

Table S1. Summary of raw reads obtained through High-throughput Sequencing of diseased tuberose samples and trimming statistics

Sample	Input Reads	Average length	No. of read after Trimming	Percentage trimmed (%)	Average length after trim
Mexican single	53,374,692	75.48	53,370,490	99.99	75.47
Hyderabad single	37,005,916	75.45	37,000,244	99.98	75.44

Table S2. Putative genes along with nine protease cleavage sites in polyprotein of TuMMV.

Region	Start-End site	Size in nt/aa	Cleavage site (C-Terminus)
5'UTR	1-138	138/-	
P1	139-1032	894/298	Y/S
HC-Pro	1033-2406	1374/458	G/G
P3	2407-3435	1029/343	Q/I
6K1	3436-3591	156/52	Q/S
CI	3592-5499	1908/636	Q/A
6K2	5500- 5661	162/54	Q/G
VPg	5662- 6237	576/192	E/S
NIa-Pro	6238-6966	729/243	Q/G
NIb	6967-8532	1566/522	Q/S
CP	8533-9351	819/273	-
3'-UTR	9352-9485	134/-	-

Table S3. Putative genes along with nine protease cleavage sites in polyprotein of TuMMoV.

Region	Start-End site	Size in nt/aa	Cleavage site (C-Terminus)
5'UTR	1-164	164/-	
P1	165-1061	897/299	Y/S
HC-Pro	1062-2435	1374/458	G/G
P3	2436-3464	1029/343	Q/A
6K1	3465-3620	156/52	Q/S
CI	3621-5528	1908/636	Q/S
6K2	5528-5687	159/53	Q/G
VPg	5688-6263	576/192	E/S
NIa-Pro	6264-6992	729/243	Q/S
NIb	6993-8555	1563/521	Q/S
CP	8556-9409	855/285	-
3'-UTR	9410-9462	53/-	-

Table S4: List of virus-specific primers designed from the coat protein (CP) region of the obtained viral genomes.

	Primer Sequence	Product Length
TuMMV	F: 5'-AAGATGATGTCAACAATGCA-3' R: 5'-TTACGCACTCCCAACAAAG-3'	~700 bp
TuMMoV	F: 5'-TCCGTAGGTGAACCTGCGG-3' R: 5'-TCCTCCGCTTATTGATATGC-3'	~700 bp

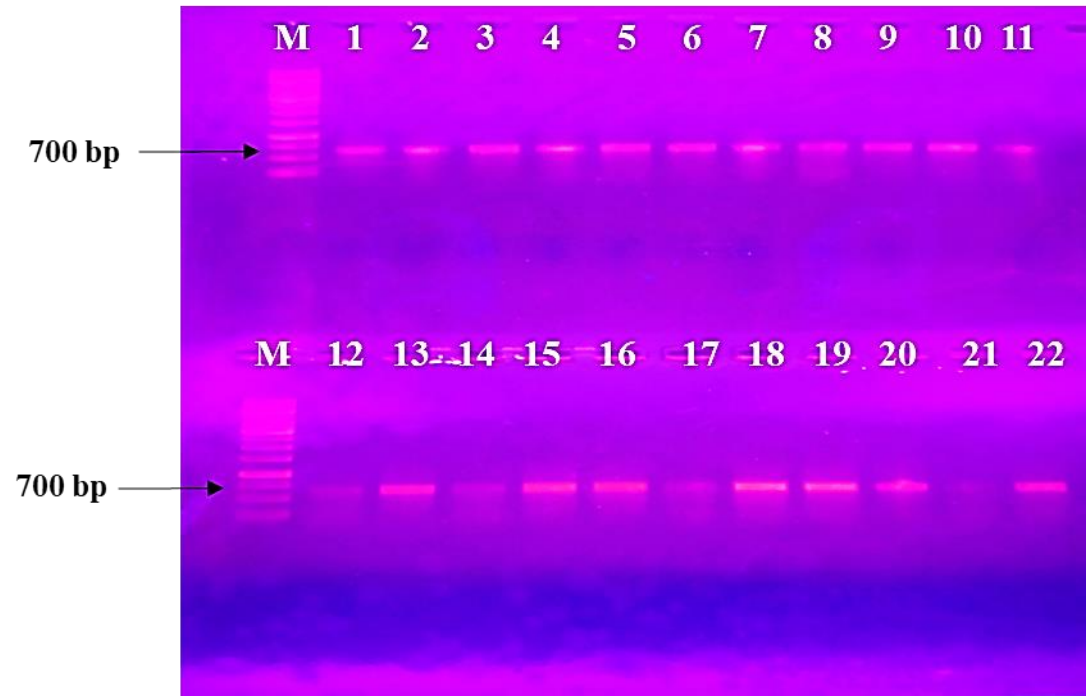


Figure S1. PCR detection of TuMMV and TuMMoV. Expected amplicon size was ~700 bp. Lane M, 1 kb DNA ladder (Cat. No. SM0311; Thermo Scientific); Lanes 2, 3, 4, 5, 6, 7, 8, 9, 10 and 11, PCR amplified products of TuMMV; Lane 12, 13, 14, 15, 16, 17, 18, 19, 20, 21 and 22, PCR amplified products of TuMMoV.