Comparison of Barley Stripe Mosaic Virus Strains

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BSMV (barley stripe mosaic virus) particles were obtained in a pure state from infected host plant tissues of *Hordeum vulgare*. The three genomic parities (α, β and γ) were amplified by PCR using specific primers for each particle; each was cloned. Partial sequence of the α, β and γ segments was determined for the Egyptian isolate of barley stripe mosaic virus (BSMV AE1). Alignment of nucleotide sequences with that of other known strains of the virus, BSMV type strains (CV17, ND18 and China), and the generation of phylogenetic trees was performed. A low level of homology was detected comparing 467 bp of the α and 643 bp of the segments to that of the other strains, and thus BSMV α and β segments were in separate clusters. However, 1154 bp of the γ segments of BSMV AE1 showed a high level of homology especially to strain BSMV ND18, as they both formed a distinct cluster. Northern blotting of pure BSMV AE1 virus and *H. vulgare*-infected tissue were compared using an α ND18 specific probe. Western blotting using antibodies specific for the coat protein (CP) and the triple gene block 1 (TGB1) protein, which are both encoded by the β ND18 segment, still indicated a high level of similarity between proteins produced by BSMV ND18 and AE1. We suggest that the BSMV AE1 isolate is a distinct strain of BSMV which reflects the genetic evolutionary divergence among BSMV strains and members of the *Hordeivirus* group.

Key words: Hordeiviruses, Egyptian BSMV AE1, Barely Stripe Mosaic Virus