGCTATCAACAGCTCCT	
S3-875F	S	AGCCCTCATCCCACCCCAATTTATGG	336
S3-1210R		CCTAGCTTTGCTGGTCTGATTGATCC	
※w1S4-916F	S	GCTAGCCCTAGCACTGGATG	517
※w1S4-1432R		GGCCTTGACTCGAGGAAACA	
S5-1333F	S	CTCTTGTCAGTGTTAGCCCGTTCC	199
S5-1531R		AACCTGATTAAGTTAGGCGGAAGT	
S6-1441F	S	TCTTCTTTGGCTTGTTACCTC	247
S6-1687R		AGCTCCCTAGTACGTTCTTGA	

Note: L, M and S represent the L, M and S gene segments of WUXV, respectively; we redesigned the primers that did not produce amplification products, the redesigned primers are labelled with “※”.

Table S2 The homology analysis of nucleotide (amino acid) sequence of *GP* gene of *M* gene of WUXV

NO	Strain	Strain			
		1	2	3	4
1	SXYQ1916	***	96.8	97.5	97.0
2	SXYQ1927-2	98.3	***	98.7	99.2
3	SXYQ1930	98.5	98.8	***	98.8
4	SXYQ1931	98.2	99.2	98.7	***

Note: The upper right side of *** is the homology analysis of the nucleotide sequence in the coding region; The lower left side of *** is the homology comparison of amino acid sequence in the coding region.

Table S3 The homology analysis of nucleotide (amino acid) sequence of *NS* gene of WUXV

NO	Strain	Strain			
		1	2	3	4
1	SXYQ1916	***	98.3	98.3	98.3
2	SXYQ1927-2	98.9	***	99.5	99.5
3	SXYQ1930	98.5	99.2	***	99.5
4	SXYQ1931	98.5	99.2	98.9	***

Note: The upper right side of *** is the homology analysis of the nucleotide sequence in the coding region; The lower left side of *** is the homology comparison of amino acid sequence in the coding region.

Table S4 The homology analysis of nucleotide (amino acid) sequence of *N* gene of WUXV

NO	Strain	Strain			
		1	2	3	4
1	SXYQ1916	***	98.8	98.8	98.2
2	SXYQ1927-2	98.8	***	99.2	98.9
3	SXYQ1930	99.6	98.8	***	98.8
4	SXYQ1931	98.8	98.8	98.8	***

Note: The upper right side of *** is the homology analysis of the nucleotide sequence in the coding region; The lower left side of *** is the homology comparison of amino acid sequence in the coding region.