

Accepted Manuscript

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PII: S2352-4073(18)30001-5
DOI: doi:[10.1016/j.plgene.2018.01.001](https://doi.org/10.1016/j.plgene.2018.01.001)
Reference: PLGENE 139
To appear in: *Plant Gene*
Received date: 24 October 2017
Revised date: 6 January 2018
Accepted date: 9 January 2018

Please cite this article as: Anurag Kumar Sahu, Rakesh Kumar Verma, R.K. Gaur, Neeti Sanan Mishra , Complexity and recombination analysis of novel begomovirus associated with Spinach yellow vein disease in India. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. *Plgene*(2017), doi:[10.1016/j.plgene.2018.01.001](https://doi.org/10.1016/j.plgene.2018.01.001)

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Complexity and recombination analysis of novel begomovirus associated with Spinach yellow vein disease in India

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Abstract:

Leaves with vein yellowing were observed on Spinach (*Spinacia oleracea*) in Rajasthan province of India. The plants were severely stunted in growth and exhibited symptoms typical of *Begomovirus* infection. Here we report a comprehensive study of complexity and recombination of novel begomovirus associated with spinach yellow vein disease. It is probably a perpetuation of *Papaya leaf curl virus* in absence of its main host and thus raises concern about its spread to other crops. Analysis of samples collected in the survey indicates that SYVD infected plants are associated with a begomoviruses (novel species showed <91% nucleotide sequence similarity) and its associated betasatellites. Interestingly, most of the begomoviruses were found to be inter-species recombinants and the betasatellites possess high nucleotide variability, due to recombination. This suggested the existence of a complex recombination pattern to form “gene pool” of the crop-infecting begomovirus–betasatellites complexes. The Nucleotide diversity (π) and nucleotide substitution rates were determined for the DNA-A of begomoviruses SYVSV is 0.10382 and 2.436×10^{-3} substitutions site⁻¹ year⁻¹ respectively. Thus mutation and recombination are driving forces for the emergence and evolution of new begomoviruses. This strengthens the hypothesis for increase

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