

عنوان مقاله:

Single nucleotide polymorphism analysis and 3D protein models predict a gap between Bean golden yellow mosaic virus isolates found in Cuba and those of the continent

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خلاصه مقاله:

Bean golden yellow mosaic virus (BGYMV) is considered the main drawback for bean production in the Caribbean basin and South Florida, where it is widely distributed. In Cuba, BGYMV disease has been reported along the entire territory and several BGYMV isolates were described in western Cuba. Now, further prospection uncovers a new BGYMV isolate in Ciego de Avila province in the center of the island, which together with the previous isolates configured a broader epidemiological picture of the country. An in-depth analysis of BGYMV genome sequences revealed many single nucleotide polymorphisms contrasting the sequences of isolates found in Cuba and those outside the island, albeit their phylogenetic closeness. An analysis of viral protein sequences disclose specific amino acids in the coat, replication enhancer, nuclear shuttle (NSP) proteins, distinguishing the new isolate from that of western Cuba and from the continental consensuses. Moreover, other amino acid substitutions were predicted in the replication associated protein (Rep) and movement proteins. The protein modeling discloses some new amino acid interactions that together with previous findings suggest a gap in gene/amino-acid sequences when compared the isolates in Cuba and those of the continent. Interesting, the transcriptional activator protein (TrAP) is the most

conservative protein in all analyzed BGYMV isolates being totally conservative. Thus, with the invariable Rep, the TrAP could be considered as suitable .supports to build molecular antiviral strategies in a way to protect local bean cultivation

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