

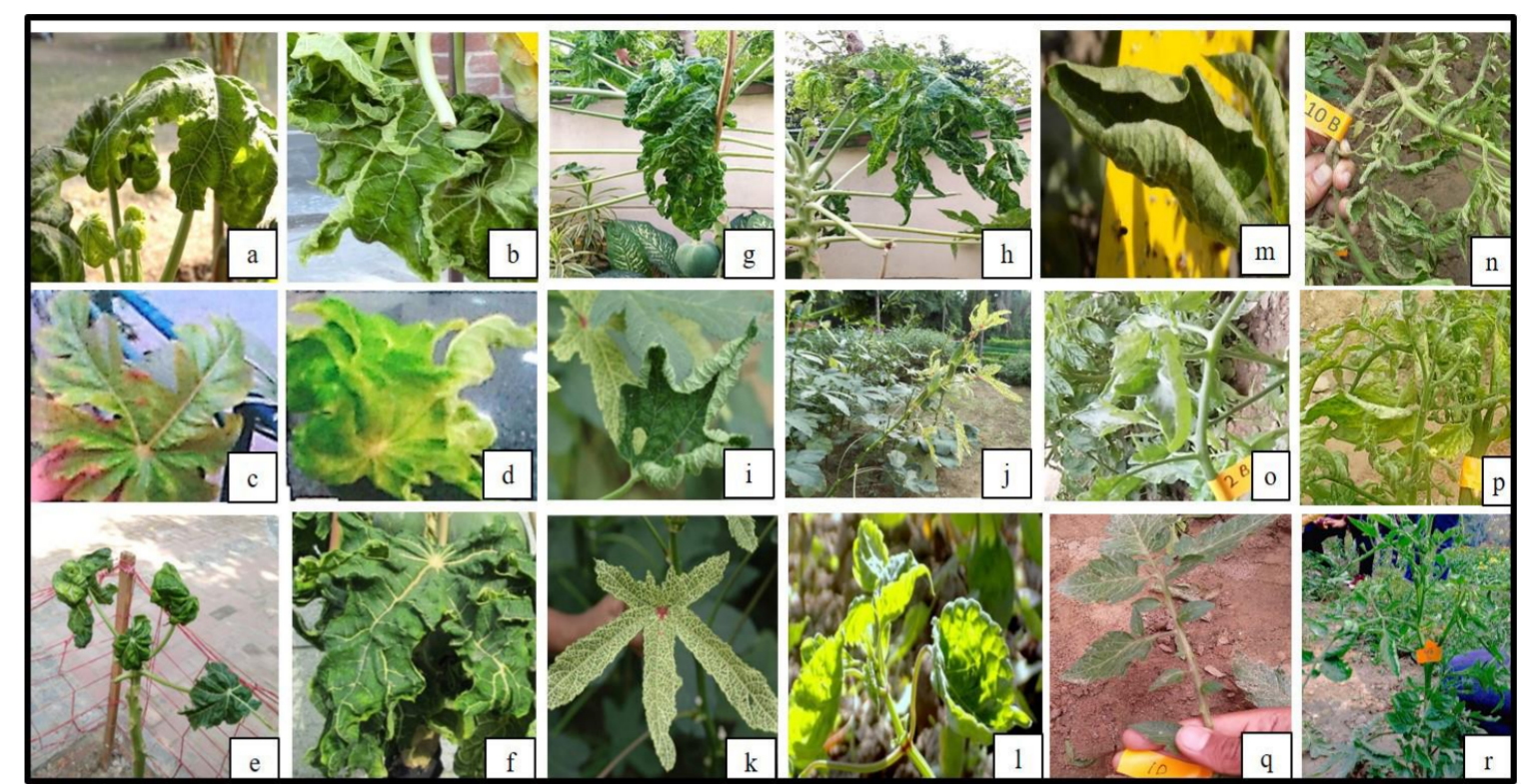


Plant-Virus Interactions

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We are trying to understand *Begomovirus* diversity, a pre-requisite for sustainable transgenic strategies for control of leaf curl disease in *Carica papaya* L. Ten year old surveys using serological and molecular tools with symptomatic papaya leaf samples and proximal weeds (Solanaceae, Malvaceae, Cucurbitaceae, Lamiaceae, Brassicaceae members) indicate high genetic diversity and an expanding host range for these viruses. The genome of a novel papaya virus *Papaya leaf crumple virus* is available in GenBank. Current research focuses on identification of prevalent and persistent begomoviruses in papaya and weeds.



Various symptoms of begomovirus infection observed in plant samples of Papaya, Okra, Tomato and weeds from 2010-2016.

Poster presentation in International Conference:
 “Understanding Persistence and Evolution of Begomoviruses infecting Feral Papaya and Solanaceous weeds by Epidemiological Screenings” in the 8th International Geminivirus Symposium & 6th International ssDNA Comparative Virology Workshop, New Delhi, India, November 7-10, 2016.

Research publication:
 Singh-Pant, P., Pant, P., Mukherjee, S. K., & Mazumdar-Leighton, S. (2012). Spatial and temporal diversity of begomoviral complexes in papayas with leaf curl disease. *Archives of virology*, 157(7), 1217-1232.



Collection of symptomatic plants samples with M.Sc. (Left) and Dissertation students (Right).



Map showing collection sites of 184 symptomatic plants sampled from 2005-2017.



Symptomatic papaya plant

