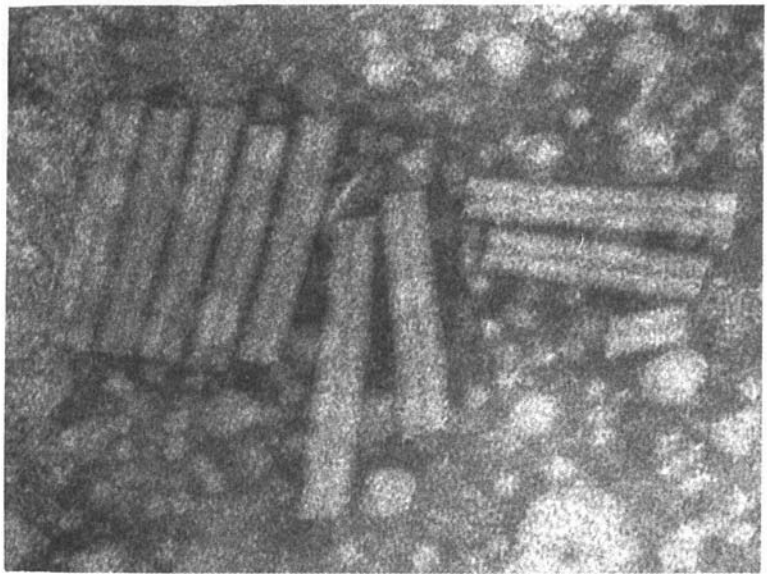

Fig. 1. Hordeivirus morphology. Electron micrograph of negatively stained particles of BSMV. The virus particles are ~25 nm in width and vary in length from ~100 to 160 nm.

The genome organization of BSMV is shown in **Fig. 2**. All three RNAs have a 7-methylguanosine cap at the 5' terminus and a conserved 3' region containing an internal poly(A) tail directly following the stop codon of the 3' proximal open reading frame (ORF). Following the poly(A) tail is a 238 nucleotide tRNA-like structure that is capable of binding tyrosine in vitro. The α, β, and γ genomes are required to establish a systemic infection in plants; the α and γ genomes are sufficient for viral RNA replication in protoplasts ***(5)***. The α genome encodes a single 130-kDa protein (αa) that contains both methyl transferase- and nucleotide-binding domains. At least four proteins are encoded by the β genome: βa (23 kDa) is followed by an intergenic region that precedes a series of overlapping genes, designated the triple gene block. The triple gene block encodes proteins of 58 kDa (βb), 14 kDa (βd), and 17 kDa (βc). The βa protein is the BSMV capsid protein, but, despite its role in formation of virus particles, it is not essential for systemic spread ***(6)***. βb is known to bind RNA and nucleotide triphosphates in vitro. Hence it is speculated that it has a role as an RNA helicase in vivo, even though in vitro helicase activity has not been associated with the purified protein ***(7)***. βd and βc are both hydrophobic proteins, and immunolocalization of βd in infected barley tissue has shown that it