

Global summit on Agriculture & Organic farming

August 25–26, 2022 | Webinar

Neha Sharma, Adv Crop Sci Tech 2022, Volume 10

Serological Identification, In silico comparison and Validation of Partial Coat Protein (CP) Gene of Zucchini Yellow Mosaic Virus (ZYMV) infecting summer squash in India

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Zucchini yellow mosaic virus (ZYMV) belonging to Potyvirus family is responsible for causing major crop losses in summer squash in India. By Direct Antigen Coating Enzyme-linked immunosorbent assay (DAC ELISA) the presence of potyvirus was confirmed and ZYMV in particular was authenticated by Double antibody Sandwich ELISA (DAS ELISA). RNA isolation of test virus cDNA showed a 700 bp amplification by using specific primers and the PCR product was outsourced for sequencing and finally a sequence of 154 bp was obtained with 50.65 % G+C content and 49.35 % A+T content. The test sequence proved 91 % alignment with D13914 (ZYMV isolate from USA) on BLASTN analysis. ExPasy tools were further used for translating the test sequence into protein sequence and it showed 75.9% similarity on BLASTP analysis. To further understand evolutionary status, on phylogenetic tree construction with other already submitted sequences at National Center for Biotechnology Information (NCBI) it clearly proved a close relation of the Indian isolate of ZYMV with ZYMV isolate of USA. 22 different restriction sites were found in In silico restriction digestion in the test ZYMV sequence via using NEB cutter. On secondary structure prediction dominance of alpha helix was reported. The present study aimed to enhance the knowledge about ZYMV and hence prevent crop losses by controlling the disease. The study would also help plant virologists and pathological researchers to work on coat protein-mediated virus resistance against ZYMV.

Biography

Dr. Neha Sharma is currently working as a assistant professor, biotechnology, IILM College of Engineering and Technology, Greater Noida, India

Received: August 22, 2022; Accepted: August 26, 2022; Published: August 26, 2022
