



Fig. 1. Genomic organization of geminiviruses. Grey boxes indicate the intergenic regions containing the origin of replication and promoters for bidirectional transcription. The part of the intergenic region whose sequence is identical in both Begomovirus genome components is called the common region (CR). The complementary strand origin of replication in Mastreviruses is in the short intergenic region (SIR). Open reading frames (ORFs) are indicated by black arrows. The convention for naming the ORFs of geminiviruses is that ORFs present in the virion sense of the genome are designated  $V_x$  and complementary sense ORFs  $C_x$ , where  $x$  is a number generally indicating the order in which the ORF occurs. In bipartite geminiviruses, the ORFs are preceded by the letter "A" or "B" to indicate on which genome component the ORF occurs. When a gene's function is known, we have replaced the ORF designation with the gene name. CP, coat protein; MP, movement protein; Rep, replication initiator protein; TrAP, *transcription activator protein*; REn, *replication enhancer protein* (5). In Curtoviruses, the AC2-encoded protein does not seem to have TrAP activity. The AV1 ORF is only present in Begomoviruses from the Old World; in monopartite Begomoviruses, the AV1 protein may have a function in movement (4). The proteins encoded by the BV1 and BV2 ORFs are both movement proteins.