In silico analysis of *Tomato Leaf Curl New Delhi Virus*

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Abstract

Tomato leaf curl New Delhi virus (ToLCNDV) belongs to genus *Begomovirus* (family Geminiviridae), with bipartite genome consisting of two components i.e. DNA A and DNA B. It causes infection and almost complete yield loss in species of many plant families including *Cucurbitaceae* and *Solanaceae* and cotton crops as well. In this study, available full-length sequences of both components of ToLCNDV (DNA A: 133 and DNA B: 115) were retrieved from GenBank, NCBI (updated upto 21st June, 17) for *In-silico* analysis. Pairwise sequence identity of DNA A isolates was obtained by MUSCLE Alignment in SDTv1.2 software in three output forms: i). Graph plot showed that most of the isolates shared identity above 91% as being isolates of ToLCNDV, with highest peak around 94%. ii). Color-encoded matrix showed 5 isolates near the threshold value 91%. iii). Sequence identity score confirmed ToLCNDV2-[IN:IANDS1:11] JQ897969, ToLCNDV3-[IN:Bij:Chi:12] KC465466, ToLCNDV4- [IN:Jun:TC306:11] KF551592 and ToLCNDV-[BD:Cuc:06] EF450316 as outliers that shared identity below 91%, thus, confirming that they were not isolates of ToLCNDV anymore. Alignment of all isolates was done by MUSCLE and Phylogenetic tree (maximum-likelihood) was generated using MEGA6 software which prominently showed the outliers of the study. The analysis revealed massive spread of virus in Asian Continent and its recent outbreak in some European countries i.e. Spain.

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Syeda Wajeeha Gillani

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List of Abbreviations

African Cassava Mosaic Virus:	ACMV
Amino acids:	aa
Approximately:	Approx./ ~
Artificial Micro RNAs:	amiRNAs/ amiRs
Bangladesh:	BD
Base pairs:	bp
Chili Leaf Curl Betasatellite:	ChLCB
Chili Leaf Curl Virus:	ChLCV
Coat Protein:	CP
Complementary DNA:	cDNA
Cotton Leaf Curl Disease:	CLCuD
Cotton Leaf Curl Virus:	CLCuV
Cotton Leaf Curl Kokhran Virus:	CLCuKoV
Cotton Leaf Curl Multan Betasatellite:	CLCuMB
Cucumber Mosaic Virus:	CMV
Cultivar:	cv
Days after Inoculation:	DAI
Days Post-Inoculation:	DPI
Deoxythymine:	dT
Double stranded DNA:	dsDNA
Double Antibody Sandwich ELISA:	DAS-ELISA
Electrophoretic Mobility Shift Assay:	EMSA
Enzyme-linked immunosorbent assay:	ELISA
Expressed Sequence Tags:	ESTs
Glutathione S-transferase:	GST

Green Florescent Protein:	GFP
Hypersensitive Response:	HR
India:	IN
Indian Cassava Mosaic Virus:	ICMV
Indian Tomato Leaf Curl Virus:	ITLCV
Indonesia:	ID
Intergenic Region:	IR
Inter Simple Sequence Repeat:	ISSR
International Committee on Taxonomy of Viruses:	ICTV
Iran:	IR
Ludwigia Leaf Distortion Betasatellite:	LuLDB
Maximum Likelihood:	ML
Mediterranean-Q1:	MED-Q1
Micro RNA:	miRNA
Mitochondrial cytochrome oxidase I:	MTCOI
Monoclonal Antibody:	mAb
Movement Protein:	MP
Multan:	Mul
National Center for Biotechnology Information:	NCBI
Next Generation Sequencing:	NGS
Non-radioactive Nucleic Acids Spot Hybridization:	NASH
Nuclear Shuttle Protein:	NSP
Nucleotide-binding site leucine-rich repeat:	NBS-LRR
Open Reading Frames:	ORFs
Origin of Replication:	*ori*
Papaya Ringspot Virus:	PRSV
Pakistan:	PK

Pepper Huasteco Yellow Vein Virus:	PHYVV
Pepper Leaf Curl Bangladesh Virus:	PLCBV
Pepper Leaf Curl Lahore Virus:	PepLCLV
Percentage:	%
Polymerase Chain Reaction:	PCR
Potato Virus X:	PVX
Potato Virus Y:	PVY
Potato Yellow Mosaic Virus:	PYMV
Print Capture PCR:	PC-PCR
Quantitative Real Time PCR:	qPCR/ qRT-PCR
Reactive Oxygen Species:	ROS
Reverse Transcriptase PCR:	RT-PCR
Replication Associated Gene:	Rep Gene
RNA Interference:	RNAi
RNA Polymerase-II:	RNA Pol-II
Rolling Circle Amplification:	RCA
Satellite conserved region:	SCR
Sequence-related Amplified Polymorphism:	SRAP
Single-chain fragment variable:	scFv
Single stranded DNA:	ssDNA
Small interfering RNA:	siRNA
Small RNA:	sRNA
Solanum lycopersicum-26S proteasomal subunit RPT4a:	SlRPT4
Spain:	ES
Specie Demarcation Tool:	SDT
Squash Leaf Curl Virus:	SLCV
Surface Plasmon Resonance Spectroscopy:	SPR Spectroscopy

Taiwan:	TW
Thailand:	TH
Tomato Leaf Curl Joydebpur Virus-Mild:	ToLCJV-Mld
Tomato Leaf Curl New Delhi Virus:	ToLCNDV
Tomato Leaf Curl Palampur Virus:	ToLCPMV
Tomato Leaf Curl Sudan Virus:	ToLCSV
Tomato Leaf Curl Virus:	ToLCV
Tomato Leaf Curl Virus-India:	ToLCV-IN
Tomato Leaf Curl Virus-New Delhi:	ToLCV-NDe
Tomato yellow leaf curl virus:	TYLCV
Tomato yellow leaf curl Sardinia virus:	TYLCSV
Transcriptional Activator Protein:	TrAP
Watermelon Cholorotic Stunt Virus:	WmCSV
Whitefly-Transmitted Geminiviruses:	WTGs
Zucchini Yellow Mosaic Virus:	ZYMV

Chapter 1

INTRODUCTION

1.1 Family *Geminiviridae*

The family *Geminiviridae* contains plant-infecting viruses of approx. 2.7–5.2 kb single-stranded and circular DNA (ssDNA) genome that is encapsidated in virions (composed of 22 pentameric capsomeres), making an ~18 to 30 nm twinned icosahedral shape (Bottcher *et al*., 2004; Ha *et al*., 2008; Varsani *et al*., 2017). It is distributed nearly worldwide and causes infection in both kind of plants i.e., dicots and monocots. In economically significant crops such as cotton, tomato, maize, cassava and chickpea, it leads towards severe yield loss (Moffat, 1999; Varsani *et al*., 2017). Geminivirus infection induces symptoms including curling, stunting, mosaic, yellowing, foliar crinkling, and/or striations (Varsani *et al*., 2017).

In accordance of factors introduced by ICTV i.e. transmission by vector, host range, genome-wide pairwise identities of sequences and organization of genome, it is distributed into seven genera: Turncurtovirus, Topocuvirus, Eragrovirus, Becurtovirus, Curtovirus, Mastrevirus and Begomovirus (Varsani *et al*., 2014; Kumar *et al*., 2015; Varsani *et al*., 2017).

1.1.1 Genus *Begomovirus*

Currently in plant viruses, begomovirus is considered as the largest genus with 288 species identified by ICTV (Brown *et al*., 2015). Begomoviruses are widely spread in nature and are transferred through the vector *Bemisia tabaci* (an arthropod).

Furthermore, they are classified as monopartite or bipartite having a DNA-A like or both DNA-A and DNA-B like components, respectively with genome size of each component about 2.5–2.7 kb (Brown *et al*., 2012; Fortes *et al*., 2016). Most of the reported begomoviruses from the ‘Old World’ are monopartite while those from the ‘New World’ are bipartite in majority (Nawaz-ul- Rehman & Fauquet, 2009; Melgarejo *et al.*, 2013; Kumar *et al.,* 2015).

1.1.1.1 Genome Organization of *Begomovirus*

DNA-A, in general, encodes six ORFs that are generally important for encapsidation, replication of virus and transcription activation. CP of bipartite begomovirus is not needed for intercellular movement because DNA-B encoded proteins i.e. MP (movement protein) and NSP (nuclear shuttle protein) help in nucleocytoplasmic and cell-to-cell viral genome trafficking. Additionally, in monopartite begomoviruses, two proteins, C4 and V1, encoded by the DNA-A like constituent control the general intracellular and intercellular movement and also carries out other functions i.e. pathogenesis and replication (Jupin *et al.,* 1994; Rojas *et al.*, 2001; Stanley *et al.*, 2005, Saeed *et al.*, 2007; Hanley-Bowdoin *et al.*, 2013; Kumar *et al.,* 2015). For transfer of virus through host plants, five encoded proteins mainly work: NSP, CP, MP, C4 and V1 proteins (Rojas *et al.*, 2005).

The ORFs of both components are present in the form of two opposite clusters separated by a conserved sequences-containing region namely common region (CR). It contains a conserved *ori* sequence that is a hairpin-shaped structure consisting of a nonanucleotide sequence (TAATATTAC) in the loop and iteron (Rep-binding) sequences situated upstream. Similar iteron sequences among DNA-A and –B ensure binding between Rep sequences of both components (Rojas *et al.*, 2005; Jyothsna *et al.*, 2013).

1.1.1.1.1 Alphasatellites and Betasatellites

Reportedly, begomoviruses are associated with single-stranded (ssDNA), satellite-like and/or satellite molecules called as **alphasatellites** and **betasatellites**, respectively (Mansoor *et al.*, 1999; Saunders *et al.*, 2000; Nawaz-ul-Rehman & Fauquet, 2009; Kumar *et al.,* 2015). Most of the monopartite begomoviruses of the ‘Old World’ co-exist along with **betasatellites**. Usually, betasatellites consists of a βC1 ORF, SCR (satellite conserved region) and an adenine-rich region. The βC1 ORF has been distinguished as a pathogenicity determinant that plays a role in virus movement and causes suppression of host's anti-viral silencing (Saunders *et al*., 2004; Cui *et al*., 2005; Li *et al*., 2014; Yang *et al*., 2011).

A group of self-replicating satellite-like components namely **alphasatellites**, need helper begomoviruses for their inter- and intra-cellular movement, and in some cases, they are also reported to enhance symptoms (Idris *et al*., 2011; Nawaz-ul-Rehman *et al*., 2010).

1.1.1.2 *Tomato Leaf Curl New Delhi Virus* (ToLCNDV)

It was initially named as tomato leaf curl geminivirus from India (ToLCV-India) or Indian-ToLCV. Its two isolates were firstly sequenced in 1995 (Padidam *et al*., 1995). It is a bipartite begomovirus which is economically-important and causes infection and almost complete yield loss in species of many plant families including *Cucurbitaceae* (Cucumber, melon, luffa and pumpkin etc.) and *Solanaceae* (Tomato, chili pepper, potato and egg plant etc.), and as well as in cotton crops in Pakistan. For causing systemic infection, it needs both of its DNA constituents (Padidam *et al*., 1995, Padidam *et al*., 1996; Sohrab *et al*., 2003; Mizutani *et al*., 2011; Pratap *et al*., 2011; Zaidi *et al*., 2016a).

1.1.1.2.1 Symptoms

It causes potential damages and almost complete yield loss in tomato plants by inducing stunting, curling of leaves (both upward and downward), vein clearing, interveinal yellowing and crinkling (Chakraborty, 2008; Fortes *et al*., 2016).

It is highly prevalent in the northern areas of India and a major cause of tomato yield loss. It was reported limited to Asian countries only till 2012, as it was then identified in southern Spain (western Mediterranean Basin) inducing infectivity in cucumber, zucchini squash and melon species. Furthermore, it has also been reported in Italy and Tunisia, causing infectivity in cucurbits (Juarez *et al*., 2014; Fortes *et al*., 2016).

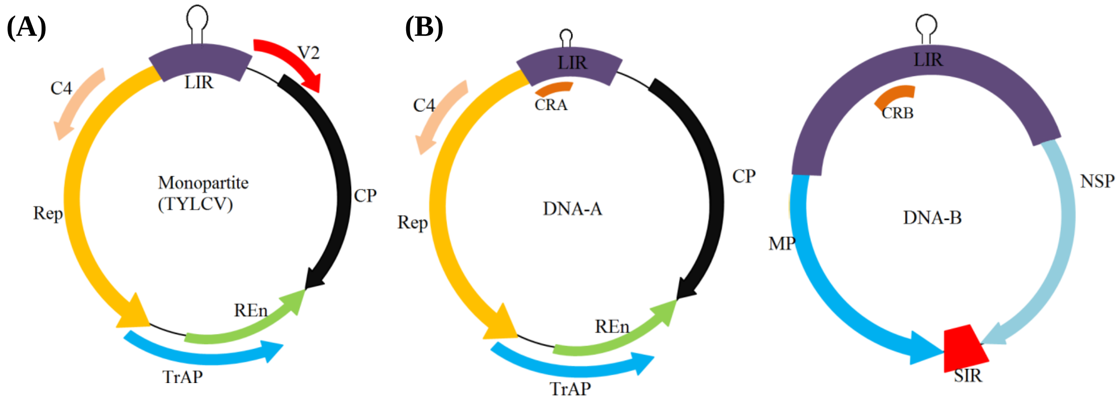

Figure 1.1 Organization of genome in the components of genus *Begomovirus* belonging to family *Geminiviridae*. (A) Monopartitie genome. (B) Bipartite Genome i.e. DNA-A and DNA-B

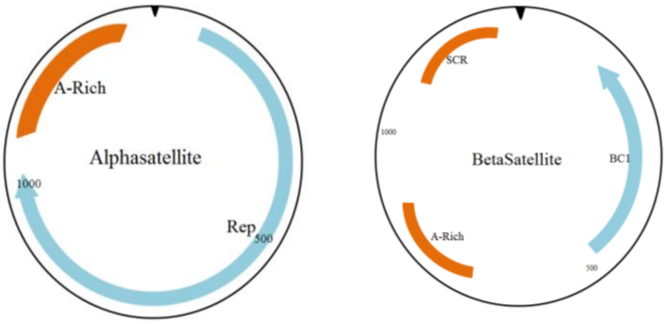

Figure 1.2 Genome organization of Alphasatellites and Betasatellites: Arrows represent ORFs (open reading frames). SCR: satellite-conserved region, A-rich: Adenosine-rich region, βC1: the gene that encodes betaC1 protein.

Figure 1.3 Upward Leaf Curling symptom induced by ToLCNDV in Cucumber (https://gd.eppo.int/taxon/TOLCND/photos; last accessed: 17th Aug, 17)

1.2 Importance of Study

ToLCNDV is a bipartite begomovirus which is economically-important and with the help of whiteflies acting as its vectors, it causes infectivity in species of many plant families including *Cucurbitaceae* (Cucumber, melon, luffa and pumpkin etc.) and *Solanaceae* (Tomato, chili pepper, potato and egg plant etc.), as well as in cotton crops in Pakistan (Pratap *et al*., 2011; Zaidi *et al*., 2016a). It causes almost complete yield loss in tomato plants by inducing symptoms such as stunting, curling of leaves etc (Fortes *et al*., 2016). For causing systemic infection, it needs both of its DNA constituents.

Present study includes the *in silico* analysis of all the ToLCNDV components. As, the measure of ToLCNDV infectivity and spread can help to overcome economical losses caused by it. Therefore, latest history of ToLCNDV spread was obtained using its all available sequences.

1.3 Aims and Objectives

Objectives of my study are:

- Analysis of DNA-A component of ToLCNDV
- Analysis of DNA-B component of ToLCNDV

Chapter 2

LITERATURE REVIEW

Figas *et al*. (2017) mechanically did sap inoculation in a susceptible type of zucchini and checked the infection rate of ToLCNDV inocula that was made with the help of three various buffers. It was then observed that buffer III (polyvinylpyrrolidone) containing inoculum was the most efficient one, displaying severe symptoms in 100% plants after 21 days of infection. 19 commercial cucurbit plants were inoculated mechanically by using this buffer and 9 various detection methods for ToLCNDV were used to diagnose infectivity and estimate the symptoms evolution. The results exhibited that among melon, zucchini and cucumber varieties, latter ones showed a lesser amount of severe symptoms, however, all varieties appeared susceptible. In zucchini and melon, all methods of detection worked efficiently, however, while using molecular hybridization and serology methods in cucumber, positive plants percentage ranged from 20.4% with SLCV antiserum, to 78.5% by DNA extract hybridization. However, PCR gave the best detection results with 92.4%, 98.4% and 92.6% melon, zucchini and cucumber tested as positive, respectively. Using WmCSV antiserum and DNA extract gave the best molecular hybridization and serology results overall.

Janssen *et al*. (2017) collected 35 populations of whiteflies from various crops of southern Spain regions to investigate if whitefly species (new in Mediterranean) were involved in the tomato leaf curl New Delhi virus (ToLCNDV) spread, as it had recently pervaded in Italy, Tunisia and Spain. After comparison of sequences of partial MTCOI (mitochondrial cytochrome oxidase I) from obtained whiteflies, 7 dissimilar haplotypes were assumed to be a part of enigmatic Mediterranean-Q1 species. It was, hence, concluded that in the ongoing increase of ToLCNDV in Spain, MED-Q1 was also involved.

Ruiz *et al*. (2017) investigated that betasatellite DNA was absent in ToLCNDV infected samples of zucchini squash and tomato collected from Spain, whereas, DNA-A and DNA-B that were inoculated through agro-infiltration were enough to recreate symptoms in both crops. Those infected crop samples being source of inoculum, helped in efficient transfer of virus by either using whiteflies or by mechanical method. Various crops were easily infected by virulent whiteflies and they exhibited symptoms right after 8–15 days of inoculation. A great genetic homogeneity (sequence identity: >99%) of new complete sequences from both crops i.e. zucchini squash and tomato was seen in ToLCNDV population in Spain indicating towards the current introduction incident.

Jeevaltha *et al*. (2017) did microarray analysis to distinguish regulatory genes that work differently among susceptible (Kufri Pukhraj) and resistant cultivar (Kufri Bahar) during infection by ToLCNDV-[Pot]. After mechanical inoculation, symptoms in Kufri-Pukhraj started to appear and gotten severe after 15 days of inoculation whereas, in Kufri-Bahar very mild or no proper symptoms were observed upto 35 days of infection. qPCR essay showed massive viral load and very minute viral load in Kufri-Pukhraj and Kufri-Bahar, respectively. Microarray analysis of Kufri-Bahar and Kufri-Pukhraj exhibited that during infection, a total number of 1111 and 2588 genes were regulated (|log2 (Fold Change)|>2) differently in them, respectively. Involvement of these altered transcripts in numerous processes i.e. biological and metabolic was diagnosed by mapman analyses and gene ontology. Expression of various genes having unidentified increased upto 5 to 10 fold after infection as well.

Zaidi *et al.* (2016) discussed in his study that ToLCNDV was exceptional bipartite Old World begomovirus that extensively spread in geographical range of Indian continent and also extended towards Far East, where satellite-associated DNA begomoviruses (monopartite) were only dominant to narrow ranges. Due to highly flexible arrangement of genome and extensive host range, ToLCNDV was prevailing: DNA-A trans-replicated, and productively cooperated with betasatellites and DNA-B constituents. By knowing the capability of ToLCNDV to cause infection, severe economic threats could also be enlightened. Therefore, history of ToLCNDV emergence and spread was reconstructed using its all present sequences.

Alfaro-Fernandez *et al.* (2016) analyzed PCR, NASH technique (Non-radioactive Nucleic Acids Spot Hybridization) and two protocols of nucleic acid extraction all together for diagnosing ToLCNDV and distinguishing it from its closely associated viruses i.e. *Tomato yellow leaf curl virus* (TYLCV) and *Tomato yellow leaf curl Sardinia virus* (TYLCSV). For PCR technique, only DNA extraction and for NASH technique, extraction of nucleic acid using silica proved to be best protocols as they allowed the precise ToLCNDV detection. Some general primers of begomoviruses detected all of the three viruses. When replicase- and coat protein gene-targeting two riboprobes of ToLCNDV were examined by NASH, no cross-reaction of ToLCNDV was diagnosed with the TYLCSV and TYLCV, getting a better limit of detection with the replicase riboprobe. Analysis of field samples i.e. 42 in number, a good-quality correlation between NASH and PCR was revealed and their use for general diagnosis of ToLCNDV was considered.

Yazdani-Khameneh *et al.* (2016) described that after field survey in Iran during 2012-2014, total 787 virus-containing samples of leaves from vegetables and other additional host-plants were collected. Those were examined by performing ELISA (enzyme-linked immunosorbent assay) in which polyclonal antibodies that were formed against TYLCV, were used. 81 samples (10.3%), in accordance of ELISA results, reacted positively with virus antibodies. By using pair of universal primers Begomo-F and Begomo-R or TYLCV-specific primers TYLCV-Sar and TYLCV-Isr in PCR, infection of begomovirus was confirmed. From tested samples (tomato, spinach, pepper and alfalfa plants), samples that were ELISA-positive, expected fragments of size *ca*. 0.67-kb were amplified while performing PCR test by primers TYLCV-Sar and TYLCV-Isr, validating TYLCV presence. Nucleotide sequences of Kz-Me198 (isolate) derived DNA amplicons were obtained and then their comparison was done with those present in GenBank. Begomovirus infection was verified by BLASTN analysis and 99% nucleotide identities with ToLCNDV were also seen; these results were also supported by phylogenetic analysis. Hence, presence of TYLCV in various host plants and outbreak of ToLCNDV in cucurbit crops of Iran was observed.

In 2016, **Luigi *et al*. (2016)** collected virulent leaf samples from three plants of zucchini squash from Sardinia, Italy, showing symptoms similar to that of ToLCNDV and isolated total DNA from them. PCR amplification with both primers i.e. degenerative for begomovirus diagnosis and specific ones for diagnosis of ToLCNDV components (DNA A and B) gave positive results. After partial characterization of amplified DNA A by sequencing in both directions, aligned sequences of all samples were found identical and hence, one sequence was submitted in GenBank as KX826050. This isolate had 99% nucleotide identity with three ToLCNDV isolates i.e. Sicilian (KU145141), Murcia, Spain (KF749223-5) and Almeria, Spain (KF891468). In amino acid sequences comparison of above mentioned isolates with Sardinian isolate, latter one showed single non-conservative replacement in AC1 and two conservative substitutions in AV1 region. The pathogen might be introduced from Spain through trading of plants therefore; the possible rapid spread of virus in Italy came under observation.

In Spain, a genetically-stable population of ToLCNDV was reported by **Fortes *et al*. (2016)**. Further analyses done on world-wide reported isolates of ToLCNDV exhibited that it had a diverse genetic pool with unclear plant host, year or geography-based phylogenetic clades. Strains from Spain seem to be emerged through recombination and modified to cause infection in cucurbits and hardly in tomatoes.

Kumar and Naqvi, (2016) investigated the activity of ToLCNDV induced RSS (RNA silencing suppressor) i.e. AC2, on the miRNA system of host. Reportedly, the deregulation of miR172 and miR319 by association with AC2 during ToLCNDV infectivity caused deregulation of miRNA. Performing *ex vivo* and *in vitro* assays confirmed that the earlier mentioned interaction was regulated by association among AC2 and AGO1. Hence, an insight on AC2 to disturb host miRNA functionality was given.

In a resistant cultivar namely H-88-78-1, **Sahu *et al.* (2016)** functionally distinguished a SlRPT4 (*Solanum* lycopersicum-26S proteasomal subunit RPT4a) gene, whose expression after infection by ToLCNDV, became different. After analysis at molecular level, a vigorous ATPase activity in SlRPT4 protein was observed. Binding precisely to the stem-loop point of IR, SlRPT4 could exist in both DNA-A and -B of bipartite genome of virus but absence of secondary structure in rep gene restricted the DNA-protein complex formation, signifying that DNA and SlRPT4 binding is limited by secondary structure. RNA Pol-II function was stopped by SlRPT4 and IR binding and hence the transcription (bi-directional) of ToLCNDV genome was reduced. Resistant features of H-88-78-1 specie turned into being susceptible by virus-induced silencing of SlRPT4 gene. *SlRPT4* transient over-expression caused programmed cell death and activation of antioxidant enzymes pathway. Anyhow, nonproteolytic activity of protein SlRPT4 and its role in defense against virus infectivity in tomato was discussed.

Zaidi *et al.* (2016a) isolated ToLCNDV from CLCuD-infected cotton. In cotton, frequency and geographic rate of ToLCNDV was checked by performing diagnostic PCR in cotton plants with CLCuD symptoms collected from Punjab and Sindh during 2013-15. CLCuKoV-Bur in all 31 plants and ToLCNDV in 20 plants was found. qRT-PCR analysis to check virus levels in co-infected plants explained that co-infectivity of ToLCNDV and CLCuKoV-Bur or CLCuMB complex increased the amount of CLCuMB, which induces infectivity (symptom) determinant of the complex.

Saez *et al*. (2016) screened accessions of *Cucurbita* spp., including wild species, commercial species and landraces, e.g. *Cucurbita moschata*, *C. pepo*, and *C. maxima*, for ToLCNDV resistance. The screening included inoculation by two means i.e. whitefly and mechanically. The resistance rate was examined by scoring severity of symptoms and by checking virus quantity in selected genotypes through qPCR. In *C. pepo*, rigorous symptoms and elevated viral quantity was observed after 30 days of inoculation. All Zucchini morphotypes and *C. maxima* were seemed susceptible showing leaf decay and severe yellowing, internode shortening and curling was also observed in *C. pepo*. *C. moschata* was resistant as in its four accessions few plants had mild symptoms, after three times mechanical inoculation with the inoculum sources differing each time, or were symptomless. Two of them exhibited no symptoms after virus inoculation with infectious whiteflies. 15 and 30 days after inoculation, ToLCNDV was obtained from these symptomless accessions but virus quantities were lower than those obtained from susceptible genotypes, defining high resistance. Susceptible species were showed specific leaf mottling, converting into a severe mosaic. *C. moschata* resistant accessions were hence considered for breeding programmes to avoid infection by ToLCNDV.

By chloroform/phenol extraction and ethanol precipitation, **Panno *et al.* (2016)** extracted total DNA from 22 young leaves infected by begomovirus reported from Tunisia. PCR with the primer set A1F and A1R for the DNA-A component and the primer set for

DNA-B mentioned by Ruiz *et al*. (2015) amplified a DNA-A and –B fragment of size ~1200-bp and ~890 bp, respectively. 10 samples were positive by PCR but amplification using primers set precise for TYLCV and ToLCSV, showed no results. For CMV, PRSV and ZYMV, DAS-ELISA analysis also gave negative results.

Sharma *et al*. (2015) used leaves with symptoms and performed ELISA against familiar cucurbit viruses such as PVX, CMV subgroups I and II, (PVY)o, ZYMV and PVYN. ELISA came positive only for ZYMV, so, total RNA was obtained from its infected samples and cDNA synthesis was done by oligo (dT) primers, and then DNA was amplified by primers set ZY-2 and ZY-3, approximately 1200 bp sized product obtained in RT-PCR. In pGEM-T, this product was cloned and sequenced. Sequence analysis showed 99.5% and 97.8% nucleotide and amino acid identities respectively, between the ZYMV isolate KJ614229 and GQ482976. Occurrence of begomovirus was checked by total DNA isolation of infected bittergourd leaves was done and PCR amplification using universal primers AV494 and AC1048. The 575 bp DNA amplicon was cloned and then sequenced. Sequence analysis exhibited that bittergourd isolate in India (KJ44258) gave 100% nucleotide and amino acid identity with ToLCNDV isolate of bittergourd in Pakistan (AJ854186). It is first report of mixed infection of ZYMV and ToLCNDV in bittergourd.

Pradhan *et al*. (2015) studied the consequences of ToLCNDV infectivity on miRNAs of tomato. Next generation sequencing was done on isolated sRNAs from healthy and ToLCNDV-infected tomato leaves. Total 112 mature miRNA sequences were predicted by using miR Deep-P program. About 53 novel miRNA sequences were screened based on the precision value. 58 out of 112 were 24-mer in size. Northern blot assay was performed on 19 sequences for expression analysis that appeared positive. By expression analysis, a reverse relation was predicted between abundance of conforming miRNAs and target transcript accumulation. To confirm the precise annotation of miRNA targets, cleavage site of target transcripts was recorded. Thus, sequencing of sRNA by NGS revealed the expression of miRNA in the host due to virus. To understand the relation between ToLCNDV and tomato plants and to develop the virus resistant plants, these authorized miRNAs (Tom 43, Tom 14, Tom 4, Tom 21, Tom 17 and Tom 29) proved to be of high importance.

Venkataravanappa *et al*. (2015) performed dot blot and PCR detection on the symptomatic okra samples collected during years 2005–2009 and determined that 75.14% of the specimen belonged to monopartite while rest of them to bipartite virus. Whitefly-mediated infection was found in three samples linked with DNA-B. After cloning and sequencing of these isolates, their DNA-A analysis showed 93% and of DNA-B showed upto 90% sequence identity with ToLCNDV. Analyses of iteron-binding sequence exhibited their compatibility with rep-binding iterons of DNA-B component of ToLCNDV, identifying that for okra infection, okra yellow vein disease interacted with DNA-B of ToLCNDV. In accordance of recombination analysis, DNA-A assumed to be obtained by inter-specific recombination among begomoviruses, DNA-B, on the other hand, was obtained from various hosts infected by ToLCNDV.

Mandal *et al*. (2015) reported that in the ToLCD-infected leaves the amount of transcript TORNADO1 (SlTRN1) readily increased. SlTRN1 promoter analysis was performed to identify functionality of various promoter elements. Salicylic acid (SA) induced WRKY proteins and elevated the level of SlTRN1 and SlWRKY16 transcript. W-boxes function to induce SlTRN1 during ToLCNDV attack or SA treatment was confirmed by mutational analysis. Hence, induction of WRKY16 that regulates encoding of SlTRN1 gene under stress was confirmed, which may have affect on infection severity.

Srivastava *et al.* (2015) detected begomovirus in unhealthy leaves of *P. somniferum* by total DNA extraction of ten unhealthy and one wild leaf samples and proceded to PCR with degenerate primers set, hence amplifying ~1.2 kb gene confirming the presence of begomovirus. RCA was used to amplify whole genome and digested by restriction enzymes (*Pst*I, *Xba*I, *Cla*I and *Msp*I). Approximately 2.7 kb band was obtained by *Xba*I digestion followed by cloning in the pCAMBIA1300 vector (at *Xba*I site) and sequencing (KC513822). It showed 96-98% identities with DNA-A of ToLCNDV isolates including AB368447,AB368448, U15016, HM007113, KC545812 and HM989845 confirming it as an isolate of ToLCNDV, named as ToLCNDV-[IN:LKO:PS:13]. For measuring prevalence of this virus, total DNA from 23 samples of *P. somniferum* plants was isolated and NASH was performed for ToLCNDV detection using α-32P radioactive probe. Positive signals from 19 out of 23 samples were obtained by NASH confirming ToLCNDV occurrence in 82.6% Papaver plants for the first time.

Ruiz *et al*. (2015) did extraction of total nucleic acid and PCR amplifications of 10 leaves from tomato using precise primers that were compatible with the DNA-A (KF891468) and -B (KF891467) components of ToLCNDV. DNA fragments of 1,260 and 890 bp, respectively, were amplified and cloned in Easy vector (pGEM-T) Products were sequenced and gave highest identity with ToLCNDV when analyzed with BLASTn. Amplification with primers that were TYLCV and TYLCSV-specific showed negative results. Primers from of complete genome sequence of ToLCNDV, reported from zucchini squash (Spain) samples, amplified 2,738 and 2,684 kb genes from two tomato samples that were then cloned and sequenced. 99% identity with the KF891468 and KF891467 isolates of Spain was obtained and they were submitted as KM977733 and KM977734 in GenBank. Five *S. lycopersicum* cv marmande young plants were infected with 15-20 ToLCNDV containing whiteflies for 48 h. By PCR analysis, all plants showed positive results for DNA-A and –B of ToLCNDV and negative for TYLCV. At 45 DAI, for 48-h, 10-15 whiteflies were exposed to tomato plants and then transferred to five young plants of zucchini squash. At fifteen DAI, resulted as positive for ToLCNDV In this case, no betasatelites and ToLCNDV interaction was detected. Hence, presence and transfer of ToLCNDV among tomato and zucchini squash plants in Spain was reported.

Mnari-Hattab *et al.* (2015) detected virus inducing infection in cucurbit plants in Tunisia by DNA purification and PCR amplification from nine unhealthy plant samples (i.e. fruit skins and leaves). Degenerate primers set for CP gene of begomovirus amplified a product of ~560 bp from symptomatic samples only. Begomovirus specie was detected by Multiplex PCR. Three amplified CP genes were cloned, sequenced and they exhibited 99% identity with each another. They were submitted in GenBank as accessions KP979713-KP979715. Their 97.6 to 99.2% nucleotide identity with CP gene (partial) from ToLCNDV isolates inducing infection in zucchini (KM977733) and tomato (KF749225) in Spain was obtained and with an Indian ToLCNDV sequence (KC846817) similarity values found were 96.9 and 97.3%.

Kushwaha *et al*. (2015) did a relative molecular analysis of ToLCNDV on various solanaceous hosts from which *N. benthamiana* was considered as the most vulnerable host, whereas *C. annuum* was resistant against a ToLCNDV isolate (U15015 and U15017). Clear symptoms and related massive virus accumulation took place in *N. tabacum* and *S. lycopersicum*. Amount of ToLCNDV-specific siRNA were also directly linked to the viral DNA level. A relative expression analysis involving defense-related genes of various hosts took place to check the variability of their response to ToLCNDV, indicating different expression rate of post-transcriptional pathway for gene silencing (SGS3, RDR6, and AGO1), host defense proteins and lipid transfer protein. NBS-LRR genes expression was clearly higher in *C. annuum* after ToLCNDV infectivity, suggesting that the level of host defense responses gave knowledge about the ToLCNDV accumulation and severity of symptom formation in plant.

After spread of ToLCNDV on melon and cucurbits in Spain, **Lopez *et al*. (2015)** discovered method of germplasm detection against this virus through mechanical inoculation that appeared positive in 4 genera and 13 species including melons, pumpkins, watermelons etc, and wild species and landraces used for breeding of cucurbits. Melon (*Cucumis melo* subsp. *agrestis* var. *momordica* and some wild species) from India showed tolerance to mechanical transfer of ToLCNDV making them a good source to generate new ToLCNDV-tolerant melon species.

Sohrab *et al.* (2014) recognized factors providing proficient sap-mediated transfer of begomovirus. In inoculum, addition of Celite, Corborundum powder, Sodium sulphite, and b-mercaptoethanol elevated the sap transmission rate. On the basis of factors such as age of inoculum, buffer combinations, and genotypes of experimental plants etc, percentage of diseased plants varied. Amplification of CP gene, its cloning and sequencing from sap-inoculated plants confirmed sap-mediated transfer of virus reported for the first time in sponge gourd in India.

Akhter *et al*. (2014) used biolistic gun method and caused infection in *Nicotiana benthamiana* by using DNA-A and –B of ToLCNDV isolated from chili and tomato and Chili leaf curl betasatellite (ChLCB). ToLCNDV components isolated from tomato and chili came out to be infectious and induced symptoms of leaf curl when inoculated by biolistic gun process. Co-inoculation of ToLCNDV with ChLCB gave severity in disease symptoms. These results showed that with bipartite begomoviruses interaction with betasatellite might enhance bipartite virus-induced symptoms. It presented another example changes in begomovirus complexes that infected significant crops in the region.

Sahu *et al.* (2014) measured the allocation of virus-derived siRNAs throughout the ToLCNDV genome together with the difference in expression of DNA methylation in IR and Rep (AC1) regions of two tomato plants showing different tolerance for ToLCNDV. Elevated accumulation of siRNA and AC1-specific 21-nt siRNA was obtained in the tolerant cultivar, along with higher methylation amount in IR regions. RNA silencing and DNA methylation pathway were differently expressed in both tomato plants at 21 dpi. Thus, it was considered that for tolerance against ToLCNDV, methylation of viral DNA and siRNA-regulated RNA breakdown were significant. Targeting the viral regions with RNAi technology could act as a defense strategy to form transgenic plants.

Rai *et al*. (2013) distinguished PCR based markers associated to gene(s) causing resistance to ToLCNDV. BC1F1 population obtained by cross between ToLCNDV tolerant LA1777 and susceptible 15SBSB tomato plants. 135 BC1F1 plants showed that, in specie LA1777, three dominant genes induced tolerance against ToLCNDV. An ISSR marker producing fragment of 564 bp in tolerant wild and bulk samples was identified by Bulk-Segregant-Analysis. The marker validated in 18 tomato isolates and could be used as a diagnostic marker.

Vu *et al.* (2013) reported the features of two amiRs that were targeting the overlapping AV1 and AV2 transcripts region and middle region of AV1 transcript of ToLCV. In T2 generation, transgenic tomato species encoded amiR-AV1-1 and were extremely tolerant to ToLCNDV, whereas those with amiR-AV1-3 showed moderate resitance. Biochemical analyses showed slicing mechanism of amiRs cleaving targets. Hence, this method could be used for tolerance against ToLCV.

Roy *et al*. (2013) used begomovirus-specific primers in PCR that gave expected amplicon fragment from all the unhealthy plants with absence of betasatellites. Whole genome was amplified by RCA, was cloned and then sequenced showing high sequence identities of DNA-A and DNA-B with various ToLCNDV isolates (AM286433 & AM286435) as 99.6 and 96.8 %, respectively and grouped with them. Sequence analysis distinguished ash gourd begomovirus as a ToLCNDV isolate. Prevalence of ToLCNDV in ash gourd genome hence, elevated concern about the spread of this virus in Indian subcontinent.

Sohrab *et al*. (2013) tried to transfer begomovirus by sap. The virulent agent was effortlessly transferred by sap to sponge gourd, *Nicotiana benthamiana* and ridge gourd. Application of inoculum, use of two abrasive (corborundum and celite) and two antioxidants (β- mercaptoethanol and sodium sulphite) on first younger leaves and cotyledons by rubbing cotton and dipping in inoculum increased the transmission rate. Due to various factors like inoculum source, combinations of buffers etc, inoculation by sap gave different infected plants percentages. Seven days old plantlet of ridge gourd got 100% infection by sap inoculation which was confirmed by PCR amplification, cloning and sequencing of CP gene from infected plants.

Sohrab *et al*. (2013a) reported that ToLCNDV was already inoculated by sap to *Nicotiana benthamiana*, ridge gourd and sponge gourd and confirmed by amplification, cloning and sequencing of CP gene. The CP sequence AY309957 gave 95.1% sequence identity with ToLCNDV-Svr sequence U15015. Factors affecting transmission of begomovirus viz., genotypes and species of plants, buffer combinations, temperature, source and age of inoculum were identified. Addition of an antioxidant and abrasive gave successful transmission. The optimal buffer combination gave 100% infectivity on 7-day-old plantlet. This was the first report of sap inoculation of a begomovirus sponge gourd in India.

Jyothsna *et al*. (2013) cloned ten begomovirus isolates infectious samples and identified them as ToLCNDV. Frequent interaction with betasatellites, LuLDB and CLCuMuB was shown by 44 % of the samples. Components of ToLCNDV were agro-infilterated in tomato and *Nicotiana benthamiana* plants with or without CLCuMuB, LuLDB or betasatellites. Level of viral genome was then observed by qPCR at various times of disease growth. Elevated symptom severity and levels of viral DNA-A and –B were observed in both plants i.e. tomato and *N. benthamiana* that were co-inoculated with betasatellites. The DNA B and betasatellites worked opposite to one another as DNA-B amount raised upto 16-fold in the presence of betasatellites, while levels of LuLDB, betasatellites and CLCuMuB and were lowered as much as 60 % in the DNA B presence. Symptoms induced by DNA-B were prominent in CLCuMuB-transmitted plants, whereas leaf abnormalities induced by betasatellite were predominant in LuLDB-co-infected plants. Hence, transmission involving cloned components considered as a good biotechnological tool in inducing resistance.

Zakri *et al*. (2012) explained that scFv, that identifies the CP of ToLCNDV *in vitro*, could also interact in plant cytosol (*in vivo*) with another recombinant CP. The scFv and its target were called as fluorescent-protein fusions in which one incorporated GFP and the other DsRed. Addition of nuclear localization signal into the construct of scFv gave nuclear transfer of the antigen- antibody complex, as shown by fluorescent signals. That showed that recombinant antibodies could be sent to nucleus and bind to CP of geminivirus interrupting the virus infection cycle.

Sahu *et al.* (2012) characterized the association of tomato and ToLCV on biochemical and molecular basis. A comparative analysis of RNA interference between two tomato species i.e. 15SBSB (susceptible) and LA1777 (tolerant) infected with ToLCNDV gave higher accumulation levels of siRNA in the tolerant plant. After 5–10 days of inoculation, ToLCNDV induced chlorotic and necrotic areas at the transmission site. Elevated levels of Caspase- 3- and caspase-9-like reactions and antioxidant enzymes detoxifying the ROS were observed in both areas of infection i.e systemic and localized. This expression was confirmed by qRT-PCR where expression levels of three pathogenicity-related genes exhibited elevated accumulation in tolerant specie. Hence, a putative ToLCNDV tolerance mechanism was discussed in the tolerant specie.

Phaneendra *et al*. (2012) reported association between ToLCNDV and pumpkin leaf curl by PCR amplification of sample with CP-specific primers. The sequences and phylogenetic analysis of the whole genome confirmed it as ToLCNDV.

Mizutani *et al*. (2011) determined the virus in cucumber plants with mosaic symptoms and high nucleotide sequence identity with ToLCNDV-[cucumber:Thailand] and considered it as a ToLCNDV isolate namely ToLCNDV-ID[ID:Jav:Cuc:08]. In Indonesia, effect of ToLCNDV on chili pepper is a major problem but ToLCNDV was also found in cucumber. Therefore, it was the first report of ToLCNDV occurrence in Indonesia.

Malik *et al*. (2011) characterized the begomovirus linked with yellow leaf curl disease occurring on muskmelon in Pakistan. Analysis of the complete nucleotide sequence of the both components of the begomovirus exhibited highest identity of DNA sequence with ToLCPMV. Agrobacterium-mediated infiltration of ToLCPMV done in *Nicotiana benthamiana* resulted symptomless. However, inoculation of DNA A of ToLCPMV and the DNA B of ToLCNDV caused systemic infection. Thus, lack of infectivity of the ToLCPMV was assumed to be due to its defective DNA B. But, when co-inoculated with DNA-A of either virus, DNA B of ToLCPMV was able to systemically move, and gave a hypersensitive response along the veins. Under the influence of 35S promoter of caulifower mosaic virus, muskmelon that was agro-infiltered with NSP gene construct of ToLCNDV, induced hypersensitive response, distinguishing that HP was induced by it. Results suggested that these species needed interaction with ZYMV for infection.

Pratap *et al*. (2011) identified and characterized begomovirus in India causing yellow mosaic disease in eggplant. Whole genome was cloned, sequenced and analyzed for nucleotide identity where its DNA-A showed maximm 97.6% and DNA-B showed 94.1% identity with ToLCNDV[India:Udaipur:Okra:2007]. Hence, named as ToLCNDV IN[IN:Nag:Egg:09], its infectivity was confirmed by symptoms produced when agrobacterium-mediated infiltraion and inoculation of DNA-A and -B dimeric clones was done in tomato and egg plants. It was first report highlighting ToLCNDV causing yellow mosaic disease in eggplant.

About 20 tomato ESTs were identified by **Naqvi *et al.* (2011)**, while performing subtractive hybridization, that were inoculated in leaves of tomato by agro-infiltration with the DNA-A and –B dimmers constructs. Induced ESTs functioned for plant metabolism, ethylene signaling and innate immunity. ESTs expression was confirmed by northern blot analysis and further checked in variety of healthy and infected plant tissues by RT-PCR showing elevated level of most of the genes while in root and stem tissues down-regulation occurred.

Islam *et al*. (2011) confirmed DSG-6, a cultivar of *L. cylindrica* Roem., resistant to ToLCNDV by PCR amplification with primers specific to CP gene. 750 bp sized product was obtained from susceptible plants (positive control) only. Resistance to ToLCNDV in plant generations was determined by inoculations in backcross (B1: resistant DSG-6 and B2: susceptible ‘Pusa Sneha’) and F2 populations. Resistance of dominant monogenic origin was observed. Two SRAP markers and ToLCNDV-non-resistant gene were closely interrelated in the non-resistant parent and bulk population and same results were obtained for resistant genes. These markers could be used in seedling selection, speeding up production of ToLCNDV-resistant Luffa cultivars thus, reducing the disease rate in this crop.

Sahu *et al*. (2010) determined the rate of replicative-intermediate constituents and siRNAs induced host plants in naturally resistant cultivar H-88-78-1 and susceptible plant Punjab Chhuhara to understand the virus tolerance mechanism in tomato at times after agro-infiltration. Lesser amount of viral replicative intermediate in the tolerant specie might have a correlation with comparatively higher levels of viral siRNAs. After ToLCNDV infection, the defense-related ToLCNDV-inoculated and agrobacterium mock-inoculated tolerant cultivar replicates were prepared at 21 DIP. 106 non-redundant transcripts in total were identified and classified into 12 categories according to their functions. By reverse Northern analysis and qRT-PCR, expression pattern of 106 transcripts were identified in which 34 should upregulation. The direct and indirect relationship of rate of siRNA accumulation and up-regulated transcripts with the ToLCNDV tolerance mechanism was discussed.

Shafiq *et al*. (2010) found a chili plant (*Capsicum annum*) containing DNA B of ToLCNDV and a betasatellite exhibiting the symptoms of ChLCV. The begomovirus had maximum 99% of sequence identity with PepLCLV-[PK: Lah: 04] AM404179. In *Nicotiana benthamiana,* very mild symptoms appeared after agroinfiltration of clone and in its leaves PCR detected low amount of viral DNA. Neither availability nor absence of betasatellite caused symptoms in chilies or *Nicotiana tabacum*. But co-infection of DNA B of ToLCNDV along with PepLCLV caused leaf curl symptoms in chilies, *N. benthamiana* and *N. tabacum*. The amount of viral DNA in the co-infected plants was higher than those only infected by PepLCLV. It was assumed that PepLCLV started infecting chilies by its association with

DNA B component of ToLCNDV. Moreover, the rep-associated iterons of PepLCLV (GGGGAC) varied from that of ToLCNDV (GGTGTC) at two base positions. Hence, from Pakistan, begomovirus causing chili leaf curl infection in chilies was first reported and highlighted its emerging complexity.

Naqvi *et al*. (2010) isolated miRNAs from the leave of tomato cv Pusa Ruby, both control and agro-infiltered with ToLCNDV and did their microarray analyses that exhibited that miRNAs from ~13 various conserved families were deregulated by the infection of ToLCNDV. Similar irregular patterns were showed by the miRNAs precursors, signifying that the respective miRNA genes deregulation was caused by their transcription regulation. miRNAs and the rate of expression of their respective targeted genes were totally opposite. After agro-inoculation of ToLCNDV in tomato (Pusa Ruby), an up rise in amount of miR172 and miR159/319 was noticed with increasing dpi. In ToLCNDV agro-inoculated chilli and tomato (JK Asha) plants, these miRNAs were also induced. Results exhibited the involvement of miR172 and miR159/319 with the leaf curling symptoms. Hence, miRNA(s) could be possibly used as specific molecules for ToLCNDV infectivity as various host miRNAs indicated viral attack and could help to prepare viral resistance.

Islam *et al*. (2010) screened and confirmed thirty genotypically assorted sponge gourd varieties collected from various locations in India for resistance for epiphytic surroundings by challenge inoculation of virus (purified strain) in insect-free environment. Under the challenge (whitefly-presence) inoculation environment, genotype DSG-6 gave the lowest susceptibility index of 3.33 along with DSG 7 of 6.0. Desirable characters containing non-resistant genotypes NSG-1-11 and Pusa Sneha' were then crossed with the two resistant varieties DSG-7 and DSG-6, and through challenge inoculation of virus (purified strain) backcross generation and segregation disease reaction were studied. The test namely chisquare (v2) exhibited the dominant Mendelian ratio (monogenic) as 3(R):1(S). All results obtained were firstly reported and they showed that single dominant allele in resistant parents controlled the resistance against ToLCNDV causing infectivity in sponge gourd and the resistant lines could be used for the formation of resistant-hybrids.

Tiwari *et al*. (2010) performed PCR using the total DNA isolated from infected leaf samples and a pair of begomovirus specific primers which resulted in the expected size (~800 bp) amplicon in 3/6 samples indicating presence of begomovirus. Then, amplicons were cloned and sequenced (EU439260). The sequence at both amino acid and nucleotide level showed maximum 93-98% identities with different isolates of ToLCNDV and closest relationship with some of its variants. Hence, it was considered as an isolates of ToLCNDV.

Zakri *et al*. (2010) reported the formation of monocolonal antibody (mAb) HAV-secreting hybridoma cell line that identifies the coat protein (AV1) of ToLCNDV. After immunizing the mice with recombinant AV1 (purified form) infused with GST (glutathione S-transferase), the cell line was established. cDNA of hybridoma was used to assemble scFv-SAV (single-chain fragment), however, sequence analysis exhibited that a frame shift causing 21' N-terminal truncation occurred due to deletion of single nucleotide. For the formation of scFv-RWAV, site-directed mutagenesis (*in-vitro*) was used for the restoration of the omitted nucleotide. ELISA, SPR spectroscopy (surface plasmon resonance) and western blot were used for the characterization of binding properties among mAb HAV and its respective scFvs. MAb HAV only attached to AV1. This revealed that a conserved linear epitope of begomovirus coat protein was only identified by the antibody.

Raj *et al*. (2008) reported association of *Tomato leaf curl New Delhi virus* with leaf curl disease of papaya (*Carica papaya* L.) that was detected by polymerase chain reaction using begomovirus-specific primers and confirmed by highest sequence similarities and close phylogenetic relationships.

Hussain *et al*. (2007) did analysis of all ToLCNDV encoded genes that pinpointed the transcriptional activator protein (TrAP) as the factor mediating the anti-HR effect. Deletion mutagenesis showed the central region of TrAP, containing a zinc finger domain and nuclear localization signal, to be important in inhibiting the HR. These results demonstrate that TrAP counters HR-induced cell death, the first such activity identified for a plant-infecting virus.

Raj *et al*. (2007) determined the causing agent of symptom yellow vein netting by total DNA isolation from both symptomatic and control *H. cannabinus* leaf samples and doing their dot blot analysis on nylon membranes and then hybridization with probes (radio-labelled) made from a cloned DNA-A of a precisely characterized ITLCV isolate. A well hybridization was seen among the entire DNA of symptomatic samples only and probes representing the existence of a begomovirus.

Chang *et al.* (2007) mechanically inocluated the infected melon-isolated virus culture (SL-1) in oriental melon and *Nicotiana benthamiana*. Amplification of viral DNAs from the infected plants was done by begomovirus specific degenerative primers and sequence analysis of amplicon DNA-A and –B showed similarity with the cucumber isolate of ToLCNDV as 97.7% and 90.6%, respectively. It was hence, named as oriental melon isolate of ToLCNDV (ToLCNDV-OM). Agroinfiltration confirmed its pathogenicity and its rate of transmission by mechanical means was greater than 93%. It caused infectivity in five more species of *Cucurbitaceae* family when mechanically inoculated. This was the first report about novel strain of ToLCNDV infecting oriental melon in Taiwan.

Gawande *et al*. (2007) developed a polymerase chain reaction based method, also known as print-capture PCR (PC-PCR), for the detection of ToLCNDV (Tomato leaf curl

New Delhi virus), responsible for potato apical leaf curl disease in potato. In this method, DNA was not extracted from symptomatic samples, instead, it included adsorption of virus from freshly cut end of infected leaf tissue on to nylon membrane (also known as “tissue printing”). The viral coat protein (CP) gene was then amplified after removing the DNA from the print in sterile distilled water at 95°C. The print-capture PCR method was considered reliable and sensitive as the conventional PCR method and was said to be appropriate for detection of virus in infected potato samples.

Maruthi *et al.* (2006) extracted total DNA from leaves with symptoms and putative viral genomes were amplified by PCR using degenerate primers specific to DNA-A and -B. Virus ToLCJV-Mld (Tomato leaf curl Joydebpur virus-Mild) was seemed linked with the mild symptoms. ToLCJV-Mld showed highest similarity of 87.1% to the PLCBV AF314531 with reference to its DNA-A component and its DNA-β satellite showed maximum nucleotide identity of 59.0% with the isolate of ToLCV-IN AY438558. However, DNA-B was absent. An additional 849 nucleotides based ORF was found on the complementary strand encircling the entire CP gene. These results concluded the presence of three begomovirus species infecting tomato in Bangladesh.

Khan *et al.* (2006) confirmed that leaf curl disease on chili crop (*Capsicum annuum*) was caused by begomovirus. Experimentally, whitefly was seemed to be involved in the transmission of disease from infected to healthy tomato and chili plants. Inoculated plants of chili showed characteristic disease symptoms but tomato plants showed severe leaf curl symptoms similar to those produced by ToLCNDV. Total DNA was isolated from naturally infected leaves of chili plant. Amplification of CP region of ToLCNDV was done by specific primer set. Amplicon obtained was of 800 bp that was then cloned and sequenced (AY883570). Sequence analyses exhibited its 89–93% nucleotide identity with different

ToLCNDV isolates (U15016, AY428769, AF448058 and X78956), but 81 and 86% identity to ChLCV-[Mul] AF336806 and PLCBV AF314531, respectively. It was then concluded that on Indian region, ToLCNDV used chili as a substitute host.

Haider *et al*. (2006) reported that yellow vein disease-causing virus on *Eclipta prostrate* was a strain of ToLCNDV. Both symptomatic and asymptomatic plants were collected and their total DNA was isolated. Degenerative primers conserved for CP gene of begomoviruses were used for PCR. Only from symptoms-containing plants, an amplicon of 750 bp was obtained, that was then cloned and sequenced in both directions (AJ889185). It exhibited the highest sequence identity of 98% to ToLCNDV isolate U15015. It was concluded by this first report that the virus causing infectivity in *Eclipta prostrate* was a strain of ToLCNDV.

Hussain *et al*. (2005) demonstrated the role of the NSP and movement protein MP in the pathogenic behavior of ToLCNDV. In *Nicotiana benthamiana*, *Lycopersicon esculentum* and *Nicotiana tabacum* plants, both MP and NSP genes were expressed through stable transformation of gene constructs in *N. tobacum*, under the control of the 35S promoter or by PVX expression vector. No phenotypic changes were observed when MP was expressed constitutively in transgenic plants or when it was expressed by expression vector (PVX). However, clear leaf curling was observed when ToLCNDV NSP was expressed with expression vector (PVX) in *N. benthamiana.* A hypersensitive response (HR) was observed by expression of NSP in *L. esculentum* and *N. tabacum* from PVX. Necrotic spots were also noted in expanded leaves when NSP was expressed as a transgene. However, by deleting the amino acids from N-terminus (60-100 amino acids), HR response was terminated, indicating that N-terminus had major importance in regulating the HR response. Results suggested the role of ToLCNDV NSP as a target of host defense responses as well as a pathogenicity determinant.

Tahir and Haider (2005) reported the virus infecting *Momordica charantia* in Pakistan. DNA was isolated from two control and four infected plant leaves and CP-specific degenerative primers of begomoviruses were used for PCR. Only from infected plants, an amplicon of size approx. 750 bp was obtained that was then cloned and sequenced (AJ854186). Amplicon showed utmost sequence identity of 95% to ToLCNDV (U15015), indicating that the virus infecting the *M. charantia* was a strain of ToLCNDV. Universal primers for DNA-β were used to detect the DNA-β in infected *M. charantia* plant samples and obtained amplicon of 0·6 kb indicated the presence of a defective DNA-β. This study report was the first report of ToLCNDV infecting *M. charantia*.

Usharani *et al*. (2004) identified the causal agent of leaf curl disease, observed on *Solanum tuberosum* (Potato) crop. From infected *N. benthamiana* and potato plants, Double-stranded viral replicative DNAs were isolated from infected plants and cloning was done at *BamH*I, *Hind* III, *Pst*I and *Xba*I sites in pUC18 vector. The nucleotide sequence of the *Xba*I and *Pst*I clones exhibited a close similarity to DNA A (AY286316) and -B (AY158080) components. Complete sequence of DNA A showed 93–95% sequence identity with ToLCNDV isolates and <75% sequence identity with PYMV and ToLCV isolates. The sequencing data showed that this strain was not sap-transmissible. It indicated the emergence of a novel strain of ToLCNDV. It was the first report about begomovirus infectivity on potato in India.

Hussain *et al*. (2004) collected the infected chili peppers samples to confirm the association of tomato begomoviruses (ToLCNDV) because both crops overlaid in the field. Total DNA was extracted from affected leaf samples and hybridization was done using radioactively labelled probe of DNA A of ToLCNDV. When blot was washed away at average stringency, the probe hybridized with bands in all the samples. Then, amplicon obtained by PCR reaction using degenerate DNA A primers was cloned and sequenced. Sequence analyses showed its 95% sequence identity to DNA-A of ToLCNDV. By using ToLCNDV DNA B as a probe in hybridization, samples were also verified. However, with DNA A probe, a positive signal was noticed in six samples. For further confirmation of ToLCNDV, PCR amplification was done using specific primers for DNA B. PCR products of predicted size were obtained from all samples positive by hybridization. These findings suggested the presence of ToLCNDV in chili pepper crops in Pakistan.

Sohrab *et al.* (2003) reported that on *L. cylindrica* (*L. aegyptiaca*) in India, tomato leaf curl virus-New Delhi (ToLCV-NDe) caused the yellow mosaic disease. Further confirmation was done through genetic analysis. It was observed that viral DNA isolated from plants showing disease symptoms corresponded to the known ToLCV-NDe strains.

Chatterji *et al.* (2001) used the co-purification assays and EMSA to determine the least DNA-binding domain of Rep protein of ToLCNDV. DNA binding action was linked to the Rep protein at 1–160 amino acids region and was seen overlapped with the domain of protein oligomerization. In *Nicotiana benthamiana* plants and protoplasts of tobacco, Rep protein showed a transitory expression that repressed the accretion of DNA of virus (homologous) by 70–86%. The obtained results exhibited that during virus attack, the N-terminal expression of Rep protein could proficiently hinder with the oligomerization and DNA binding activities. Reduction in the accretion of ACMV, PHYVV and PYMV was observed by 22–48% due to this protein. In *in vitro* analysis, co-purification and EMSA assays exhibited that Rep-(1–160 aa) linked with heterologous geminiviruses with low affinity and shaped oligomers by linking with the Rep proteins of various geminiviruses.

Results suggested that the virus accumulation regulation might include the Rep-binding to the target DNA and various Rep components during replication of virus.

Chatterji *et al*. (2000) determined the sites of DNA binding for the Rep proteins of 2 strains of ToLCV-Nde by performing EMSAs. Sequence specificity while recognition of iterons was observed for Rep proteins of both strains, however, they shared sequence identity of 91% in total. In EMSAs, a synthetic oligonucleotides series was used as probe that determined that the dependence of Rep protein and its binding site interaction was on sequence, size and number of 2 iterons. Alteration in arrangement and mutations in the repeat iterons affected the Rep protein capability to bind with the sequence of DNA and in protoplasts, lowered the accretion of viral DNA, declaring Rep protein binding to its iterons is a necessary action in replication of virus.

Chatterji *et al*. (1999) used 2 strains of ToLCV-Nde to determine the replication specificity of their respective genomes. They shared sequence identity of 94% and were named as mild and severe strains due to symptoms rate on tobacco and tomato plants. In tobacco plants and protoplasts, replication process determined that single change in an amino acid, such as Asn10 converted to Asp in the Rep protein (N terminus), limited the replication specificity of both strains on the basis of its linkage with *ori* equences. In mild strain, the above mentioned change incorporated with 3rd and 20th number nucleotide point mutations and altered the ability of replication of 13-mer binding site that resulted in the raised amount of virus accretion. Similarly, this change in severe strain disabled the virus replication and in plants, changed its severe phenotype. Mutations (site-directed) in *ori* sequences and Rep protein (in Asn10) described that in the severe strain, Asn10 identified the 3rd base pair of the binding site sequence (GGTGTCGGAGTC).

Padidam *et al.* (1996) analyzed different mutants of ToLCV-IN to determine the role of ORFs: AV3, AV2, and coat protein (CP) in viral replication, movement, and symptom development. Results showed that no protein was encoded by AV3 and AV2 was found to be very significant. So, by inoculating plants with DNA (with AV2 absent), very insignificant symptoms were determined and a little (ss) and (ds) viral DNA was found. Both ss- and ds-DNA were present in higher quantity in the protoplast, signifying that AV2 was a key component for virus movement. Substitution, frameshift or other mutations in AV2, accreted very minute amount of DNA of virus in both plants and protoplasts. Mutations in the CP exhibited an elevation in accretion of dsDNA in protoplasts and reduction of ssDNA in the plants. In both mutated AV2 and CP, gave AV2 mutants and CP mutants in plants and protoplasts, respectively. In results, different functions were exhibited by BC1, BV1 and AV2 that are significant for the changes in the DNA-A virion-sense mRNA organization or translation effect, viral replication and for viral movement.

Padidam *et al.* (1995) sequenced the two isolates of ToLCV-India and found two components (A and B) that were responsible for symptom development and systemic movement of virus. Two isolates showed nucleotide sequence identity of 94%; however, only one isolate induced the mild symptoms in *Nicotiana benthamiana* and tomato plants. ToLCV-India showed almost similar genome to WTGs except an additional ORF, AV3 that was absent in others. However, its CP sequence was similar to that of ICMV (90%). Mutations after 65 or 172 amino acids of CP had no effect on symptom development and systemic movement. Mutant viruses had less amount of single-stranded viral DNA and showed different symptoms as compared to unmodified viruses. Sequence comparison confirmed that ToLCV-India was a distinct virus, associated to the WTGs from the Old World and was similar to the ACMV in its requirement for -B component as compared to the other geminiviruses. From the results, it was concluded that unlike other geminiviruses of the old world, ToLCV-India evolved more recently.

Srivastava *et al*. (1995) isolated the replicative form of ds-viral DNA by cloning of DNA-A and DNA-B components of a whitefly transmitted virus responsible for leaf curl and yellowing symptoms in tomato plants (ITLCV). Total DNA was isolated and replicative form of ds-viral DNA was concentrated using alkaline denaturation process similar to plasmid isolation from *E. coli*. Cloning results confirmed the presence of an insert of either DNA-B (2.55 kb) or DNA-A (2.75 kb) in the plasmids of 95 % of transformants. In total nucleic acid, DNA-A and DNA-B clones could distinguish DNA-A/DNA-B, required for infection. Both DNA-A and DNA-B shared a common region of 166 bases and showed nucleotide sequence identity of 94%. Amino acid sequence of coat protein product of ITLCV exhibited 86% identity with *Indian cassava mosaic virus* (ICMV).

Chapter 3

METHODOLOGY

3.1 Data Collection

All accessible complete sequences of ToLCNDV (DNA A and DNA B) were retrieved from GenBank, NCBI (https://www.ncbi.nlm.nih.gov/) and previously published data i.e. a total of 133 sequences of DNA A and 115 sequences of DNA B (Appendix I). All sequences were submitted from 8 different countries namely Spain, Iran, Indonesia, Bangladesh, Taiwan, Thailand, and a most of them were from India and Pakistan. The all general available information of both components obtained from GenBank and ORF Finder (https://www.ncbi.nlm.nih.gov/orffinder/) was then arranged in the form of data tables (Table 4.1 and 4.2).

3.1.1 Renaming of Sequences

Following the ICTV guidelines for naming of begomoviruses discussed by Brown *et al*. (2015), all sequences were renamed as follows:

ToLCNDV-[Country:City:Host:Year]-Accession Number

3.2 Analysis of Pairwise Sequence Identity

Pairwise identity of DNA-A isolates was only obtained. All DNA-A isolates were together saved in the FASTA format (.fas) and by using MUSCLE alignment in SDTv1.2 (Specie Demarcation Tool), results were generated in three output formats:

- Graph Plot
- Color-coded matrix
- Sequence Distance Score, which was originally generated by the formula (http://web.cbio.uct.ac.za/~brejnev/):

1-(M/N)

Here, **M** designates the overall number of mismatched nucleotides and

N is overall number of sites in alignment with no gap character.

The graph plot gave the range of isolates lying above and below the demarcation values: 91 and 94 (Figure 4.1). Matrix was also obtained in 3-color mode with cut-off values 94 and 91, identifying the isolates that lie within the criterion and those behaving as outliers (Figure 4.2). A file (.csv) containing scores of pairwise sequence identities was also generated providing precise knowledge about percentage sequence identities of isolates (Appendix II).

3.3 Alignment of Sequences

Alignment of ToLCNDV components was done by MUSCLE in MEGA6 software. Which was further proceeded for phylogenetic analysis.

3.4 Phylogenetic Analysis by Maximum Likelihood Tree

By using MUSCLE alignment in MEGA6, maximum likelihood trees of both ToLCNDV components were generated. The obtained trees were then labeled and interpreted accordingly (Figure 4.3 and 4.4).

Chapter 4

RESULTS

ToLCNDV (bipartite) belongs to begomoviruses and it needs both of its DNA constituents for causing systemic infection (Padidam *et al*., 1995; Padidam *et al*., 1996). By knowing the capability of ToLCNDV to cause infection, possible economical threats could also be enlightened. Therefore, history of ToLCNDV spread was reconstructed using its all present sequences (Zaidi *et al*., 2016).

4.1 Data Collection of Isolates

Data regarding isolates of DNA-A and DNA-B was retrieved from GenBank, NCBI and ORF Finder, NCBI, and two data tables were generated i.e. Data table of DNA-A and DNA–B, respectively. That gave all the basic knowledge about the origin, host and molecular information about the isolates used.

Table 4.1 Data Table of DNA-A Isolates.

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
1.	U15015	India	Tomato	2739	99%	ToLCNDV-[PK:Fai:Sol:09] FN435310	Coat Protein (CP)	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.4
							V3	99%	V3 / ToLCNDV-[PK:Sol:09] CBA13464	41-427: 387	128	14.7
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							TrAP	99%	Transcriptor activator protein / ToLCNDV AER93214	1177-1596: 420	139	15.7
							REn	99%	Rep protein 3 / ToLCNDV-[Luc] CAA76214	1047-1457: 411	136	16.1
							C4	98%	AC4 Protein / ToLCNDV CAQ19352	2251-2427: 177	58	65.9
							Rep	98%	Replication associated protein / ToLCNDV ABA00492	1499-2584: 1086	361	40.8
2.	FN435310	Pakistan	Tomato	2739	99%	ToLCNDV-IN[IN:ND:Svr:92] U15015	CP	99%	AV1 protein / ToLCNDV NP_803220	280-1050: 771	256	29.4
							V3	99%	AV3 protein / ToLCNDV NP_803218	41-427: 387	128	14.8
							V2	99%	AV2 protein / ToLCNDV NP_803219	120-458: 339	112	12.9
							TrAP	99%	TrAP / ToLCNDV AER93214	1177-1596: 420	139	15.7
							C4	98%	AC4 Protein / ToLCNDV CAQ19352	2251-2427: 177	58	65.9
							REn	99%	Rep protein 3 / ToLCNDV-[Luc] CAA76214	1047-1457: 411	136	16.1
							Rep	98%	Replication associated protein / ToLCNDV ABA00492	1499-2584: 1086	361	40.8
3.	AM258977	Pakistan	Tomato	2739	99%	ToLCNDV-IN[IN:ND:Svr:92] U15015	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.4
							V3	96%	V3 / ToLCNDV-[PK:Sol:97] ABB52058	41-427: 387	128	14.6
							V2	97%	Pre-Coat Protein / ToLCNDV CRI05839	120-458: 339	112	13
							TrAP	98%	TrAP / ToLCNDV AER93214	1177-1596: 420	139	15.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C4	97%	AC4 Protein / ToLCNDV NP_803225	2251-2427: 177	58	65.4
							REn	98%	Replication Enhancer Protein / ToLCNDV AER93213	1047-1457: 411	136	16.1
							Rep	98%	AC1 Protein / ToLCNDV NP_803224	1499-2584: 1086	361	40.9
4.	HM159454	India	Tomato	2739	98%	ToLCNDV-IN[IN:ND:Svr:92] U15015	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.4
							V3	98%	AV3 protein / ToLCNDV NP_803218	41-427: 387	128	14.8
							V2	99%	Pre-Coat Protein / ToLCNDV-[IN:Tum:Chi:08] AEA76850	120-458: 339	112	12.9
							TrAP	98%	TrAP / ToLCNDV-IN[PK:Sol:97] CAF04470	1177-1596: 420	139	15.6
							C4	95%	PTGS Suppressor / ToLCNDV-JID27 ADT70817	2251-2427: 177	58	66.6
							REn	97%	AC3 Protein / ToLCNDV-IN[PK:Isl:T1/8:00] AAN76350	1047-1457: 411	136	16
							Rep	98%	Replication associated protein / ToLCNDV ABB77270	1499-2584: 1086	361	41.2
5.	DQ116880	Pakistan	Chilli	2739	98%	ToLCNDV-IN[IN:ND:05] DQ169056	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.4
							V3	98%	V3 / ToLCNDV-[PK:Sol:97] ABB52058	41-427: 387	128	14.7
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							TrAP	96%	TrAP / ToLCNDV AER93214	1177-1596: 420	139	15.8
							C4	98%	AC4 Protein / ToLCNDV-[IN:Bha:12] AGV02038	2251-2427: 177	58	65.8
							REn	96%	REn / ToLCNDV AER93213	1047-1457: 411	136	15.9
							Rep	98%	Replication associated protein / ToLCNDV ABA00492	1499-2584: 1086	361	41
6.	KC960492	Pakistan	*Convolvulus arvensis*	2728	99%	ToLCNDV-[PK:Fai:Sol:09] FN435310	CP	99%	AV1 protein / ToLCNDV NP_803220	278-1048: 771	256	29.4
							V2	99%	AV2 protein / ToLCNDV NP_803219	118-456: 339	112	12.9
							C5	99%	AC5 Protein / ToLCNDV NP_803221	308-670: 363	120	13.2

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	99%	TrAP / ToLCNDV AER93214	1175-1594: 420	139	15.7
							C4	98%	AC4 Protein / ToLCNDV CAQ19352	2249-2425: 177	58	65.9
							REn	99%	Rep protein 3 / ToLCNDV-[Luc] CAA76214	1045-1455: 411	136	16.1
							Rep	98%	Replication associated protein / ToLCNDV ABA00492	1497-2582: 1086	361	40.8
7.	JN129254	India	Pumpkin	2740	98%	ToLCNDV-IN[IN:ND:05] DQ169056	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.5
							V3	98%	AV3 protein / ToLCNDV-Svr ADM36024	41-427: 387	128	14.8
							V2	98%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.8
							Rep	98%	Replication associated protein / ToLCNDV ABA00492	1499-2674: 1176	391	44.6
							C4	95%	C4 Protein / ToLCNDV-[PK:Sol:97] CAF04472	2251-2427: 177	58	66.5
							C5	98%	C5 / ToLCNDV-[PK:Kha:Chi] ABB52030	310-795: 486	161	17.9
							TrAP	99%	AC2 / ToLCNDV ABA00495	1177-1596: 420	139	15.7
							REn	99%	AC3 Protein / ToLCNDV NP_803222	1047-1457: 411	136	16.1
8.	KF551592	India	Tomato	2739	88%	ToLCNDV-[IN:Mah:Svr:08] HM345979	CP	83%	AV1 Protein / ToLCNDV-[IN:Bha:12] AGV02034	280-1050: 771	256	29.5
							V2	72%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	13
							C5	73%	AC5 / ToLCNDV-[IN:Aur:OY164A:06] ADO41081	310-795: 486	161	18.2
							TrAP	81%	AC2 / ToLCNDV AJW80911	1177-1596: 420	139	15.7
							C4	72%	AC4 / ToLCNDV ACZ63316	2251-2427: 177	58	66.4
							REn	99%	AC3 / ToLCNDV AHA82178	1047-1457: 411	136	16.1
							Rep	82%	AC1 / ToLCGV-[IN:Pun:08] ADK55535	1499-2584: 1086	361	40.5

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
9.	DQ169056	India	Tomato	2739	98%	ToLCNDV-[Pum:IARI:06] JN129254	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.5
							V3	97%	AV3 / ToLCNDV AEF38353	41-427: 387	128	14.7
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							C5	97%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.8
							C4	97%	AC4 Protein / ToLCNDV-[IN:Bha:12] AGV02038	2251-2427: 177	58	65.9
							TrAP	99%	TrAP / ToLCNDV AER93214	1177-1596: 420	139	15.7
							REn	99%	REn / ToLCNDV AER93213	1047-1457: 411	136	16.1
							Rep	99%	Rep / ToLCNDV-[PK:Sol:97] CAF04471	1499-2584: 1086	361	41
10.	AJ620187	Pakistan	*Solanum nigrum*	2740	98%	ToLCNDV-IN[PK:Kha:Chi:04] DQ116880	CP	99%	CP / ToLCNDV ABB52025	281-1051: 771	256	29.5
							V3	98%	V3 / ToLCNDV-[PK:Sol:97] ABB52058	42-428: 387	128	14.6
							V2	99%	Pre-Coat Protein / ToLCNDV-[PK:Mul:Luf:05] CAL22868	121-459: 339	112	12.9
							C5	94%	AC5 Protein / ToLCNDV-[PK:Mul:Luf:05] CAL22870	311-796: 486	161	17.8
							TrAP	96%	TrAP / ToLCNDV CAO98745	1178-1597: 420	139	15.6
							C4	95%	AC4/ ToLCNDV AER93216	2252-2428: 177	58	65.8
							REn	97%	REn / ToLCNDV-[IN:Tum:Chi:08] AEA76854	1048-1458: 411	136	16.2
							Rep	99%	Rep / ToLCNDV ABA00492	1500-2585: 1086	361	40.9
11.	HM345979	India	Tomato	2739	99%	ToLCNDV-[IN:Pun:08] HQ141673	CP	99%	CP / ToLCNDV-JID27 ADT70813	280-1050: 771	256	29.4
							V2	99%	Pre-Coat Protein / ToLCNDV-IN [IN:Tum:Chi:08] AEA76850	120-458: 339	112	12.9
							C5	97%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.8
							TrAP	99%	TrAP / ToLCNDV ACK44131	1177-1596: 420	139	15.8
							C4	98%	PTGS Suppressor / ToLCNDV-JID27 ADT70817	2251-2427: 177	58	66.1

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	REn	99%	REn / ToLCNDV-JID27 ADT70816	1047-1457: 411	136	16.1
							Rep	99%	Rep / ToLCNDV-JID27 ADT70814	1499-2584: 1086	361	40.9
12.	HG316125	Pakistan	*Rumex dentatus*	2735	99%	ToLCNDV-[PK:Fai:09] FN435310	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.4
							V2	99%	AV2 / ToLCNDV NP_803219	120-458: 339	112	12.9
							V3	95%	V3 / ToLCNDV-[PK:Sol:09] CBA13464	89-427: 339	112	12.9
							C5	99%	AC5 / ToLCNDV NP_803221	310-672: 363	120	13.2
							C4	98%	AC4 Protein / ToLCNDV CAQ19352	2251-2427: 177	58	65.9
							TrAP	99%	TrAP / ToLCNDV AER93214	1177-1596: 420	139	15.7
							REn	99%	Rep protein 3 / ToLCNDV-[Luc] CAA76214	1047-1457: 411	136	16.1
							Rep	98%	Rep / ToLCNDV-[PK:Sol:97] CAF04471	1499-2584: 1086	361	40.8
13.	AM947506 FN435309	Pakistan	Tomato	2736	97%	ToLCNDV-IN[IN:ND:Svr:92] U15015	CP	96%	CP / ToLCNDV AJY58643	280-1050: 771	256	29.4
							V2	96%	AV2 / ToLCNDV CAX51842	120-458: 339	112	12.9
							V3	90%	V3 / ToLCNDV-[PK:Sol:97] ABB52044	41-397: 357	118	13.4
							C5	91%	AC5 / ToLCNDV CAJ90653	310-795: 486	161	18.1
							C4	98%	AC4 Protein / ToLCNDV NP_803225	2248-2424: 177	58	66
							TrAP	97%	AC2 / ToLCNDV-Svr ADM36030	1177-1593: 417	138	15.5
							REn	97%	AC3 / ToLCNDV NP_803222	1047-1457: 411	136	16
							Rep	98%	Rep / ToLCNDV ABB52024	1499-2581: 1083	360	40.8
14.	HQ141673	India	Tomato	2739	99%	ToLCNDV-[IN:Mah:Svr:08] HM345979	CP	99%	CP / ToLCNDV ANS81420	280-1050: 771	256	29.4
							V2	99%	AV2 / ToLCNDV AHA82166	120-458: 339	112	12.9
							C5	97%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.8
							TrAP	99%	TrAP / ToLCNDV ACK44131	1177-1596: 420	139	15.8

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C4	95%	AC4 / ToLCNDV-Svr ADM36028	2251-2427: 177	58	65.8
							REn	99%	Transcription Enhancer Protein / ToLCNDV ADN65586	1047-1457: 411	136	16.1
							Rep	99%	Replication Initiation Protein / ToLCNDV ADN65588	1499-2584: 1086	361	40.9
15.	KP195262	India	Tomato	2739	98%	ToLCNDV-[IN:Mah:Svr:08] HM345979	CP	99%	CP / ToLCNDV AJE24778	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	13
							C5	96%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.7
							C4	97%	AC4 Protein / ToLCNDV ABA00499	2251-2427: 177	58	66.1
							TrAP	96%	TrAP / ToLCNDV CAO98745	1177-1596: 420	139	15.8
							REn	99%	AC3 / ToLCNDV-IN [IN:His:Cot:05] ABK41854	1047-1457: 411	136	16
							Rep	99%	Replication Initiation Protein / ToLCNDV ADN65588	1499-2584: 1086	361	40.9
16.	KF515617	India	Tomato	2739	98%	ToLCNDV-[IN:Mah:Svr:08] HM345979	CP	99%	AV1 / ToLCNDV-[IN:Bha:12] AGV02034	280-1050: 771	256	29.4
							V2	99%	Pre-Coat Protein / ToLCNDV-IN [IN:Tum:Chi:08] AEA76850	120-458: 339	112	12.9
							C5	97%	Unknown / ToLCNDV ADN65589	310-795: 486	161	17.7
							TrAP	98%	TrAP / ToLCNDV-[ND:Pum] CAL15160	1177-1596: 420	139	15.7
							C4	97%	AC4 Protein / ToLCNDV-[IN:Bha:12] AGV02038	2251-2427: 177	58	65.8
							REn	99%	AC3 / ToLCNDV AHA82178	1047-1457: 411	136	16
							Rep	98%	Replication associated Protein / ToLCNDV-[PK:Sol:97] CAF04471	1499-2584: 1086	361	40.9
17.	KF515616	India	Tomato	2739	99%	ToLCNDV-[IN:Jun:12] KF515617	CP	99%	AV1 Protein / ToLCNDV-[IN:Jun:12] AGV02040	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	13
							C5	98%	Unknown / ToLCNDV ADN65589	310-795: 486	161	17.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	98%	AC2 / ToLCNDV AHA82177	1177-1596: 420	139	15.7
							C4	97%	AC4 Protein / ToLCNDV ABA00499	2251-2427: 177	58	66.1
							REn	99%	AC3 / ToLCNDV AHA82178	1047-1457: 411	136	16
							Rep	98%	AC1 Protein / ToLCNDV-[IN:Jun:12] AGV02043	1499-2584: 1086	361	40.8
18.	HM007120	India	Chilli	2740	99%	ToLCNDV-[IN:Chi:09] KP235542	CP	99%	AV1 Protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							V3	98%	AV3 / ToLCNDV-Svr ADM36024	41-427: 387	128	14.8
							C5	99%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.8
							TrAP	99%	TrAP / ToLCNDV AKN79147	1177-1596: 420	139	15.7
							C4	98%	AC4 / ToLCNDV AKM49927	2251-2427: 177	58	65.8
							REn	99%	REn / ToLCNDV AKN79148	1047-1457: 411	136	16.1
							Rep	97%	Replication associated protein / ToLCNDV AJE24768	1499-2584: 1086	361	40.9
19.	KP235542	India	Chilli	2740	99%	ToLCNDV-[IN:Tum:Chi:08] HM007120	CP	99%	AV1 Protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							V3	98%	AV3 / ToLCNDV-Svr ADM36024	41-427: 387	128	14.8
							C5	99%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.8
							C4	98%	AC4 / ToLCNDV AKM49927	2251-2427: 177	58	65.8
							TrAP	99%	TrAP / ToLCNDV AKN79147	1177-1596: 420	139	15.7
							REn	99%	REn / ToLCNDV AKN79148	1047-1457: 411	136	16.1
							Rep	97%	Replication associated protein / ToLCNDV AJE24768	1499-2584: 1086	361	40.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
20.	FJ468356	India	Tomato	2739	99%	ToLCNDV-[IN:Mah:Svr:08] HM345979	CP	99%	CP / ToLCNDV-JID27 ADT70813	280-1050: 771	256	29.4
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	13
							C5	97%	Unknown / ToLCNDV ADN65589	310-795: 486	161	17.8
							C4	95%	AC4 / ToLCNDV-Svr ADM36028	2251-2427: 177	58	65.8
							TrAP	99%	Transcription Enhancer Protein / ToLCNDV ADN65587	1177-1596: 420	139	15.8
							REn	99%	Transcription Enhancer Protein / ToLCNDV ADN65586	1047-1457: 411	136	16
							Rep	99%	Replication Initiation Protein / ToLCNDV ADN65588	1499-2584: 1086	361	41
21.	KP235540	India	Chilli	2740	99%	ToLCNDV-[IN:Tum:Chi:08] HM007120	CP	99%	AV1 Protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV-IN [IN:Tum:Chi:08] AEA76850	120-458: 339	112	12.9
							V3	98%	AV3 / ToLCNDV-Svr ADM36024	41-427: 387	128	14.7
							C5	99%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.8
							C4	98%	AC4 / ToLCNDV AKM49927	2251-2427: 177	58	65.8
							TrAP	99%	TrAP / ToLCNDV-IN[IN:Tum:Chi:08] AEA76853	1177-1596: 420	139	15.6
							REn	99%	REn / ToLCNDV-IN[IN:Tum:Chi:08] AEA76854	1047-1457: 411	136	16.1
							Rep	97%	Replication associated Protein / ToLCNDV AJE24768	1499-2584: 1086	361	40.9
22.	AF448059	Pakistan	Tomato	2739	97%	ToLCNDV-IN[PK:Sol:97] AJ620187	CP	98%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.5
							V2	96%	Pre-Coat Protein / ToLCNDV ABA00498	120-458: 339	112	13
							V3	95%	AV3 / ToLCNDV AEF38353	41-427: 387	128	14.5
							C5	96%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.8
							C4	95%	PTGS Suppressor / ToLCNDV-JID27 ADT70817	2251-2427: 177	58	65.5
							TrAP	97%	AC2 / ToLCNDV-Svr ADM36030	1177-1596: 420	139	15.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	REn	97%	AC3 / ToLCNDV-Svr ADM36029	1047-1457: 411	136	16
							Rep	98%	Replication associated Protein / ToLCNDV-[PK:Sol:97] CAF04471	1499-2584: 1086	361	41
23.	AM286434	India	Pumpkin	2739	99%	ToLCNDV-[IN:ND:Pum:01] AM286433	CP	99%	AV1 / ToLCNDV-Mld AAA92817	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							V3	97%	V3 / ToLCNDV-[Chi] ABB52029	41-427: 387	128	14.7
							C5	98%	AC5 Protein / ToLCNDV ABA00494	310-672: 363	120	13.2
							C4	98%	AC4 / ToLCNDV AEX15668	2251-2427: 177	58	65.8
							TrAP	99%	TrAP / ToLCNDV-IN AGK29963	1177-1596: 420	139	15.7
							REn	99%	REn / ToLCNDV AEX15666	1047-1457: 411	136	16.1
							Rep	99%	Replication associated Protein / ToLCNDV-[ND:Pum] CAL15161	1499-2584: 1086	361	40.9
24.	AM286433	India	Pumpkin	2738	99%	ToLCNDV-[IN:ND:Ash:11] JN208136	CP	99%	CP / ToLCNDV AEX15665	280-1050: 771	256	29.4
							V2	99%	AV2 / ToLCNDV AEX15664	120-458: 339	112	12.8
							V3	99%	AV3 / ToLCNDV AEX15669	41-427: 387	128	14.7
							C5	98%	AC5 Protein / ToLCNDV ABA00494	310-672: 363	120	13.2
							C4	98%	AC4 / ToLCNDV AEX15668	2251-2427: 177	58	65.8
							TrAP	99%	TrAP / ToLCNDV AGK29963	1177-1596: 420	139	15.7
							REn	99%	REn / ToLCNDV AEX15666	1047-1457: 411	136	16.1
							Rep	99%	Replication associated Protein / ToLCNDV-[ND:Pum] CAL15167	1499-2584: 1086	361	40.9
25.	JX232220	India	Tomato	2736	97%	ToLCNDV-[IN:ND:Pum:01] AM286434	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							V3	98%	AV3 / ToLCNDV-[IN:ND:Pap:05] ABJ97333	41-427: 387	128	14.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C4	98%	AC4 Protein / ToLCNDV-[IN:ND:Pum] CAL15162	2248-2424: 177	58	65.9
							C5	99%	AC5 / ToLCNDV-Mld AAA92818	310-795: 486	161	17.8
							TrAP	99%	AC2 / ToLCNDV AJW80911	1174-1593: 420	139	15.7
							REn	90%	AC3 / ToLCNDV AJW80912	1047-1454: 408	135	16.1
							Rep	98%	AC1 / ToLCNDV AJW80910	1496-2581: 1086	361	40.8
26.	KF551577	India	Tomato	2739	98%	ToLCNDV-[IN:Bha:12] KF515616	CP	97%	CP / ToLCNDV CAH17798	280-1050: 771	256	29.4
							V2	88%	Pre-Coat Protein / ToLCNDV-IN [IN:Tum:Chi:08] AEA76850	120-458: 339	112	12.9
							V3	87%	AV3 / ToLCNDV-Svr ADM36024	41-427: 387	128	14.3
							C5	96%	Unknown / ToLCNDV ADN65589	310-795: 486	161	17.7
							C4	95%	AC4 / ToLCNDV AHA82171	2251-2427: 177	58	66.3
							TrAP	98%	AC2 Protein / ToLCNDV-[IN:Bha:12] AGV02036	1177-1596: 420	139	15.8
							REn	99%	AC3 Protein / ToLCNDV-[IN:Bha:12] AGV02035	1047-1457: 411	136	16.1
							Rep	94%	AC1 Protein / ToLCNDV-[IN:Bha:12] AGV02037	1499-2584: 1086	361	40.7
27.	AM292302	Pakistan	*Luffa cylindrica*	2739	98%	ToLCNDV-[PK:Swa:15] LT556081	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.5
							V2	99%	V2 Protein / ToLCNDV-[PK:Sol:97] CAF04467	120-458: 339	112	12.9
							V3	98%	AV3 Protein / ToLCNDV SAM29899	41-427: 387	128	14.7
							C5	96%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.7
							C4	93%	C4 Protein / ToLCNDV-[PK:Sol:97] CAF04472	2251-2427: 177	58	66.9
							TrAP	97%	TrAP / ToLCNDV AGK29963	1177-1596: 420	139	15.6
							REn	96%	Transcripton Enhancer Protein / ToLCNDV ADN65586	1047-1457: 411	136	16
							Rep	99%	Replication associated Protein / ToLCNDV SAM29932	1499-2584: 1086	361	41

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
28.	AF448058	Pakistan	Tomato	2740	96%	ToLCNDV-[IN:Tum:Chi:08] HM007120	CP	99%	AV1 / ToLCNDV AHB37373	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCNDV AHA82194	120-458: 339	112	13
							V3	96%	V3 / ToLCNDV-[PK:Sol:97] ABB52044	41-427: 387	128	14.5
							C5	94%	AC5 Protein / ToLCNDV CRI05841	310-795: 486	161	17.8
							C4	95%	AC4 Protein / ToLCNDV-IN [IN:Tum:Chi:08] AEA76855	2251-2427: 177	58	66.2
							TrAP	97%	TrAP / ToLCNDV-[PK:Sol:97] CAF04470	1177-1596: 420	139	15.7
							REn	96%	AC3 / ToLCNDV ABU95064	1047-1457: 411	136	16.1
							Rep	98%	Rep / ToLCNDV-IN[IN:Tum:Chi:08] AEA76852	1499-2584: 1086	361	40.9
29.	KP178729	India	Tomato	2739	97%	ToLCNDV-[IN:12] JX232220	CP	99%	CP / ToLCNDV-[PK:Sol:97] ABB52054	280-1050: 771	256	29.4
							V2	96%	Pre-Coat Protein / ToLCNDV CRI05839	120-458: 339	112	13
							V3	95%	AV3 / ToLCNDV AFQ62670	41-427: 387	128	14.5
							C5	94%	C5 / ToLCNDV-[PK:Kha:Chi] ABB52030	310-795: 486	161	17.9
							C4	93%	AC4 Protein / ToLCNDV AHJ80140	2251-2427: 177	58	65.8
							TrAP	99%	AC2 / ToLCNDV AFQ62675	1177-1596: 420	139	15.7
							REn	97%	REn / ToLCNDV CAJ90654	1047-1457: 411	136	16
							Rep	98%	Replication initiator Protein / ToLCNDV-[Pot] AGR88343	1499-2584: 1086	361	40.8
30.	JN208136	India	*Benincasa hispida* (ash gourd)	2738	99%	ToLCNDV-[IN:ND:Pum:01] AM286433	CP	99%	CP / ToLCNDV-[IN:ND:Pum] CAL15158	280-1050: 771	256	29.3
							V2	99%	AV2 / ToLCNDV-[IN:ND:Pum] CAL15157	120-458: 339	112	12.9
							V3	92%	AV3 / ToLCNDV AEF38353	41-427: 387	128	14.8
							C5	97%	AC5 Protein / ToLCNDV ABA00494	310-672: 363	120	13.3

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C4	98%	AC4 Protein / ToLCNDV [IN:ND:Pum] CAL15162	2251-2427: 177	58	65.6
							TrAP	99%	TrAP / ToLCNDV-[IN:ND:Pum] CAL15160	1177-1596: 420	139	15.8
							REn	99%	REn / ToLCNDV-[IN:ND:Pum] CAL15159	1047-1457: 411	136	16
							Rep	99%	Replication associated protein / ToLCNDV-[ND:Pum] CAL15161	1499-2584: 1086	361	40.9
31.	HM989845	India	*Luffa acutangula*	2739	99%	ToLCNDV-[PK:Rwp:Cuc:12] KT948072	CP	99%	AV1 Protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V2	98%	Pre-Coat Protein / ToLCNDV ABA00498	120-458: 339	112	12.9
							C5	96%	AC5 / ToLCNDV-IN[IN:His:Cot:05] ABK41852	310-795: 486	161	17.9
							C4	98%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66
							TrAP	99%	AC2 / ToLCNDV-IN[IN:His:Cot:05] ABK41855	1177-1596: 420	139	15.7
							REn	99%	Ren Protein / ToLCNDV AER93213	1047-1457: 411	136	16.1
							Rep	99%	AC1 / ToLCNDV AAY44735	1499-2584: 1086	361	40.9
32.	KC874507	India	Potato	2739	99%	ToLCNDV-[IR:Zab:Cuc:14] KP641675	CP	99%	CP / ToLCNDV-[Pot] AGG20240	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 Protein / ToLCNDV CAO98805	310-795: 486	161	18.3
							C4	97%	AC4 / ToLCNDV AKM49927	2251-2427: 177	58	65.8
							TrAP	99%	TrAP / ToLCNDV-[Pot] ABL09092	1177-1596: 420	139	15.8
							REn	99%	REn Protein / ToLCNDV CAO98806	1047-1457: 411	136	16.1
							Rep	99%	Replication initiator Protein / ToLCNDV-[Pot] ABL09091	1499-2584: 1086	361	41

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
33.	KC874502	India	Potato	2739	99%	ToLCNDV-IN[IN:Mer:Pot:05] EF043231	CP	99%	AV1 / ToLCNDV-[Pot] AAP37406	279-1049: 771	256	29.5
							V2	98%	Pre-Coat Protein / ToLCNDV-[Pot] ABL09097	119-457: 339	112	12.9
							C5	98%	AC5 Protein / ToLCNDV-[Pot] AGR88312	309-794: 486	161	18.3
							C4	98%	AC4 Protein / ToLCNDV-[Pot] ABL09101	2250-2426: 177	58	65.2
							TrAP	99%	AC2 / ToLCNDV-[Pot] AAP37409	1176-1595: 420	139	15.8
							REn	99%	REn Protein / ToLCNDV-[Pot] ABL09093	1046-1456: 411	136	16.1
							Rep	99%	AC1 / ToLCNDV-[Pot] AAP37410	1498-2583: 1086	361	41
34.	KC545812	India	*Cucumis sativus*	2739	98%	ToLCNDV-[IN:ND:Luf:10] HM989845	CP	99%	AV1 / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.4
							V2	99%	Pre-Coat Protein / ToLCNDV ABA00498	120-458: 339	112	12.8
							C5	98%	AC5 / ToLCNDV AAY44736	310-672: 363	120	13.2
							C4	98%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66
							TrAP	99%	TrAP / ToLCNDV-JLX10 ADT70804	1177-1596: 420	139	15.7
							REn	99%	Ren Protein / ToLCNDV CAJ90654	1047-1457: 411	136	16.2
							Rep	99%	AC1 ToLCNDV AAY44735	1499-2584: 1086	361	40.9
35.	KP641675	Iran	Cucumber	2739	99%	ToLCNDV-[IN:Mod:Pot:11] KC874507	CP	99%	CP / ToLCNDV-[Pot] AGG20240	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 Protein / ToLCNDV CAO98805	310-795: 486	161	18.3
							C4	97%	AC4 / ToLCNDV AKM49927	2251-2427: 177	58	65.8
							TrAP	99%	TrAP / ToLCNDV-[Pot] ABL09092	1177-1596: 420	139	15.8
							REn	99%	REn Protein / ToLCNDV CAO98806	1047-1457: 411	136	16.1

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	Rep	99%	Replication Initiator Protein / ToLCNDV-[Pot] ABL09091	1499-2584: 1086	361	41
36.	KC874505	India	Potato	2740	99%	ToLCNDV-[IN:Gwa:Pot:10] KC874504	CP	99%	CP / ToLCNDV-[Pot] AGG20247	280-1050: 771	256	29.5
							V2	99%	AV2 Protein / ToLCNDV-[PkT5/6] AAL60212	120-458: 339	112	13
							V3	92%	AV3 Protein / ToLCNDV-[PkT5/6] AAL60211	41-427: 387	128	14.5
							C4	98%	AC4 / ToLCNDV AHA61379	2251-2433: 183	60	70
							C5	98%	AC5 Protein / ToLCNDV-[Pot] AGR88319	310-795: 486	161	18
							TrAP	96%	TrAP / ToLCNDV-[Pot] AGR88321	1177-1596: 420	139	15.6
							REn	96%	AC3 / ToLCNDV-[Pot] AAP37408	1047-1457: 411	136	16
							Rep	99%	Replication Initiator Protein / ToLCNDV-[Pot] AGR88322	1499-2584: 1086	361	40.9
37.	EF620534	Pakistan	Tomato	2740	96%	ToLCNDV-[IN:ND:Luf:10] HM989845	CP	99%	AV1 Protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV-[PK:Mul:Luf:05] CAL22868	120-458: 339	112	12.9
							V3	97%	V3 / ToLCNDV-[PK:Sol:97] ABB52044	41-427: 387	128	14.6
							C5	94%	AC5 / ToLCNDV AAR28542	310-795: 486	161	17.9
							C4	91%	AC4 / ToLCNDV AJW80913	2251-2427: 177	58	66.2
							TrAP	97%	TrAP / ToLCNDV-[PK:Sol:97] CAF04470	1177-1596: 420	139	15.6
							REn	96%	AC3 Protein / ToLCNDV-[PkT5/6] AAN76346	1047-1457: 411	136	16.1
							Rep	98%	AC1 / ToLCNDV AAY44735	1499-2584: 1086	361	40.9
38.	DQ116883	Pakistan	Tomato	2739	97%	ToLCNDV-IN[PK:RYK:04] DQ116885	CP	99%	CP / ToLCNDV-[PK:Sol:97] ABB52054	280-1050: 771	256	29.4
							V2	99%	Pre-Coat Protein / ToLCNDV-[PK:Mul:Luf:05] CAL22868	120-458: 339	112	12.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	V3	98%	V3 / ToLCNDV-[PK:Sol:97] ABB52058	41-427: 387	128	14.5
							C5	98%	AC5 Protein / ToLCNDV SAM29891	310-672: 363	120	13.2
							TrAP	95%	AC2 / ToLCNDV AJW80817	1192-1596: 405	134	15.2
							C4	97%	AC4 Protein / ToLCNDV-[Pot] ABL09094	2251-2427: 177	58	66.3
							REn	97%	C3 / ToLCNDV-[PK:Sol:97] ABB52055	1047-1457: 411	136	16.1
							Rep	98%	Replication asociated protein / ToLCNDV ABA00492	1499-2584: 1086	361	41
39.	KC513822	India	*Papaver somniferum* (poppy)	2739	98%	ToLCNDV-[IN:Chi:09] KU196750	CP	99%	AV1 Protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							V3	98%	AV3 / ToLCNDV AFQ62670	41-427: 387	128	14.7
							C5	95%	AC5 / ToLCNDV-[IN:ND:Pap:05] ABJ97336	310-795: 486	161	18.1
							C4	98%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66
							TrAP	99%	TrAP / ToLCNDV-[IN:ND:Pum] CAL15160	1177-1596: 420	139	15.7
							REn	99%	REn / ToLCNDV-[IN:ND:Pum] CAL15159	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV AAY44735	1499-2584: 1086	361	40.9
40.	KC874506	India	Potato	2740	99%	ToLCNDV-IN[IN:Hap:Pot:05] EF043230	CP	99%	CP / ToLCNDV-[Pot] AGG20240	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 Protein / ToLCNDV CAO98805	310-795: 486	161	18.3
							TrAP	99%	TrAP / ToLCNDV-[Pot] ABL09092	1177-1596: 420	139	15.9
							C4	97%	AC4 protein / ToLCNDV-[Pot] AGR88309	2251-2427: 177	58	65.5
							REn	99%	Ren Protein / ToLCNDV CAO98806	1047-1457: 411	136	16.1

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	Rep	99%	Replication intiator protein / ToLCNDV-[Pot] ABL09091	1499-2584: 1086	361	41
41.	EF043230	India	Potato	2739	99%	ToLCNDV-[IN:Dee:Pot:11] KC874506	CP	99%	CP / ToLCNDV-[Pot] AGG20240	280-1050: 771	256	29.5
							V2	98%	Pre-Coat Protein / ToLCNDV-[Pot] ABL09097	120-458: 339	112	13
							C5	99%	AC5 / ToLCNDV CAO98805	310-795: 486	161	18.2
							C4	97%	AC4 protein / ToLCNDV-[Pot] AGR88309	2251-2427: 177	58	65.5
							TrAP	99%	TrAP / ToLCNDV-[Pot] AGR88342	1177-1596: 420	139	15.8
							REn	99%	REn Protein / ToLCNDV CAO98806	1047-1457: 411	136	16.1
							Rep	99%	Replication intiator protein / ToLCNDV-[Pot] AGR88336	1499-2584: 1086	361	41
42.	KM383736	Bangladesh	Tomato	2739	98%	ToLCNDV-[BD:Syl:06] KM383737	CP	99%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV ABA00498	120-458: 339	112	12.9
							C5	98%	AC5 Protein / ToLCNDV AJE24752	310-672: 363	120	13
							C4	97%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	67.3
							TrAP	99%	TrAP / ToLCNDV AJE24802	1192-1596: 405	134	15.2
							REn	99%	AC2 / ToLCNDV-[Luf] AAD14626	1047-1457: 411	136	16.1
							Rep	98%	Replication associated protein / ToLCNDV AJE24761	1499-2584: 1086	361	40.9
43.	KC874503	India	Potato	2740	99%	ToLCNDV-IN[IN:Mee:Po12:02] AY286316	CP	99%	AV1 / ToLCNDV-[Pot] AAP37406	280-1050: 771	256	29.4
							V2	98%	Pre-Coat Protein / ToLCNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 Protein / ToLCNDV-[Pot] AGR88347	310-795: 486	161	18.1
							C4	98%	AC4 / ToLCNDV-[Pot] AAP37411	2251-2427: 177	58	65.4
							TrAP	99%	TrAP / ToLCNDV-[Pot] AGR88349	1177-1596: 420	139	15.8

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	REn	99%	AC3 / ToLCNDV ADP44681	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV-[Pot] AAP37410	1499-2584: 1086	361	41
44.	AM850115	India	Potato	2740	99%	ToLCNDV-[IR:Zab:14] KP641677	CP	99%	CP / ToLCNDV-[Pot] ABL09089	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 Protein / ToLCNDV-[Pot] AGR88333	310-795: 486	161	18.3
							C4	97%	AC4 Protein / ToLCNDV-[Pot] AGR88309	2251-2427: 177	58	65.5
							TrAP	99%	TrAP / ToLCNDV-[Pot] ABL09092	1177-1596: 420	139	15.8
							REn	99%	REn / TOLCNDV-[Pot] ABL09093	1047-1457: 411	136	16.1
							Rep	99%	Replication initiator protein / ToLCNDV-[Pot] ABL09091	1499-2584: 1086	361	41.1
45.	KM383738	Bangladesh	Tomato	2739	99%	ToLCNDV-[BD:Syl:06] KM383737	CP	99%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV ABA00498	120-458: 339	112	12.9
							C4	98%	AC4 / ToLCNDV-Mld AAA92822	2251-2427: 177	58	66.3
							TrAP	99%	TrAP / ToLCNDV AJE24774	1192-1596: 405	134	15.2
							REn	99%	REn Protein / ToLCNDV AJE24746	1047-1457: 411	136	16.1
							Rep	99%	Replication associated protein / ToLCNDV AJE24755	1499-2584: 1086	361	40.8
46.	Y16421	India	Tomato	2739	97%	ToLCNDV-[IN:Bwp:Chi:06] EU309045 HQ658479	CP	99%	CP / ToLCNDV ABB52025	280-1050: 771	256	29.4
							V2	99%	Pre-Coat Protein / ToLCNDV ABO31249	120-458: 339	112	12.9
							V3	94%	V3 / ToLCNDV ABB52029	41-427: 387	128	14.7
							C4	95%	AC4 / ToLCNDV AHA61379	2251-2427: 177	58	66.2
							TrAP	99%	TrAP / ToLCNDV AAR28539	1177-1596: 420	139	15.6

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	REn	99%	Transcription enhancer protein / ToLCNDV ABO31252	1047-1457: 411	136	16.1
							Rep	97%	Replication associated protein / ToLCNDV AJE24768	1499-2584: 1086	361	40.9
47.	EF043231	India	Potato	2740	99%	ToLCNDV-[IN:Dee:Pot:11] KC874506	CP	97%	CP / ToLCNDV CAO00517	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV CAO98803	120-458: 339	112	12.9
							C5	98%	AC5 / ToLCNDV CAO98805	310-795: 486	161	18.2
							C4	98%	AC4 Protein / ToLCNDV-[Pot] AGR88309	2251-2427: 177	58	65.5
							TrAP	99%	AC2 / ToLCNDV-[Pot] AAP37409	1177-1596: 420	139	15.9
							Rep	99%	Replication initiator protein / ToLCNDV-[Pot] AGR88308	1499-2584: 1086	361	41
48.	LT556081	Pakistan	Tomato	2739	100%	ToLCNDV-[PK:Lhr:15] LT556076	CP	99%	CP / ToLCNDV ABB52025	280-1050: 771	256	29.4
							V2	99%	V2 Protein / ToLCNDV-[PK:Sol:97] CAF04467	120-458: 339	112	12.9
							V3	98%	AV3 Protein / ToKLCNDV-[PK:Mul:Luf] CAL22867	41-427: 387	128	14.7
							C5	98%	AC5 Protein / ToLCNDV SAM29891	310-795: 486	161	17.8
							C4	93%	C4 Protein / ToLCNDV-[PK:Sol:97] CAF04472	2251-2427: 177	58	66.9
							TrAP	93%	AC2 / ToLCNDV AJW80911	1177-1596: 420	139	15.6
							REn	93%	REn Protein / ToLCNDV-[PK:Mul:Luf] CAL22871	1047-1457: 411	136	16
							Rep	99%	Replication associated protein / ToLCNDV-[PK:Mul:Luf] CAL22873	1499-2584: 1086	361	41
49.	LT556076	Pakistan	Tomato	2739	100%	ToLCNDV-[PK:Swa:15] LT556081	CP	99%	CP / ToLCNDV ABB52025	280-1050: 771	256	29.4
							V2	99%	V2 Protein / ToLCNDV-[PK:Sol:97] CAF04467	120-458: 339	112	12.9
							V3	98%	AV3 Protein / ToKLCNDV-[PK:Mul:Luf] CAL22867	41-427: 387	128	14.7
							C5	98%	AC5 Protein / ToLCNDV SAM29891	310-795: 486	161	17.8

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C4	93%	C4 Protein / ToLCNDV-[PK:Sol:97] CAF04472	2251-2427: 177	58	66.9
							TrAP	93%	AC2 / ToLCNDV AJW80911	1177-1596: 420	139	15.6
							REn	93%	REn Protein / ToLCNDV-[PK:Mul:Luf] CAL22871	1047-1457: 411	136	16
							Rep	99%	Replication associated protein / ToLCNDV-[PK:Mul:Luf] CAL22873	1499-2584: 1086	361	41
50.	LT556074	Pakistan	Tomato	2739	100%	ToLCNDV-[PK:Swa:15] LT556081	CP	99%	CP / ToLCNDV ABB52025	280-1050: 771	256	29.4
							V2	99%	V2 Protein / ToLCNDV-[PK:Sol:97] CAF04467	120-458: 339	112	12.9
							V3	98%	AV3 Protein / ToKLCNDV-[PK:Mul:Luf] CAL22867	41-427: 387	128	14.7
							C5	98%	AC5 Protein / ToLCNDV SAM29891	310-795: 486	161	17.8
							C4	93%	C4 Protein / ToLCNDV-[PK:Sol:97] CAF04472	2251-2427: 177	58	66.9
							TrAP	93%	AC2 / ToLCNDV AJW80911	1177-1596: 420	139	15.6
							REn	93%	REn Protein / ToLCNDV-[PK:Mul:Luf] CAL22871	1047-1457: 411	136	16
							Rep	99%	Replication associated protein / ToLCNDV-[PK:Mul:Luf] CAL22873	1499-2584: 1086	361	41
51.	KT948072	Pakistan	*Cucurbita pepo*	2739	99%	ToLCNDV-[IN:ND:Luf:10] HM989845	CP	99%	AV1 Protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV ABA00498	120-458: 339	112	12.9
							C5	98%	Unknown / ToLCNDV-JLX10 ADT70807	310-795: 486	161	17.9
							C4	98%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66
							TrAP	99%	TrAP / ToLCNDV-JLX10 ADT70804	1177-1596: 420	139	15.7
							REn	98%	REn / ToLCNDV-[IN:ND:Pum] CAL15159	1047-1457: 411	136	16

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	Rep	99%	Replication initiation Protein / ToLCNDV-JLX10 ADT70803	1499-2584: 1086	361	41
52.	KM383740	Bangladesh	Tomato	2739	99%	ToLCNDV-[BD:Joy:06] KM383738	CP	99%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.5
							V2	98%	Pre-Coat Protein / ToLCNDV AJE24743	120-458: 339	112	13
							V3	96%	V3 / ToLCNDV ABB52029	41-427: 387	128	14.7
							C5	94%	AC5 Protein / ToLCNDV AJE24745	310-672: 363	120	13
							C4	98%	C4 Protein / ToLCNDV-Mild AAA92822	2251-2427: 177	58	66.3
							TrAP	99%	Transcriptional activator protein / ToLCNDV AJE24754	1192-1596: 405	134	15.2
							REn	99%	REn Protein / ToLCNDV AJE24746	1047-1457: 411	136	16.1
							Rep	99%	Replication associated protein / ToLCNDV AJE24755	1499-2584: 1086	361	40.8
53.	KM383737	Bangladesh	Tomato	2739	99%	ToLCNDV-[BD:Joy:06] KM383738	CP	99%	AV1 / ToLCNDV-[TH:Cuc] BAF69030	280-1050: 771	256	29.5
							V2	99%	Pre-Coat Protein / ToLCNDV ABA00498	120-458: 339	112	12.9
							C5	98%	AC5 Protein / ToLCNDV AJE24745	310-672: 363	120	13.1
							C4	98%	C4 Protein / ToLCNDV-Mild AAA92822	2251-2427: 177	58	66.3
							TrAP	99%	TrAP / ToLCNDV AJE24774	1192-1596: 405	134	15.2
							REn	99%	REn Protein / ToLCNDV AJE24746	1047-1457: 411	136	16.1
							Rep	99%	Replication associated protein / ToLCNDV AJE24761	1499-2584: 1086	361	40.8
54.	AY286316	India	Potato	2740	99%	ToLCNDV-[IN:His:Pot:10] KC874503	CP	99%	CP / ToLCNDV-[Pot] AGG20216	280-1050: 771	256	29.4
							V2	98%	Pre-Coat Protein / ToLCNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	98%	AC5 Protein / ToLCNDV-[Pot] AGR88312	310-795: 486	161	18.2

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C4	98%	AC4 Protein / ToLCNDV-[Pot] AGR88316	2251-2427: 177	58	65.2
							TrAP	99%	TrAP / ToLCNDV-[Pot] AGR88349	1177-1596: 420	139	15.8
							REn	99%	AC3 / ToLCNDV ADP44681	1047-1457: 411	136	16
							Rep	99%	Replication initiator protein / ToLCNDV-[Pot] AGR88315	1499-2584: 1086	361	41
55.	KC874504	India	Potato	2740	99%	ToLCNDV-[IN:Fai:Pot:11] KC874505	CP	99%	CP / ToLCNDV AGH07934	280-1050: 771	256	29.5
							V2	99%	AV2 Protein / ToLCNDV-[PkT5/6] AAL60212	120-458: 339	112	13
							C5	98%	AC5 Protein / ToLCNDV-[Pot] AGR88326	310-795: 486	161	18
							C4	97%	AC4 / ToLCNDV AHA61379	2251-2433: 183	60	69.2
							TrAP	96%	TrAP / ToLCNDV-[Pot] AGR88328	1177-1596: 420	139	15.7
							REn	97%	AC3 / ToLCNDV AHA82258	1047-1457: 411	136	16
							Rep	99%	Replication initiator protein / ToLCNDV-[Pot] AGR88329	1499-2584: 1086	361	40.9
56.	KF551587	India	Tomato	2740	97%	ToLCNDV-[IN:His:Pot:10] KC874503	CP	97%	AV1/ToLCNDV-[Pot] AAP37406	280-1050: 771	256	29.3
							V2	92%	AV2/ToLCNDV-[Pot] AAP37405	120-458: 339	112	13
							C5	94%	AC5/ ToLCNDV-[Pot] AGR88312	795-310: 486	161	18.2
							C4	98%	AC4 Protein / ToLCNDV-[Pot] AGR88316	2251-2427: 177	58	65.2
							TrAP	99%	TrAP / ToLCNDV-[Pot] AGR88349	1177-1596: 420	139	15.8
							REn	99%	AC3/ ToLCNDV ADP44681	1047-1457: 411	136	16
							Rep	99%	AC1/ ToLCNDV-[Pot] AAP37410	1499-2584: 1086	361	40.9
57.	KM383741	Bangladesh	Tomato	2740	98%	ToLCNDV-[BD:Jam:10] KM383742	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.5
							V2	99%	AV2 / ToLCKV AHA82181	120-449: 330	109	12.6
							C5	93%	AC5 / ToLCNDV AAR28542	310-588: 279	92	99
							C4	98%	AC4 Protein / ToLCNDV AJE24790	2251-2427: 177	58	65.6

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	99%	TrAP / ToLCNDV-Svr [Jes] CAI44690	1177-1596: 420	139	15.6
							REn	97%	REn protein / ToLCNDV AJE24766	1047-1457: 411	136	16.2
							Rep	98%	Replication-associated protein / ToLCNDV AJE24796	1499-2584: 1086	361	40.9
58.	AB613825	Indonesia	Cucumber	2739	96%	ToLCNDV-[TH:Cuc] AB330079	CP	99%	AV1/ ToLVNDV AHA82167	280-1050: 771	256	29.5
							V3	88%	AV3 / ToLCNDV ABU95060	41-427: 387	128	14.4
							V2	99%	Pre-Coat Protein / ToLCNDV ABA00498	120-458: 339	112	13
							C5	92%	AC5 / ToLVNDV AJE24800	310-672: 363	120	13.2
							C4	96%	AC4 / ToLCNDV- Mild AAA92822	2251-2433: 183	60	69.2
							TrAP	96%	AC2 / ToLCNDV AHA82257	1177-1596: 420	139	15.7
							REn	95%	AC3 / ToLCNDV AHA82198	1047-1457: 411	136	16
							Rep	95%	Replication associated protein / TolCNDV AJE24748	1499-2584: 1086	361	41
59.	GU180095	Taiwan	*Cucumis melo*	2739	98%	ToLCNDV-[TH:Cuc] AB330079	CP	99%	CP / ToLCNDV AJE24744	280-1050: 771	256	29.6
							V3	88%	AV3 protein / ToLCNDV CRI05838	41-127: 387	128	14.7
							V2	99%	AV2 protein / ToLCNDV-[TH:Cuc] BAF93941	120-458: 339	112	12.9
							C5	93%	AC4 / ToLCNDV-[Luf] AAD14628	310-795: 486	161	17.9
							C4	98%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66.1
							TrAp	96%	AC2 / ToLCNDV-[TH:Cuc] BAF69032	1192-2596: 405	134	15.1
							REn	99%	AC3 / ToLCNDV-[TH:Cuc] BAF69031	1047-1457: 411	136	16
							Rep	98%	AC1 / ToLCNDV-[TH:Cuc] BAF69033	1499-2584: 1086	361	41

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
60.	KM383742	Bangladesh	Tomato	2740	98%	ToLCNDV-[BD:Jes:10] KM383741	CP	99%	Coat protein / ToLCNDV AAY44733	280-1050: 771	256	29.5
							V3	91%	AV3 / ToLCNDV-Mild AAA92815	41-427: 387	128	14.7
							V2	99%	AV2 / ToLCNDV AAR28537	120-458: 339	112	12.9
							C4	96%	AC4 / ToLCNDV AAR28541	2251-2556: 306	101	11.7
							TrAP	98%	TrAP / ToLCNDV-Svr [Jes] CAI44690	1177-1596: 420	139	15.6
							REn	97%	REn protein / ToLCNDV AJE24780	1047-1457: 411	136	16.3
							Rep	98%	Replictaion-associated protein / ToLCNDV AJE24768	1499-2584: 1086	361	40.8
61.	LT556071	Pakistan	Tomato	2740	97%	ToLCNDV-[IN:ND:06] EF068246	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.4
							V2	99%	Pre-coat protein / ToLCNDV ABO31249	120-458: 339	112	12.9
							C5	98%	AC5 / ToLCNDV ABO31254	310-795: 486	161	17.9
							C4	96%	AC4 Protein / ToLCNDV ABO31253	2251-2427: 177	58	65.8
							TrAP	96%	TrAP / ToLCNDV ABO31251	1177-1596: 420	139	15.6
							REn	99%	Transcription enhancer protein / ToLCNDV ABO31252	1047-1457: 411	136	16
							Rep	99%	Replication-associated protein / ToLCNDV AJE24768	1499-2584: 1086	361	40.9
62.	KC914896	Pakistan	*Chenopodium album*	2745	100%	ToLCNDV-[PK:Mul:BG:05] AM747291	CP	99%	CP / ToLCNDV AJE24764	285-1055: 771	256	29.5
							V2	80%	Pre-coat protein / ToLCNDV AAY44734	44-463: 420	139	15.9
							C5	95%	AC5 protein / ToLCNDV AJE24745	315-677: 363	120	13.1
							C4	93%	AC4 Protein / ToLCNDV-IN [IN:Tum:Chi:08] AEA76855	2256-2432: 177	58	66.7
							TrAP	94%	TrAP protein / ToLCNDV AIX97575	1182-1601: 420	139	15.6
							REn	93%	REn protein / BGYVV YP_009058922	1052-1462: 411	136	16.1

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	Rep	96%	Replication-associated protein / ToLCNDV AJE24761	1504-2589: 1086	361	40.9
63.	AM747291	Pakistan	Bitter Gourd	2742	100%	ToLCNDV-[PK:Che:12] KC914896	CP	99%	CP / ToLCNDV AJE24764	282-1052: 771	256	29.5
							V2	80%	Pre-coat protein / ToLCNDV AAY44734	41-460:420	139	15.9
							C5	95%	AC5 protein / ToLCNDV AJE24745	312-674: 363	120	13.1
							C4	93%	AC4 Protein / ToLCNDV-IN [IN:Tum:Chi:08] AEA76855	2253-2429: 177	58	66.7
							TrAP	94%	TrAP / ToLCNDV AIX97575	1179-1598: 420	139	15.6
							REn	93%	REn protein / BGYVV YP_009058922	1049-1459: 411	136	16.1
							Rep	96%	Replication-associated protein / ToLCNDV AJE24761	1501-2586: 1086	361	40.9
64.	JN809814	Thailand	*Sauropus androgynus*	2739	98%	ToLCNDV-[TH:Cuc] AB330079	CP	99%	CP / ToLCNDV AJE24744	280-1050: 771	256	29.5
							V2	98%	AC2 / ToLCNDV-[TH:Cuc] BAF69029	120-458: 339	112	12.9
							C5	93%	AC4 / ToLCNDV-[Luf] AAD14628	310-795: 486	161	17.9
							C4	98%	AC4 / ToLCNDV- Mild AAA92822	2251-2427: 177	58	66.3
							TrAP	98%	AC2 / ToLCNDV-[TH:Cuc] BAF69032	1177-1596: 420	139	15.6
							REn	99%	REn Protein / ToLNDV-[TH:Cuc] BAF93943	1047-1457: 411	136	16
							Rep	98%	AC1 / ToLCNDV-[TH:Cuc] BAF69033	1499-2674: 1176	391	44.2
65.	KP178727	India	Tomato	2740	98%	ToLCNDV-IN [BD:Jes:Svr:03] AJ875157	CP	99%	CP / ToLCNDV AJE24778	280-1050: 771	256	29.5
							V3	98%	AV3 protein / ToLCNDV ABM21599	41-427: 387	128	14.7
							V2	97%	Pre-coat protein / BYVDV-[ND:04] YP_002519376	120-458: 339	112	12.9
							C5	97%	AC5 protein / ToLCNDV AGO64031	310-588: 279	92	99.1
							C4	95%	Pathogenecity Determinant Protein / ToLCNDV AGO64033	2251-2433: 183	60	69.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	99%	TrAP /ToLCNDV AJE24781	1177-1596: 420	139	15.6
							REn	96%	REn protein / ToLCNDV AJE24766	1047-1457: 411	136	16.1
							Rep	96%	Replication initiator protein / ToLCNDV AII96793	1499-2674: 1176	391	44.5
66.	AF102276	Thailand	*Luffa cylindrica*	2746	97%	ToLCNDV-[TH:Cuc] AB330079	CP	99%	AV1 / ToLVNDV-[TH:Cuc] BAF69030	286-1056: 771	256	29.6
							V2	89%	Pre-coat protein / ToLCNDV AJE24743	120-464: 345	114	13.3
							C5	92%	AC5 protein / ToLCNDV ABA00494	316-801: 486	161	17.9
							C4	98%	AC4 / ToLCNDV-Mld AAA92822	2258-2434: 177	58	66.3
							REn	99%	REn protein / ToLCNDV AJE24746	1053-1463: 411	136	16
							Rep	98%	AC1 / ToLCNDV-[TH:Cuc] BAF69033	1506-2591: 1086	361	40.8
67.	KF537780	India	Tomato	2740	97%	ToLCNDV-IN [BD:Jes:Svr:03] AJ875157	CP	99%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.6
							V3	89%	V3 / ToLCNDV ABB52029	41-427:387	128	14.6
							V2	98%	AV2 / ToLCKV AHA82181	120-458: 339	112	12.9
							C5	94%	AC5 protein / ToLCNDV AJE24793	310-795: 486	161	17.9
							C4	98%	AC4 / ToLCNDV-Svr [Jes] CAI44692	2251-2427: 177	58	66.4
							TrAP	96%	TrAP / ToLCNDV-[ND: Pum] CAL15160	1177-1596: 420	139	15.7
							REn	98%	REn protein / ToLCNDV AGK29962	1047-1457: 411	136	16
							Rep	98%	Replication-associated protein /ToLCNDV AJE24768	1499-2584: 1086	361	40.9
68.	GU112084	India	*Abelmoschus esculentus*	2743	98%	ToLCNDV-[IN:Uda:Okr:06] EF035482	CP	98%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.5
							V3	98%	AV3 protein / ToLCNDV ABM21599	41-427:387	128	14.6

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	V2	98%	Pre-coat protein / ToLCNDV-[IN:Kar:OY81A:04] ADO41052	120-458: 339	112	13
							C5	91%	AC5 / ToLCNDV AHB37379	310-984: 675	224	20.5
							C4	99%	AC4 Protein / ToLCNDV-[IN:Aur:OY164A:06] ADO41085	2125-2433: 309	102	118.8
							TrAP	98%	TrAP / ToLCNDV-[IN:Aur:OY164A:06] ADO41083	1177-1596: 420	139	15.6
							REn	95%	AC3 / ToLCNDV AHB37377	1047-1457: 41	136	16
							Rep	99%	Replicase / ToLCNDV-[IN:Aur:OY164A:06] ADO41084	1499-2584: 1086	361	40.9
169.	AJ875157	Bangladesh	Tomato	2740	98%	ToLCNDV-[IN:Ori:09] KP178727	CP	99%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.5
							V3	92%	V3 / ToLCNDV ABB52029	41-427: 387	128	14.8
							V2	99%	AV2 / ToLCNDV AAR28537	120-458:339	112	12.9
							C5	99%	AC5 / ToLCNDV AAR28542	310-588: 279	92	98
							C4	98%	AC4 / ToLCNDV AHA61379	2251-2427: 177	58	66.5
							TrAP	99%	TrAP / ToLCNDV AJE24781	1177-1596: 420	139	15.6
							REn	96%	REn protein / ToLCNDV AJE24766	1047-1457: 411	136	16.1
							Rep	97%	Rep / ToLCNDV-[PK:Sol:97] ABB52053	1499-2584: 1086	361	41
70.	DQ116885	Pakistan	Tomato	2740	97%	ToLCNDV-IN [PK:Mul:Sol:PT10: 04] DQ116883	CP	99%	AV1 / ToLCNDV AJW80908	280-1050:771	256	29.5
							V3	98%	V3 / ToLCNDV-[PK:Sol:97] ABB52044	41-427: 387	128	14.7
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							C5	98%	C5 / ToLCNDV ABB52030	310-672: 363	120	13.2
							C4	98%	AC4 / ToLCNDV AJW80819	2251-2427: 177	58	65
							TrAP	98%	AC2 / ToCNDV AJW80817	1192-1596: 405	134	15.2
							REn	97%	C3 / ToLCNDV-[PK:Sol:97] ABB52042	1047-1457: 411	136	16

Sr #	**Accession Number**	**Country**	**Host**	**Nucleotide Number**	**Nucleotide Sequence Identity**	**Nucleotide identity with Virus**	**Proteins**	**Proteins Percentage Identity**	**Protein / Identity with Virus**	**Nucleotide Length**	**Number of Amino acids**	**Molecular Weight (kDa)**
	//	//	//	//	//	//	Rep	99%	AC1 / ToLCNDV AJW80816	1499-2584: 1086	361	41
71.	KM383743	Bangladesh	Tomato	2740	99%	ToLCNDV-[BD:Joy:06] KM383739	CP	99%	AV1 / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V3	91%	V3 / ToLCNDV ABB52029	41-427: 387	128	14.7
							V2	99%	Pre-coat protein / ToLCNDV ABO31249	120-458:339	112	12.9
							C5	97%	AC5 protein / ToLCNDV AJE24765	310-795: 486	161	17.9
							C4	98%	AC4 Protein / ToLCNDV-Svr [Jes] CAI44692	2251-2427: 177	58	66.4
							TrAP	99%	TrAP / ToLCNDV AJE24767	1177-1596: 420	139	15.7
							REn	99%	REn protein / ToLCNDV AJE24766	1047-1457: 411	136	16.1
							Rep	99%	Replication-associated protein / ToLCNDV AJE24768	1499-2584: 1086	361	40.9
72.	KP868764	India	Bitter gourd	2742	95%	ToLCNDV-[IN:Chi:09] KP235542	CP	98%	CP / ToLCNDV CAO00517	280-1050: 771	256	29.6
							V2	98%	Pre-coat protein / ToLCNDV CBJ17648	120-458: 339	112	12.9
							C5	90%	AC5 / ToLCNDV-Svr ADM36027	310-795: 486	161	17.9
							C4	98%	AC4 Protein / ToLCNDV-IN [IN:Tum:Chi:08] AEA76855	2251-2427: 177	58	66
							TrAP	98%	TrAP / ToLCNDV AIX97575	1177-1596: 420	139	15.5
							REn	98%	REn Protein / ToLCNDV AIX97576	1047-1457: 411	136	15.9
							Rep	98%	AC1 / ToLCNDV AAY44735	1499-2584: 1086	361	40.8
73.	AB368447	Thailand	Bottle Gourd	2739	99%	ToLCNDV-[TH:Cuc] AB330079	CP	99%	AV1 / ToLCNDV ACZ63311	280-1050: 771	256	29.6
							V3	91%	AV3 / ToLCNDV ABU95060	41-427: 387	128	14.6
							V2	99%	AC2 / ToLCNDV-[TH:Cuc] BAF69029	120-458: 339	112	13
							C5	94%	AC4 / ToLCNDV-[Luf] AAD14628	310-795: 486	161	17.8
							C4	98%	AC4 / ToLCNDV-Mld AAA92822	2251-2427: 177	58	66.3

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	99%	AC2 / ToLCNDV-[TH:Cuc] BAF69032	1177-1596: 420	139	15.7
							REn	99%	REn Protein / ToLCNDV-[TH:Cuc] BAF93943	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV-[TH:Cuc] BAF69033	1499-2584: 1086	361	41
74.	AB368448	Thailand	Muskmelon	2739	99%	ToLCNDV-[TH:Cuc] AB330079	CP	99%	CP / ToLCNDV AJE24744	280-1050: 771	256	29.5
							V3	91%	AV3 / ToLCNDV ABU95060	41-427: 387	128	14.5
							V2	99%	AC2 / ToLCNDV-[TH:Cuc] BAF69029	120-458: 339	112	12.9
							C5	95%	AC4 / ToLCNDV-[Luf] AAD14628	310-795: 486	161	17.9
							C4	98%	AC4 / ToLCNDV-Mld AAA92822	2251-2427: 177	58	66.3
							TrAp	99%	TrAP / ToLCNDV-[TH:Cuc] BAF93939	1177-1596: 420	139	15.6
							REn	99%	AC3 / ToLCNDV BAF69031	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV-[TH:Cuc] BAF69033	1499-2584: 1086	361	40.9
75.	KM383739	Bangladesh	Tomato	2740	99%	ToLCNDV-[BD:Jam:10] KM383743	CP	99%	CP / ToLCNDV AIW42891	280-1050: 771	256	29.5
							V3	88%	AV3 / ToLCNDV-[IN:Pap:05] ABJ97333	41-427: 387	128	14.6
							V2	99%	Pre-coat protein / ToLCNDV AJE24791	120-458: 339	112	13
							C5	97%	AC5 protein / ToLCNDV AJE24793	310-795: 486	161	18.1
							C4	98%	AC4 Protein / ToLCNDV-Svr [Jes] CAI44692	2251-2427: 177	58	66.4
							TrAP	99%	TrAP / ToLCNDV AJE24795	1177-1596: 420	139	15.6
							REn	99%	REn protein / ToLCNDV AJE24794	1047-1457: 411	136	16.1
							Rep	99%	Replication-associated protein / ToLCNDV-Svr [Jes] CAI44691	1499-2584: 1086	361	41

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
76.	EF068246	India	Tomato	2740	97%	ToLCNDV-[PK:Swa:13] LT556071	CP	99%	CP / ToLCNDV AAY44733	280-1050:771	256	29.4
							V2	99%	Pre-coat protein / ToLCNDV AJE24791	120-458: 339	112	12.9
							C5	98%	AC5 protein / ToLCNDV SAM29888	310-795: 486	161	17.8
							C4	97%	AC4 / ToLCNDV AHA61379	2251-2427: 177	58	66.9
							TrAP	99%	AC2 / ToLCNDV AAR28539	1177-1596: 420	139	15.6
							REn	99%	Rep protein 3 / ToLCNDV-[Luc] CAA76214	1047-1457: 411	136	16
							Rep	98%	Replication-associated protein / ToLCNDV AJE24768	1499-2584: 1086	361	40.9
77.	KP195259	India	Tomato	2740	99%	ToLCNDV-[IN:Gun:08] KP178728	CP	99%	AV1 / ToLCNDV AJW80902	280-1050: 771	256	29.6
							V3	96%	AV3 / ToLCNDV AJW80900	41-427: 387	128	14.6
							V2	99%	AV2 / ToLCNDV AJW80901	120-458: 339	112	13
							C4	97%	AC4 / BYVHV-[Kar:03] ACT67441	2134-2433: 300	99	115.4
							TrAP	97%	AC2 / ToLCNDV-Sev ADM36030	1177-1596: 420	139	15.7
							REn	97%	AC3 / ToLCNDV-Sev ADM36029	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV AJW80903	1499-2674: 1176	391	44.5
78.	AB330079	Thailand	Cucumber	2739	99%	ToLCNDV-[TH:Kam:Bot:96] AB368447	CP	99%	CP / ToLCNDV AJE24744	280-1050: 771	256	29.5
							V3	91%	AV3 / ToLCNDV ABU95060	41-427: 387	128	14.6
							V2	99%	AV2 protein / ToLCNDV-[TH:Cuc] BAF93941	120-458: 339	112	12.9
							C5	95%	AC4 / ToLCNDV-[Luf] AAD14628	310-795: 486	161	17.9
							C4	98%	AC4 / ToLCNDV-Mld AAA92822	2284-2427: 144	47	53.8
							TrAP	99%	TrAP / ToLCNDV-[TH:Cuc] BAF93939	1177-1596: 420	139	15.6
							REn	99%	REn Protein / ToLCNDV-[TH:Cuc] BAF93943	1047-1457: 411	136	16

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	Rep	99%	Replication-associated protein / ToLCNDV-[TH:Cuc] BAF93940	1499-2584: 1086	361	40.9
79.	KF551580	India	Tomato	2740	97%	ToLCNDV-[IN:ND:06] EF068246	CP	99%	AV1 protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V3	91%	AV3 / ToLCNDV-Mild AAA92815	41-427: 387	128	14.7
							V2	99%	AV2 protein / ToLCNDV [PkT5/6] AAL60212	120-458: 339	112	13
							C5	95%	AC5 protein / ToLCNDV SAM29888	310-795: 486	161	18
							C4	95%	AC4 / ToLCNDV AHA61379	2251-2427: 177	58	66.9
							TrAP	97%	TrAP / ToLCNDV ABO31251	1177-1596: 420	139	15.6
							REn	99%	REn protein / ToLCNDV CBJ17678	1047-1457: 411	136	16
							Rep	94%	Replication-associated protein / ToLCNDV CAO00520	1499-2584: 1086	361	41.1
80.	KP178728	India	Tomato	2740	99%	ToLCNDV-[IN:Ama:08] KP195259	CP	99%	AV1 / TLCNDV AJW80776	280-1050: 771	256	29.6
							V2	99%	AV2 / ToLCNDV AJW80775	120-458: 339	112	13.1
							C4	97%	AC4 / BYVHV-[Kar:03] ACT67441	2251-2433: 183	60	69.1
							TrAP	97%	AC2 / ToLCNDV-Svr ADM36030	1177-1596: 420	139	15.7
							REn	97%	AC3 / ToLCNDV-Svr ADM36029	1047-1457: 411	136	16
							Rep	97%	AC3 / ToLCNDV-Svr ADM36029	1499-2674: 1176	391	40.5
81.	GQ865546	India	Tomato	2740	98%	ToLCNDV-[IN:Uda:Okr:06] EF035482	CP	97%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.5
							V3	93%	AV3 / ToLCNDV AJW80900	41-427: 387	128	14.7
							V2	96%	AV2 / ToLCKV AHA82181	120-458: 339	112	13.1
							C4	97%	Pathogenecity Determinant Protein / ToLCNDV AGO64033	2251-2433: 183	60	69.6
							C5	90%	AC5 / ToLCNDV AGO64031	310-672: 363	120	13.2

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	94%	AC2 / ToLCNDV AHB37376	1177-1596: 420	139	15.6
							REn	96%	REn Protein / ToLCNDV AER93213	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV AHB37374	1499-2584: 1086	361	40.9
82.	AY428769	India	Tomato	2738	98%	ToLCNDV-IN [BD:Jes:Svr:03] AJ875157	CP	99%	AV1 protein / ToLCNDV [PkT5/6] AAL60213	280-1050: 771	256	29.5
							V3	93%	V3 / ToLCNDV ABB52029	41-427: 387	128	14.7
							V2	99%	AV2 / ToLCKV AHA82181	120-458: 339	112	12.9
							C4	98%	AC4 Protein / ToLCNDV-Svr [Jes] CAI44692	2249-2554: 306	101	117.9
							C5	97%	AC5 / ToLCNDV ABY40424	310-795: 486	161	17.8
							TrAP	99%	Rep protein 2 / ToLCNDV-[Luc] CAA76213	1176-1595: 420	139	15.6
							Rep	99%	Replication-associated protein / ToLCNDV AJE24768	1614-2582: 969	322	36.7
83.	AY939926	India	*Luffa cylindrica*	2684	98%	ToLCNDV-[IN:ND:Luf:10] HM989845	CP	99%	AV1 protein / ToLCNDV [PkT5/6] AAL60213	225-995: 771	256	29.5
							V2	99%	AV2 / ToLCNDV-Sev ADM36025	41-403: 363	120	13.8
							C5	98%	AC5 / ToLCNDV-[IN:Pap:05] ABJ97336	255-617: 363	120	13.2
							C4	98%	C4 Protein/ ToLCNDV-[PK:Lah:Sol:04] CAO98747	2196-2372: 177	58	66.6
							TrAP	99%	TrAP / ToLCNDV CAO98745	1122-1541: 420	139	15.7
							REn	99%	AC3 protein / ToLCNDV NP_803222	992-1402: 411	136	16
							Rep	99%	Replication initiation protein / ToLCNDV-JLX10 ADT70803	1444-2529: 1086	361	40.9
84.	HG932559	India	Tomato	2739	99%	ToLCNDV-[IN:His:Pot:10] KC874503	CP	99%	AV1 / ToLCNDV-[Pot] AAP37406	280-1050: 771	256	29.4
							V2	99%	AV2 protein / ToLCNDV-[Pot] AAP37405	120-458: 339	112	12.9
							C5	98%	AC5 / ToLCNDV ADP44680	442-795: 354	117	13.6
							C4	98%	AC4 / ToLCNDV-[Pot] AAP37411	2250-2426: 177	58	64.6

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	99%	AC2 protein / ToLCNDV-[Pot] AAP37409	1177-1596: 420	139	15.8
							REn	99%	AC3 / ToLCNDV ADP44681	1047-1457: 411	136	15.9
							Rep	97%	AC1 / ToLCNDV-[Pot] AAP37410	2155-2583: 429	142	16
85.	HQ658479 EU309045	India	Chilli	2740	98%	ToLCNDV-IN[BD:Jes:Svr:03] AJ875157	CP	99%	CP / SLCCNV AIW42883	280-1050: 771	256	29.5
							V3	91%	V3 / ToLCNDV ABB52029	41-427: 387	128	14.8
							V2	99%	AV2 / ToLCKV AHA82181	120-458: 339	112	12.9
							C5	97%	AC5 / ToLCNDV AAR28542	310-795: 486	161	17.9
							C4	97%	AC4 / ToLCNDV AHA61379	2251-2427: 177	58	67.1
							TrAP	99%	AC2 / ToLCNDV AAR28539	1177-1596: 420	139	15.6
							REn	99%	TrAP / ToLCNDV ABO31252	1047-1457: 411	136	16.1
							Rep	98%	Replication-associated protein / ToLCNDV AJE24768	1499-2584: 1086	361	41
86.	JX460805	India	Tomato	2730	95%	ToLCNDV-[PK:Fai:09] FN435310	CP	97%	V1 protein / ToLCNDV-[PK:Sol:09] CBA13466	280-1050: 771	256	29.4
							V3	99%	AV3 protein / ToLCNDV NP_803218	41-427: 387	128	14.8
							V2	99%	AV2 protein / ToLCNDV NP_803219	120-458: 339	112	12.9
							C5	99%	AC5 protein / ToLCNDV NP_803221	310-672: 363	120	13.2
							C4	100%	AC4 Protein / ToLCNDV-[Pot] AGR88344	2302-2427: 126	41	45.8
							TrAP	94%	AC2 / ToLCNDV-Svr ADM36030	1192-1596: 405	134	15
							REn	84%	AC3 / PLCV-[IN:Tom:05] ABF71088	1047-1457: 411	136	15.9
							Rep	98%	AC1 / ToLCNDV-Svr ADM36031	1499-2584: 1086	361	41

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
87.	KF551589	India	Tomato	2739	99%	ToLCNDV-[IN:Kol:11] KF551590	CP	98%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.5
							V3	92%	V3 protein / ToLCNDV-[PK:Sol:97] ABB52058	41-427: 387	128	14.8
							V2	98%	Pre-coat protein / ToLCNDV ABO31249	120-458: 339	112	13
							C5	91%	AC5 protein / ToLCNDV AJE24772	400-672: 273	90	99.1
							C4	97%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66.2
							TrAP	99%	AC2 / ToLCNDV AAY44737	1177-1596: 420	139	15.7
							REn	99%	REn protein / ToLCNDV AJE24746	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV AHA82262	1499-2584: 1086	361	40.8
88.	LT556070	Pakistan	Tomato	2739	97%	ToLCNDV-[PK:Swa:15] LT556081	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.4
							V3	97%	V3 / ToLCNDV-[PK:Sol:97] ABB52044	41-427: 387	128	14.6
							V2	99%	Pre-coat protein / ToLVNDV-[PK:Mul:Luf] CAL22868	120-458: 339	112	12.9
							C5	98%	AC5 protein / ToLCNDV SAM29919	310-795: 486	161	17.9
							C4	97%	AC4 / ToLCNDV ABU95067	2251-2427: 177	58	66.2
							TrAP	88%	AC2 / ToLCNDV AJW80911	1192-1596: 405	134	15.2
							REn	91%	C3 / ToLCNDV-[PK:Sol:97] ABB52055	1047-1457: 411	136	16.1
							Rep	98%	Replication-associated protein / ToLCNDV SAM29932	1499-2584: 1086	361	41
89.	LT556082	Pakistan	Tomato	2739	100%	ToLCNDV-[PK:Swa:15] LT556070	CP	99%	CP / ToLCNDV AAY44733	280-1050: 771	256	29.4
							V3	97%	V3 / ToLCNDV-[PK:Sol:97] ABB52044	41-427: 387	128	13.6
							V2	99%	Pre-coat protein / ToLVNDV-[PK:Mul:Luf] CAL22868	120-458: 339	112	12.9
							C5	98%	AC5 protein / ToLCNDV SAM29919	310-795: 486	161	17.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C4	97%	AC4 / ToLCNDV ABU95067	2251-2427: 177	58	66.2
							TrAp	88%	AC2 / ToLCNDV AJW80911	1192-1596: 405	134	15.2
							REn	91%	C3 / ToLCNDV-[PK:Sol:97] ABB52055.	1047-1457: 411	136	16.1
							Rep	98%	Replication-associated protein / ToLCNDV SAM29932	1499-2584: 1086	361	41
90.	KF551590	India	Tomato	2741	99%	ToLCNDV-[IN:Kol:11] KF551589	CP	98%	AV1 / ToLCNDV AHA82255	280-1050: 771	256	29.4
							V3	90%	V3 / ToLCNDV-[PK:Sol:97] ABB52058	41-427: 387	128	14.8
							V2	97%	AV2 / ToLCNDV AHA82254	120-458: 339	112	12.9
							C5	90%	AC5 protein / ToLCNDV AJE24772	400-672: 273	90	10
							C4	97%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66.2
							TrAP	99%	AC2 / ToLCNDV AAY44737	1177-1596: 420	139	15.7
							REn	99%	Replication enhancer protein / ToLCNDV AJE24746	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV AHA82256	1499-2584: 1086	361	40.9
91.	KJ000564	India	Tomato	2740	98%	ToLCNDV-[IN:09] KF571461	CP	99%	AV1 protein / ToLCNDV NP_803220	280-1050: 771	256	29.4
							V3	98%	AV3 protein / ToLCNDV AHB37375	41-427: 387	128	14.4
							V2	98%	Pre-coat protein / ToLVNDV CRI05839	120-458: 339	112	12.9
							C5	96%	AC5 / ToLCNDV AHB37379	310-795: 486	161	17.9
							C4	98%	AC4 / ToLCNDV AJW80780	2251-2427: 177	58	66.7
							TrAP	99%	AC2 / ToLCNDV AHB37376	1177-1596: 420	139	15.7
							REn	99%	AC3 / ToLCNDV AHB37377	1047-1457: 411	136	16.1
							Rep	97%	AC1 / ToLCNDV AHB37374	1499-2584: 1086	361	41

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
92.	GU112088	India	*Abelmoschus esculentus*	2742	97%	ToLCNDV-[IN:Uda:Okr:06] EF035482	CP	99%	CP / ToLCNDV ACK44128	282-1052: 771	256	29.3
							V2	96%	V2 / ToLCNDV-[PK:Sol:97] CAF04467	74-460: 387	128	14.9
							C5	93%	AC5 / ToLCNDV NP_803221	312-797: 486	161	18.1
							C4	99%	AC4 Protein / ToLCNDV-[IN:Ban:OY135:05] ADO41067	2127-2435: 309	102	119
							TrAP	98%	TrAP / ToLCNDV-[IN:OY135:05]	1179-1598: 420	139	15.6
							REn	96%	AC3 protein / ToLCNDV NP_803222	1049-1459: 411	136	16.1
							Rep	97%	Replication-initiator protein / ToLCNDV AII96793	1501-2676: 1176	391	44.4
93.	EF035482	India	Okra cultivar : Parbhani Kranthi	2740	98%	ToLCNDV-[IN:Kar:Okr:05] GU112084	CP	98%	CP / ToLNDV-[IN: OY136B:06] ADO41071	280-1050: 771	256	29.6
							V3	98%	AV3 / ToLCNDV AJW80900	41-427: 387	128	14.5
							V2	99%	Pre-coat protein / ToLVNDV-[IN:OY81A:04]	120-458: 339	112	13.1
							C5	98%	AC5 protein / ToLCNDV-[IN:OY135:05]	406-672: 267	88	99.7
							C4	95%	Pathogenecity Determinant Protein / ToLCNDV AGO64033	2251-2433: 183	60	69.9
							TrAP	99%	TrAP / ToLCNDV-[IN:OY164A:06] ADO41083	1177-1596: 420	139	15.6
							REn	99%	REn protein / ToLCNDV AER93213	1047-1457: 411	136	16.1
							Rep	98%	Replication initiator protein / ToLCNDV AII96793	1499-2674: 1176	391	44.4
94.	HM007113	India	Chilli	2739	99%	ToLCNDV-[IN:Chi:09] KU196750	CP	99%	CP / SLCCV AIW42879	280-1050: 771	256	29.5
							V3	97%	AV3 / ToLCNDV-Mild AAA92815	41-427: 387	128	14.7
							V2	99%	Pre-coat protein / ToLVNDV ABA00498	120-458: 339	112	12.9
							C4	98%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66
							C5	97%	AC5 / ToLCNDV-[IN:Cot:05] ABK41852	310-795: 486	161	17.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	99%	TrAP / ToLCNDV-JLX10 ADT70804	1177-1596: 420	139	15.7
							REn	99%	AC3 / ToLCNDV-[IN:Cot:05] ABK41854	1047-1457: 411	136	16
							Rep	99%	Replication associated protein / ToLCNDV CAO98746	1499-2584: 1086	361	41.1
95.	KM383744	Bangladesh	Tomato	2739	98%	ToLCNDV-[BD:Joy:06] Km383738	CP	99%	CP / SLCCNV-[IN:Var:Pum] ACE79034	280-1050: 771	256	29.5
							V2	99%	Pre-coat protein / ToLVNDV ABA00498	120-458: 339	112	12.9
							C5	97%	AC4 / ToLNDV-[Luffa] AAD14628	310-672: 363	120	13.1
							C4	98%	AC4 / ToLCNDV-Mld AAA92822	2251-2427: 177	58	66.3
							TrAP	99%	AC2 / ToLCNDV AHA82257	1192-1596: 405	134	15.2
							REn	99%	AC2 / ToLNDV-[Luffa] AAD14626	1047-1457: 411	136	16.1
							Rep	99%	Replication associated protein / ToLCNDV AJE24755	1499-2584: 1086	361	40.7
96.	U15016	India	Tomato	2739	98%	ToLCNDV-[IN:Chi:09] KU196750	CP	99%	AV1 protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V3	97%	AV3 / ToLCNDV AEF38353	41-427: 387	128	14.7
							V2	99%	Pre-coat protein / ToLVNDV ABA00498	120-458: 339	112	12.9
							C5	99%	AC5 / ToLCNDV AFQ62673	310-795: 486	161	17.9
							C4	98%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2430: 180	59	67.3
							TrAP	98%	TrAP / ToLCNDV-JLX10 ADT70804	1177-1596: 420	139	15.7
							REn	99%	REn Protein / ToLCNDV-[IN:Chilli:09] AEA76824	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV AAY44735	1499-2584: 1086	361	40.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
97.	KJ778692 KJ778694	Iran	Egg plant	2741	99%	ToLCNDV-[IN:Mah:Egg:09] HQ264185	CP	98%	AV1 protein / ToLCNDV-[PkT5/6] AAL60213	281-1051: 771	256	29.5
							V2	98%	V2 protein / ToLCNDV-[PK:Sol:97] CAF04467	121-459:339	112	13
							C5	93%	AC5 protein / ToLCNDV-[IN:OY81A:04] ADO41054	311-673: 363	120	13.3
							C4	97%	AC4 Protein / ToLCNDV AJW80780	2252-2434: 183	60	69.2
							TrAP	96%	AC2 / ToLCNDV AHB37376	1178-1597: 420	139	15.7
							REn	97%	AC3 / ToLCNDV AHB37377	1048-1458: 411	136	16
							Rep	97%	AC1 / ToLCNDV AHB37374	1500-2675: 1176	391	44.5
98.	KU196750	India	Chilli	2739	99%	ToLCNDV-[IN:ND:Chi:09] HM007113	CP	99%	CP / SLCCV AIW42879	280-1050: 771	256	29.5
							V3	98%	AV3 / ToLCNDV-Mild AAA92815	41-427: 387	128	14.7
							V2	99%	AV2 / ToLCNDV-Svr ADM36025	120-458: 339	112	12.9
							C5	97%	AC5 / ToLCNDV-[IN:Cot:05] ABK41852	310-795: 486	161	18
							C4	98%	C4 Protein / ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66
							TrAP	99%	TrAP / ToLCNDV-JLX10 ADT70804	1177-1596: 420	139	15.7
							REn	99%	AC3 / ToLCNDV-[IN:Cot:05] ABK41854	1047-1457: 411	136	16
							Rep	99%	Replication association protein / ToLCNDV CAO98746	1499-2584: 1086	361	41.1
99.	HQ264185	India	Egg plant	2741	99%	ToLCNDV-[IR:Zab:Egg:13] KJ778692	CP	98%	AV1 protein / ToLCNDV-[PkT5/6] AAL60213	281-1051: 771	256	29.5
							V2	98%	V2 protein / ToLCNDV-[PK:Sol:97] CAF04467	121-459:339	112	13
							C5	93%	AC5 protein / ToLCNDV-[IN:OY81A:04] ADO41054	311-673: 363	120	13.3
							C4	97%	AC4 / ToLCNDV AJW80780	2252-2434: 183	60	69.2

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	96%	AC2 / ToLCNDV AHB37376	1178-1597: 420	139	15.7
							REn	97%	AC3 / ToLCNDV AHB37377	1048-1458: 411	136	16
							Rep	97%	AC1 / ToLCNDV AHB37374	1500-2675: 1176	391	44.5
100.	KP641673	Iran	Melon	2740	99%	ToLCNDV-[IN:Jal:Pot:10] KC874509	CP	99%	CP / ToLCNDV-[Pot] AGG20240	280-1050: 771	256	29.5
							V2	98%	Pre-coat protein / ToLVNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 protein / ToLCNDV CAO98805	310-795: 486	161	18.3
							C4	97%	AC4 Protein / ToLCNDV-[Pot] AGR88309	2251-2427: 177	58	65.5
							TrAP	99%	AC2 / ToLCNDV-[Pot] AAP37409	1177-1596: 420	139	15.8
							REn	99%	REn protein / ToLCNDV-[Pot] ABL09093	1047-1457: 411	136	16.1
							Rep	99%	Replication initiator protein / ToLCNDV-[Pot] ABL09091	1499-2584: 1086	361	41.1
101.	KC874508	India	Potato	2740	99%	ToLCNDV-[IN:His:Pot:10] KC874503	CP	99%	AV1 / ToLCNDV-[Pot] AAP37406	280-1050: 771	256	29.4
							V2	98%	Pre-coat protein / ToLVNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 protein / ToLCNDV-[Pot] AGR88312	310-795: 486	161	18.2
							C4	98%	AC4 Protein / ToLCNDV-[Pot] AGR88316	2251-2427: 177	58	65.2
							TrAP	99%	AC2 / ToLCNDV-[Pot] AAP37409	1177-1596: 420	139	15.8
							REn	99%	AC3 / ToLCNDV ADP44681	1047-1457: 411	136	16
							Rep	99%	AC1 / ToLCNDV-[Pot] AAP37410	1499-2584: 1086	361	41
102.	KC874509	India	Potato	2740	99%	ToLCNDV-[IR:Zab:Mel:14] KP641673	CP	99%	CP / ToLCNDV-[Pot] AGG20240	280-1050: 771	256	29.5
							V2	99%	Pre-coat protein / ToLVNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 protein / ToLCNDV CAO98805	310-795: 486	161	18.3

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C4	97%	AC4 Protein / ToLCNDV-[Pot] AGR88309	2251-2427: 177	58	65.5
							TrAP	99%	AC2 / ToLCNDV-[Pot] AAP37409	1177-1596: 420	139	15.8
							REn	99%	REn protein / ToLCNDV-[Pot] ABL09093	1047-1457: 411	136	16.1
							Rep	99%	Replication initiator protein / ToLCNDV-[Pot] ABL09091	1499-2584: 1086	361	41.1
103.	KF571461	India	Tomato	2740	98%	ToLCNDV-[IN:Hes:13] KJ000564	CP	99%	AV1 protein / ToLCNDV-[PkT5/6] AAL60213	280-1050: 771	256	29.5
							V3	98%	AV3 / ToLCNDV AHN13900	41-427: 387	128	14.4
							V2	98%	AV2 protein / ToLCNDV-[PkT5/6] AAL60212	120-458: 339	112	13
							C5	91%	AC5 protein / ToLCNDV-[IN:OY135:05] ADO41063	310-795: 486	161	17.9
							C4	97%	AC4 / BYVHV-[Kar:03] ACT67441	2251-2427: 177	58	66.5
							TrAP	99%	AC2 / ToLCNDV AHN13902	1177-1596: 420	139	15.7
							REn	99%	AC3 / ToLCNDV AHN13903	1047-1457: 411	136	16.1
							Rep	97%	Replication initiator protein / ToLCNDV AII96793	1499-2674: 1176	391	44.7
104.	AM849548	Pakistan	*Solanum nigrum*	2739	97%	ToLCNDV-[IN:ND:Luf:10] HM989845	CP	98%	CP / ToLCNDV-[Chilli pep] ABB52025	280-1050: 771	256	29.4
							V2	97%	Pre-coat protein / ToLVNDV CRI05839	120-458: 339	112	12.9
							TrAP	98%	AC2 / ToLCNDV-[IN:Cot05] ABK41855	1177-1596: 420	139	15.7
							C4	98%	AC4 / ToLCNDV-Mld AAA92822	2251-2427: 177	58	66.3
							REn	99%	REn / ToLCNDV-[IN:Chilli:09] AEA76824	1095-1457: 363	120	14.2
							Rep	99%	AC1 / ToLCNDV AAY44735	1499-2584: 1086	361	41

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
105.	KP641677	Iran	Tomato	2740	99%	ToLCNDV-[IN:Him:Pot:06] AM850115	CP	99%	CP/ ToLCNDV-[Pot] ABL09089	280-1050: 771	256	29.5
							V2	99%	Pre-coat protein / ToLVNDV-[Pot] ABL09097	120-458: 339	112	12.9
							C5	99%	AC5 protein / ToLCNDV-[Pot] AGR88333	310-795: 486	161	18.3
							C4	97%	AC4 Protein / ToLCNDV-[Pot] AGR88309	2251-2427: 177	58	65.5
							TrAP	99%	TrAP / ToLCNDV-[Pot] ABL09092	1177-1596: 420	139	15.8
							REn	99%	REn protein / ToLCNDV-[Pot] ABL09093	1047-1457: 411	136	16.1
							Rep	99%	Replication initiator protein / ToLCNDV-[Pot] ABL09091	1499-2584: 1086	361	41.1
106.	KC465466	India	Chilli	2766	94%	ToLCNDV-[PK:Lhr:Sol:04] AM849548	CP	96%	CP / ToLCNDV CAO98743	307-1077: 771	256	29.3
							V2	95%	V2 / ChLCPKV ABB52010	147-503: 357	118	13.6
							C5	73%	AC5 Protein / ToLCNDV-[Pot] AGR88326	298-615: 318	105	11.6
							C4	71%	AC4 / ToLCNDV-Mld AAA92822	2278-2454: 177	58	65.7
							TrAP	96%	TrAP / ToLCNDV AER93214	1204-1623: 420	139	15.7
							REn	96%	REn Protein / ToLCNDV CAO98744	1122-1484: 363	120	14.2
							Rep	88%	AC1 / ToLCNDV AAY44735	1526-2611: 1086	361	40.7
107.	JQ897969	India	Tomato	2735	88%	CLCuBaV-[IN] AY705380	CP	98%	CP / BYVIV-[IN:Var:14] ALB26354	276-1046: 771	256	29.7
							C4	95%	C4 Protein / CLCuMV-[IN:Hib:11] AFA26458	2126-2434: 309	102	11.1
							V2	92%	AV2 Protein / CLCuBV-[IN:Mal:14] BAU61800	116-463: 348	115	13.3
							REn	92%	REn Protein / BYVIV-[IN:Var:14] ALB26355	1060-1452: 393	130	15.2
							TrAP	90%	AC2 Protein / MaYVYnV-[CN:Yun] YP_184753	1145-1597: 453	150	17.2
							Rep	93%	Replicase / BYVMV-[IN:Kar:06] AFU61928	1494-2582: 1089	362	40.8

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
108.	KF749224	Spain	Zucchini	2738	99%	ToLCNDV-[ES:Alm:TomA4:14] KM977733	CP	99%	Coat Protein / ToLCNDV-[ES:Zuc:13] KF749223	279-1049: 771	256	29.6
							C5	86%	AC5 Protein/ ToLCNDV-[IN:Ker:RG:13] AMB18904	309-794: 486	161	18.1
							C4	93%	AC4 Protein/ ToLCNDV-[PK:Che:Sol:11 CUU64521	2250-2426: 177	58	62.9
							V2	99%	Precoat Protein/ ToLCNDV-[ES:Zuc:13] AHJ80134	119-457: 339	112	13
							REn	99%	Replication enhancer protein/ ToLCNDV-[ES:Alm:Mel:14] ALP06192	1046-1456: 411	136	15.8
							TrAP	99%	Suppressor Protein/ ToLCNDV-[ES:Alm:Mel:14] ALP06193	1191-1595: 405	134	15.2
							Rep	99%	Replication Associated Protein/ ToLCNDV-[ES:Zuc:13] AHM26187	1498-2583: 1086	361	40.9
109.	KT175406	Spain	Tomato	2738	99%	ToLCNDV-[ES:Alm:661:Sq:13] KF749223	CP	99%	Coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18871	279-1049: 771	256	29.6
							C5	87%	AC5 Protein/ ToLCNDV-[IN:Ker:RG:13] AMB18904	309-794: 486	161	18
							C4	93%	AC4 Protein/ ToLCNDV-[PK:Che:Sol:11] CUU64521	2250-2426: 177	58	66.1
							V2	99%	AV2 Protein/ ToLCNDV-[ES:Zuc:12] AHM26189	119-457: 339	112	13
							REn	99%	Replication enhancement protein/ ToLCNDV-[ES:Zuc:13] AHM26185	1046-1456: 411	136	15.8
							TrAP	99%	Suppressor Protein/ ToLCNDV-[ES:Alm:Zuc:13] AHJ80138	1191-1595: 405	134	15.2
							Rep	99%	Replication initiation protein/ ToLCNDV-[ES:Alm:Zuc:13] AHJ80139	1498-2583: 1086	361	40.9
110.	KF749225	Spain	Zucchini	2738	99%	ToLCNDV-[ES:Alm:TomA4:14] KM977733	CP	99%	Coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18871	279-1049: 771	256	29.6
							C4	93%	AC4 Protein/ ToLCNDV-[PK:Che:Sol:11 CUU64521	2250-2426: 177	58	66.1
							C5	87%	AC5 Protein/ ToLCNDV-[IN:Ker:RG:13] AMB18904	309-794: 486	161	18

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	V2	99%	AV2 Protein/ ToLCNDV-[ES:Zuc:12] AHM26189	119-457: 339	112	13
							REn	99%	Replication enhancer protein/ ToLCNDV-[ES:Alm:Mel:14] ALP06192	1046-1456: 411	136	15.8
							TrAP	99%	Suppressor Protein/ ToLCNDV-[ES:Alm:Mel:14] ALP06193	1191-1595: 405	134	15.2
							Rep	99%	Replication associated protein/ ToLCNDV-[ES:Zuc:12] AHM26193	1498-2583: 1086	361	40.9
111.	KF891468	Spain	Zucchini	2738	99%	ToLCNDV-[ES:Alm:661:Sq:13] KF749223	CP	99%	Coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18871	279-1049: 771	256	29.6
							C4	93%	AC4 Protein/ ToLCNDV-[PK:Che:Sol:11] CUU64521	2250-2426: 177	58	66.1
							C5	87%	AC5 Protein/ ToLCNDV-[IN:Ker:RG:13] AMB18904	309-794: 486	161	18
							V2	99%	AV2 Protein/ ToLCNDV-[ES:Zuc:12] AHM26189	119-457: 339	112	13
							REn	99%	Replication enhancement protein/ ToLCNDV-[ES:Zuc:13] AHM26185	1046-1456: 411	136	15.8
							TrAP	99%	Suppressor protein/ ToLCNDV-[ES:Alm:14] ALP06199	1191-1595: 405	134	15.2
							Rep	99%	Replication associated protein/ ToLCNDV-[ES:Zuc:13] AHM26187	1498-2583: 1086	361	40.9
112.	KM977733	Spain	Tomato	2738	99%	ToLCNDV-[ES:Alm:661:Sq:13] KF749223	CP	99%	Coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18871	279-1049: 771	256	29.6
							C4	93%	AC4 Protein/ ToLCNDV-[PK:Che:Sol:11] CUU64521	2250-2426: 177	58	66.1
							C5	87%	AC5 Protein/ ToLCNDV-[IN:Ker:RG:13] AMB18904	309-794: 486	161	18
							V2	99%	AV2 Protein/ ToLCNDV-[ES:Zuc:12] AHM26189	119-457: 339	112	13
							REn	99%	Replication enhancement protein/ ToLCNDV-[ES:Zuc:12] AHM26191	1046-1456: 411	136	15.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	99%	Transactivator protein/ ToLCNDV-[ES:Zuc:12] AHM26192	1191-1595: 405	134	15.1
							Rep	99%	Replication associated protein/ ToLCNDV-[ES:Zuc:13] AHM26187	1498-2583: 1086	361	40.9
113.	GU112082	India	*Abelmoschus esculentus* cultivar US7109	2740	96%	ToLCNDV-[IN:Kar:Okr:05] GU112084	CP	98%	Coat Protein/ ToLCNDV-[IN:Kar:Abe:05] ADO41062	280-1050:771	256	29.5
							C4	100%	AC4 Protein/ ToLCNDV-[IN:Har:Abe:04] ADO41058	2125-2433: 309	102	11.7
							C5	100%	AC5 Protein/ ToLCNDV-[IN:Har:Abe:04] ADO41054	310-984: 675	224	25.1
							V2	99%	Pre-coat Protein/ ToLCNDV-[IN:Uda:Okr] ABM21600	120-458:339	112	13
							V3	99%	AV3 Protein/ ToLCNDV-[IN:Uda:Okr] ABM21599	41-427:387	128	14.6
							REn	100%	Replication enhancer protein/ ToLCNDV-[IN:Har:Abe:04] ADO41055	1047-1457: 411	136	16.1
							TrAP	88%	AC2/ ToLCNDV-[IN:Cha:09] AJW80911	1144-1596: 453	150	16.8
							Rep	96%	Replication initiator protein/ ToLCNDV-[IR:Zab:Egg:13] AII96793	1499-2674: 1176	391	44.5
114.	GU112086	India	2742	*Abelmoschus esculentus* (okra)	95%	ToLCNDV-[IN:Uda:Okr:06] EF035482	CP	98%	Coat Protein/ ToLCNDV-[IN:Uda:Okr] ABM21601	282-1052: 771	256	29.5
							C4	100%	AC4 Protein/ ToLCNDV-[IN:Kar:Abe:04] ADO41058	2127-2435: 309	102	11.7
							C5	86%	AC5 Protein/ ToLCNDV-[IN:Ban:Abe:05] ADO41063	312-797: 486	161	18.4
							V3	95%	AV3/ ToLCNDV-[IN:Ori:09] AJW80900	43-429: 387	128	14.6
							V2	97%	AV2/ ToLCNDV-[IN:Ori:09] AJW80894	122-460: 339	112	12.9
							REn	100%	Replication enhancer protein/ ToLCNDV-[IN:Gun:Abe:06] ADO41073	1049-1459: 411	136	16
							TrAP	91%	AC2/ ToLCNDV-[IN:Lyc:12] AFQ62675	1179-1598: 420	139	15.5

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	Rep	96%	AC1/ ToLCNDV-[IN:Ori:09] AJW80896	1501-2676: 1176	391	44.5
115.	KP195265	India	2740	Tomato	94%	ToLCNDV-IN[PK:RYK:04] DQ116885	CP	95%	AV1 Protein/ ToLCNDV-[Svr] NP_803220	280-1050: 771	256	29.4
							C4	88%	AC4/ ToLCNDV-[IN:Cha:09] AJW80913	2251-2427: 177	58	64.7
							C5	94%	Gemini_AC_4_5/ SLCCNV-[IN:Ben:13] AGT98645	310-795: 486	161	18.1
							V2	82%	AV2/ ToLCNDV-[IN:Rau:09] AHA82228	120-458: 339	112	13
							REn	91%	C3/ ToLCNDV-[PK:RYK] ABB52055	1047-1457: 411	136	15.9
							TrAP	98%	C2/ ToLCNDV-[PK:RYK] ABB52056	1192-1596: 405	134	15.2
							Rep	99%	Rep/ ToLCNDV-[PK:RYK] ABB52053	1499-2584: 1086	361	41
116.	KP235541	India	2740	Chilli	99%	ToLCNDV-[IN:Chi:09] KP235542	CP	99%	Coat Protein/ ToLCNDV-[PK:Fsd:Gly:15] AQT38104	280-1050: 771	256	29.5
							C4	98%	AC4/ ToLCNDV-[IN:Pha:BG:14] AKM49927	2251-2427: 177	58	65.8
							C5	99%	AC5/ ToLCNDV-[IN:ND:Sol] ADM36027	310-795: 486	161	17.8
							V2	99%	AV2/ ToLCNDV-[IN:Sol] ADM36025	120-458: 339	112	12.9
							V3	98%	AV3/ ToLCNDV-[IN:ND:Sol] ADM36024	41-427: 387	128	13.5
							REn	99%	Replication enhancer protein/ ToLCNDV-[PK:Cal:15] AQY45833	1047-1457: 411	136	16.1
							TrAP	99%	TrAP/ ToLCNDV-[IN:Chi:09] AKN79147	1177-1596: 420	139	15.7
							Rep	98%	Replication associated protein/ ToLCNDV SAM29896	1499-2584: 1086	361	40.9
117.	KF551582	India	2741	Tomato	94%	ToLCNDV-[IN:ND:06] EF068246	CP	96%	AV1 Protein/ ToLCNDV-[PK:Dar:01] AAL60213	280-1050: 771	256	29.6
							C4	93%	AC4 Protein/ ToLCNDV ABO31253	2251-2427: 177	58	66.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	C5	100%	AC5/ ToLCNDV-[IN:Rau:09] AHA82210	310-828: 519	172	19.1
							V2	98%	Pre-coat Protein/ ToLCNDV-[IN:MP:Pot:10] AGR88317	120-458: 339	112	13
							V3	93%	AV3/ ToLCNDV AAA92815	41-427: 387	128	13.7
							REn	99%	AC3/ ToLCNDV-[IN:10] AGG13395	1047-1457: 411	136	15.9
							TrAP	99%	Transcriptional activator protein/ MLCV-[PK:Pun:Cuc:05] CAM56760	1177-1596: 420	139	15.8
							Rep	95%	AC1/ ToLCNDV-[IN:Var:11] AHA61376	1499-2584: 1086	361	40.9
118.	FN645905	India	2737	*Lagenaria siceraria*	97%	BGYVV-[IN:BG:12] KJ862841	CP	99%	AV1/ ToLCNDV-[Mld] AAA92817	280-1050: 771	256	29.5
							C4	95%	AC4 Protein/ BGYVV-[IN:Kan:Len:13] AIS68776	2134-2427: 294	97	11.1
							C5	96%	AC5/ ToLCNDV-[IN:Luf] AAY44736	310-534: 225	74	80.6
							V2	99%	Pre-coat Protein/ ToLCNDV-[IN:ND] ABA00498	120-458: 339	112	12.9
							V3	91%	V3/ ToLCNDV-[PK:RYK] ABB52058	41-427: 387	128	14.7
							REn	98%	AC3/ ToLCNDV-[IN:Ker:BG:14] AKM49924	1047-1457: 411	136	15.9
							TrAP	96%	Transcription activator protein/ ToLCNDV-[IN:TN:BG:13] AIX97575	1177-1596: 420	139	15.5
							Rep	98%	Replication-associated protein/ BGYVV-[BD:BG:12] YP_009058924	1499-2584: 1086	361	40.9
119.	KF551576	India	2739	Tomato	93%	ToLCNDV-[IN:Jun:11] KP195262	CP	99%	AV1/ ToLCNDV-[Mld] AAA92817	280-1050: 771	256	29.5
							C4	95%	C4 Protein/ ToLCNDV-[PK:Lah:Sol:04] CAO98747	2251-2427: 177	58	66.6
							C5	95%	C5/ ToLCNDV-[PK:Kha:Chi] ABB52030	310-795: 486	161	17.7
							V2	99%	Precoat Protein/ ToLCNDV-[IN:Pun:08] ADT70812	120-458: 339	112	12.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	V3	95%	AV3/ ToLCNDV-[Mld] AAA92815	41-427: 387	128	14.5
							REn	99%	AC3/ ToLCNDV-[IN:His:Cot:05] ABK41854	1047-1457: 411	136	16
							TrAP	95%	AC2/ ToLCNDV-[IN:Cha:09] AJW80911	1177-1596: 420	139	15.8
							Rep	94%	Replication initiator protein/ ToLCPMV SAM29870	1499-2584: 1086	361	41
120.	KT426907	India	2739	Ridge Gourd	99%	ToLCNDV-[IN:RG4:13] KT426906	CP	99%	Coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18871	280-1050: 771	256	29.6
							C4	97%	AC4 Protein/ ToLCNDV-[IN:AP:RG:13] AMB18896	2251-2427: 177	58	65.8
							C5	94%	AC5 Protein/ ToLCNDV-[IN:AP:RG:13] AMB18890	310-795: 486	161	18.1
							V2	99%	Pre-coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18870	120-458: 339	112	13
							REn	99%	Replication enhancer protein/ ToLCNDV-[IN:Kar:RG:13] AMB18872	1047-1457: 411	136	15.7
							TrAP	99%	Transcription activator protein/ ToLCNDV-[IN:AP:RG:13] AMB18887	1192-1596: 405	134	15.2
							Rep	99%	Replication associated protein/ ToLCNDV-[IN:AP:RG:13] AMB18888	1499-2584: 1086	361	40.8
121.	KT426906	India	2739	Ridge Gourd	99%	ToLCNDV-[IN:RG1:13] KT426903	CP	99%	Coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18871	280-1050: 771	256	29.6
							C4	97%	AC4 Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18875	2251-2427: 177	58	66.7
							C5	98%	AC5 Protein/ ToLCNDV-[IN:AP:RG:13] AMB18890	310-795: 486	161	17.8
							V3	92%	AV3/ ToLCNDV-[IN:Cha:09] AJW80909	41-427: 387	128	14.3
							V2	99%	Pre-coat Protein/ ToLCNDV-[IN:Ker:RG:13] AMB18898	120-458: 339	112	13
							REn	99%	Replication enhancer protein/ ToLCNDV-[IN:Kar:RG:13] AMB18872	1047-1457: 411	136	15.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	TrAP	99%	Transcription activator protein/ ToLCNDV-[IN:Ker:RG:13] AMB18901	1192-1596: 405	134	15.2
							Rep	99%	Replication associated protein/ ToLCNDV-[IN:AP:RG:13] AMB18888	1499-2584: 1086	361	40.9
122.	KT426904	India	2739	Ridge Gourd	98%	ToLCNDV-[IN:RG1:13] KT426903	CP	98%	Coat Protein/ ToLCNDV-[ES:Alm:Zuc:13] AHJ80135	280-1050: 771	256	29.7
							C4	90%	AC4/ ToLCNDV-[TW:07] ACZ63316	2251-2427: 177	58	66.5
							C5	94%	AC5 Protein/ ToLCNDV-[IN:AP:RG:13] AMB18897	310-795: 486	161	17.8
							V3	89%	AV3/ ToLCNDV-[IN:Cha:09] AJW80909	41-427: 387	128	14.3
							V2	99%	Pre-coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18870	120-458: 339	112	13
							REn	96%	Replication enhancer protein/ ToLCNDV-[IN:AP:RG:13] AMB18893	1047-1457: 411	136	15.8
							TrAP	99%	Transcription activator protein/ ToLCNDV-[IN:AP:RG:13] AMB18887	1192-1596: 405	134	15.2
							Rep	99%	Replication associated protein/ ToLCNDV-[IN:AP:RG:13] AMB18888	1499-2584: 1086	361	40.9
123.	KT426905	India	2739	Ridge Gourd	99%	ToLCNDV-[IN:RG4:13] KT426906	CP	99%	Coat Protein/ ToLCNDV-[ES:Alm:Zuc:13] AHJ80135	280-1050: 771	256	29.6
							C4	90%	AC4/ ToLCNDV-[IN:BG:Ker:14] AKM49927	2251-2427: 177	58	67
							C5	98%	AC5 Protein/ ToLCNDV-[IN:AP:RG:13] AMB18897	310-795: 486	161	17.9
							V2	99%	Pre-coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18870	120-458: 339	112	13.1
							REn	99%	Replication enhancer protein/ ToLCNDV-[IN:AP:RG:13] AMB18893	1047-1457: 411	136	15.7
							TrAP	99%	Transcription activator protein/ ToLCNDV-[IN:Ker:RG:13] AMB18901	1192-1596: 405	134	15.2

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	Rep	99%	Replication associated protein/ ToLCN/DV-[IN:AP:RG:13] AMB18895	1499-2584: 1086	361	40.8
124.	KT426903	India	2739	Ridge Gourd	99%	ToLCNDV-[IN:RG4:13] KT426906	CP	99%	Coat Protein/ ToCNDV-[ES:Alm:Zuc:13] AHJ80135	280-1050: 771	256	29.6
							C4	97%	AC4 Protein/ ToLCNDV-[IN:AP:RG:13] AMB18896	2251-2427: 177	58	67
							C5	98%	AC5 Protein/ ToLCNDV-[IN:AP:RG:13] AMB18890	310-795: 486	161	17.8
							V3	91%	AV3/ ToLCNDV-[IN:Cha:09] AJW80909	41-427: 387	128	14.3
							V2	99%	Pre-coat Protein/ ToLCNDV-[IN:Ker:RG:13] AMB18898	120-458: 339	112	13
							REn	99%	Replication enhancer protein/ ToLCNDV-[IN:AP:RG:13] AMB18893	1047-1457: 411	136	15.7
							TrAP	99%	Transcription activator protein/ ToLCNDV-[IN:Ker:RG:13] AMB18901	1192-1596: 405	134	15.2
							Rep	99%	Replication associated protein/ ToLCNDV-[IN:AP:RG:13] AMB18888	1499-2584: 1086	361	40.9
125.	KF749223	Spain	2738	Zucchini	99%	ToLCNDV-[ES:Alm:TomA5:14] KT175406	CP	99%	Coat Protein/ ToLCNDV-[IN:Kar:RG:13] AMB18871	279-1049: 771	256	29.6
							C4	93%	AC4 Protein/ ToLCNDV-[PK:Che:Sol:11] CUU64521	2250-2426: 177	58	66.1
							C5	87%	AC5 Protein/ ToLCNDV-[IN:Ker:RG:13] AMB18904	309-794: 486	161	18
							V2	99%	AV2 Protein/ ToLCNDV-[ES:Zuc:12] AHM26189	119-457: 339	112	13
							REn	99%	Replication enhancer protein/ ToLCNDV-[ES:Alm:Zuc:13] AHJ80137	1046-1456: 411	136	15.8
							TrAP	99%	Suppressor Protein/ ToLCNDV-[ES:Alm:14] ALP06199	1191-1595: 405	134	15.2
							Rep	99%	Replication initiation protein/ ToLCNDV-[ES:Alm:Zuc:13] AHJ80139	1498-2583: 1086	361	40.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
126.	EF450316	Bangladesh	2738	Cucumber	90%	ToLCNDV-IN [PK:RYK:04] DQ116885	CP	99%	Coat Protein/ ToLCNDV-[IN:Luf] AAY44733	278-1048: 771	256	29.5
							C5	79%	AC5 Protein/ ToLCNDV-[IN:MP:Pot:10] AGR88319	308-793: 486	161	18.4
							C4	88%	AC4/ ChEYMV- [IN:TN:Cha:15] APF30593	2249-2425: 177	58	67
							V2	95%	Pre-coat protein/ ToLCNDV-[IN:MP:Pot:10] AGR88317	118-447: 330	109	12.6
							REn	87%	Replication enhancer protein/ ToLCNDV-[ES:Alm:Mel:14] ALP06192	1045-1455: 411	136	15.7
							TrAP	83%	AC2/ ToLCNDV-[IN:Guj:11] AHA82169	1190-1594: 405	134	15.2
							Rep	93%	AC1 Protein/ ToLCNDV-[IN:Var:11] AHA61376	1497-2582: 1086	361	41
127.	KF002409	Pakistan	2743	*Parthenium hysterophorus*	98%	ToLCNDV-[IR:Zab:Egg:13] KJ778692 KJ778694	CP	99%	CP/ ToLCNDV-[PK:RYK] ABB52054	287-1057: 771	256	29.5
							C5	93%	AC5 Protein/ ToLCNDV-[IN:Kar:Abe:04] ADO41054	317-679: 363	120	13.3
							C4	97%	AC4/ ToLCNDV-[IN:AP:08] AJW80780	2280-2462: 183	60	69.2
							V2	98%	V2 protein / ToLCNDV-[PK:Sol:97] CAF04467	127-465: 339	112	13
							REn	97%	AC3/ ToLCNDV-[IN:09] AHB37377	1054-1464: 411	136	16
							TrAP	96%	AC2/ ToLCNDV-[IN:09] AHB37376	1184-1603: 420	139	15.7
							Rep	100%	Replication initiator protein/ ToLCNDV-[IN:Mah:Egg:09] ADY75699	1506-1949: 444	147	16.8
128.	KP191047	India	2739	*Sechium edule* (Chayote)	98%	ChEYMV-[IN:TN:Cha:15] KX259336	CP	99%	Coat Protein/ ToLCNDV-[ES:Alm:Zuc:13] AHJ80135	280-1050: 771	256	29.6
							C5	88%	AC5 Protein/ ToLCNDV-[IN:AP:RG:13] AMB18890	310-795: 486	161	18.1
							C4	95%	AC4, ChEYMV-[IN:TN:Cha:15] APF30593	2251-2427: 177	58	66.2
							V2	97%	AV2/ ChEYMV-[IN:TN:Cha:15] APF30582	120-458: 339	112	12.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
	//	//	//	//	//	//	REn	98%	AC3/ ChEYMV-[IN:TN:Cha:15] APF30586	1047-1457: 411	136	15.9
							TrAP	94%	AC2/ ChEYMV-[IN:TN:Cha:15] APF30585	1192-1596: 405	134	15.1
							Rep	98%	AC1/ ChEYMV-[IN:TN:Cha:15] APF30584	1499-2584: 1086	361	40.8
129.	KX827602	India	2735	Carica papaya cultivar Pusa dwarf	97%	ToLCNDV-[IN:ND:Pap:05] DQ989325	CP	99%	Coat Protein/ ToLCNDV-[IN:Luf] AAY44733	287-1057: 771	256	29.5
							C5	96%	AC5/ ToLCNDV-[IN] ADM36027	317-802: 486	161	18.4
							V3	95%	AV3/ ToLCNDV-[PK:Bwp:Gos:13] CRI05838	48-434: 387	128	15.1
							REn	99%	AC3/ ToLCNDV-[IN:ND:Pap:05] ABJ97337	1054-1464: 411	136	16.2
							TrAP	96%	AC2/ ToLCNDV-[IN:ND:Pap:05] ABJ97338	1199-1603: 405	134	15.9
							V2	99%	V2 Protein/ ToLCNDV-[PK:Sol] CAF04467	127-465: 339	112	13.4
							Rep	95%	AC1/ ToLCNDV-[IN:ND:Pap:05] ABJ97339	1506-2597: 1092	363	42.2
							C4	97%	C4 Protein/ ToLCNDV-[PK:Gly:15] AQT3101	2440-2264: 177	58	68.7
130.	DQ989325	India	2735	Carica papaya cultivar Pusa dwarf	97%	ToLCNDV-[PK:Fsd:Gly:15] KX827602	CP	99%	Coat Protein/ ToLCNDV-[PK:Fsd:15] AQT3104	287-1057: 771	256	29.6
							V3	98%	AV3/ ToLCNDV-[IN:12] AFQ62670	48-434: 387	128	15.2
							C5	93%	AC5/ ToLCNDV-[IN:Guj:11] AHA82172	317-802: 486	161	18.4
							V2	98%	Pre-Coat Protein/ ToLCNDV-[IN:ND] ABA00498	127-465: 339	112	13.2
							REn	99%	Replication Enhancer Protein/ ToLCNDV-[PK:Fsd:Gly:15] AQT38108	1054-1464: 411	136	16.2
							TrAP	96%	Transcriptional Activation Protein/ ToLCNDV-[PK:Fsd:Gly:15] AQT38107	1199-1603: 405	134	15.9
							C4	91%	C4 Protien/ ToLCNDV-[PK:Lhr:Sol:04] CAO98747	2264-2440: 177	58	69.2
							Rep	95%	Replication-Associated Protein/ ToLCNDV-[PK:Fsd:15] AQT38106	1506-2597: 1092	363	42.2

Table 4.2 Data Table of Isolates of DNA-B

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
1.	KF749226	Spain	Zucchini	2684	99%	ToLCNDV-[ES:Alm:Zuc:13] KF891467	Movement Protein	95%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05817	1290-2135: 846	281	31.4
							Nuclear Shuttle Protein	90%	Nuclear shuttle protein/ ToLCNDV-[PK:Rwp:Cuc:13] AMW03298	430-1236: 807	268	30.9
2.	KF749227 KF749228	Spain	Zucchini	2684	99%	ToLCNDV-[ES:Zuc:13] KF749226	Movement Protein	95%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05817	1290-2135: 846	281	31.4
							Nuclear Shuttle Protein	90%	Nuclear shuttle protein/ ToLCNDV-[PK:Rwp:Cuc:13] AMW03298	430-1236: 807	268	30.9
3.	KF891467	Spain	Zucchini	2684	99%	ToLCNDV-[ES:Zuc:13] KF749226	Movement Protein	95%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05817	1290-2135: 846	281	31.4
							Nuclear Shuttle Protein	90%	Nuclear shuttle protein/ ToLCNDV-[PK:Rwp:Cuc:13] AMW03298	430-1236: 807	268	30.9
4.	KM977734	Spain	Zucchini	2684	99%	ToLCNDV-[ES:Zuc:13] KF749226	Movement Protein	95%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05817	1290-2135: 846	281	31.4
							Nuclear Shuttle Protein	90%	Nuclear shuttle protein/ ToLCNDV-[PK:Rwp:Cuc:13] AMW03298	430-1236: 807	268	30.9
5.	KT175407	Spain	Zucchini	2684	99%	ToLCNDV-[ES:Alm:Zuc:13] KF891467	Movement Protein	95%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05817	1290-2135: 846	281	31.4
							Nuclear Shuttle Protein	90%	Nuclear shuttle protein/ ToLCNDV-[PK:Rwp:Cuc:13] AMW03298	430-1236: 807	268	30.9
6.	U15017	India	*Lycopersicon esculentum*	2696	99%	ToLCNDV-[IN:Chi:09] JN663871 KF471060	Movement Protein	99%	MP/ ToLCNDV-[IN:Chi:09] AGA60307	1276-2154: 879	292	32.8
							Nuclear Shuttle Protein	99%	BV1/ ToLCNDV-[IN:Svr] ADM36032	405-1250: 846	281	32.5
7.	JN663871 KF471060	India	Chilli	2696	99%	ToLCNDV-[IN:ND:Svr:92] U15017	Movement Protein	99%	Movement Protein/ ToLCNDV-[Svr] NP_803227	1276-2154: 879	292	32.8
							Nuclear Shuttle Protein	99%	BV1/ ToLCNDV-[IN:Svr] ADM36032	405-1250: 846	281	32.5

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
8.	JN663848 KP235543	India	Chilli	2696	99%	ToLCNDV-[IN:ND:Svr:92] U15017	Movement Protein	99%	MP/ ToLCNDV-[IN:Chi:09] AGA60307	1276-2154: 879	292	32.8
							Nuclear Shuttle Protein	99%	BV1/ ToLCNDV-[IN:Svr] ADM36032	405-1250: 846	281	32.5
9.	FN435312	Pakistan	*Lycopersicon esculentum*	2696	99%	ToLCNDV-[IN:ND:Svr:92] U15017	Movement Protein	99%	Movement Protein/ ToLCNDV-[Svr] NP_803227	1276-2154: 879	292	32.8
							Nuclear Shuttle Protein	99%	BV1/ ToLCNDV-[IN:Svr] ADM36032	405-1250: 846	281	32.5
10.	JN663867	India	Chilli	2696	99%	ToLCNDV-[IN:ND:Svr:92] U15017	Movement Protein	99%	MP/ ToLCNDV-[IN:Chi:09] AGA60307	1276-2154: 879	292	32.8
							Nuclear Shuttle Protein	99%	BV1/ ToLCNDV-[IN:Svr] ADM36032	405-1250: 846	281	32.5
11.	HM159455	India	*Lycopersicon esculentum*	2696	99%	ToLCNDV-[IN:ND:Svr:92] U15017	Movement Protein	99%	MP/ ToLCNDV-[IN:Chi:09] AGA60307	1276-2154: 879	292	32.8
							Nuclear Shuttle Protein	99%	Nuclear shuttle protein/ ToLCNDV-[Svr] NP_803226	405-1250: 846	281	32.5
12.	DQ169057	India	*Lycopersicon esculentum*	2693	99%	ToLCNDV-[IN:ND:Luf:10] HM989846	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Luf:10] ADT70809	1306-2151: 846	281	31.3
							Nuclear Shuttle Protein	100%	Nuclear shuttle protein/ ToLCNDV-[Svr] NP_803226	443-1249: 807	268	31
13.	HM989846	India	*Luffa acutangula*	2692	99%	ToLCNDV-[IN:ND] DQ169057	Movement Protein	99%	BC1 Protein/ ToLCNDV-[IN:ND] ABA00500	1305-2150: 846	281	31.3
							Nuclear Shuttle Protein	100%	Nuclear Shuttle Protein/ ToLCNV-[Svr] NP_803226	442-1248: 807	268	31
14.	KC545813	India	*Cucumis sativus*	2694	99%	ToLCNDV-[IN:ND] DQ169057	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Luf:10] ADT70809	1306-2151: 846	281	31.3
							Nuclear Shuttle Protein	99%	BV1 Protein/ ToLCNDV-[IN:ND] ABA00501	443-1249: 807	268	31
15.	KC969439	Pakistan	*Convolvulus arvensis*	2681	98%	ToLCNDV-[PK:Fas:Sol:09] FN435312	Movement Protein	99%	Movement Protein/ ToLCNDV-[Svr] NP_803227	1273-2151: 879	292	32.8
							Nuclear Shuttle Protein	99%	BV1/ ToLCNDV-[IN:Svr] ADM36032	397-1242: 846	281	32.5

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
16.	AY939924	India	*Luffa cylindrica*	2643	98%	ToLCNDV-[IN:ND] DQ169057	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Luf:10] ADT70809	1306-2151: 846	281	31.2
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Svr] ABA00501	395-1249: 855	284	32.8
17.	HG316126	Pakistan	*Rumex dentatus*	2651	96%	ToLCNDV-[PK:Fas:Sol:09] FN435312	Movement Protein	99%	Movement Protein/ ToLCNDV-[Svr] NP_803227	1276-2154: 879	292	32.8
							Nuclear Shuttle Protein	99%	BV1/ ToLCNDV-[IN:Svr] ADM36032	405-1250: 846	281	32.5
18.	AM778833	Pakistan	*Solanum esculentum*	2800	98%	ToLCNDV-[IN:ND] DQ169057	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Luf:10] ADT70809	1413-2258: 846	281	31.3
							Nuclear Shuttle Protein	99%	BV1 Protein/ ToLCNDV-[IN:ND] ABA00501	550-1356: 807	268	31
19.	DQ020490	India	Bitter gourd	2706	93%	ToLCNDV-[IN:ND] DQ169057	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Luf:10] ADT70809	1321-2166: 846	281	31.1
							Nuclear Shuttle Protein	97%	Nuclear Shuttle Protein/ BGYVV-[BD:12] YP_009058926	458-1264: 807	268	30.9
20.	HQ141674	India	Tomato	2695	96%	ToLCNDV-[IN:Pun:08] HM803117	Movement Protein	99%	Movement Protein/ BYVMV-[IN:Kar:Okr:06] AFS63513	1302-2147: 846	281	31.3
							Nuclear Shuttle Protein	96%	BV1 Protein/ ToLCNDV-[IN:Guj:12] AGV02073	400-1245: 846	281	32.4
21.	HM803117	India	Tomato	2699	96%	ToLCNDV-[IN:Pun:08] HQ141674	Movement Protein	95%	Movement Protien/ ToLCNDV-[Svr] NP_803227	1304-2149: 846	281	31.6
							Nuclear Shuttle Protein	96%	Nuclear Shuttle Protein/ ToLCNDV-[Svr] NP_803226	402-1247: 846	281	32.5
22.	KF515623	India	Tomato	2700	94%	ToLCNDV-[IN:Pun:08] HQ141674	Movement Protein	99%	BC1/ ToLCNDV-[IN:Guj:11] AHA98625	1307-2152: 846	281	31.4
							Nuclear Shuttle Protein	97%	Nuclear Shuttle Protein/ ToLCNDV-[Svr] NP_803226	404-1249: 846	281	32.5
23.	AM286435	India	Pumpkin	2694	97%	ToLCNDV-[IN:ND:AG:11] JN208137	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:AG:11] AEX15671	1306-2151: 846	281	31.2
							Nuclear Shuttle Protein	98%	Nuclear Shuttle Protein/ ToLCNDV-[IN:ND:AG:11] AEX15670	442-1248: 807	268	30.8

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
24.	KC874496	India	Potato	2692	99%	ToLCNDV-[INHim:Sol:06] FN356024	Movement Protein	100%	Movement Protien/ ToLCNDV-[IN:MP:Pot:10] AGR88292	1303-2289: 987	328	36.7
							Nuclear Shuttle Protein	99%	Nuclear shuttle protein/ ToLCNDV-[IN:Dee:Pot:11] AGR88295	440-1246: 807	268	30.9
25.	FN356024 KP709056	India	*Solanum tuberosum*	2693	99%	ToLCNDV-[IN:Har:Pot:10] KC874494	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Dee:Pot:11] AGR88296	1303-2148: 846	281	31.4
							Nuclear Shuttle Protein	99%	Nuclear shuttle protein/ ToLCNDV-[IN:Dee:Pot:11] AGR88295	440-1246: 807	268	30.9
26.	KC874494	India	Potato	2693	99%	ToLCNDV-[INHim:Sol:06] FN356024	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Dee:Pot:11] AGR88296	1303-2148: 846	281	31.4
							Nuclear Shuttle Protein	99%	Nuclear shuttle protein/ ToLCNDV-[IN:Him:Pot:06] CAX83211	440-1246: 807	268	30.9
27.	KC874499	India	Potato	2693	99%	ToLCNDV-[IR:Zab:Cuc:14] KP641676	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Dee:Pot:11] AGR88296	1303-2148: 846	281	31.4
							Nuclear Shuttle Protein	99%	Nuclear shuttle protein/ ToLCNDV-[IN:Him:Pot:06] CAX83211	440-1246: 807	268	30.9
28.	GU112085	India	*Abelmoschus esculentus* cultivar Arka Anamika	2692	97%	BYVDV-[IN:ND:Okr:07] HQ542082	Movement Protein	98%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1305-2150: 846	281	31.2
							Nuclear Shuttle Protein	97%	Bv1/ BYVDV-[IN:ND:Okr:07] AEP31932	442-1248: 807	268	31
29.	KP641676	Iran	Cucumber	2693	99%	ToLCNDV-[IN:Mod:Pot:11] KC874499	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Dee:Pot:11] AGR88296	1303-2148: 846	281	31.4
							Nuclear Shuttle Protein	99%	Nuclear shuttle protein/ ToLCNDV-[IN:Him:Pot:06] CAX83211	440-1246: 807	268	30.9
30.	KC874495	India	Potato	2693	99%	ToLCNDV-[INHim:Sol:06] FN356024	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Dee:Pot:11] AGR88296	1303-2148: 846	281	31.4
							Nuclear Shuttle Protein	99%	Nuclear shuttle protein/ ToLCNDV-[IN:Him:Pot:06] CAX83211	440-1246: 807	268	30.9
31.	AY158080	India	Potato	2693	98%	ToLCNDV-[IN:Dee:Pot:11] KC874498	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Him:Pot:06] CAX83212	1303-2148: 846	281	32.4
							Nuclear Shuttle	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:UP:Pot:11]	440-1246: 807	268	31.7

							Protein		AGR88293			
Sr #	**Accession Number**	**Country**	**Host**	**Nucleotide Number**	**Nucleotide Sequence Identity**	**Nucleotide Identity with Virus**	**Proteins**	**Proteins Percentage Identity**	**Protein / Identity with Virus**	**Nucleotide Length**	**Number of Amino acids**	**Molecular Weight (kDa)**
32.	HG932560	India	Tomato	2694	99%	ToLCNDV-[INHim:Sol:06] FN356024	Movement Protein	97%	Movement Protien/ ToLCNDV-[IN:Him:Pot:06] CAX83212	1382-2149: 768	255	29.7
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Guj:Pot:11] AGR88295	440-1246: 807	268	31.8
33.	KC874501	India	Potato	2693	99%	ToLCNDV-[IR:Zab:Mel:14] KP641674	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Guj:Pot:11] AGR88296	1303-2148: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Guj:Pot:11] AGR88295	440-1246: 807	268	31.7
34.	EF043233	India	Potato	2693	97%	ToLCNDV-[IN:MP:Pot:10] KC874496	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Guj:Pot:11] AGR88296	1303-2148: 846	281	32.4
							Nuclear Shuttle Protein	97%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Guj:Pot:11] AGR88295	440-1246: 807	268	31.7
35.	KC874497	India	Potato	2694	98%	ToLCNDV-[IN] AY158080	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Him:Pot:06] CAX83212	1303-2148: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN] AAO06845	440-1246: 807	268	31.7
36.	JN208137	India	*Benincasa hispida* (Ash gourd)	2694	97%	ToLCNDV-[IN:ND:Pum] AM286435	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	98%	Nuclear Shuttle Protein/ ToLCNDV-[IN:ND:Pum] CAL15169	442-1248: 807	268	31.8
37.	KC874498	India	Potato	2693	99%	ToLCNDV-[IR:Zab:14] KP641678	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Him:Pot:06] CAX83212	1303-2148: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Pun:Pot:10] AGR88301	440-1246: 807	268	31.7
38.	KF577603	India	Tomato	2699	93%	ToLCNDV-[IN:Jun:12] KF515623	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Luf:10] ADT70809	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	79%	Nuclear Shuttle Protein/ ToLCNDV-[Svr] NP_803226	403-1248: 846	281	32.8
39.	EF043232	India	Potato	2693	99%	ToLCNDV-[IN:Mod:Pot:10] KC874500	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:UP:Pot:10] AGR88300	1303-2148: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Him:Pot:06] CAX83211	440-1246: 807	268	31.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
40.	AY150305	Pakistan	Tomato	2686	94%	ToLCNDV-[PK:Add:Gos:13] HG983285	Movement Protein	97%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1299-2144: 846	281	32.4
							Nuclear Shuttle Protein	97%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Add:Gos:13] CDP90410	436-1242: 807	268	31.8
41.	KP641674	Iran	Melon	2693	99%	ToLCNDV-[IN:Jal:Pot:10] KC874501	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Guj:Pot:11] AGR88296	1303-2148: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Guj:Pot] AGR88295	440-1246: 807	268	31.7
42.	KC874500	India	Potato	2693	99%	ToLCNDV-[IN:Pot:05] EF043232	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Him:Pot:06] CAX83212	1303-2148: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Him:Pot:06] CAX83211	440-1246: 807	268	31.8
43.	LN845960	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845947	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.7
44.	LN845963	Pakistan	*Gossypium hirsutum*	2697	98%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	98%	Nuclear Shuttle Protein/ ToLCNDV-[IN:ND:AG:11] AEX15670	442-1248: 807	268	31.7
45.	LN845947	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05834	442-1248: 807	268	31.7
46.	LN845942	Pakistan	*Abelmoschus esculentus*	2696	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05835	1305-2150: 846	281	31.2
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05784	441-1247: 807	268	30.9
47.	LN845935	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845936	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
48.	LN845950	Pakistan	*Abelmoschus esculentus*	2696	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1305-2150: 846	281	31.2
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05784	441-1247: 807	268	30.9
49.	LN845939	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.7
50.	LN845938	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05784	442-1248: 807	268	31.7
51.	LN845954	Pakistan	*Abelmoschus esculentus*	2695	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05835	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.6
52.	LN845941	Pakistan	*Abelmoschus esculentus*	2698	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1304-2152: 849	282	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05784	443-1249: 807	268	31.7
53.	KP641678	Iran	Tomato	2693	99%	ToLCNDV-[IN:Dee:Pot:11] KC874498	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Him:Pot:06] CAX83212	1303-2148: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Pun:Pot:10] AGR88301	440-1246: 807	268	31.7
54.	LN845943	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05835	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.7
55.	LN713274	Pakistan	*Abelmoschus esculentus*	2700	99%	ToLCNDV-[PK:Goj:Abe:13] LN845935	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
56.	LN845936	Pakistan	*Abelmoschus esculentus*	2695	99%	ToLCNDV-[PK:Goj:Abe:13] LN845935	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.7
57.	LN845946	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.2
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.6
58.	LN845953 LN845952	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.7
59.	AJ875158	Bangladesh	Tomato	2688	91%	ToLCNDV-[IN:Pun:09] KF571462	Movement Protein	98%	BC1/ ToLCNDV-[IN:Pun:09] AHB37381	1301-2146: 846	281	36.8
							Nuclear Shuttle Protein	93%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Gun:Abe:06] ADO41077	312-1244: 933	310	32.4
60.	FN435311	Pakistan	*Solanum lycopersicum*	2736	98%	ToLCNDV-[PK:Che:12] KC969440	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Gly:15] AQT38103	1351-2196: 846	281	32.5
							Nuclear Shuttle Protein	93%	BV1/ ToLCNDV-[PK:Kha:Chi] ABB52038	486-1292: 807	268	31.6
61.	KC969440	Pakistan	*Chenopodium album*	2736	98%	ToLCNDV AM947507	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Gly:15] AQT38103	1343-2188: 846	281	32.5
							Nuclear Shuttle Protein	94%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05816	478-1284: 807	268	31.6
62.	KF002410	Pakistan	*Parthenium hysterophorus*	2689	99%	ToLCNDV-[IR:Zab:Egg:13] KJ778693 KJ778695	Movement Protein	96%	BV1/ ToLCNDV-[IN:09] AHA98620	1310-2151: 846	281	33.5
							Nuclear Shuttle Protein	98%	BC1/ BYVMV-[IN:Kar:Okr:06] AEP31937	408-1253: 846	281	32.4
63.	EF408038	India	Tomato	2693	94%	ToLCGV-[Var:01] AY190291	Movement Protein	99%	Movement Protein/ TLCGV NP_783159	1304-2149: 846	281	32.4
							Nuclear Shuttle Protein	96%	BC1/ ToLCNDV-[IN:Pun:09] AHB37380	441-1247: 807	268	31.8

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
64.	KF571462	India	Tomato	2693	93%	ToLCNDV EF408038	Movement Protein	98%	Movement Protein/ ToLCNDV-[BD:Jes] CAI44694	1304-2149: 846	281	32.4
							Nuclear Shuttle Protein	96%	Nuclear Shuttle Protein/ ToLCNDV ABO13956	441-1247: 807	268	31.9
65.	AB613826	Indonesia	*Cucumis sativus*	2690	91%	ToLCNDV-[TH:Cuc] AB330080	Movement Protein	98%	BC1/ ToLCNDV-[TH:Cuc] BAF69035	1305-2150: 846	281	32.2
							Nuclear Shuttle Protein	91%	BV1/ ToLCNDV-[TW:Mel:07] ACZ63317	442-1248: 807	268	31.6
66.	LN845951	Pakistan	*Abelmoschus esculentus*	2703	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2157: 852	283	32.5
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05834	442-1248: 807	268	31.7
67.	LN845948	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	98%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2157: 852	283	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05784	442-1248: 807	268	31.7
68.	LN845945	Pakistan	*Abelmoschus esculentus*	2697	99%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2157: 852	283	32.2
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05834	442-1248: 807	268	31.6
69.	LN845949	Pakistan	*Abelmoschus esculentus*	2698	99%	ToLCNDV-[PK:Goj:Abe:13] LN845950	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1304-2149: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	440-1246: 807	268	31.7
70.	AM947507	India	Tomato	2736	98%	ToLCNDV-[PK:Che:12] KC969440	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Gly:15] AQT38103	1351-2196: 846	281	32.5
							Nuclear Shuttle Protein	93%	BV1/ ToLCNDV-[PK:Kha:Chi] ABB52038	486-1292: 807	268	31.6
71.	HG983285	Pakistan	*Gossypium hirsutum*	2688	99%	ToLCNDV-[PK:Bah:Gos:13] LN845934	Movement Protein	100%	Movement Protein/ ToLCNDV-[PK:Add:Gos:13] CDP90411	1301-2287: 987	328	38.2
							Nuclear Shuttle Protein	97%	BV1 Protein/ ToLCNDV-[PK:Dar] AAO32353	438-1244: 807	268	31.8

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
72.	LN845934	Pakistan	*Gossypium hirsutum*	2687	99%	ToLCNDV-[PK:Add:Gos:13] HG983285	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Add:Gos:13] CDP90411	1301-2146: 846	328	32.4
							Nuclear Shuttle Protein	97%	BV1 Protein/ ToLCNDV-[PK:Dar] AAO32353	438-1244: 807	268	31.8
73.	GU112089	India	*Abelmoschus esculentus* (okra)	2695	91%	ToLCNDV-[IN:Gun:OY136B:06] GU112087	Movement Protein	98%	Movement Protein/ ToLCNDV-[IN] AAO06846	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	100%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Aur:Abe:06] ADO41086	403-1248: 846	281	33.3
74.	KT948071	Pakistan	*Duranta repens*	2702	96%	ToLCNDV-[PK:Mul:Dur:05] AM392426	Movement Protein	96%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRL52725	1315-2160: 846	281	32.5
							Nuclear Shuttle Protein	97%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Mul:Dur:05] CAL36103	452-1258: 807	268	31.9
75.	KT948073	Pakistan	*Cucurbita pepo*	2693	95%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1304-2149: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05786	442-1248: 807	268	31.6
76	LN845961	Pakistan	*Abelmoschus esculentus*	2698	98%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	93%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05835	1337-2152: 816	271	31.7
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05782	442-1248: 807	268	31.7
77.	LN845937	Pakistan	*Abelmoschus esculentus*	2690	98%	ToLCNDV-[PK:Goj:Abe:13] LN845940	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05786	440-1246: 807	268	31.7
78.	LN845940	Pakistan	*Abelmoschus esculentus*	2690	98%	ToLCNDV-[PK:Goj:Abe:13] LN845937	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1305-2150: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05780	440-1246: 807	268	31.7
79.	GU112087	India	*Abelmoschus esculentus* (okra)	2695	99%	ToLCNDV-[IN:Kar:OY81A:04] GU112083	Movement Protein	99%	Movement Protein/ BYVMV-[IN:Kar:Okr:07] AEP31935	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Kar:Abe:04] ADO41059	442-1248: 807	268	31.7

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
80.	GU112083	India	*Abelmoschus esculentus* cultivar US7109 (okra)	2695	99%	ToLCNDV-[IN:Kar:OY81A:04] GU112083	Movement Protein	99%	Movement Protein/ BYVMV-[IN:Kar:Okr:07] AEP31935	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:AP:Abe:06] ADO41077	442-1248: 807	268	31.8
81.	AM392426	Pakistan	*Duranta repens*	2724	96%	ToLCNDV-[PK:Bhe:Dur:14] KT948071	Movement Protein	96%	Movement Protein/ ToLCNDV-[PK:Bhe:Dur:14] AMW03291	1314-2159: 846	281	32.6
							Nuclear Shuttle Protein	97%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Bhe:Dur:14] AMW03290	451-1257: 807	268	31.9
82.	LN845944	Pakistan	*Abelmoschus esculentus*	2698	97%	ToLCNDV-[PK:Goj:Abe:13] LN845960	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05791	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05834	442-1248: 807	268	31.7
83.	KF577604	India	Tomato	2694	92%	ToLCNDV-[IN:ND:Pum] AM286435	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	96%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Goj:Abe:13] CRI05780	442-1248: 807	268	31.6
84.	DQ116882	Pakistan	Chilli	2683	91%	ToLCNDV-[PK:Bah:Gos:13] LN845955	Movement Protein	98%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05817	1297-2142: 846	281	32.5
							Nuclear Shuttle Protein	96%	BV1/ ToLCNDV-[IN:ND] ABA00501	432-1238: 807	268	31.8
85.	HQ264186	India	Egg Plant	2698	99%	ToLCNDV-[IR:Zab:Egg:13] KJ778693 KJ778695	Movement Protein	98%	BC1/ BYVMV-[IN:Kar:Okr:06] AEP31937	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	96%	BV1/ ToLCNDV-[IN:09] AHA98620	403-1248: 846	281	33.5
86.	EF043394	India	Okra	2695	98%	ToLCNDV-[IN:Gun:OY136B:06] GU112087	Movement Protein	99%	BC1/ BYVMV-[IN:Kar:Okr:07] AEP31935	1305-2150: 846	281	32.3
							Nuclear Shuttle Protein	100%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Raj:Okr] ABM21602	442-1248: 807	268	31.8
87.	KJ778693 KJ778695	Iran	Egg Plant	2698	99%	ToLCNDV-[IN:Mah:Egg:09] HQ264186	Movement Protein	98%	BC1/ BYVMV-[IN:Kar:Okr:06] AEP31937	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	96%	BV1/ ToLCNDV-[IN:09] AHA98620	403-1248: 846	281	33.5

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
88.	LM645012	Pakistan	*Cestrum nocturnum*	2693	99%	ToLCNDV-[PK:Mul:Mom:05] AM849547	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Mul:Mom:05] CAO98741	1303-2148: 846	281	32.5
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Mul:Mom:05] CAO98740	439-1245: 807	268	31.8
89.	AY150304	Pakistan	Tomato	2728	91%	ToLCNDV-[IN:ND:Luf:10] HM989846	Movement Protein	98%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1335-2180: 846	281	32.4
							Nuclear Shuttle Protein	89%	Nuclear Shuttle Protein/ ToLCNDV-[Svr] NP_803226	402-1277: 876	291	34.5
90.	AY438563	India	Tomato	2693	95%	ToLCNDV-[PK:Bah:Gos:13] LN845956	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Hes:13] AJG05602	1304-2149: 846	281	32.4
							Nuclear Shuttle Protein	97%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Yaz:Gos:13] CEK41036	441-1247: 807	268	31.4
91.	AM849547	Pakistan	*Momordica charantia*	2694	99%	ToLCNDV-[PK:Isl:Ces:13] LM645012	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Isl:Ces:13] CDW74352	1304-2149: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Isl:Ces:13] CDW74351	440-1246: 807	268	31.8
92.	EF620535	Pakistan	Tomato	2693	93%	BYVDV-[IN:Kar:Okr:06] HQ586006	Movement Protein	90%	Movement Protein/ ToLCNDV-[Svr] NP_803227	1273-2151: 879	292	33.8
							Nuclear Shuttle Protein	91%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Hes:13] AJG05601	402-1247: 846	281	33.1
93.	LM645011	Pakistan	*Cestrum nocturnum*	2692	99%	ToLCNDV-[PK:Isl:Ces:13] LM645012	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Isl:Ces:13] CDW74352	1303-2148: 846	281	31.5
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Mul:Mom:05] CAO98740	439-1245: 807	268	31
94	KF577601 KF577602	India	Tomato	2695	97%	ToLCNDV-[IN:Hess:13] KM921670	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:Hes:13] AJG05602	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[IN:Hes:13] AJG05601	403-1248: 846	281	33.3
95.	KF577605	India	Tomato	2695	91%	ToLCNDV-[IN:ND] AY438563	Movement Protein	99%	Movement Protein/ ToLCNDV-[IN:ND:Pum] CAL15170	1306-2151: 846	281	32.3
							Nuclear Shuttle Protein	82%	Nuclear Shuttle Protein/ ToLCNDV-[IN:ND] AAR84223	442-1248: 807	268	31.3

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
96.	LN713270	Pakistan	*Gossypium* sp.	2692	99%	ToLCNDV-[PK:Bah:Gos:13] LN845956	Movement Protein	98%	BC1/ BYVMV-[IN:Kar:Okr:06] AEP31937	1304-2149: 846	281	31.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[Pak:Bwp:Gos:13] CRI05818	441-1247: 807	268	31
97.	AB330080	Thailand	Cucmber	2694	92%	ToLCNDV-[TH:Cuc:12] KU992384	Movement Protein	99%	Movement Protein/ ToLCNDV-[TH:Cuc:12] APC57610	1306-1249: 846	281	32.3
							Nuclear Shuttle Protein	100%	BV1/ ToLCNDV-[TH:Cuc] BAF69034	359-1249: 891	296	34.9
98.	LN845956	Pakistan	*Gossypium hirsutum*	2692	99%	ToLCNDV-[PK:Yaz:Gos:13] LN713270	Movement Protein	98%	BC1/ BYVMV-[IN:Kar:Okr:06] AEP31937	1304-2149: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Yaz:Gos:13] CEK41036	441-1247: 807	268	31.4
99.	KM921670	India	Tomato	2694	97%	ToLCNDV-[IN:09] KF577601 KF577602	Movement Protein	98%	BC1/ BYVMV-[IN:Kar:Okr:06] AEP31937	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	99%	BV1/ ToLCNDV-[IN:09] AHA98620	403-1248: 846	281	33.3
100.	FN432357 AJ620188	Pakistan	*Sonchus arvensis*	2702	95%	ToLCNDV-[PK:Gly:15] KX827600	Movement Protein	97%	Movement Protein/ ToLCNDV-[PK:Gly:15] AQT38103	1305-2150: 846	281	32.4
							Nuclear Shuttle Protein	93%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Gly:15] AQT38102	440-1126: 687	228	26.9
101.	LN845955	Pakistan	*Gossypium hirsutum*	2693	99%	ToLCNDV-[PK:Add:Gos:13] LN713269	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRL52725	1304-2149: 846	281	32.3
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRL52724	440-1246: 807	268	31.8
102.	KX827600	Pakistan	*Glycine max*	2702	95%	ToLCNDV-[PK:Sol:97] AJ620188	Movement Protein	99%	Movement Protein/ ToLCNDV CAQ19354	1305-2150: 846	281	32.5
							Nuclear Shuttle Protein	93%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Sol] CAF04473	439-1125: 687	228	26.7
103.	LN713269	Pakistan	*Gossypium hirsutum*	2695	99%	ToLCNDV-[PK:Bah:Gos:13] LN845955	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05817	1305-2150: 846	281	32.3
							Nuclear Shuttle Protein	100%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05816	440-1126: 687	228	26.9

Sr #	Accession Number	Country	Host	Nucleotide Number	Nucleotide Sequence Identity	Nucleotide Identity with Virus	Proteins	Proteins Percentage Identity	Protein / Identity with Virus	Nucleotide Length	Number of Amino acids	Molecular Weight (kDa)
104.	LN845959 LN854628	Pakistan	*Abelmoschus esculentus*	2694	99%	ToLCNDV-[PK:Bah:Gos:13] LN845955	Movement Protein	99%	Movement Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05817	1304-2149: 846	281	32.4
							Nuclear Shuttle Protein	99%	Nuclear Shuttle Protein/ ToLCNDV-[PK:Bwp:Gos:13] CRI05816	440-1246: 807	268	31.8
105.	KU992384	Thailand	*Cucumis sativus*	2690	94%	ToLCNDV-[TW:Cuc:07] GU180096	Movement Protein	99%	BC1/ ToLCNDV-[TH:Cuc] BAF69035	1304-2149: 846	281	32.3
							Nuclear Shuttle Protein	98%	BV1/ ToLCNDV-[TW:Mel:07] ACZ63317	402-1247: 846	281	33.5
106.	GU180096	Taiwan	*Cucumis melo* var. makuwa cv. Silver Light (oriental melon)	2673	94%	ToLCNDV-[TH:Cuc:12] KU992384	Movement Protein	99%	Movement Protein/ ToLCNDV-[TH:Cuc:12] APC57610	1304-2149: 846	281	32.2
							Nuclear Shuttle Protein	98%	Nuclear Shuttle Protein/ ToLCNDV-[TH:Cuc:12] APC57609	441-1247: 807	268	31.8

4.2 Pairwise sequence Identity Analysis

After analysis of all DNA-A isolates by SDTv1.2:

- Graph plot
- Color-encoded matrix with cut off values 94 and 91
- Scores of pairwise sequence identities; were obtained

4.2.1 Graph Plot Interpretation

It exhibited that most of the isolates came above the demarcation cut-off value (for isolates): 91%, showing that maximum number of isolates belonged to ToLCNDV whereas, highest peak was seen at demarcation cut-off value (for strains): 94%, highlighting the presence of numerous isolates as different strains of ToLCNDV (Fig.4.1).

4.2.2 Interpretation of Color-encoded Matrix

Isolates ToLCNDV3-[IN:Bij:Chi:12] KC465466, ToLCNDV2-[IN:IANDSI:11] JQ897969, ToLCNDV4-[IN:Jun:TC306:11] KF551592, ToLCNDV-[BD:Cuc:06] EF450316 and ToLCNDV-[IN:Har:Luc:07] FN645905 showed color pattern i.e. royal blue, falling in 91 cut-off range and behind (Fig.4.2). Therefore, for precise differentiation, sequence identity scores (Appendix II) obtained along with matrix were interpreted.

4.2.3 Interpretation of Pairwise Sequence Identity by Sequence Distance Scores

Overall pairwise sequence identity showed by:

- ToLCNDV2-[IN:IANDSI:11] JQ897969 was upto 74%,
- ToLCNDV3-[IN:Bij:Chi:12] KC465466 was upto 90%,
- ToLCNDV4-[IN:Jun:TC306:11] KF551592 upto 87%,
- ToLCNDV-[BD:Cuc:06] EF450316 upto 90%, and
- ToLCNDV- [IN:Har:Luc:07] FN645905 91%, with all other DNA-A isolates of ToLCNDV.

According to ICTV guidelines discussed by Brown *et al*. (2015), in this study, these isolates were not considered as a part of ToLCNDV anymore, and generally they all need to be reclassified.

4.3 Phylogenetic Analysis by Maximum Likelihood

After alignment of isolates done by MEGA6, those alignments were used for the generation of phylogenetic trees i.e. Maximum-likelihood (ML). ML tree of DNA-A isolates (Fig 4.3) did not give any clear clade formation with respect to area of distribution and host specificity. Moreover, similar isolates were seemed close to each other. The ML tree of DNA-B (Fig 4.4), however, showed a few clades formation with respect to area of distribution.

On the whole, the spread of ToLCNDV in the Asian continent and in some countries of Europe i.e. Spain, was noticeable.

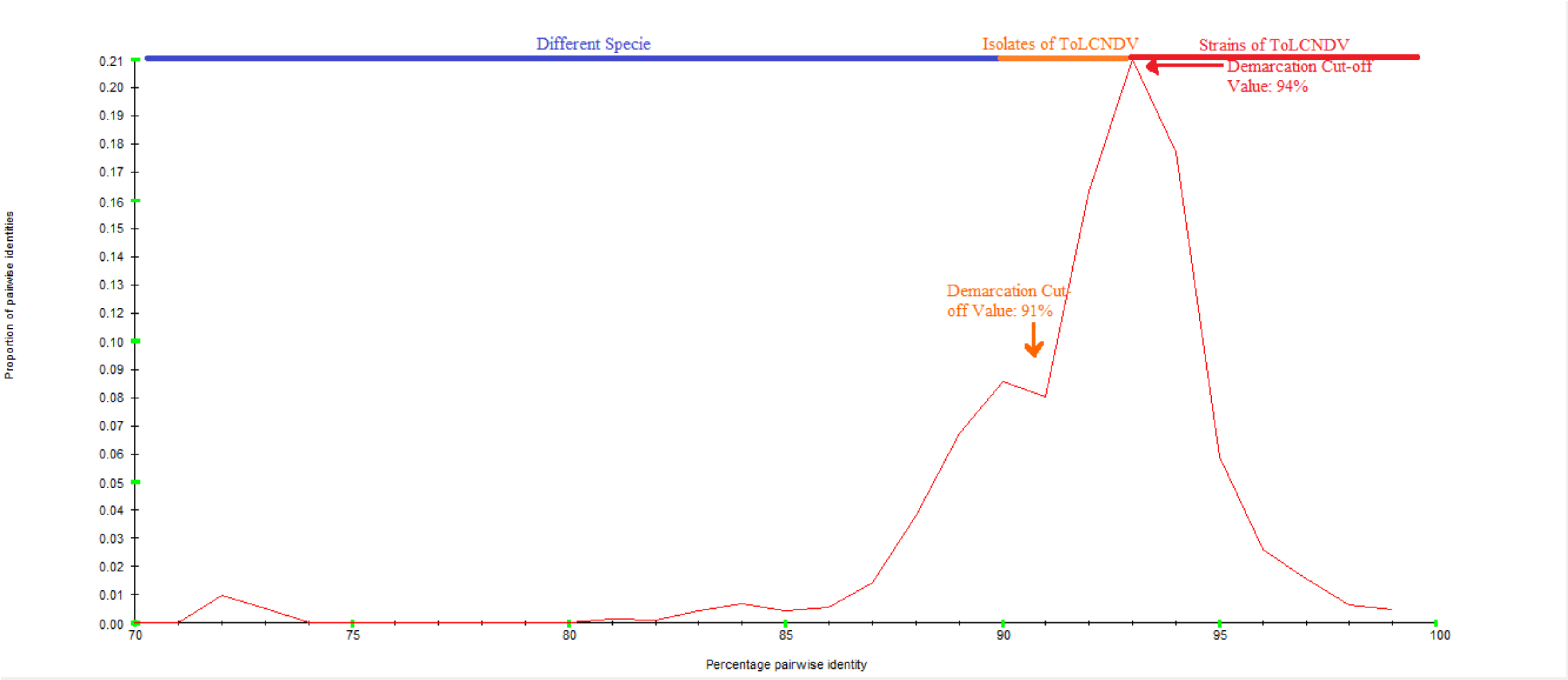

Figure 4.1 Graph plot of all DNA-A isolates of ToLCNDV, obtained by SDT analysis. Most of the isolates lay above the isolates demarcation value: 91%, and gave a highest peak at 94% exhibiting that most of the isolates were different strains of ToLCNDV.

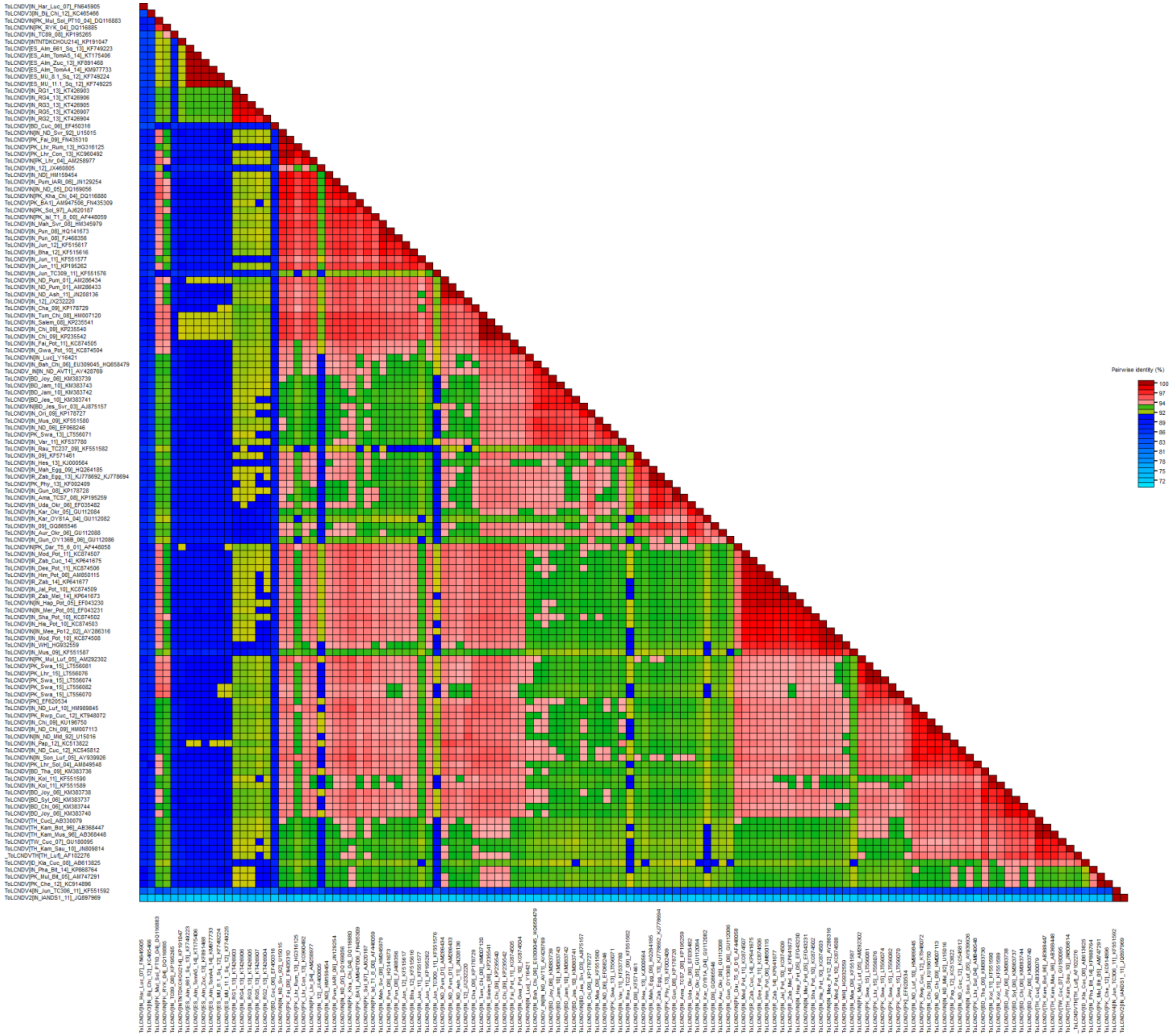

Figure 4.2 Color-encoded Matrix of all DNA-A isolates of ToLCNDV obtained by SDT analysis. Light Blue and Royal Blue colored blocks showed isolates having pairwise sequence identity below and near the isolate demarcation value: 91%, respectively. Pink colored blocks showed isolates having the sequence identity: 94% (Strain Demarcation Value). Whereas, Maroon colored blocks exhibit 100% sequence identity between isolates.

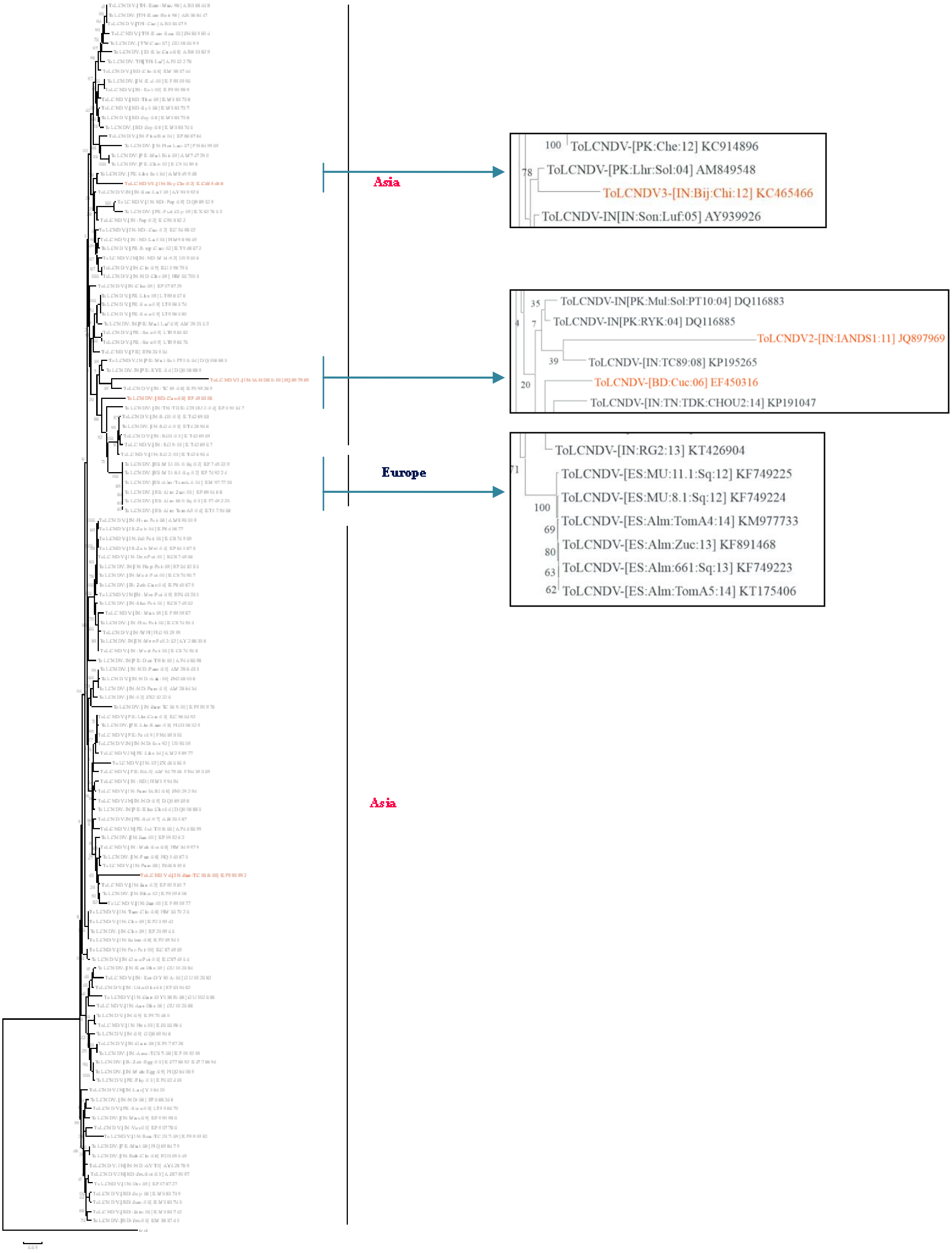

Figure 4.3 Maximum Likelihood tree of All 133 isolates of DNA-A generated by MEGA6 Software with Bootstrap (with 1000 replicates) values are presented in percentages. Scale bar at the bottom show value of nucleotide substitution per site i.e. 0.05

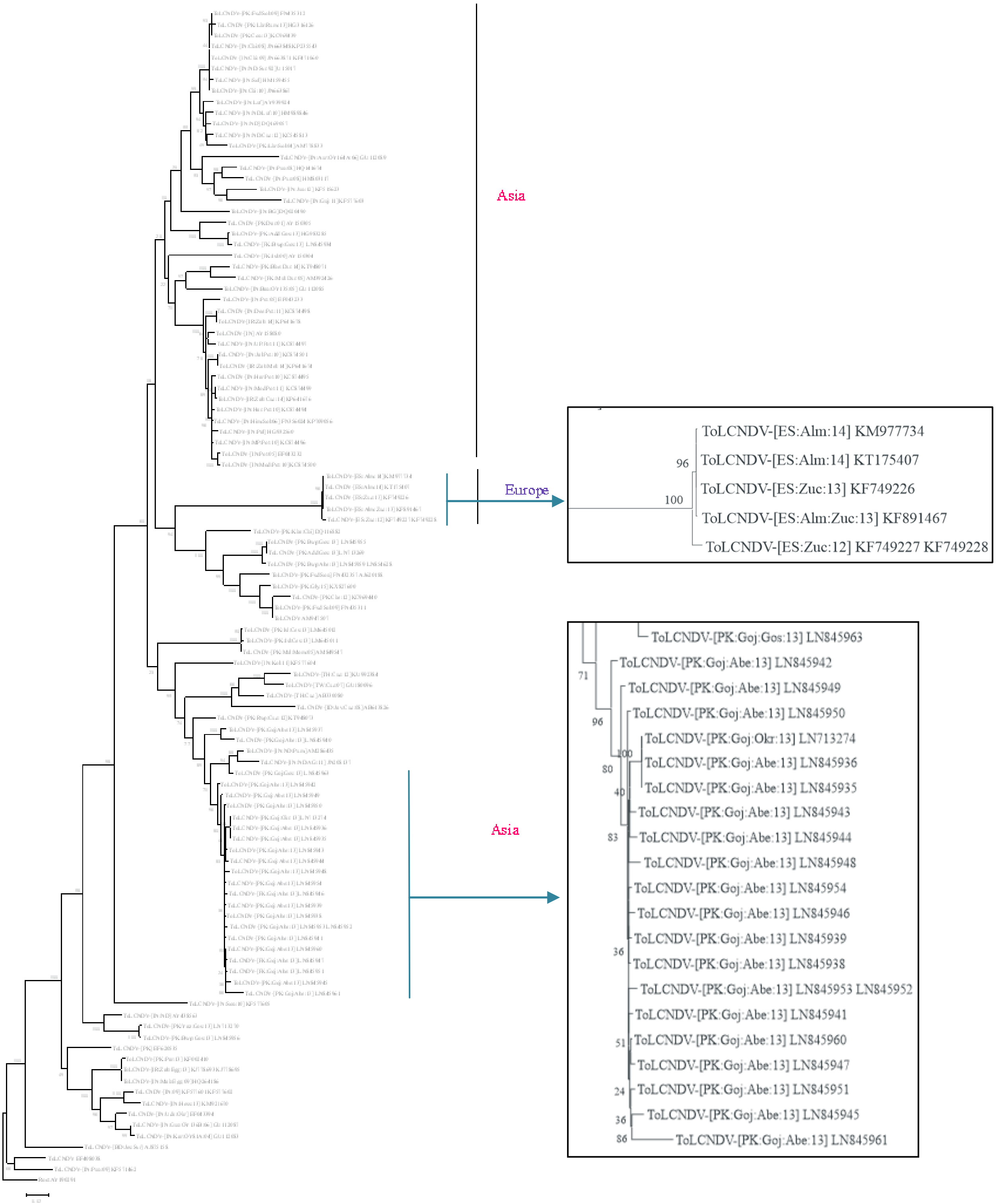

Figure 4.4 Maximum Likelihood tree of All 115 isolates of DNA-B generated by MEGA6 Software with Bootstrap (with 1000 replicates) values are presented in percentages. Scale bar at the bottom show value of nucleotide substitution per site i.e. 0.02

Chapter 5

DISCUSSION

ToLCNDV has been found prevailing among most of the Asian countries mostly India and Pakistan infecting many plant families such as *Solanaceae*, *Cucurbitaceae* and some members of family *Malvaceae*. It has also recently shown emergence in the European countries such as Spain, Southern Italy and Tunisia infecting plants such as zucchini squash and cucurbits (Juarez *et al.*, 2014; Mnari-Hattab *et al.*, 2015; Ruiz *et al.*, 2015; Luigi *et al.*, 2016; Panno *et al.*, 2016; Janssen *et al.*, 2017; Ruiz *et al.*, 2017).

In Pakistan, ToLCNDV has been immensely reported to cause yield loss in many regions especially Sindh and Punjab, infecting plants/crops such as Bitter gourd, *Calotropis procera*, *Chenopodium album*, Chili pepper, *Convolvulus arvensis*, Cotton, *Cucurbita pepo*, *Eclipta prostrate*, *Luffa cylindrica*, *Parthenium hysterophorus*, *Rumex dentatus*, *Solanum nigrum*, Tomato (Hussain *et al.*, 2004; Tahir and Haider, 2005; Haider *et al.*, 2006; Zaidi *et al.*, 2016a; Zaidi *et al.*, 2017).

ToLCNDV and its components has also being reported to individually cause mixed infection in association with other plant viruses or betasatellites such as PepLCLV, ZYMV and ChLCB (Shafiq *et al.*, 2010; Akhter *et al.*, 2014; Sharma *et al.*, 2015)

Measure of ToLCNDV infectivity and spread can help to overcome economical losses caused by it. Therefore, latest history of ToLCNDV spread was obtained using its all available sequences (Appendix I).

Data tables of DNA-A and DNA-B (Table 4.1 and 4.2) included the basic information about respective isolate's host, country of origin, its highest nucleotide identity with another virus isolate and also the genomic information about its ORFs. Such information was provided with reference to the work of Fortes *et al*. (2016), who also made such information mandatory in his work.

SDT analysis (Figure 4.1, 4.2 & Appendix I) showed clear demarcation between isolates that showed 91% or more pairwise sequence identity with each other and those that had identity below 90% behaving as outliers that means that they need to get reclassified. Isolates ToLCNDV2-[IN:IANDSI:11] JQ897969, ToLCNDV3-[IN:Bij:Chi:12] KC465466, ToLCNDV4-[IN:Jun:TC306:11] KF551592 and ToLCNDV-[BD:Cuc:06] EF450316 were hence said to be the different species rather than being isolates of ToLCNDV. Same method for the reclassification of determination of isolates was done by Brown *et al.* (2015) for the revision of taxonomy of *Begomovirus*.

Maximum-likelihood analysis of DNA-A isolates gave the knowledge about outliers of the study and similar to the results of Fortes *et al*. (2016), the isolates gave random distribution throughout the continent irrespective of the similar host and country of origin, except one clade formed by the similar isolates originated from Europe.

Maximum-likelihood tree of DNA-B isolates was also made that however, gave the various clades formation including one large clade containing isolates originated from Pakistan and other from Europe. However, the selection of isolates and strains of ToLCNDV depends mainly on the distribution and results of DNA-A isolates, therefore, information obtained by DNA-B was not so impactful.

5.1 Conclusion

Whole genome analysis of ToLCNDV described various and latest aspects of infectivity and spread of ToLCNDV. That can be helpful for further classification and disease control of many closely related isolates of ToLCNDV together.

References

Akhter, A., Akhtar, S., Saeed, M. and Mansoor, S. (2014). Chili Leaf Curl Betasatellite Enhances Symptoms Induced by Tomato Leaf Curl New Delhi Virus, a Bipartite Begomovirus. *International Journal of Agriculture and Biology*, 16: 1225-1228.

Alfaro-Fernandez, A., Sanchez-Navarro, J. A., Landiera, M., Font, M. I., Hernandez-Llopis, D. and Pallas, V. (2016). Evaluation of PCR and non-radioactive molecular hybridization techniques for the routine diagnosis of *Tomato Leaf Curl New Delhi Virus*, *Tomato Yellow Leaf Curl Virus* and *Tomato Yellow Leaf Curl Sardinia Virus*. *Journal of Plant Pathology*, 98(2), 245-254.

Bottcher, B., Unseld, S., Ceulemans, H., Russell, R. B. and Jeske, H. (2004). Geminate structures of African cassava mosaic virus. *Journal of Virology*, 78: 6758–6765.

Brown, J. K., Fauquet, C. M., Briddon, R. W., Zerbini, F. M., Moriones, E. & Navas-Castillo, J. (2012). Family Geminiviridae, In Virus Taxonomy: Classification and Nomenclature of Viruses – Ninth Report of the International Committee on Taxonomy of Viruses. (M. Q. King, M. J. Adams, E. B. Carstens & E. J. Lefkowitz). London: Elsevier. 351–373.

Brown, J. K., Zerbini, F. M., Navas-Castillo, J., Moriones, E., Ramos-Sobrinho, R., Silva, J. C. F., Fiallo-Olive, E., Briddon, R. W., Hernandez-Zepeda, C., Idris, A., Malathi, V. G., Martin, D. P., Rivera-Bustamante, R., Ueda, S. and Varsani, A. (2015). Revision of Begomovirus taxonomy based on pairwise sequence comparisons. *Archives of Virology*, 160: 1593–1619.

Chakraborty, S. (2008). Tomato leaf curl viruses from India (*Geminiviridae*). In, Enciclopedy of Virology. (Mahy, B.W.J., van Regenmortel, M.H.V). Elsevier: Amsterdam, The Netherlands. 124–133.

Chang, H-H., Chien, R-C., Tsai, W. S. and Jan, F-J. (2007). Molecular and biological characterization of a mechanically transmissible *Tomato leaf curl New Delhi virus* infecting oriental melon plants. *Plant Virology & Genetic Engineering Lab,.*

Chatterji, A., Beachy, R. N. and Fauquet, C. M. (2001). Expression of the Oligomerization Domain of the Replication associated Protein (Rep) of *Tomato Leaf Curl New Delhi Virus* Interferes with DNA Accumulation of Heterologous Geminiviruses. *The Journal of Biological Chemistry,* 276(27): 25631-25638.

Chatterji, A., Padidam, M., Beachy, R. N. and Fauquet, C. M. (1999). Identification of Replication Specificity Determinants in Two Strains of Tomato Leaf Curl Virus from New Delhi. *Journal of Virology*, 73(7): 5481-5489.

Cui, X., Li, G., Wang, D., Hu, D. and Zhou, X. (2005). A Begomovirus DNA-β encoded protein binds DNA, functions as a suppressor of RNA silencing, and targets the cell nucleus. *Journal of Virology*, 79: 10764–10775.

Figas, M. R., Alfaro-Fernandez, A.,Font, M. I., Borras, D., Casanova, C., Hurtado, M., Plazas, M., Prohens, J. and Soler, S. (2017). Inoculation of cucumber, melon and zucchini varieties with *Tomato leaf curl New Delhi virus* and evaluation of infection using different detection methods. *Annals of Applied Biology,.*

Fortes, I. M., Sanchez-Campos, S., Fiallo-Olive, E., Diaz-Pendon, J.A., Navas-Castillo, J. and Moriones, E. (2016). A novel strain of Tomato Leaf Curl New Delhi Virus has spread to the Mediterranean Basin. *Viruses*, 8: 307.

Gawande, S. J., Kaundal, P., Kaushal, N. and Garg, I. D. (2007). Print capture PCR – A simple technique for the detection of Tomato leaf curl New Delhi virus – causal agent of Potato apical leaf curl disease in India. *Potato Journal,* 34(1-2): 87-88.

Ha, C., Coombs, S., Revill, P., Harding, R., Vu, M. and Dale, J. (2008). Molecular characterization of begomoviruses and DNA satellites from Vietnam: additional evidence that the New World geminiviruses were present in the Old World prior to continental separation. *Journal of General Virology,* 89: 312-326.

Haider, M. S., Tahir, M., Latif, S. and Briddon, R. W. (2006). First report of *Tomato leaf curl New Delhi virus* infecting *Eclipta prostrate* in Pakistan. *Plant Pathology,* 55: 285.

Hanley-Bowdoin, L., Bejarano, E. R., Robertson, D. and Mansoor, S. (2013). Geminiviruses: masters at redirecting and reprogramming plant processes. *Nature Reviews: Microbiology,* 11: 777–788.

https://gd.eppo.int/taxon/TOLCND/photos (Last accessed on: 17-8-17)

https://www.ncbi.nlm.nih.gov/ (Last accessed on: 17-7-17)

http://web.cbio.uct.ac.za/~brejnev/ (Last accessed on: 17-7-17)

https://talk.ictvonline.org/taxonomy/ (Last accessed on: 17-7-17)

Hussain, M., Mansoor, S., Iram, S., Fatima, A. N. and Zafar, Y. (2005). The Nuclear Shuttle Protein of *Tomato Leaf Curl New Delhi Virus* is a Pathogenicity Determinant. *Journal of Virology,* 79(7): 4434-4439.

Hussain, M., Mansoor, S., Iram, S., Zafar, Y. and Briddon, R. W. (2004). First report of *Tomato leaf curl New Delhi virus* affecting chilli pepper in Pakistan. *Plant Pathology: Disease Notes,* 53: 794.

Hussain, M., Mansoor, S., Iram, S., Zafar, Y. and Briddon, R. W. (2007). The Hypersensitive Response to *Tomato leaf curl New Delhi virus* Nuclear Shuttle Protein is inhibited by Transcriptional Activator Protein. *Molecular Plant-Microbe Interactions,* 20(12): 1581-1588.

Idris, A. M., Shahid, M. S., Briddon, R. W., Khan, A. J., Zhu, J. K. and Brown, J. K. (2011). An unusual alphasatellite associated with monopartite begomoviruses attenuates symptoms and reduces betasatellite accumulation. *Journal of General Virology,* 92: 706–717.

Islam, S., Munshi, A. D., Verma, M., Arya, L., Mandal, B., Behera, T. K., Kumar, R. and Lal, S. K. (2011). Screening of *Luffa cylindrica* Roem. for resistance against *Tomato Leaf Curl New Delhi Virus,* inheritance of resistance, and identification of SRAP markers linked to the single dominant resistance gene. *Journal of Horticultural Science & Biotechnology,* 86 (6) 661–667.

Islam, S., Munshi, A. D., Mandal, B., Kumar, R. and Behera, T. K. (2010). Genetics of resistance in *Luffa cylindrica* Roem. against *Tomato Leaf Curl New Delhi Virus*. *Euphytica,* 174: 83-89.

Jupin, I., De Kouchkovsky, F., Jouanneau, F. and Gronenborn, B. (1994). Movement of tomato yellow leaf curl geminivirus (TYLCV): involvement of the protein encoded by ORF C4. *Virology,* 204: 82–90.

Janssen, D., Simon, A., Crespo, O. and Ruiz, L. (2017). Genetic Population Structure of *Bemisia tabaci* in Spain Associated with *Tomato Leaf Curl New Delhi Virus* – Short Communication. *Plant Protection Science,* 53(1): 25-31.

Jeevaltha, A., Siddappa, S., Kumar, A., Kaundal, P., Guleria, A., Sharma, S., Nagesh, M. and Singh, B. P. (2017). An insight into differentially regulated genes in resistant and susceptible genotypes of potato in response to *Tomato leaf curl New Delhi virus*-[*potato*] infection. *Virus Research,*.

Juarez, M., Tovar, R., Fiallo-Olive, E., Aranda, M.A., Gosalvez, B., Castillo, P., Moriones, E. and Navas-Castillo, J. (2014). First detection of Tomato leaf curl New Delhi virus infecting zucchini squash in Spain. *Plant Disease,* 98.

Jyothsna, P., Haq, Q. M. I., Singh, P., Sumiya, K. V., Praveen, S., Rawat, R., Briddon, R. W. and Malathi, V. G. (2013). Infection of tomato leaf curl New Delhi virus (ToLCNDV), a bipartite begomovirus with betasatellites, results in enhanced level of helper virus components and antagonistic interaction between DNA B and betasatellites. *Applied Microbiology and Biotechnology*, 97: 5457-5471.

Khan, M. S., Raj, S. K. and Singh, R. (2006). First report of *Tomato Leaf Curl New Delhi Virus* infecting chilli in India. *Plant Pathology,* 55: 289.

Kumar, R. V., Singh, A. K., Singh, A. K., Yadav, T., Basu, S., Kushwaha, N., Chattopadhyay, B. and Chakraborty, S. (2015). Complexity of begomovirus and betasatellite populations associated with chilli leaf curl disease in India. *Journal of General Virology,* 96: 3143-3158.

Kumar, V. and Naqvi, A. R. (2016). Tomato leaf curl New Delhi virus (ToLCNDV) encoded AC_2 associates with host miRNAs by directly interacting with AGO_1. *Journal of RNAi and Gene Silencing*, 12: 515-520.

Leke, W. N., Mignouna, D. B., Brown, J. K. and Kvarnheden, A. (2015). Begomovirus disease complex: emerging threat to vegetable production systems of West and Central Africa. *Agriculture and Food Security,* 4(1).

Li, F., Huang, C., Li, Z. and Zhou, X. (2014). Suppression of RNA silencing by a plant DNA virus satellite requires a host calmodulinlike protein to repress RDR6 expression. *PLoS Pathogens*, 10: e1003921.

Luigi, M., Manglli, A., Valdes, M., Sitzia, M., Davino, S. and Tomassoli, L. (2016). Occurrence of *Tomato leaf curl New Delhi virus* infecting Zucchini in Sardinia (Italy). *Journal of Plant Pathology: Disease Note,* 98(3): 677-697.

Malik, A. H., Briddon, R. W. and Mansoor, S. (2011). Infectious clones of Tomato leaf curl Palampur virus with a defective DNA B and their pseudorecombination with Tomato leaf curl New Delhi virus. *Virology Journal,* 8: 173.

Mandal, A., Sarkar, D., Kundu, S. and Kundu, P. (2015). Mechanism of regulation of tomato TRN1 gene expression in late infection with tomato leaf curl New Delhi virus (ToLCNDV). *Plant Science,* 241: 221-237.

Mansoor, S., Khan, S. H., Bashir, A., Saeed, M., Zafar, Y., Malik, K. A., Briddon, R., Stanley, J. and Markham, P. G. (1999). Identification of a novel circular single-stranded DNA associated with cotton leaf curl disease in Pakistan. *Virology,* 259: 190–199.

Maruthi, M. N., Rekha, A. R., Alam, S. N., Kader, K. A., Cork, A. and Colvin, J. (2006). A novel begomovirus with distinct genomic and phenotypic features infects tomato in Bangladesh. *Plant Pathology,* 55: 290.

Melgarejo, T. A., Kon, T., Rojas, M. R., Paz-Carrasco, L., Zerbini, F. M. and Gilbertson, R. L. (2013). Characterization of a New World monopartite begomovirus causing leaf curl disease of tomato in Ecuador and Peru reveals a new direction in geminivirus evolution. *Journal of Virology,* 87: 5397–5413.

Mizutani, T., Daryono, B. S., Ikegami, M. and Natsuaki, K. T. (2011). First report of Tomato leaf curl New Delhi virus infecting cucumber in central Java, Indonesia. *Plant Disease,* 95.

Mnari-Hattab, M., Zammouri, S., Belkadhi, M. S., Bellon Dona, D., ben Nahia, E. and Hajlaoui, M. R. (2015). First report of *Tomato leaf curl New Delhi virus* infecting cucurbits in Tunisia. *New Disease Reports*, 31: 21.

Moffat, A. S. (1999). Plant pathology- geminiviruses emerge as serious crop threat. *Science*, 286: 1835.

Naqvi, A. R., Haq, Q. M. R. and Mukherjee, S. K. (2010). MicroRNA profiling of tomato leaf curl new delhi virus (ToLCNDV) infected tomato leaves indicates that deregulation of mir159/319 and mir172 might be linked with leaf curl disease. *Virology Journal*, 7: 281.

Naqvi, A. R., Sarwat, M., Pradhan, B., Choudhury, N. R., Haq, Q. M. R. and Mukherjee, S. K. (2011). Differential expression analyses of host genes involved in systemic infection of Tomato leaf curl New Delhi virus (ToLCNDV). *Virus Research,* 160: 395-399.

Nawaz-ul-Rehman, M. S. and Fauquet, C. M. (2009). Evolution of geminiviruses and their satellites. *FEBS Letters*, 583: 1825–1832.

Padidam, M., Beachy, R. N. and Fauquet, C. M. (1995). Tomato leaf curl geminivirus from India has a bipartite genome and coat protein is not essential for infectivity. *Journal of General Virology,* 76: 25-35.

Padidam, M., Beachy, R. N. and Fauquet, C. M. (1996). The Role of AV2 (‘‘Precoat’’) and Coat Protein in Viral Replication and Movement in Tomato Leaf Curl Geminivirus. *Virology,* 224, 390-404.

Panno, S., Iacono, G., Davino, M., Marchione, S., Zappardo, V., Bella, P., Tomassoli, L., Accotto, G. P. and Davino, S. (2016). First report of *Tomato leaf curl New Delhi virus* affecting zucchini squash in an important horticultural area of southern Italy. *New Disease Reports,* 33: 6.

Phaneendra, C., Rao, K. R. S. S., Jain, R. K. and Mandal, B. (2012). Tomato leaf curl New Delhi virus is associated with Pumpkin Leaf Curl: A New Disease in Northern India. *Indian Journal of Virology,* 23(1): 42-45.

Pradhan, B., Naqvi, A. R., Saraf, S., Mukherjee, S. K., Dey, N. (2015). Prediction and characterization of Tomato leaf curl New Delhi virus (ToLCNDV) responsive novel microRNAs in *Solanum lycopersicum*. *Virus Research,* 195: 183-195.

Pratap, D., Kashikar, A. R. and Mukherjee, S. K. (2011). Molecular characterization and infectivity of a Tomato leaf curl New Delhi virus variant associated with newly emerging yellow mosaic disease of eggplant in India. *Virology Journal,* 8: 305.

Rai, N. K., Sahu, P. P., Gupta, S., Reddy, M. K., Ravishankar, K. V., Singh, M., Sadashiva, A. T. and Prasad, M. (2013). Identification and validation of an ISSR marker linked to Tomato leaf curl New Delhi virus resistant gene in a core set of tomato accessions. *Vegetable Science*, 40(1): 1-6.

Raj, S. K., Khan, M. S., Snehi, S. K. and Roy, R. K. (2007). Yellow vein netting of Bimili jute (*Hibiscus cannabinus* L.) in India caused by a strain of *Tomato leaf curl New Delhi virus* containing DNA β. *Australasian Plant Disease Notes*, 2: 45-47.

Raj, S. K., Snehi, S. K., Khan, M. S., Singh, R. and Khan, A. A. (2008). Molecular evidence for association of *Tomato leaf curl New Delhi virus* with leaf curl disease of papaya (*Carica papaya* L.) in India. *Australian Plant Disease Notes,* 3: 152-155.

Rojas, M. R., Hagen, C., Lucas, W. J. and Gilbertson, R. L. (2005). Exploiting chinks in the plant's armor: evolution and emergence of geminiviruses. *Annual Review of Phytopathology,* 43: 361–394.

Rojas, M. R., Jiang, H., Salati, R., Xoconostle-Cazares, B., Sudarshana, M. R., Lucas, W. J. and Gilbertson, R. L. (2001). Functional analysis of proteins involved in movement of the monopartite begomovirus, Tomato yellow leaf curl virus. *Virology*, 291: 110–125.

Roy, A., Spoorthi, P., Panwar, G., Bag, M. K., Prasad, T. V., Kumar, G., Gangopadhyay, K. K. and Dutta, M. (2013). Molecular Evidence for Occurrence of Tomato leaf curl New Delhi virus in Ash Gourd (*Benincasa hispida*) Germplasm Showing a Severe Yellow Stunt Disease in India. *Indian Journal of Virology,* 24(1): 74-77.

Ruiz, L., Simon, A., Velasco, L. and Janssen, D. (2017). Biological characterization of *Tomato Leaf Curl New Delhi Virus* from Spain. *Plant Pathology*, 66: 376-382.

Ruiz, M. L., Simon, A., Velasco, L., Garcia, M. C. and Janssen, D. (2015). First Report of *Tomato leaf curl New Delhi virus* Infecting Tomato in Spain. *Disease Notes*, 99(6): 894.

Saeed, M., Zafar, Y., Randles, J. W. and Rezaian, M. A. (2007). A monopartite begomovirus-associated DNA β satellite substitutes for the DNA B of a bipartite begomovirus to permit systemic infection. *Journal of General Virology*, 88: 2881-2889.

Saez, C., Martinez, C., Ferriol, M., Manzano, S., Velasco, L., Jamilena, M., Lopez, C. and Pico, B. (2016). Resistance to Tomato leaf curl New Delhi virus in *Cucurbita* spp. *Annals of Applied Biology*, 169: 91-105.

Sahu, P. P., Rai, N. K., Chakraborty, S., Singh, M., Chandrappa, P. H., Ramesh, B., Chattopadhyay, D. and Prasad, M. (2010). Tomato cultivar tolerant to *Tomato leaf curl New Delhi virus* infection induces virus-specific short interfering RNA accumulation and defence-associated host gene expression. *Molecular Plant Pathology*, 11(4): 531-544.

Sahu, P. P., Rai, N. K., Puranik, S., Roy, A., Khan, M. and Prasad, M. (2012). Dynamics of Defense-Related Components in Two Contrasting Genotypes of Tomato upon Infection with Tomato Leaf Curl New Delhi Virus. *Molecular Biotechnology*, 52: 140-150.

Sahu, P. P., Sharma, N., Puranik, S. and Prasad, M. (2014). Post-transcriptional and Epigenetic Arms of RNA Silencing: A Defense Machinery of Naturally Tolerant Tomato Plant against Tomato Leaf Curl New Delhi Virus. *Plant Molecular Biology Reporter*, 32: 1015-1029.

Sahu, P. P., Sharma, N., Puranik, S., Chakraborty, S. and Prasad, M. (2016). Tomato 26S Proteasome subunit RPT4a regulates ToLCNDV transcription and activates hypersensitive response in tomato. *Nature: Scientific Reports*,.

Saunders, K., Bedford, I. D., Briddon, R. W., Markham, P. G., Wong, S. M. and Stanley, J. (2000). A unique virus complex causes Ageratum yellow vein disease. *Proceedings of National Academy of Sciences USA,* 97, 6890–6895.

Saunders, K., Norman, A., Gucciardo, S. and Stanley, J. (2004). The DNA β satellite component associated with ageratum yellow vein disease encodes an essential pathogenicity protein (bC1). *Virology*, 324: 37–47.

Sharma, S., Kang, S. S. and Sharma, A. (2015). First report of mixed infection of *zucchini yellow mosaic virus a*nd *tomato leaf curl New Delhi virus* in bitter gourd in India. *Journal of Plant Pathology,* 97(2): 391-403.

Shafiq, M., Asad, S., Zafar, Y., Briddon, R. W. and Mansoor, S. (2010). Pepper leaf curl Lahore virus requires the DNA B component of Tomato leaf curl New Delhi virus to cause leaf curl symptoms. *Virology Journal,* 7: 367.

Sohrab, S. S., Karim, S., Varma, A., Abuzenadah, A. M., Chaudhury, A. G., Damanhouri, G. A. and Mandal, B. (2013). Characterization of *Tomato Leaf Curl New Delhi Virus* infecting cucurbits: Evidence for sap transmission in a host specific manner. *African Journal of Biotechnology,* 12(32): 5000-5009.

Sohrab, S. S., Karim, S., Varma, A., Azhar, E. I., Mandal, B., Abuzenadah, A. M., Chaudhary, A. G. (2013a). Factors affecting sap transmission of Tomato leaf curl New Delhi begomovirus infecting sponge gourd in India. *Phytoparasitica,* 41: 591-592.

Sohrab, S. S., Karim, S., Varma, A., Azhar, E. I., Abuzenadah, A. M. and Mandal, B. (2014). Sap transmission of Tomato leaf curl New Delhi virus infecting sponge gourd in northern India. *Journal of Plant Interactions*, 9(1): 241-248. .

Sohrab, S. S., Mandal, B., Pant, R. P. and Varma, A. (2003). First report of association of Tomato leaf curl virus-New Delhi with yellow mosaic disease of *Luffa cylindrica* in India. *Plant Disease,* 87.

Srivastava, A., Kumar, S., Jaidi, M., Raj, S. K. and Shukla, S. K. (2015). First report of tomato leaf curl New Delhi virus on opium poppy (*Papaver somniferum* L.) in India. *Plant Disease*,.

Srivastava, K. M., Hallan, V., Raizada, R. K., Chandra, G., Singh, B. P., Sane, P. V. (1995). Molecular cloning of Indian tomato leaf curl virus genome following a simple method of concentrating the supercoiled replicative form of viral DNA. *Journal of Virological Methods*, 51: 297-304.

Stanley, J., Bisaro, D. M., Briddon, R. W., Brown, J. K., Fauquet, C. M., Harrison, B. D., Rybicki, E. P. & Stenger, D. C. (2005). Geminiviridae, In Virus Taxonomy-VIIIth Report of the International Committee on Taxonomy of Viruses, (C. M. Fauquet, M. A. Mayo, J. Maniloff, U. Desselberger & L. A. Ball). London: Elsevier/ Academic Press. 301–326.

Tahir, M. and Haider, M. S. (2005). First report of *Tomato Leaf Curl New Delhi Virus* infecting bitter gourd in Pakistan. *Plant Pathology,* 54: 807.

Tiwari, A. K., Sharma, P. K., Khan, M. S., Snehi, S. K., Raj, S. K. and Rao, G. P. (2010). Molecular detection and identification of *Tomato leaf curl New Delhi virus* isolate causing yellow mosaic disease in Bitter gourd (*Momordica charantia*), a medicinally important plant in India. *Medicinal Plants - International Journal of Phytomedicines and Related Industries,* 2(2).

Usharani, K. S., Surendranath, B., Paul-Khurana, S. M., Gar, I. D. and Malathi, V. G. (2004). Potato leaf curl – a new disease of potato in northern India caused by a strain of *Tomato leaf curl New Delhi virus. Plant Pathology,* 53: 235.

Varsani, A., Navas-Castillo, J., Moriones, E., Hernandez-Zepeda, C., Idris, A., Brown, J. K., Murilo Zerbini, F. and Martin, D. P. (2014). Establishment of three new genera in the family Geminiviridae: Becurtovirus, Eragrovirus and Turncurtovirus. *Archives of Virology*, 159: 2193–2203.

Varsani, A., Roumagnac, P., Fuchs, M., Navas-Castillo, J., Moriones, E., Idris, A., Briddon, R. W., Rivera-Bustamante, R., Zerbini, F. M. and Martin, D. P. (2017). *Capulavirus* and *Grablovirus*: two new genera in the family *Geminiviridae*. *Archives of Virology*,.

Venkataravanappa, V., Reddy, C. N. L., Jalali, S. and Reddy, M. K. (2015). Association of tomato leaf curl New Delhi virus DNA-B with bhendi yellow vein mosaic virus in okra showing yellow vein mosaic disease symptoms. *Acta virologica,* 59: 125-139.

Vu, T. V., Choudhury, N. R. and Mukherjee, S. K. (2013). Transgenic tomato plants expressing artificial microRNAs for silencing the pre-coat and coat proteins of a begomovirus, Tomato leaf curl New Delhi virus, show tolerance to virus infection. *Virus Research,* 172: 35-45.

Yang, X., Xie, Y., Raja, P., Li, S., Wolf, J. N., Shen, Q., Bisaro, D. M. and Zhou, X. (2011). Suppression of methylation-mediated transcriptional gene silencing by bC1-SAHH protein interaction during geminivirus betasatellite infection. *PLoS Pathogens*, 7: e1002329.

Yazdani-Khameneh, S., Aboutorabi, S., Shoori, M., Aghazadeh, A., Jahanshahi, P., Golnaraghi, A. and Maleki, M. (2016). Natural Occurrence of *Tomato leaf curl New Delhi virus* in Iranian Cucurbit crops. *The Plant Pathology Journal,* 32(3): 201-208.

Zaidi, S. S-e-A., Martin, D. P., Amin, I., Farooq, M. and Mansoor, S. (2016). Tomato leaf curl New Delhi virus: a widespread bipartite begomovirus in the territory of monopartite begomoviruses. *Molecular Plant Pathology: Pathogen Profile,*.

Zaidi, S. S-e-A., Shafiq, M., Amin, I., Scheffler, B. E., Scheffler, J. A., Briddon, R. W. and Mansoor, S. (2016a). Frequent Occurrence of Tomato Leaf Curl New Delhi Virus in Cotton Leaf Curl Disease Affected Cotton in Pakistan. *PLoS ONE*, 11(5): e0155520.

Zaidi, S. S-e-A., Shakir, S., Malik, H. J., Farooq, M., Amin, I. and Mansoor, S. (2017). First report of Tomato leaf curl New Delhi virus *Calotropis procera* in Pakistan. *The American Phytopathological Society*: *Plant Disease,*.

Zakri, A. M., Ziegler, A., Commandeur, U., Fischer, R. and Torrance, L. (2012). In *vivo* expression and binding activity of scFv-RWAV, which recognizes the coat protein of tomato leaf curl New Delhi Virus (family *Geminiviridae*). *Archives of Virology,*.

Zakri, A. M., Ziegler, A., Torrance, L., Fischer, R. and Commandeur, U. (2010). Generation and characterization of a scFv against recombinant coat protein of the geminivirus tomato leaf curl New Delhi virus. *Archives of Virology,*.