Peer Community In Infections

A smooth takeover in tomato begomovirus populations: when selection pressure drives independent recombinant shifts in the Mediterranean bassin

Sebastien Massart *based on peer reviews by* ***Jean-Michel Lett*** *and* ***Arvind Varsani***

Martine Granier, Mohamed Faize, Sandie Passera, Cica Urbino, Michel Peterschmitt (2024) Population shifts in begomoviruses associated with tomato yellow leaf curl disease in western Mediterranean countries. bioRxiv, ver. 2, peer-reviewed and recommended by Peer Community in Infections. https://doi.org/10.1101/2024.08.09.607290

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The tomato yellow leaf curl disease (TYLCD) has long plagued tomato crops across the western Mediterranean. The virus landscape has long included both native (TYLCSaV) and introduced (TYLCV) begomoviruses (Lefeuvre et al., 2010), along with a mosaic of recombinants, firstly detected in 1998 for TYLCSaV/TYLCV (Monci et al., 2002).

Despite shared vectors and active trade between Spain, Italy, and Morocco, regional differences in virus populations were evident through 2014 with distinct recombinants between countries (Belabess et al., 2015; Pano et al., 2018). The recommended publication (Garnier et al., 2024) therefore addresses the question of whether these patterns have persisted over time.

To find out, researchers analyzed 105 tomato samples collected between 2015 and 2019, using targeted PCR assays to distinguish between virus species, strains, and recombinants, especially the so-called Srec (short-fragment) and Lrec (long-fragment) recombinants.

The findings reveal two key insights: (1) Geographic signatures persist as Morocco harbors TYLCV-IS76 exclusively and Italy hosts TYLCV-IS141 and a newly identified Srec recombinant, TYLCV-IMS60-2400; (2) A striking population shift across all countries as Srec recombinants now dominate, with no Lrec forms detected, resulting in a marked change from earlier decades.

So, selective pressures independently favored the same recombinant genomic configuration, yet with distinct strains. One hypothesis from the authors is that the selective sweep might have been driven by Ty-1 resistance genes in modern tomato cultivars. As breeders deploy resistance, viruses evolve in turn, highlighting a classic case of adaptive viral evolution under host-imposed pressure.

References:

Belabess, Z., Dallot, S., El-Montaser, S., Granier, M., Majde, M., Tahiri, A., Blenzar, A., Urbino, C., Peterschmitt, M., 2015. Monitoring the dynamics of emergence of a non-canonical recombinant of Tomato yellow leaf curl virus and displacement of its parental viruses in tomato. Virology 486, 291-789. https://doi.org/10.1016/j.virol.2015.09.011

Granier, M., Tomassoli, L., Manglli, A., Nannini, M., Peterschmitt, M., Urbino, C., 2019. First Report of TYLCV-IS141, a Tomato Yellow Leaf Curl Virus Recombinant Infecting Tomato Plants Carrying the Ty-I821 Resistance Gene in Sardinia (Italy). Plant Dis 103, 1437-1437. https://doi.org/10.1094/PDIS-09-18-1558-PDN

Granier, M., Faize, M., Passera, S., Urbino, C.,Peterschmitt, M. (2024) Population shifts in begomoviruses associated with tomato yellow leaf curl disease in western Mediterranean countries. bioRxiv, ver.3 peer-reviewed and recommended by PCI Infections https://doi.org/10.1101/2024.08.09.607290

Lefeuvre P, Martin DP, Harkins G, Lemey P, Gray AJA, et al. (2010) The Spread of Tomato Yellow Leaf Curl Virus from the Middle East to the World. PLOS Pathogens 6(10): e1001164. https://doi.org/10.1371/journal.ppat.1001164 https://doi.org/10.1371/journal.ppat.1001164 https://doi.org/10.1371/journal.ppat.1001164https://doi.org/10.1371/journal.ppat.1001164

Monci, F., Sanchez-Campos, S., Navas-Castillo, J., Moriones, E., 2002. A natural recombinant between the geminiviruses Tomato yellow leaf curl Sardinia virus and Tomato yellow leaf curl virus exhibits a novel pathogenic phenotype and is becoming prevalent in Spanish populations. Virology 303, 317-326. https://doi.org/10.1006/viro.2002.1633

Panno, S., Caruso, A.G. & Davino, S. The nucleotide sequence of a recombinant tomato yellow leaf curl virus strain frequently detected in Sicily isolated from tomato plants carrying the Ty-1 resistance gene. Arch Virol 163, 795–797 (2018). https://doi.org/10.1007/s00705-017-3674-9

Reviews

Evaluation round #1

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Version of the preprint: 1

Authors' reply, 18 June 2025

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Montpellier, June 17, 2025

Dear Recommender,

Our manuscript entitled “Population shifts in begomoviruses associated with tomato yellow leaf curl disease in western Mediterranean countries” has been revised according to the suggestions and comments of the recommender and the two reviewers. All comments and issues raised by the recommender and the reviewers were addressed point by point in the attached file. Virtually all the suggested corrections were included in the revised manuscript and for those that were not included, we explained why they were not included.

We are very thankful to the recommender and the reviewers for the time they spend to carefully read and comment our manuscript and we acknowledge that their valuable input has substantially improved the quality of our manuscript. Thus, we hope that the revised manuscript will be suitable for publication in PCI-Infections.

With best regards,

Michel Peterschmitt (Corresponding author)

Download author’s reply
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Decision by Sebastien Massart, posted 25 November 2024, validated 26 November 2024

Dear authors,

Thank you very much for submitting your research paper to PCI Infection.

Following the in-depth review of a reviewer and my analysis of the document, we invite you to improve the manuscript through a new version answering the comments raised.After improving the manuscript, it will be reviewed again. You will find my own comments (both minor and major) at the bottom of this message.

Kind regards,

Sébastien Massart

Comment from recommender

L24 : could you indicate the number of samples analysed in this study ?

L25: could you cite the countries (Italy and Morrocco are cited further on but no information on 3rd)

L28: are TYLCV-IS76 and Srec the same or from the same origin ? It is stated next line but, to clarify the message, maybe the line 17 should be adapted to introduce Srec term and give one example (IS76)

L39: Solanum lycopersicum L. (adding the author)

L43: could you cite the number of the report from ICTV ?

L44-48: this information is still referenced from ICTV or another reference should be added ?

L55-57: please rephrase the sentence using both viruses and both dates in a row and ending by “respectively”

L67-68: indicate clearly that ToLCNDV is also a non-native LC virus and its origin (if its introduction is not linked to introduction of TYLCV)

L72, 76: past tense

L82: “bean growing” : latin name (with author) at first occurrence and rather cultivation than growing and specific it is a host for LC viruses

L87 and 93: what does mean “autonomous” spreading ? should it be “epidemics” or something related ? Autonomous could be understood as spreading autonomously without vector

L122: what does mean “protected tomato crops” ? Under net ? with insecticides ?

Plant material: it lacks important information (or the information is very unequal between countries, Morrocco being well detailed, other countries not) related to details about samples (or at least a mention of the result table (n°2) where the number of samples, their location and sampling dates are clearly indicated).

L139: why the initial amount of material is so variable ? Why explaining this protocol if failed ?

L165: I understand that the test distinguishing Srec and Lrec has been designed in this publication but the details of the protocol should be stated in material and methods, reporting the software used to design the primers, the optimization carried out (temperature, primer concentration…), the validation with reference isolates and final PCR protocol… while the obtained results of these steps would remain in result section.

L169: give the size of the PCR product. Why not making both strand sequencing as double check for errors ?

L167-171: this analysis has been carried out whatever the origin of the sample (contrary to next paragraph focused on Spain). Please specify

L172-191: state clearly if the IM650R primer is designed during this study and state the length of the PCR product (so just stating 11 positions in the next sentence is fine)

L202: the virus specific primers should be indicated as not communicated

L207-234: I understand that there is no optimization of the protocol (PCR mix and cycling). So it can be described in M&m (see previous comment)

L220-222: what were the results of in silico specificity analyses? How many mismatches with non-targets? Which primers were evaluated: all of them (old and newly designed)?

L226-227: first occurrence of the terms Lerc-IL and Lrec-Mld -> please describe them properly (here or before). Same point for line 236 with Lrec-IL PCR test

L235-248: it is unclear how the validation was carried out. It seems only sample containing the target were used -> validation of the ability to detect (inclusivity) but what about exclusivity (no detection of non target) and not only for one negative control (empty vector). Even though it is partially stated in the legend of fig 1, the exact validation scheme should be better specified in the text (also in M&m with the information on the clones used).

L236: no description of the viral clone (and their reference) in material and methods

L241: it can be guessed that R11 represents one of the plants Pristyle agroinoculated. Can it be specified clearly if it is the case?

L242: a detection with Sanger sequencing is not enough described: sequencing is applied on PCR product generated by a PCR test. Please clarify

Fig 1B & D: could you show the full agarose gel as the ladder is not completely visible and the image has been cut. The stated marker starts at 250 nt.

Fig 1D: it seems there are aspecific bands for Sar599F/Mld2310R while it is not stated nor discussed in the text.

Table 2: why some samples were sequenced and other samples not? For example, why Oualida – Antalya cultivar from Morrocco were not sequenced while from Calvi it was? The rationale behind is not stated.

Table 2: when there are several samples (8 for Calvi in Oualida): it means that all 8 samples were sequenced if there is a + on partial genome sequence?

L343: rephrase the sentence with the verb after the two observations and before the coma

L349-350: between coma can be deleted: whereas all the other samples were positive for the presence of IL/Sar or Mld/Sar recombinants

L351: all the recombinant-positive samples corresponded to Srec recombinants.

L353-354: what is the rationale in the sample selection ? Please state it

L365-367: this statement relies on only 2 samples for 2015. If the prevalence of IS60 is low, there is a low probability of detecting it. This should be nuanced properly or deleted

L370-371: it is an hypothesis, so conditional tense should be used

L372: stress such as … (Reference)

Figure 2: the sequence should be longer to see better what are the homologies after position 80 (for example from 1 to 120, so 60 is in the middle).

Recombination analysis: there are several algorithms to give confidence on the occurrence of a recombination event (Recombination Detection Program (RDP)). Did you use it? What was the confidence in the results?

L387-390: as for previous country, there are very few samples analysed and it should be stated (not only in the discussion). A solution might be to indicate the number of samples in brackets for the reader to understand that these observations are coming from few samples

L402-405: hypothesis so using conditional tense

L405: same comment as before for non specificity of symptoms

Fig 4: a curve joining dots might be more readable than histogram ?

Fig 4: the title is not appropriate: this is the dynamics of the viruses in the infected plants, not the infected plants

Fig 4: could be moved to results section with a specific mention there (yet still discussed in the discussion section)

L547: the dominant species rather ?

Reviewed by Jean-Michel Lett, 13 November 2024

Download the review

Reviewed by Arvind Varsani, 12 November 2024

This MS is well written and i do not have any major concerns with reagrds to the research methods and the interpretation of the data. Thanks for making the reviewers job relatively easy - much appreciated.

Some minor points -

1) Line 14 - Geminiviridae should be in italics.

2) line 45 and 46 for some odd reason leaf curl is in bold - unblod please.

3) Line 121: A map of the samplling locaitons may be helpful. Overlaying the results sumamried in table 2 onto this map would would be very useful for the reader and the authors to have visual representation of the TYLCV variants / recombinants and also the tomato genotypes. You can use the shapes for tomato genotypes and perhaps colour fill for different TYLCV variants / recombiants.