

LETTER TO THE EDITOR

Soybean and radish as new hosts of Begomoviruses in Cuba

Soya y rábano como nuevos hospedantes de Begomovirus en Cuba

Dear Sir,

Emerging whitefly transmitted begomoviruses are major pathogens of the Solanaceae plant family throughout the world, particularly in tropical and sub-tropical regions. Mutation, recombination and pseudorecombination are driving forces associated with the emergence and evolution of new crop-infecting begomoviruses.

At present, Begomovirus is the largest genus of the plant virus family Geminiviridae whose members infect only dicotyledonous plants and are transmitted by the whitefly (*Bemisia tabaci* Gen). Most of the begomoviruses have a bipartite genome with two components of about 2.6-2.8 kb each one, which are referred to as DNA-A, required for replication and encapsidation, and DNA-B, required for virus movement. Some species present a monopartite genome with all the genes residing on one (DNA A-like) ssDNA of about 2.8 kb.

The presence of begomoviruses in radish (*Raphanus sativus* L.) and soybean (*Glycine max* L.) crops has been reported worldwide, but in Cuba the presence of begomoviruses in these crops was unknown.

Soybean plants, from Mayabeque and Las Tunas provinces, and radish plants, from plantations of the organoponic crop system in the province of Matanzas, were found showing symptoms similar to those reported for begomovirus infections, interveinal chlorosis, stunting and mosaic leaf symptoms. Ten foliar samples were collected from these plants and taken to the laboratory. Molecular analyses were performed using a universal primer set for begomovirus infection, and the infection with begomoviruses was detected.

Having in mind the worldwide emergence and incidence of these pathogens, we consider very important to continue studies on the identification and characterization of the associated etiological agents in these infections, a priority aspect for establishing rapid and sure management practices for these crops in Cuba.

Sincerely yours,

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