

## Relationships among Bean-Infecting Geminiviruses

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Bean golden mosaic (BGM) disease has become one of the major constraints on dry bean production in South America, Central America and the Caribbean. The disease is induced by bean golden mosaic geminivirus (BGMV), which is whitefly-transmitted. The geminiviruses are small plant viruses that possess a single-stranded circular DNA genome and derive their name from their unique twin icosahedral particles. The genome of BGMV and other whitefly-transmitted geminiviruses is bipartite, composed of two 2.6 kilobase pair components, DNAs A and B.

It has become apparent, based on differences in symptomatology, sap transmissibility and bean genotype reaction, that there are differences among geminiviruses that cause BGM and that different geminiviruses infect beans in various bean growing regions in the tropics. Therefore, bean cultivars that are resistant or tolerant to infection by geminiviruses endemic to a given region may be susceptible to those in other regions. One of the objectives of this project is to provide the molecular characterization of bean-infecting geminiviruses and to determine their relationship to each other and to other whitefly-transmitted geminiviruses.

In a previous report, the cloning and sequencing of DNA components A and B of a nonmechanically transmissible isolate of BGMV from Brazil, BGMV-BZ, was described (Gilbertson et al., 1989). The nucleotide sequences of these components were entirely different except for a 181 nucleotide region that is shared between the two molecules and is referred to as the common region. The common region is characteristic of the genomes of all whitefly-transmitted geminiviruses and is highly conserved between the components of a given geminivirus, but is divergent among different geminiviruses. DNA sequence analysis of the BGMV-BZ genome demonstrated a surprisingly level of divergence from a previously characterized mechanically transmissible isolate of BGMV from Puerto Rico, BGMV-PR (Howarth et al. 1985).

In this report we present the cloning of the entire bipartite genomes of three other bean-infecting geminiviruses: mechanically transmissible BGMV isolates from Guatemala (BGMV-GA) and the Dominican Republic (BGMV-DR) and an isolate of bean dwarf mosaic virus (BDMV) from Colombia. BDMV causes a striking dwarfing and distortion of infected beans, but no golden mosaic symptoms. The nucleotide sequences of BGMV-GA and BGMV-DR have been determined and that of BDMV partially determined. Computer-assisted analysis of the BGMV-GA and BGMV-DR sequences revealed that both isolates have a genetic organization that is similar to that of BGMV-BZ and other whitefly-transmitted bipartite geminiviruses. There are two DNA components, which are completely different in nucleotide sequence except

for an approximately 200 nucleotide common region, and there are four open reading frames or genes on DNA component A and two on DNA component B. The nucleotide sequences of BGMV-GA, BGMV-DR, and BGMV-PR DNA component A are very similar (>95%), and are divergent from component A of BGMV-BZ (75% similar); similar results were obtained when component B sequences were compared. A phylogenetic tree was constructed based on computer-assisted comparisons of the common regions of BGMV-GA, BGMV-DR, BGMV-BZ, BDMV

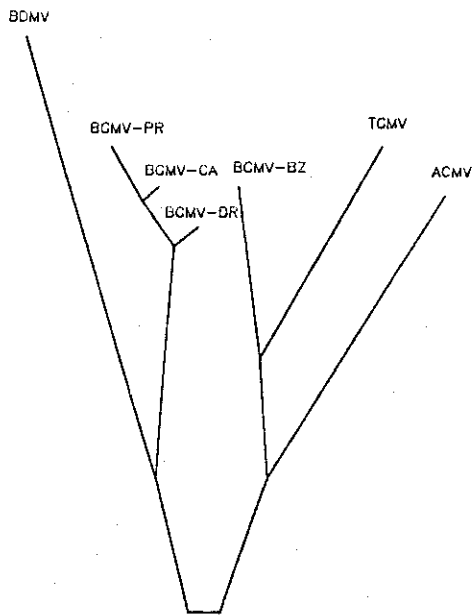


Fig. 1. Phylogenetic tree showing relationships among whitefly-transmitted geminiviruses

tomato golden mosaic geminivirus (TGMV), and African cassava mosaic geminivirus (ACMV) (Fig. 1). ACMV which is believed to have originated in Africa, is most distantly related to the other geminiviruses, which have New World origins. BGMV-GA, BGMV-DR, and BGMV-PR form a closely related group (Fig. 1) that share a common geographical origin and sap transmission. BGMV-BZ has a different geographical origin, is not sap transmissible, and is more closely related to TGMV (Fig. 1) but infects a different host. BDMV falls into its own group and is not closely related to any of the other geminiviruses.

Although BGMV-BZ is sufficiently divergent from the mechanically transmissible BGMV isolates to possibly be considered a different geminivirus, we propose that it be considered a distinct strain of BGMV and be referred to as BGMV-BZ. This would avoid the confusion generated by having two names for geminiviruses that cause the same disease.

The major practical implication of these results and the observation that bean genotypes react differently to BGMV strains is that more than one BGMV strain should be used when breeding for disease resistance to bean golden mosaic.

#### References

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