Metagenomic analyses and genetic diversity of Tomato leaf curl virus complex affecting tomato plants in Kenya

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Research

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Abstract

Background

Tomato production is threatened worldwide by the occurrence of begomoviruses which are associated with tomato leaf curl diseases. There is little information on the molecular properties of tomato begomoviruses in Kenya, hence we investigated the population and genetic diversity of begomoviruses associated with tomato leaf curl in Kenya.

Methods

In 2018, we obtained tomato leaf samples with virus-like symptoms from farmers’ fields across Kenya and used Illumina sequencing to identify associated begomoviruses. Using the sequences, we determined the genetic diversity of begomoviruses. Additionally, selection pressure and recombinant isolates within the population were evaluated.

Results

Twelve complete begomovirus genomes were obtained from our samples with an average coverage of 99.9%. The sequences showed 95.7–99.7% identity among each other and 95.9–98.9% similarities with a Tomato leaf curl virus Arusha virus (ToLCArV) isolate from Tanzania. When we analyzed the amino acid sequences, we detected the highest identities in the regions coding for the coat protein gene (98.5–100%) within the isolates, and with the C4 gene of ToLCArV (97.1–100%). Phylogenetic algorithms clustered all Kenyan isolates in the same clades with ToLCArV, thus confirming the isolates to be a variant of the virus. Recombination analyses identified four putative events (P ≤ 0.05) among the isolates. Estimation of selection pressure within the virus population revealed the occurrence of negative or purifying selection in 5 out of the 6 coding regions.

Conclusions

The begomovirus associated with tomato leaf curl diseases in Kenya is a variant of ToLCArV possibly originating from Tanzania. Recombinant virus strains were detected within the population and there are divergence evolutionary events within the coding regions of the virus in Kenya. This information is useful in the development of appropriate management strategies for the disease.

Background

Tomato (Solanum lycopersicum) is an important vegetable grown worldwide for its commercial and high nutritional value [1, 2]. Tomato fruits are rich in ascorbic acid, retinol and lycopene with antioxidant properties that fight cancer [3]. In Kenya, the annual tomato production is approximately 410,033 tons,
valued at Ksh. 14 billion [4, 5]. The crop is a major source of income for smallholder rural farmers and it is produced predominantly for the domestic market [6]. The main producing counties are Kirinyaga, Kajiado, Nakuru, Meru, Bungoma and Taita Taveta. Despite the intensified production of tomato in Kenya, yields from tomato farms are low due to biotic and abiotic constraints. Biotic constraints include insect pests and diseases caused by various bacteria, fungi, nematodes and viruses [7]. Although diseases caused by bacteria, fungi and nematodes cause significant yield losses in tomato production, the effect of virus infections on production has been given relatively low attention.

Virus diseases are considered as the third significant constraint to tomato production [8]. There are about 136 viruses that infect tomato [9] of which 60 belong to the genus Begomovirus and family Geminiviridae [10]. Begomoviruses are transmitted by whitefly (Bemisia tabaci Gennadius) in a persistent manner, leading to yield losses of up to 100% in tropical and subtropical regions [11, 12]. They possess circular single-stranded DNA (ssDNA) genomes, classified as either mono- or bipartite [13]. Bipartite begomoviruses possess two ssDNA molecules, identified as DNA-A and -B whereas, monopartite begomoviruses have only DNA-A which is capable of solely inducing diseases [14]. Most begomoviruses from the Old World (mainly Africa and Asia) are monopartite and possess satellites known as alpha-, beta- or delta- satellites [15, 16]. The genomes of monopartite begomoviruses are ~ 2.8 kb in size with genes in both directions that diverge from a non-coding intergenic region (IR). The region has promoter elements including the ori of virion-strand DNA replication [17]. The DNA-A component of begomoviruses contains five or six open reading frames (ORFs) that encode ~ 10 kDa proteins [18]. These proteins play various roles in virus assembly, virus replication, host gene regulation, silencing suppression and vector transmission [11]. Like most plant viruses, begomoviruses evolve rapidly through recurrent mutations and recombination events, leading to the emergence of novel pathotypes that exploit new environments and challenge host resistance [19–22]. Natural occurrences of recombinants are known to lead to emergence of more virulent viruses or novel strains with new hosts and properties [22].

The leaf curl disease of tomato, caused by several begomoviruses, is a widespread threat to tomato production in many tropical and subtropical regions worldwide [9, 23]. Symptoms include yellowing of upper leaves, excessive branching, reduced leaf sizes, puckering of leaves, curling upwards of margins, stunting and flower abscission [9]. In Kenya, the disease symptoms were first observed in 1997 across tomato fields and Tomato yellow leaf curl virus (TYLCV) was identified as its causative agent [23, 24]. However, there has been no effort afterwards to characterize the virus populations. Several approaches are available for begomovirus identification, ranging from serological techniques to deep sequencing approaches [25]. Since begomoviruses species and strains cause diseases with similar symptoms in tomato, the use of serological assays has limitations as antibodies are able to cross-react with closely-related viruses or virus strains, thus making strain identification difficult. Recent advances in sequencing technologies have provided better approaches for identification and characterization of plant viruses [26–29].

Metagenomics is the analysis of microbial and virus populations in environmental samples through nucleic acid sequencing methods [30]. Motivations for performing plant virus metagenomics include the
identification of causal organisms associated with virus diseases in crops, screening for specific viruses when their presence is suspected, detection of asymptomatic or cryptic viruses, and the discovery of novel viruses and other microorganisms [27]. In this study, we used a metagenomics approach to investigate the occurrence of Tomato leaf curl viruses in tomato plants from farmers’ fields in Kenya. The virus populations were further evaluated for their genetic diversity, evidence of recombination and occurrence of selection pressure.

**Methods**

**Sample collection and extraction of nucleic acids**

Field surveys and sampling were carried out between January and May 2018 in four major tomato growing regions in Kenya, with different agro-ecological and climatic conditions (Figure 1). Tomato fields were randomly selected based on crop availability, with 30 plants randomly assessed per field. From each field, young, trifoliate leaf samples (n=5) were obtained only from plants showing symptoms such as chlorosis, reduced leaf size, upward leaf curling, stunting and flower abscission (Figure 2). A total of 515 leaf samples were obtained from 259 fields, carried in paper bags and stored at -80°C till further analysis. DNA extraction was done on pooled samples from each field.

Extraction of total genomic DNA was performed as described [31]. Briefly, about 150 mg of leaf tissues were homogenized using a mortar and pestle with 1.5 ml of pre-warmed extraction buffer (2% cetyl trimethyl ammonium bromide w/v; 100 mM Tris-HCl, 1.4 M NaCl, 20 mM EDTA, pH 8.0 + 50 mg PVP + 0.2% v/v β-mercaptoethanol added just before use). The samples were transferred into 1.5 ml microtubes and incubated at 65°C for 30 mins while mixing at 10 mins interval. The tubes were centrifuged at 10,000 rpm for 5 secs and supernatants (750 µl) were transferred into fresh microtubes. Chloroform and isoamyl alcohol (750 µl) in the ratio 24:1 was added to the tubes, mixed and centrifuged at 10,000 rpm for 15 mins. The aqueous layers were transferred into new microtubes and ice cold isopropanol (300 µl) were added and mixed by inverting the tube slowly. Tubes were incubated overnight at -20°C and the nucleic acids were pelleted by centrifugation at 10,000 rpm for 15 mins. The supernatants were discarded, pellets washed with 500 µl of 70% (v/v) ethanol and dried at room temperature. These were dissolved in 100 µL of Tris-EDTA buffer (10mM Tris-HCl [pH 8.0] + 1 mM EDTA), incubated at 37°C for 30 mins and stored at -20°C. A Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific, MA, USA) was used to determine the quality of the nucleic acids.

**Library preparation and sequencing**

Genomic DNA of 48 samples were randomly selected per region and used for library preparation. These were quantified using a Qubit™ fluorometer (Thermo Fisher Scientific, MA, USA) and normalized to 2.5 ng/µl. Libraries were prepared using Nextera DNA library preparation kit (Illumina, CA, USA) according to the manufacturer’s instructions. Briefly, enzymatic fragmentation was carried out on normalized genomic DNA samples (20 µl) via addition of TD buffer (25 µl) and TDE (5 µl). Mixture were centrifuged (Hettich
Centrifugen, D–78532, Germany) at 14,000 rpm at 20 °C for 1 min and transferred into PCR tubes.
Tagmentation was carried out in a pre-programmed thermocycler at 55 °C lid and 55 °C incubation temperature, while holding at 10 ºC. The tagmented DNA was barcoded using indexed adapters then cleaned with AMPure XP magnetic beads (Beckman Coulter, Inc. Indianapolis, IN) to remove shorter DNA fragments and other impurities. Library quality was confirmed with the Agilent Tape Station 2200 System (Agilent Technologies, Santa Clara, CA). All the 48 libraries were quantified using the Qubit™ fluorometer (Thermo Fisher Scientific Inc., Waltham, MA). The indexed DNA libraries of 48 biological samples were each normalized to a concentration of 4 nm before being pooled together. High-throughput sequencing was performed on an Illumina MiSeq System using 2 × 251 v2 kit and 12 pM of 1% PhiX v3 spike to create paired-end reads. Sequencing was performed at the facility of the Biosciences Eastern and Central Africa International Livestock Research Institute (BecA-ILRI) Hub, Nairobi, Kenya.

**Sequence processing and assembly**

After sequencing, quality control of fastq paired end reads was performed using FastP v.0.20.0 [32] to remove adapters, poly-N sequences (≥15%) and filter low quality reads. The resulting lengths after quality control and the N50 varied amongst the samples (Table 1). Individual sequences were assembled de novo and the resulting contigs were submitted to BLAST analysis.Q≤5). High-quality reads were mapped to the tomato genome (GenBank RefSeq accession number GCA_000188115.3) using Bowtie v.2.3.4.3 [33] under default parameters. Unmapped reads were assembled into contigs de novo using MEGAHIT v.1.1.3 [34] with default settings and those representing ssDNA sequences verified using Kaiju virus database [35]. The sequences were then subjected to BLASTN 2.9.0+ [36] to determine similarity match and virus identification (Additional File 1: Figure S1). Protein prediction of ORFs was determined using ORF Finder (http://www.ncbi.nlm.nih.gov/projects/gorf).

**Sequence alignment, distance matrix and phylogeny**

Sequences of monopartite begomoviruses found in tomato were retrieved from GenBank (Additional File 2: Table S1) and aligned with virus contigs using ClustalW multiple sequence alignment program as implemented in BioEdit v.7.2.3 [37] using default parameters. Deduced amino acids from the ToLCV genomes were compared with GenBank isolates while sequence pairwise identities were performed using SDT v1.2 with pairwise gap deletions [38]. A phylogenetic tree was constructed using the maximum likelihood method based on Jukes-Cantor model in MEGA v.6.06 [39]. Bootstrap replicate values were set at 1,000 while a strain of *Tomato leaf curl purple vein virus* (KY196216) was selected as an outgroup.

**Genetic diversity, population genetic analysis and detection of recombination events**

Genetic structure and diversity within ToLCV populations in Kenya were investigated to understand potential evolutionary dynamics that produce variations. Population structure parameters estimated included average nucleotide diversity (π), haplotype diversity (Hd), number of polymorphic or segregating sites (S), the statistic estimate of population mutation based on the number of segregating sites (θ-W), total number of mutations (Eta), the average number of nucleotide differences between sequences (k)
and the statistic estimate of population mutation based on the total number of mutations (θ-Eta). These were estimated using complete genome and protein coding sequences in DnaSP v5.10.01 [40].

The possible occurrences of selection pressure on individual genes and sites within the ToLCV populations were obtained using the single-likelihood ancestor counting (SLAC) method [41] in the HyPhy package [42] as implemented on the Datamonkey software [43] at http://www.datamonkey.org. The ratio of average number of nucleotide differences between the sequences per nonsynonymous site (\(d_N\)) to the average number of nucleotide differences between the sequences per synonymous site (\(d_S\)) were calculated as an indicator of natural selection. These were used to estimate the occurrence of positive and negative selection at typical begomovirus amino acid ORF sites: the movement protein (MP) or V1 protein, coat protein (CP) or V2 protein, replication protein (Rep) or C1 protein, transcription activator protein (TrAP) or C2 protein, Rep enhancer protein (REn) or C3 protein and the C4 protein. Depending on the \(d_N/d_S\) values, the selection pressure was considered negative or purifying (\(d_N/d_S < 1\)), neutral (\(d_N/d_S = 1\)), or diversifying or positive (\(d_N/d_S > 1\)) for data sets of each coding region. The DNAsp v5.10.01 was used to calculate the Tajima's D, Fu and Li's F* and D*, and Fu's Fs to determine the deviation of ToLCV populations from neutrality assuming a constant population size, with zero recombination and migration [44]. A negative Tajima's D statistic indicates superfluous low-frequency polymorphism triggered by background selection, genetic hitchhiking, or population expansions [45]. Conversely, positive values of Tajima's D statistic suggests minimal levels of low and high frequency polymorphisms, indicating a reduction in population size and/or balancing selection.

A scan for recombination signatures were performed on each protein-coding sequence data using the single breakpoint scanning (SBP) and genetic algorithm recombination detection (GARD) methods [46]. These two methods were implemented by the Datamonkey software [43]. Potential recombination events were further investigated using the default settings of detection algorithms BoostScan [47], Chimaera [48], GENCONV [19], MaxChi [49], RDP [50], SiScan [51] and 3Seq which were implemented in the RDP v 4.13 software [52]. Putative recombination events, potential recombinants, and their parental sequences were deemed acceptable only when signals were identified by at least four of the seven detection methods, with strong levels of significance (P≤0.05).

**Results**

**Sequence data and de novo assembly of DNA viruses**

After mapping of sequence reads from tomato leaf samples to the tomato reference genome, unmapped reads were subsequently assembled into contigs. The de novo assembly yielded several number of contigs, with the largest contigs having sizes of >45 kb while N50 values ranged from 135 - 270 bp (Table 1). After Kaiju analyses (see Materials and Methods), all assembled virus contigs were subjected to BLASTN 2.9.0+ searches. The results revealed twelve contig matches of lengths >2.7 kb from eleven samples with complete begomovirus genomes within the database (see Additional File 3: Table S2) while several other partial contigs matching DNA viruses were also present. Raw reads from these positive
samples have been deposited at the SRA archive (Bioproject number PRJNA646848). Across all the samples, only monopartite begomoviruses with DNA-A-like sequences were recovered. The presence of beta-satellites was not evaluated in this study. However, a sample (Tom54) produced the full-length genome of a separate begomovirus, *Chickpea chlorotic dwarf virus*, which we recently described [53].

**The begomoviruses in Kenyan tomato are a variant of ToLCArV**

In all, the full-length genomes of the begomoviruses varied from 2,760 to 2,765 bp (Additional File 2: Table S1). These were deposited in GenBank database under the accession numbers MN894493 to MN894504. Sequence analyses showed that these genomes encoded the six ORFs (V1, V2, C1, C2, C3 and C4) that are typical of monopartite begomoviruses while the intergenic regions ranged from 245-250 nt. Pairwise alignments of begomoviruses with pairwise deletion of gaps using MUSCLE revealed the highest full genome similarity (95.9-98.9%) with an isolate of *Tomato leaf curl Arusha virus* (ToLCArV, GenBank accession EF194760) from Arusha, Tanzania (Table 2). This was followed by *Tomato leaf curl Toliara virus* (ToLCToV, GenBank accession AM701768) with 95.9-98.9 % identity and another isolate of *Tomato leaf curl virus Arusha virus* (ToLCArV, GenBank accession DQ519575) at 89.8-90.5% similarity. Furthermore, all isolates exhibited less than 80% pairwise sequence identity to other begomovirus sequences (see Additional File 4: Figure S2). Based on the species demarcation criteria of the International Committee for the Taxonomy of Viruses set for begomoviruses at <91% nucleotide sequence identity [54], the Kenyan begomoviruses were considered as a variant of ToLCArV. Similar patterns were observed for deduced amino acids as the highest identity was observed with ToLCArV (GenBank accession EF194760) across all the six coding regions (93.3-99.1 for MP, 97.3-98.9% for CP, 95.4-98.6% for Rep, 94.2-97.8% for TrAP, 96.0-98.0% for REn and 97.1-100% for C4 protein). Pairwise comparison across amino acids of other tomato infecting monopartite begomoviruses revealed similar patterns (Table 3). Further analyses revealed 95.7-99.7% pairwise nucleotide sequence identities within the twelve Kenyan ToLCArV-like isolates while amino acid residues also revealed high similarities at the MP (94.1-100%), CP (98.5-100%), Rep (94.1-99.4%), TrAP (94.3-100%), REn (95.6-100%) and C4 (95.1-100%) coding regions (Table 5).

**Recombination analyses**

Evidence of recombination events were found within the CP and Rep genomic regions of ToLCArV-like populations using the automated SBP and GARD tools within the Datamonkey software (data not shown). Further analyses revealed putative recombination events and potential parental isolates using the programs implemented in the RDP3 software (Table 5). The detection threshold of at least four of the seven programs revealed three recombination events among the ToLCArV-like populations from Kenya. Two isolates, Tom5a and Tom39 collected from Kirinyaga and Makueni counties respectively, were identified as putative recombinants and parental isolates (P≤0.05) while Tom28, Tom35 and Tom45 were only detected as potential major and minor parental sequences (Table 5). One of the putative recombinants (Tom5a) was identified as an intra-isolate recombination event (P≤0.05), possibly as a result of multiple co-infections of the parental isolates within affected plants.
Phylogenetic relationships and genetic diversity of Kenyan tomato begomoviruses

A phylogenetic analysis was done using the full genome sequences of the 12 ToLCArV isolates from Kenya, together with TYLCV-like sequences and other tomato begomoviruses from GenBank. Expectedly, all TYLCV-like isolates (n=25) clustered separately from ToLCV-like sequences (n=46) with a clear geographical segregation (Figure 3). African ToLCV-like sequences (n=26) were separated from those of Asian origins (n=20) while isolates from Kenya formed a monophyletic cluster with isolates from Tanzania (ToLCArV, EF194760 and DQ519575) (Figure 3). Similar results were obtained when isolates identified as putative recombinant sequences by the RDP3-implemented programs were excluded from these analyses (data not shown). This finding strengthens the hypothesis that Kenyan ToLCArV-like isolates are closely related to ToLCArV from Tanzania, with both strains having a common ancestor.

Analyses of haplotype number and haplotype diversity, represented by ‘h’ and ‘Hd’, respectively revealed varying values among the 12 Kenyan ToLCArV-like sequences and also among other ToLCV-like sequences from GenBank, based on the six coding regions evaluated (Table 6). Based on the total ToLCV-like sequences (n=46), haplotypes number ranged from 43 in the MP region to 46, obtained at the CP, Rep and whole genomes. Similarly, among the Kenyan ToLCArV-like isolates (n=12), ‘h’ values ranged from 9 (MP gene) to 12 (CP, Rep and complete genomes). Thus, across ToLCV-like sequences from the Genbank and the Kenyan ToLCArV-like sequences, each isolate represented a haplotype at both CP and Rep genes and reveals high genetic variation within the coding regions of each group. This therefore indicates that genetic variation was highest within the CP and Rep coding regions. Interestingly, Hd values were highest for the CP and REn gene and lowest for MP gene, both across ToLCV-like isolates obtained from GenBank and among the 12 Kenyan ToLCArV-like sequences obtained in this study (Table 6). Furthermore, genetic distances for each gene-specific data set were calculated, with highest π values obtained within the REn gene (0.2458) across the ToLCV-like isolates (n=46). The C4 gene and Rep gene recorded the lowest π values i.e. 0.21015 and 0.21165, respectively. Remarkably, the π value of the C4 gene within the 12 Kenyan ToLCArV-like isolates (0.00869) was more than half the π values of other coding regions, indicating that these coding regions were more variable than the C4 gene (Table 6). Collectively, these results show high genetic variability among the CP and Rep coding regions across both ToLCV groups, with C4 gene having the least variation across the isolates.

Tajima’s D and estimation of selection pressure

Tajima’s D statistical test [55] was used to evaluate the nucleotide polymorphism occurring within each gene and on the complete genomes of Kenyan ToLCArV-like isolates and other ToLCV-like isolates. The Tajima’s D, Fu and Li’s D and Fu and Li’s F statistic revealed negative values for the complete genome datasets which did not statistically deviate from zero (P > 0.10) (Table 6). Within Kenyan isolates, similar trends were observed for gene-specific datasets except the MP and CP genes which revealed positive values that are not significantly (P > 0.10) different. These results indicate an excess of low-frequency polymorphism caused by background selection, genetic hitchhiking, or population increases.
In order to understand the selection pressure acting on the different coding regions within our ToLCArV-like sequences, the ratios of nonsynonymous substitution per nonsynonymous site (dN) and synonymous substitutions per synonymous sites (dS) were calculated (Table 7). The dN/dS ratio is an estimator of the evolutionary constraints imposed on a coding region with a value >1 considered as evidence for positive selection, values <1 show evidence of negative selection while values of 1 indicate neutral selection [56]. Across the Kenyan ToLCArV-like sequences, the dN/dS ratio was 0.2067 for the MP gene, 0.067 for the CP gene, 0.3986 for Rep gene, 0.2590 for REn Gene, 0.2908 for TrAP gene and 1.1491 for C4 gene (Table 7). Thus, contrasting patterns of evolution were obtained for the coding region datasets as all except the C4 gene had dN/dS ratio of <1. This indicates a negative or purifying selection among five out of six coding regions. In addition, these results show that although the MP, CP, Rep, TrAP and REn coding regions are under strong purifying selection, the purifying selective pressure is not distributed uniformly across the genes. The protein encoded by the C4 gene appears to be selectively neutral. The dN/dS values for the CP gene had the lowest values, with other gene sets having at least more than thrice its dN/dS ratio (Table 7).

Discussion

Tomato production in Kenya is widespread and has been limited by the impact of the tomato leaf curl disease. Because of the typical yellow leaf curl symptoms commonly associated with tomato in Africa, it is assumed that the causal organism is *Tomato yellow leaf curl virus*. Indeed, a tomato leaf curl-like virus infecting tomato in Kenya has previously been reported [57]. The paucity of information on viruses of high economic importance is compounded by the fact that only a few studies from Kenya have described the genomic properties of begomoviruses from cassava [58], sweet potato [59] and a non-cultivated weed host [60]. Using a metagenomics approach, we have described the occurrence of monopartite begomoviruses associated with the leaf curl disease of tomato in Kenya. Our results show that a genetically distinct begomovirus is associated with the disease in Kenya. Analyses of the complete genomes and coding regions of these begomoviruses, together with the failure to detect the presence of DNA-B component affirms that these virus populations were members of the Old World monopartite begomovirus species. Our findings represent the first comprehensive description of full begomovirus genomes from tomato in Kenya. This information is crucial for understanding the causal agents associated with the tomato leaf curl disease and its properties as a first step towards appropriate robust disease management. The availability of full genome sequences will help to elucidate further the evolutionary behavior of the virus.

All the Kenyan ToLArV-like sequences obtained in this study shared very high nucleotide and amino acid sequence similarities, indicating low intra-population genetic diversity. Similar conclusions have been reached in other studies on tomato begomoviruses [61, 62]. Curiously, we observed that the nucleotide sequences of the 12 ToLCArV-like isolates shared high identities among themselves but shared lower sequence identities with other begomoviruses (Table 3). This is likely as a result of the genetic bottleneck imposed through the method of begomovirus transmission by whiteflies [63]. Our study did not investigate virus occurrence within vectors. Nevertheless, the high genetic similarity within the population
in our result could be due to a ‘founder effect’ arising from ecological and epidemiological factors such as vector or seed-mediated spread possibly from Tanzania. The derived amino acid sequences of the population in our results show homologous characteristic with other monopartite begomoviruses, indicating possible similar biological behaviors.

Results from sequence similarity indices together with phylogenetic inferences suggests that the ToLCArV-isolates associated with tomato leaf curl diseases in Kenya were likely of Tanzanian origin. The homogeneity of nucleotide and amino acids as well as phylogenetic inferences supports a single introduction of the tomato begomovirus into Kenya. Intriguingly, five algorithms detected recombination signals ($P \leq 0.05$) from a Tanzanian ToLCArV isolate (GenBank number DQ519575), identifying one of our Kenyan isolates (GenBank number MN894493) as a major parent (Table 5). This suggests that although the Kenyan isolates are just being characterized in this study, they could be the parents that contributed to the emergence of the ToLCArV that was initially described by [64]. It is thus possible, that the Kenyan ToLCV population could pre-date the Tanzanian isolates which were only reported earlier than our Kenyan isolates. Since our analyses reveal clustering of isolates from geographically proximal countries, the dissemination of the ToLCArV-like isolates is likely to have occurred via virus-infected planting material or spread by cross-border spread of viruliferous whiteflies, leading to genetic similarity among these isolates. Although, our study did not investigate mode of virus transmission, evidence of seed transmission has recently been reported in other closely related begomovirus species from tomato [65] and other hosts [66–69]. Thus, further research is required to understand how specific begomovirus species are spread across various borders in East Africa and to determine the epidemiological and ecological implications. Additionally, we propose studies to investigate the effect of whitefly-mediated transmission on begomovirus diversity in Kenya.

Interestingly, our results show that the begomovirus sequences from Kenya have discernible patterns of geographical structuring with other ToLCV-like isolates of African origin. This is in agreement with previous studies that have shown geographical structuring of African Old World begomovirus sub-populations into clear genetically distinct categories [70, 71]. This suggests that these viruses perhaps came from a common ancestor that was introduced to the continent and speciation arose as they interacted with various hosts across different geographical locations. In this study, we determined the genetic diversity of ToLCArV-like sequences from Kenyan within tomato fields using coding regions and complete genome sequences. Over the years, tomato begomoviruses in Kenya have received little or no attention in previous studies [72]. Our current findings will deepen the knowledge on genetic diversity of tomato begomoviruses, therefore allowing for better diagnostics and appropriate management options. Our results indicate that although there is low intra-specific diversity among our isolates, the haplotype number and haplotype diversity analyses revealed varying homogenous levels within the coding regions. Thus, the non-coding regions could have contributed to the overall low diversity indices, similar to the observations of [73].

Our results have identified the occurrence of putative recombinants within the virus population (Table 5). Recombination has been shown to crucially contribute to the evolution of tomato-infecting
begomoviruses [17, 20, 22, 74] with far-reaching implications. A distinct begomovirus has recently been identified from tomato plants in Kenya [53]. Thus, the existence of these naturally-occurring recombinant isolates could evolve into the existence of virus complexes with significant effect on disease development, and evolution of virus populations. As intensive tomato cultivation continues in Kenya and as climate-driven changes influence the spread of whitefly populations across East Africa, more virus-vector-host interplays could give rise to further recombination events, leading to further virus evolution. In addition, begomovirus populations within close geographical delineations are known to possess distinct genetic properties as a result of frequent recombination events [71].

Our results show that varying natural selection pressures appear to be acting on the coding regions of the Kenya ToLCaRV-like isolates, indicating independent coevolution of these genes. Our analyses of synonymous and nonsynonymous substitutions revealed that, except the C4 gene, all coding regions appear to be under strong negative or purifying selection to conserve its encoded amino acid sequence. This is in line with similar observations for other related tomato begomovirus species from the Old World [75] and New World [76]. The evolutionary constraints on these coding regions could be intended to preserve their biological functions which include virus replication, accumulation and fidelity to vector transmission. For example, the CP gene has been reported to mediate interactions between begomoviruses and their whitefly vectors [77, 78]. Any alterations in the CP sequence could subsequently alter their virus-vector interactions or other associated biological functions [79]. This is probably why this phenomenon is more in the CP region with the lowest mean dN/dS values, indicating that it is undergoing a stronger purifying selection. Other studies have also indicated similar patterns within begomoviruses, with the CP gene having the strongest evolutionary constraint [80–82]. dN/dS ratios are estimators of evolutionary bottlenecks imposed on a coding region at intra-specific levels. Because natural selection functions largely on these regions, synonymous and nonsynonymous mutations are usually under varying selective pressures and are fixed at different rates within begomovirus genomes [83–85]. Thus, comparison of synonymous and nonsynonymous substitution rates can reveal the direction and strength of natural selection acting on virus proteins. Importantly, we found the C4 gene within the Kenyan isolates to be selectively neutral as its estimated dN/dS ratio (1.1491) suggests that neither purifying nor diversifying selection was ongoing. This neutral selection could be as a result of its divergent but crucial role in modulating disease severity, determination of host range, virus movement and suppression of host silencing mechanisms [86, 87].

**Conclusions**

This study investigated the identity, full sequence properties, genetic diversity, population genetics and recombination analyses of monopartite begomoviruses associated with leaf curl diseases of tomato in Kenya. Nucleotide and amino acid sequence analyses together with phylogenetic inferences identified the begomoviruses as variants of ToLCaRV with origins from Tanzania. Genome analyses revealed low genetic diversity within the population with contrasting evolutionary patterns among the coding regions. The information obtained in this research will assist in the design and implementation of quarantine plans to manage virus and vector dynamics. Sequence information and genetic diversity data obtained in
this study are also important for the development of rapid and robust detection tools towards the production of virus-free tomato seedlings for farmers. This will ultimately improve tomato production across the country for better food security.

**Abbreviations**

*Tomato leaf curl virus* Arusha virus; ToLCArV: *Tomato leaf curl virus*; ToLCV: *Tomato yellow leaf curl virus*; TYLCV: *Tomato leaf curl Toliara virus*; ToLCToV: Deoxyribonucleic acid; DNA: Intergenic region; IR: Open reading frames; ORF: Tris-Hcl; Tris-*Hydrochloride*: Sodium Chloride; NaCl: Ethylenediaminetetraacetic acid; EDTA: Polyvinylpyrrolidone; PVP: Tagmented DNA Buffer; TD: Tagment DNA Enzyme; TDE: Sequence Demarcation Tool; SDT: single breakpoint scanning; SBP: genetic algorithm recombination detection; GARD: recombination detection program; RDP: Coat protein; CP: Replication gene; Rep: shortest contig length that covers 50% of the genome; N50: average nucleotide diversity: $\pi$: haplotype diversity; Hd: number of polymorphic or segregating sites; S: number of segregating sites; ($\theta$-W: total number of mutations; Eta: the average number of nucleotide differences between sequences; k: total number of mutations; $\theta$-Eta: single-likelihood ancestor counting; SLAC: Hypothesis testing using phylogenies; HyPhy: DNA Sequence Polymorphism; DnaSP: movement protein; MP: coat protein; CP: transcription activator protein; TrAP: Rep enhancer protein; REn: nonsynonymous substitution per nonsynonymous site; dN: synonymous substitutions per synonymous sites; dS:

**Declarations**

**Ethical approval and consent to participate**

Not applicable.

**Consent for publication**

Not applicable

**Data Availability**

The datasets supporting the conclusions of this article are available in the NCBI repository at [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA646848](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA646848). All the datasets supporting the conclusions of this article are included within the article and its additional files. Raw sequence data are accessible at NCBI under the BioSample accession numbers SAMN15566931-SAMN15566941 with SRA accession numbers SRR12245789-SRR12245799. Complete genomes of ToLCV were deposited to GenBank under Accession Numbers MN894493-MN894502.

**Competing interests**

The authors declare that they have no competing interests.
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Authors’ contributions

Conceived and designed experiments: EKA, IM, FMO, CDK and JMM. Collected and processed samples, performed experiments: EKA, EMM and JMM. Contributed reagents/materials/analysis tools: EKA, AOA, IM, EMA and JMM. Analyzed the data: EKA and AOA. Prepared figures and/or tables: EKA and AOA. Wrote the manuscript: EKA and AOA. All authors read and approved the final draft.

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**Tables**

*Table 1* NGS statistics of collected samples before and after quality control showing the number of reads, the N50, and the maximum contig length (bp)
| Sample ID | County   | AEZ | Reads before QC | Reads after QC | N50 after de novoassembly | Average length after de novoassembly | Max contig length |
|-----------|----------|-----|----------------|---------------|---------------------------|-------------------------------------|------------------|
| Tom 2     | Kirinyaga| UM  | 740            | 593           | 147                       | 148                                 | 1023             |
| Tom 3     | Kirinyaga| UM  | 319816         | 314602        | 157                       | 157                                 | 5262             |
| Tom 4     | Kirinyaga| UM  | 712833         | 698797        | 172                       | 171                                 | 8902             |
| Tom 5     | Kirinyaga| UM  | 478717         | 468508        | 235                       | 231                                 | 13612            |
| Tom 6     | Meru     | LM  | 926762         | 910347        | 182                       | 178                                 | 10110            |
| Tom 7     | Kirinyaga| UM  | 685854         | 673575        | 182                       | 182                                 | 7946             |
| Tom 8     | Nakuru   | LH  | 228919         | 223686        | 180                       | 178                                 | 7153             |
| Tom 9     | Nakuru   | UM  | 234634         | 230096        | 183                       | 182                                 | 6069             |
| Tom 10    | Kirinyaga| UM  | 666739         | 687749        | 184                       | 182                                 | 6290             |
| Tom 11    | Kirinyaga| UM  | 513780         | 510356        | 175                       | 175                                 | 7911             |
| Tom 12    | Nakuru   | UM  | 518378         | 510356        | 175                       | 175                                 | 6450             |
| Tom 13    | Baringo  | LH  | 1294432        | 1274379       | 201                       | 214                                 | 10139            |
| Tom 14    | Baringo  | LH  | 1315827        | 1298815       | 201                       | 207                                 | 44887            |
| Tom 15    | Baringo  | LH  | 681944         | 672083        | 159                       | 162                                 | 3864             |
| Tom 16    | Nakuru   | UM  | 923671         | 908547        | 186                       | 182                                 | 17400            |
| Tom 17    | Kwale    | Coastal | 534566       | 527106        | 162                       | 162                                 | 7417             |
| Tom 18    | Nakuru   | UM  | 352911         | 347096        | 181                       | 181                                 | 11029            |
| Tom 20    | Baringo  | LH  | 609870         | 597102        | 166                       | 165                                 | 5871             |
| Tom 21    | Nakuru   | UM  | 243975         | 240633        | 135                       | 138                                 | 947              |
| Tom 22    | Baringo  | LH  | 253971         | 251006        | 135                       | 138                                 | 947              |
| Tom 23    | Meru     | LM  | 989149         | 975057        | 163                       | 164                                 | 7104             |
| Tom 24    | Meru     | LM  | 786980         | 774322        | 171                       | 171                                 | 7102             |
| Tom 26    | Baringo  | LH  | 728499         | 719324        | 164                       | 166                                 | 42790            |
| Tom 27    | Meru     | LH  | 1058065        | 1039347       | 187                       | 190                                 | 42301            |
| Tom 28    | Baringo  | LH  | 339590         | 324853        | 170                       | 173                                 | 7369             |
| Tom 33    | Makueni  | UM  | 1093634        | 1078116       | 147                       | 149                                 | 5805             |
| Tom 34    | Kirinyaga| UM  | 619068         | 610590        | 152                       | 152                                 | 7151             |
| Tom 35    | Nakuru   | LH  | 322666         | 317651        | 159                       | 160                                 | 5398             |
| Tom 36    | Nakuru   | LH  | 605642         | 597918        | 151                       | 152                                 | 3604             |
| Tom 37    | Baringo  | LH  | 161895         | 158650        | 201                       | 206                                 | 3608             |
| Tom 39    | Makueni  | LM  | 638580         | 630445        | 146                       | 149                                 | 7957             |
| Tom 40    | Baringo  | LH  | 359195         | 353997        | 201                       | 208                                 | 40180            |
| Tom 41    | Machakos | LM  | 424094         | 418916        | 173                       | 173                                 | 5839             |
| Tom 42    | Nakuru   | LH  | 286302         | 282623        | 168                       | 167                                 | 7249             |
| Tom 43    | Kirinyaga| UM  | 478583         | 470428        | 173                       | 173                                 | 7405             |
| Tom 44    | Nakuru   | LH  | 225820         | 222387        | 191                       | 199                                 | 4190             |
| Tom 45    | Baringo  | LH  | 547166         | 540173        | 208                       | 211                                 | 9004             |
| Tom 46    | Meru     | LM  | 484669         | 477311        | 176                       | 178                                 | 6633             |
| Tom 47    | Meru     | LM  | 492672         | 486329        | 161                       | 162                                 | 4876             |
| Tom 48    | Meru     | LM  | 656855         | 649550        | 270                       | 237                                 | 14432            |
| Tom 49    | Meru     | LM  | 99706          | 98214         | 168                       | 169                                 | 5196             |
| Tom 50    | Kirinyaga| UM  | 576946         | 568993        | 166                       | 167                                 | 7263             |
| Tom 51    | Nakuru   | LH  | 236211         | 232201        | 160                       | 162                                 | 7294             |
| Tom 52    | Baringo  | LH  | 369927         | 364146        | 201                       | 212                                 | 6670             |
|    |     |     |      |      |      |      |      |      |
|----|-----|-----|------|------|------|------|------|------|
| Tom 53 | Meru | LM | 590600 | 581771 | 179 | 181 | 7083 |
| Tom 54 | Nakuru | UM | 320207 | 314556 | 174 | 174 | 7225 |
| Tom 55 | Nakuru | LH | 387684 | 382226 | 165 | 167 | 7218 |
| Tom 56 | Baringo | LH | 219381 | 214875 | 224 | 223 | 8109 |

Lower Midland (LM), Upper Midland (UM), Lower Highland (LH)

**Table 2** Percentage nucleic acid similarities between full and individual genomic regions of *Tomato leaf curl Arusha virus*-like isolates from Kenya with DNA-A component of tomato begomoviruses
| Begomovirus species a | Complete genome | Genomic regions b |
|----------------------|-----------------|-------------------|
| ToLCarV              | 95.9-98.9       | 91.8-97.1, 95.5-99.4, 96.2-98.9, 96.3-99.4, 95.7-98.3, 97.1-98.7, 98.4-99.7 |
| ToLCCMV              | 79.7-80.1       | 66.5-70.3, 79.2-81.7, 79.0-80.4, 82.2-83.7, 74.8-76.7, 76.5-77.1, 87.1-88.8 |
| ToLCAnV              | 77.0-77.8       | 69.3-74.9, 78.0-80.5, 79.6-80.1, 75.4-76.4, 73.9-74.8, 72.4-73.5, 75.8-76.8 |
| ToLCBaV/A            | 72.9-74.0       | 68.4-75.4, 69.2-72.3, 71.5-72.2, 75.1-77.0, 70.4-71.6, 70.0-70.9, 75.6-77.0 |
| ToLCBV               | 74.7-75.5       | 64.8-67.5, 75.6-77.8, 74.0-75.1, 77.1-78.1, 68.7-72.1, 70.6-72.6, 75.0-76.0 |
| ToLCMV               | 79.5-80.3       | 75.6-80.6, 82.6-84.4, 82.3-82.9, 77.3-78.2, 73.9-75.6, 74.2-74.9, 76.6-77.9 |
| ToLCDIV              | 75.9-77.2       | 64.6-67.1, 73.6-75.3, 74.7-75.9, 79.8-81.4, 73.9-75.7, 74.9-76.0, 86.2-86.8 |
| ToLCGV               | 77.9-78.2       | 71.0-73.9, 80.0-82.3, 78.0-78.9, 78.3-79.6, 74.8-76.5, 74.2-75.6, 80.4-81.1 |
| ToLCGdV              | 75.6-76.6       | 62.3-67.2, 72.8-73.9, 75.4-76.1, 79.9-80.9, 71.9-73.4, 74.7-75.2, 84.9-85.9 |
| ToLCHaiV             | 73.2-74.0       | 61.2-65.2, 75.8-76.6, 71.7-72.5, 77.9-78.9, 71.5-73.7, 70.5-71.5, 80.7-81.4 |
| ToLCHAiV             | 74.4-75.1       | 66.3-74.4, 75.8-77.0, 73.7-74.0, 77.5-78.8, 70.1-71.3, 70.0-70.8, 75.7-77.3 |
| ToLCIRV              | 73.8-74.6       | 64.2-72.0, 75.3-76.8, 71.5-72.3, 77.5-78.4, 72.0-73.5, 70.4-72.0, 76.0-77.3 |
| ToLCJv/A             | 76.1-76.9       | 65.5-71.0, 73.8-75.0, 74.1-75.1, 80.9-82.0, 71.9-72.7, 71.3-72.2, 83.9-85.3 |
| ToLCV-K3             | 74.6-75.6       | 67.7-71.6, 75.3-76.5, 73.7-74.5, 77.0-80.0, 71.1-73.0, 71.5-73.5, 80.0-81.3 |
| ToLCLV               | 74.5-75.4       | 63.5-68.6, 69.6-71.8, 74.0-75.2, 78.1-79.5, 71.7-73.4, 72.1-73.8, 81.4-82.7 |
| ToLCMGV/Men          | 78.6-79.3       | 70.2-75.5, 82.2-83.6, 79.8-80.3, 78.2-79.5, 75.1-77.2, 74.0-75.1, 80.6-82.0 |
| ToLCMIV              | 75.1-75.7       | 61.4-67.7, 73.0-74.6, 72.4-74.8, 79.1-79.1, 72.5-73.9, 72.3-73.1, 80.4-81.7 |
| ToLCMohV             | 78.0-78.9       | 70.0-76.7, 82.9-84.4, 82.1-82.7, 74.5-75.5, 74.4-76.3, 74.9-75.3, 68.3-69.2 |
| ToLCNaV              | 79.8-80.3       | 75.4-80.0, 84.3-87.3, 81.9-89.9, 77.2-78.7, 74.6-76.5, 75.3-76.2, 79.5-81.1 |
| ToLCNDC2             | 73.6-74.3       | 66.7-69.8, 71.1-73.6, 72.1-73.3, 76.9-77.8, 73.0-74.2, 70.0-72.9, 79.5-80.1 |
| ToLCNDC5             | 71.3-72.2       | 66.7-72.1, 69.8-70.4, 71.1-71.8, 72.8-73.9, 68.2-70.0, 66.8-68.5, 75.3-76.3 |
| ToLCJV               | 71.9-73.4       | 58.3-69.8, 68.8-71.0, 73.3-74.4, 76.1-78.1, 66.2-68.6, 68.7-70.5, 78.6-79.3 |
| ToLCKV2              | 74.1-74.8       | 71.9-76.0, 67.7-69.3, 72.1-73.0, 78.1-79.2, 72.5-73.5, 70.4-72.2, 76.6-78.0 |
| ToLCKV3              | 73.4-74.0       | 62.9-71.3, 73.5-75.8, 72.3-73.2, 75.7-76.5, 70.9-71.5, 70.2-72.0, 77.3-78.6 |
| ToLCNGV              | 78.1-78.9       | 68.4-71.9, 78.8-80.7, 78.8-79.9, 78.8-80.1, 75.1-77.0, 74.2-78.1, 83.0-83.6 |
| ToLCPaV              | 70.1-70.5       | 61.6-65.4, 67.7-68.3, 70.8-71.5, 70.9-72.1, 68.9-70.6, 70.3-72.2, 75.0-76.3 |
| ToLCp PatV           | 74.5-75.1       | 62.1-65.7, 72.6-73.2, 73.6-74.2, 78.7-79.6, 71.2-73.1, 70.6-71.3, 78.5-79.8 |
| Virus Name          | Range       |
|---------------------|-------------|
| ToLCRaV             | 72.4-72.9   |
| ToLCSCV             | 76.7-77.4   |
| ToLCLKV             | 73.8-74.4   |
| ToLCTV/A            | 74.1-74.7   |
| ToLCTZV             | 89.8-90.5   |
| ToLCToV             | 95.9-98.9   |
| ToLCUV              | 78.9-79.3   |

Table 3 Percentage amino acid sequence similarities between open reading frames of *Tomato leaf curl Arusha virus*-like isolates from Kenya with DNA-A component of tomato begomoviruses

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**Table 3** Percentage amino acid sequence similarities between open reading frames of *Tomato leaf curl Arusha virus*-like isolates from Kenya with DNA-A component of tomato begomoviruses

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\( ^a \) ToLCaV: *Tomato leaf curl virus Arusha virus*, ToLCaV: *Tomato leaf curl Cameroon virus*, ToLCaV: *Tomato leaf curl Anjouan virus*, ToLCaV: *Tomato leaf curl Arusha virus*, ToLCaV: *Tomato leaf curl Bangladesh virus*, ToLCaV: *Tomato leaf curl Comoros virus*, ToLCaV: *Tomato leaf curl Hainan virus*, ToLCaV: *Tomato leaf curl Hanoi virus*, ToLCaV: *Tomato leaf curl Iran virus*, ToLCaV: *Tomato leaf curl Java virus*, ToLCaV: *Tomato leaf curl Kerala virus*, TLC-NA: *Tomato leaf curl Laos virus*, ToLCaV: *Tomato leaf curl Madagascar virus*, ToLCaV: *Tomato leaf curl Mindanao virus*, ToLCaV: *Tomato leaf curl Moheli virus*, ToLCaV: *Tomato leaf curl Namakely virus*, ToLCaV: *Tomato leaf curl New Delhi virus 2*, ToLCaV: *Tomato leaf curl New Delhi virus 5*, ToLCaV: *Tomato leaf curl Joydebpur virus*, ToLCaV: *Tomato leaf curl Karnataka virus 2*, ToLCaV: *Tomato leaf curl Karnataka virus 3*, ToLCaV: *Tomato leaf curl Nigeria virus*, ToLCaV: *Tomato leaf curl Palampur virus*, ToLCaV: *Tomato leaf curl Patna virus*, ToLCaV: *Tomato leaf curl Rajasthan virus*, ToLCaV: *Tomato leaf curl Seychelles virus*, ToLCaV: *Tomato leaf curl Sri Lanka virus*, ToLCaV: *Tomato leaf curl Taiwan virus*, ToLCaV: *Tomato leaf curl Arusha virus*, ToLCaV: *Tomato leaf curl Toliara virus*, ToLCaV: *Tomato leaf curl Uganda virus.*

\( ^b \) IR: Intergenic region, V1: Movement protein gene, V2: Coat protein gene, C1: Replication-associated protein gene, C2: Transcriptional activator protein gene, C3: Replication enhancer protein gene, C4: C4 protein gene
| Begomovirus  | Genomic regions b |
|-------------|------------------|
| species a   | V1   | V2   | C1   | C2   | C3   | C4   |
| TolCArV     | 93.3-99.1      | 97.3-98.9 | 95.4-98.6 | 94.2-97.8 | 96.0-98.0 | 97.1-100.0 |
| TolCCMV     | 74.5-76.3      | 86.6-87.8 | 81.9-85.4 | 64.3-68.6 | 66.2-68.2 | 69.2-73.1 |
| TolCArV     | 75.0-76.7      | 88.2-88.9 | 70.6-72.2 | 62.1-64.3 | 65.2-68.1 | 50.6-53.3 |
| TolCBAV/A   | 63.0-64.7      | 73.9-74.3 | 75.3-76.9 | 58.5-60.0 | 63.0-65.2 | 52.9-56.5 |
| TolCBV      | 67.7-68.6      | 78.1-79.3 | 75.7-77.6 | 57.0-59.3 | 65.2-68.8 | 50.0-52.9 |
| TolCVMV     | 80.6-82.3      | 93.1-93.9 | 76.5-77.9 | 63.6-65.0 | 66.0-69.6 | 54.8-56.7 |
| TolCDiV     | 66.3-67.2      | 81.7-82.9 | 80.1-81.7 | 64.7-66.9 | 71.9-74.8 | 72.5-73.5 |
| TolCGV      | 74.8-76.5      | 86.2-87.4 | 78.2-80.1 | 64.7-68.4 | 67.5-69.6 | 56.7-58.6 |
| TolCGdV     | 71.4-73.1      | 79.0-80.5 | 80.7-81.6 | 61.0-63.2 | 62.7-66.7 | 72.9-76.5 |
| TolCHaV     | 71.2-74.3      | 75.5-75.9 | 79.3-80.7 | 59.2-60.0 | 57.3-59.4 | 60.8-61.7 |
| TolCHaV     | 72.2-73.9      | 79.0-80.1 | 76.4-77.8 | 56.3-58.5 | 63.0-64.5 | 46.1-50.9 |
| TolCIRV     | 67.7-68.6      | 73.5-73.9 | 73.3-74.4 | 59.2-61.5 | 65.2-66.7 | 48.1-51.0 |
| TolCJaV/A   | 67.7-69.5      | 78.2-79.4 | 81.8-82.9 | 56.6-58.8 | 65.9-66.7 | 70.6-73.5 |
| TolCV-K3    | 67.7-68.6      | 76.2-77.4 | 75.1-76.8 | 62.9-64.4 | 65.2-66.7 | 58.6-62.1 |
| TolCLV      | 55.0-56.7      | 81.2-82.4 | 77.4-78.6 | 56.6-59.5 | 62.0-65.2 | 59.6-62.5 |
| TolCMGV/Men | 82.5-84.2      | 88.5-90.0 | 77.7-78.5 | 67.1-69.3 | 66.2-68.8 | 57.6-61.2 |
| TolCMiV     | 68.6-69.4      | 77.8-79.0 | 77.5-78.9 | 59.5-61.7 | 65.2-66.7 | 62.5-65.4 |
| TolCMohV    | 79.8-84.0      | 91.6-92.4 | -      | 65.4-66.9 | 66.0-69.6 | 37.5-38.5 |
| TolCNAaV    | 81.5-83.2      | 91.6-92.4 | 76.8-78.2 | 66.1-66.9 | 70.2-73.2 | 60.0-64.7 |
| TolCNDC2    | 61.0-63.5      | 76.6-77.8 | 78.0-79.7 | 61.1-63.3 | 56.8-58.9 | 56.7-58.6 |
| TolCNDC5    | 61.4-62.2      | 79.3-80.1 | 73.8-75.7 | 50.7-51.5 | 54.6-57.3 | 62.1-67.2 |
| TolCJV      | 70.8-73.5      | 78.3-78.7 | 75.5-77.6 | 52.0-54.4 | 55.7-57.2 | 55.1-56.5 |
| TolCKV2     | 56.7-57.6      | 77.8-78.5 | 77.6-78.7 | 62.2-63.7 | 64.5-66.7 | 49.0-51.9 |
| TolCKV3     | 63.5-64.4      | 79.7-80.4 | 74.3-77.3 | 52.9-53.7 | 62.0-63.7 | 50.0-52.9 |
| TolCNGV     | 73.9-75.6      | 87.4-88.5 | 78.6-80.7 | 67.6-69.1 | 67.5-68.9 | 62.7-63.7 |
| TolCPaIV    | 56.8-58.5      | 76.2-77.4 | 72.0-73.4 | 52.9-54.5 | 60.0-62.3 | 62.1-67.2 |
| TolCPatV    | 70.3-74.5      | 79.4-80.1 | 76.6-77.7 | 59.5-61.7 | 56.7-60.9 | 56.3-59.7 |
| Virus Name     | Percentage Identities |
|---------------|-----------------------|
| ToLCRaV       | 62.5-66.1             |
| ToLCSCV       | 81.7-84.2             |
| ToLCLKV       | 63.6-65.4             |
| ToLCTV/A      | 67.7-68.6             |
| ToLCTZV       | 82.5-84.1             |
| ToLCToV       | 68.3-70.9             |
| ToLCUV        | 79.8-81.5             |

**Table 4** Percentage pairwise sequence identities among the twelve *Tomato leaf curl virus Arusha virus*-like isolates from Kenya

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*a ToLCArV: Tomato leaf curl virus Arusha virus, ToLCCMV: Tomato leaf curl Cameroon virus, ToLCAnV: Tomato leaf curl Anjouan virus, ToLCBaV/A: Tomato leaf curl Bangalore virus, ToLCBV: Tomato leaf curl Bangladesh virus, ToLCKMV: Tomato leaf curl Comoros virus, ToLCDIV: Tomato leaf curl Diana virus, ToLCGV: Tomato leaf curl Ghana virus, ToLCGdV: Tomato leaf curl Guangdong virus, ToLCHaV: Tomato leaf curl Hanoi virus, ToLCHaV: Tomato leaf curl Hanoi virus, ToLCIRV: Tomato leaf curl Iran virus, ToLCjaV/A: Tomato leaf curl Java virus, ToLCV-K3: Tomato leaf curl Kerala virus, TLCV-LA: Tomato leaf curl Laos virus, ToLCMGV: Tomato leaf curl Madagascar virus, ToLCMiV: Tomato leaf curl Mindanao virus, ToLCMohV: Tomato leaf curl Moheli virus, ToLCNaV: Tomato leaf curl Namakely virus, ToLCND2: Tomato leaf curl New Delhi virus 2, ToLCND5: Tomato leaf curl New Delhi virus 5, ToLCJV: Tomato leaf curl Joydebpur virus, ToLCKV2: Tomato leaf curl Karnataka virus 2, ToLCKV3: Tomato leaf curl Karnataka virus 3, ToLCNGV: Tomato leaf curl Nigeria virus, ToLCPaV: Tomato leaf curl Palampur virus, ToLCPatV: Tomato leaf curl Patna virus, ToLCRaV: Tomato leaf curl Rajasthan virus, ToLCSCV: Tomato leaf curl Seychelles virus, ToLCLKV: Tomato leaf curl Sri Lanka virus, ToLCTV/A: Tomato leaf curl Taiwan virus, ToLCTZV: Tomato leaf curl Arusha virus, ToLCToV: Tomato leaf curl Toliara virus, ToLCUV: Tomato leaf curl Uganda virus.*

b V1: Movement protein gene, V2: Coat protein gene, C1: Replication-associated protein gene, C2: Transcriptional activator protein gene, C3: Replication enhancer protein gene, C4: C4 protein gene
| Segment<sup>b</sup> | Nucleotide (%) | Amino acid (%) |
|-------------------|----------------|----------------|
| Genome            | 95.7-99.7      | -              |
| V1                | 95.0-100       | 94.1-100       |
| V2                | 95.0-100       | 98.5-100       |
| C1                | 95.7-99.6      | 94.1-99.4      |
| C2                | 95.0-100       | 94.3-100       |
| C3                | 96.8-100       | 95.6-100       |
| C4                | 98.7-100       | 95.1-100       |

<sup>b</sup> V1: Movement protein gene, V2: Coat protein gene, C1: Replication-associated protein gene, C2: Transcriptional activator protein gene, C3: Replication enhancer protein gene, C4: C4 protein gene

ecombination events identified in *Tomato leaf curl virus Arusha virus*-like isolates from Kenya using algorithms within the RDP 4 software
| Recombinants | Potential parents | Recombination breakpoints | Average $p$ values in detecting algorithms |
|--------------|------------------|---------------------------|-------------------------------------------|
| ToLCArV      | ToLCArV          | 60-570                    | 1.00E-02, 1.01E-04, 6.80E-07, 9.32E-07     |
| Tom5a-Kenya  | Tom45-Kenya      | 1386-1974                 | 7.86E-04, 8.81E-06, 1.61E-04, 5.20E-05     |
| (MN894493)   | (MN894498)       |                           |                                           |
| Tom39-Kenya  | Kenya (MN894451) |                           |                                           |
| (MN894499)   | Tanzania         |                           |                                           |
| ToLCArV      | ToLCArV          | 158-524                   | 2.42E-06, 2.04E-04, 7.13E-09, 1.68E-12     |
| TZTen05-Tanzania | Kenya (MN894493) |     |                                           |
| (DQ519575)   | Uganda           |                           |                                           |
| ToLCDiV      | ToLCArV          | 1091-1583                 | 1.48E-12, 4.75E-12, 1.32E-10, 1.17E-05     |
| Namakely-Madagascar | Kenya (MN894499) |  |                                           |
| (AM701765)   | Comoros          |                           |                                           |

$^a$ ToLCArV: *Tomato leaf curl virus Arusha virus*, ToLCDiV: *Tomato leaf curl Diana virus*.

$^b$ ToLCUV: ToLCUV: *Tomato leaf curl Uganda virus*, ToLCMohV: ToLCMohV: *Tomato leaf curl Moheli virus*.

$^c$ R: RDP, G: GENCOV, B: BoostScan, M: MaxChi, C: Chimera, S: SiScan, T: 3Seq

**Table 6** Genetic variability determinants and neutrality tests on *Tomato leaf curl virus Arusha virus*-like populations from Kenya with other worldwide tomato begomoviruses
| Gene | N  | h  | S  | Hs | Eta | \(\theta\)-W | \(\theta\)-Eta | Tajima's \(D\) | Fu and Li's \(D\) | Fu and Li's \(F\) |
|------|----|----|----|----|-----|-----------|-----------|-------------|---------------|---------------|
| Genome | 2920 | 46 | 1666 | 1.000 | 2985 | 0.22424 | 569.5749 | 0.14924 | 0.2674 | -0.5971 | -0.2912 | -0.4859 |
| **Oviruses** | | | | | | | | | | |
| V1 | 372 | 43 | 241 | 0.996 | 419 | 0.22538 | 76.1768 | 0.16224 | 0.28206 | -0.7389 | -0.8229 | -0.9463 |
| V2 | 1261 | 46 | 752 | 1.000 | 1334 | 0.22421 | 271.971 | 0.14106 | 0.25023 | -0.3842 | -0.0052 | -0.1764 |
| C1 | 1179 | 46 | 692 | 1.000 | 1213 | 0.21165 | 225.4106 | 0.14784 | 0.25915 | -0.6771 | -0.3609 | -0.5737 |
| C2 | 431 | 45 | 264 | 0.999 | 458 | 0.23777 | 97.486 | 0.14651 | 0.25417 | -0.2374 | -0.0923 | -0.1752 |
| C3 | 469 | 45 | 303 | 0.999 | 550 | 0.24589 | 108.1903 | 0.15669 | 0.28442 | -0.4989 | -0.3631 | -0.4949 |
| C4 | 316 | 44 | 210 | 0.997 | 360 | 0.21015 | 65.1459 | 0.15414 | 0.26423 | -0.7516 | -0.4512 | -0.6736 |
| **ToLCArV.-** Genome | 2766 | 12 | 211 | 1.000 | 224 | 0.0264 | 72.955 | 0.0253 | 0.0268 | -0.0774 | -0.4189 | -0.3751 |
| s (n=12) | | | | | | | | | | |
| V1 | 360 | 9 | 22 | 0.939 | 24 | 0.02298 | 8.2727 | 0.02024 | 0.02208 | 0.1819 | 0.1216 | 0.1564 |
| V2 | 1239 | 12 | 71 | 1.000 | 72 | 0.0209 | 25.8788 | 0.01899 | 0.01926 | 0.3958 | -0.0631 | 0.0659 |
| C1 | 1116 | 12 | 94 | 1.000 | 102 | 0.02744 | 30.6212 | 0.02789 | 0.03027 | -0.4355 | -0.7775 | -0.7841 |
| C2 | 422 | 11 | 39 | 0.985 | 40 | 0.02761 | 11.6515 | 0.0306 | 0.03139 | -0.5481 | -1.072 | -1.065 |
| C3 | 450 | 11 | 23 | 0.985 | 23 | 0.01872 | 8.4242 | 0.01692 | 0.01692 | 0.4703 | -0.3193 | -0.1286 |
| C4 | 312 | 10 | 11 | 0.955 | 11 | 0.00869 | 2.7121 | 0.01167 | 0.01167 | -1.0628 | -1.4718 | -1.552 |

\(^a\) V1: Movement protein gene, V2: Coat protein gene, C1: Replication-associated protein gene, C2: Transcriptional activator protein gene, C3: Replication enhancer protein gene, C4: C4 protein gene

- **N** number of nucleotide sites
- **h** type number
- **S** number of variable or segregation sites
- **Hs** polymorphism number
- **Eta** polymorphism diversity
- **\(\theta\)-W** number of mutations
- **\(\theta\)-Eta** nucleotide diversity
- **\(\theta\)** age number of nucleotide differences between sequences
- **D** Fu and Li's estimate of population mutation rate based on the total number of segregating sites
Waterson's estimate of population mutation rate based on the total number of mutations

Estimates of selection pressure on the coding regions of twelve *Tomato leaf curl virus Arusha virus*-like isolates from Kenya

| Coding region a | Number of sites b |
|-----------------|-------------------|
|                 | Total number | \( \log L \) | \( d_N \) | \( d_S \) | \( d_N/d_S \) | Positive or diversifying selection | Negative or purifying selection |
| V1              | 114          | -651.20     | 0.0363 | 0.1757 | 0.2067 | 0 | 1 |
| V2              | 258          | -1483.95    | 0.0150 | 0.2212 | 0.0677 | 0 | 3 |
| C1              | 364          | -2392.81    | 0.0847 | 0.2124 | 0.3986 | 0 | 11 |
| C2              | 135          | -856.05     | 0.0607 | 0.2085 | 0.2908 | 0 | 1 |
| C3              | 134          | -708.30     | 0.0307 | 0.1184 | 0.2590 | 0 | 2 |
| C4              | 85           | -509.31     | 0.0392 | 0.0341 | 1.1491 | 0 | 0 |

a V1: Movement protein gene, V2: Coat protein gene, C1: Replication-associated protein gene, C2: Transcriptional activator protein gene, C3: Replication enhancer protein gene, C4: C4 protein gene.

b Selected at \( p \leq 0.1 \)

**Figures**
Figure 1

Map of Kenya showing geography of tomato fields sampled for this study and photos of symptomatic plants
Figure 2

Photos of tomato leaf curl symptomatic plants from farmer fields
Figure 3

Phylogenetic analyses of tomato leaf curl virus from Kenya (n=12) with selected worldwide begomoviruses based on alignment of complete DNA-A nucleotide sequences. The tree was generated using the maximum likelihood inference based on the Jukes-Cantor model as implemented in MEGA v.6.06 [39]. Percentage bootstrap support values (1,000 iterations) are indicated at the branch nodes. The tree is rooted with Tomato leaf curl purple vein virus (accession number KY196216) as an outgroup. The
scale bar shows the number of nucleotide substitutions power site. Details of the isolates are provided in Additional File 3: Table S1

**Supplementary Files**

This is a list of supplementary files associated with this preprint. Click to download.

- Additionalfile1.FigureS1.pdf
- Additionalfile2.xlsx
- Additionalfile3.xlsx
- Additionalfile4.FigureS2.bmp
- Additionalfile5.File1.fas
- Additionalfile6.File2.fas