

***Characterization of the *Triticum* mosaic virus genome and interactions between *Triticum* mosaic virus and wheat streak mosaic virus.***

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The complete genome sequence of *Triticum* mosaic virus (TriMV) has been determined to be 10,266 nucleotides encoding a large polyprotein of 3,112 amino acids. The proteins of TriMV possess only 33–44% (with N1b protein) and 15–29% (with P1 protein) amino acid identity with the reported members of Potyviridae. These results suggest that TriMV should be classified in a new genus, and we propose the genus *Poacevirus* in the family Potyviridae with TriMV as the type member.

TriMV and wheat streak mosaic virus (WSMV), distinct potyvirus species, infect wheat naturally in the Great Plains and are transmitted by wheat curl mites. We examined the interaction between WSMV and TriMV in three wheat cultivars at two temperature regimens (19°C and 20–26°C). Double infections in wheat cultivars Arapahoe and Tomahawk at both temperature regimens induced disease synergism with severe leaf deformation, bleaching, and stunting with a 2.2- to 7.4-fold increase in accumulation of both viruses over single infections at 14 days post-inoculation (dpi). However, at 28 dpi, in double infections at 20–26°C, TriMV concentration increased by 1.4- to 1.8-fold in Arapahoe and Tomahawk, but WSMV concentration decreased to 0.5-fold. WSMV and/or TriMV replicated poorly in Mace at 19°C with no synergistic interaction, whereas both viruses accumulated at moderate levels at 20–26°C and induced mild to moderate disease synergism in doubly infected Mace when compared to Arapahoe and Tomahawk. Co-infections in Mace at 20–26°C caused increased TriMV accumulation at 14 dpi and 28 dpi by 2.6- and 1.4-fold, and WSMV accumulated at 0.5- and 1.6-fold over single infections, respectively. Our data suggest that WSMV and TriMV induced cultivar-specific disease synergism in Arapahoe, Tomahawk, and Mace, and these findings could have several implications on management of wheat viruses in the Great Plains.

***Biology, phylogenetics, and distribution of wheat curl mite population.***

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Wheat streak mosaic has long been recognized as one of the most important diseases of winter wheat in the Great Plains. However, the identification of High Plains virus in the mid 1990s and *Triticum* mosaic in 2008 create a complicated virus complex in wheat. All three of these viruses are vectored by the wheat curl mite, and management of this virus complex is dependent on cultural practices that reduce the probability of mite infestation. Research into aspects of the biology and ecology of the mite has provided valuable insights into the potential for success of various management tactics. The development of resistant wheat varieties has had an impact on the virus but has not resulted in stable control. Distribution of mite biotypes explains the limited success of varietal mite resistance. Mite biotypes have shown differences in the mite's ability to transmit virus but also differences in survival on virus infected plants. Thus, one biotype is better adapted to the presence of these viruses. Recent studies on the movement of the mite also have provided better understanding of virus epidemiology and have improved recommendations for the management of this virus complex.