S-methyl (ASM). TSWV resistant varieties of tomato and pepper are commercially available. INSV has been primarily a pathogen of ornamentals though it was found in peanut and in greenhouse-grown pepper. A combination of sound production practices including sanitation and thrips control can reduce the incidence of INSV in greenhouse operations. IYSV is the most recently reported tospovirus in the US. Initially confined to onion crops in southern Idaho for over a decade, the virus has rapidly spread to several states in the western US in the past four years and is an economically important pathogen of onion in Colorado, Oregon and Washington. There are limited control options to manage this virus at the moment. Thrips management and use of SAR-inducers such as ASM and host plant resistance. While thrips-borne topsoviruses continue to present challenges to crop production, significant progress has been made in reducing their impact.

S.16. Pigeonpea sterility mosaic disease: challenges in understanding etiology and possible solutions – P. Lava Kumar, A. Teifion Jones[1], K.B. Saxena and F. Waliyar, *International Crops Research Institute for the Semi-Arid Tropics, Patancheru-502324, Andhra Pradesh, [1]Scottish Crop Research Institute, Invergowrie DD2 5DA, Dundee, UK* Sterility mosaic (SMD) is the most damaging disease of pigeonpea in the Indian subcontinent, seems to be native to pigeonpea growing countries of Asia, and has not been recorded elsewhere. The disease described in 1930s, but its causal agent, Pigeonpea sterility mosaic virus (PPSMV), vectored by an eriophyid mite, *Aceria cajani,* was characterized recently. Serological- and nucleic acid-based diagnostic tools were developed for the virus detection. The virus has novel properties with similarities in transmission and cytopathology with the eriophyid mite-transmitted High Plains virus and the agents of unidentified etiology associated with rose rosette, fig mosaic, thistle mosaic, wheat spot chlorosis and yellow ringspot of budwood. The virus occurs as several geographically distinct isolates and knowledge on genome properties and distribution of various PPSMV isolates, its relationships with other viruses and SMD epidemiology is limited. Characterization of various PPSMV isolates to identify the basis for the differences is essential to develop diagnostic tools for the precise identification of the virus isolates to conduct comprehensive surveys to assess the prevalence of various PPSMV isolates and their impact on pigeonpea cultivars. Current knowledge on PPSMV and methods for its detection are providing opportunities for new initiatives to study these aspects. This presentation will review the highlights of progress achieved on PPSMV and future challenges.

S.17. Vector-borne viruses of banana and plantain (*Musa* spp.) occurring in semi-arid tropics – P. Sreenivasulu, B. Ramesh and P. Lava kumar[1], *Department of Virology, Sri Venkateswara University, Tirupati-517502, Andhra Pradesh, India; [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru-502324, AP*

Banana bunchy top virus (BBTV; *Babuvirus*), *Banana streak virus* (BSV; *Badnavirus*), *Banana bract mosaic virus* (BBrMV; *Potyvirus*), Banana mild mosaic virus (BanMMV, an unassigned member of the family *Flexiviridae*), Banana virus X (BVX, a new unassigned species in the family *Flexiviridae*), *Cucumber mosaic virus* (CMV; *Cucumovirus*), *Abaca mosaic virus* (AbaMV; *Potyvirus*) *Tobacco mosaic virus* (TMV; *Tobamovirus*) Banana die-back virus (BDBV, a probable species in *Nepovirus*) and a bacilliform shaped rhabdo-like virus have been reported to naturally infect banana and plantain (*Musa spp.*) cultivated in the tropical and subtropical parts of the world. BBTV and BSV are economically very important, whereas BBrMV, BanMMV and CMV can cause significant damage when they occur in mixed infections. All the viruses infecting *Musa spp.* are transmitted vertically through vegetative propagules and BSV has the ability to integrate into the host genome. Among the viruses BBTV (circulative), BBrMV (non-persistent), AbaMV (non-persistent) and CMV (non-persistent) are vectored by aphid species (*Pentalonia nigronervosa, Rhopalosiphum maides, Aphis gossypii, A. craccivora, Myzus persicae*), while the BSV is transmitted by mealy bugs (*Planococcus citri*). The distribution and incidence, economic impact, etiology and management of vector-borne viruses infecting banana and plantain in semi-arid tropics will be discussed.

S.18. Population structure and evolutionary biology of *Tomato Spotted Wilt Virus:* pathways to understanding virus vector interactions – J.W. Moyer, S.H. Sin and G.G. Kennedy, *Departments of Plant Pathology and Entomology, North Carolina State University, Raleigh, NC, USA*

Tomato spotted wilt virus (TSWV) is the type member of the *Tospovirus* genus of the *Bunyaviridae* virus family. It has a tripartite genome, two of which have an ambisense genome organization that has a replication strategy typical of negative sense viruses. Natural populations (single isolates) are very heterogeneous and consist of one or two dominant haplotypes and many haplotypes of lesser frequency. One of the questions we have been attempting to address is the molecular basis of viral phenotypes. We are particularly interested in those that are quantitative in nature, specifically insect vector transmission efficiency. Changes in transmission efficiency overtime may be due to selection of mutant haplotypes that are less efficiently transmitted or it might be due to changes in the proportion of transmissible haplotypes in the viral population. We have found that when TSWV is subjected to serial, mechanical transfers, transmission efficiency by the thrips vector declines. Molecular genetic analysis of these populations revealed the accumulation of an array of mutant haplotypes consisting of single nucleotide mutations at many positions