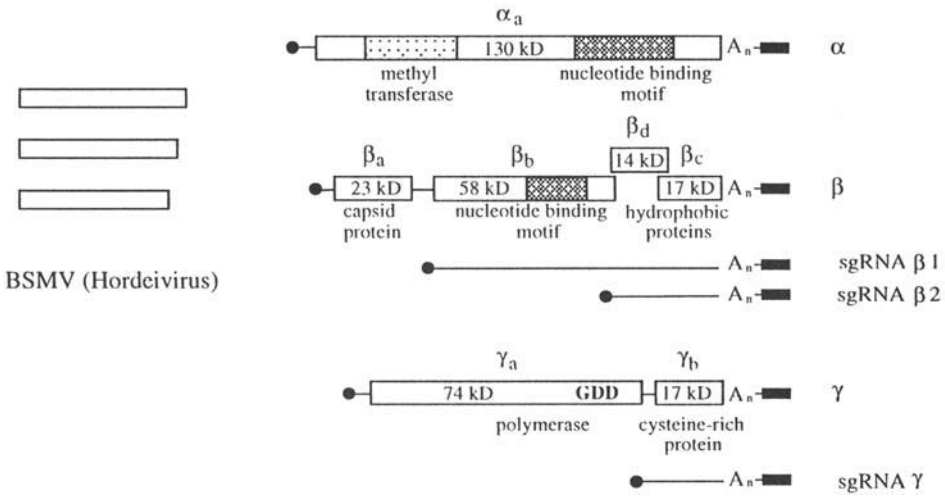

Fig. 2. Genetic organization of BSMV. The filled circles and rectangles represent a cap structure and a tRNA-like structure, respectively. The sgRNAs utilized for expression of the 3' proximal genes are depicted directly beneath the genomes.

is associated with the cell wall and membrane fractions ***(8)***. Mutational analysis of the triple gene block has shown that βb, βd, and βc are each essential for systemic infectivity in barley ***(6)***. It is postulated that βb, βd, and βc are expressed in vivo from two subgenomic (sg) RNAs that are 2.5 and 0.96 kb in size ***(9)***. When in vitro generated transcripts of the 3.3 kb genomic RNA and the 2.5 kb sgRNA containing authentic 5' termini were used to program in vitro translation reactions, the coat protein, and the βb protein, respectively, were detected. However, the 0.96 kb RNA served as an mRNA for synthesis of the βd protein, minor amounts of a translational readthrough product, βd', and βc ***(9)***.

The γ genome encodes two proteins of 74 kDa (γa) and 17 kDa (γb) in size. The γa protein contains the GDD domain present in polymerase proteins of single-stranded positive-sense RNA viruses, and is strictly required, in concert with αa, for viral replication ***(10)***. The γb protein is cysteine-rich and is expressed from a sgRNA ***(11)***. γb is known to affect virulence and expression of genes encoded by RNAβ; however, its biochemical function in infection is unclear at this time. It has been demonstrated that γb protein can bind nucleic acid ***(12)*** and that deletion of this gene attenuates viral replication; mutations in the cysteine-rich domain affect the symptom phenotype in barley ***(13)***. Thus far, all the proteins encoded by BSMV, except for βc, have been detected in infected barley tissue during infection.