

H₂O cm⁻¹ MPa⁻¹) and hydraulic capacity (Q_L; g H₂O cm⁻¹ MPa⁻¹) were calculated. The E of galled and control trees in the GH and GC was constant until the soil water content reached 11%, after which E decreased linearly with decreasing soil WC. The data were analyzed separately for well-watered (soil WC ≥ 11%) and water-limited (soil WC ≤ 8%) conditions. Analysis of variance was performed on the natural log transformed (ln) variables comprising K_{psi} and Q_L, to partition lnK_{psi} and lnQ_L into lnK_{psi} = lnE + lnL - lnA_S - lnDelta psi, and lnQ_L = lnE + lnL - lnA_L - lnDelta psi, respectively (A_S and A_L are the sapwood area and leaf area, respectively). Under well-watered conditions, galled trees had reduced A_L relative to control trees, likely because of reduced K_{psi}. However, the reduction in A_L of galled trees did not compensate for their lower K_{psi} values, and thus galled trees had lower Q_L and greater Delta psi than control trees. Under water-limited conditions galled and control trees responded similarly. The similar short term behavior of galled and control trees to drought stress suggests that gall-induced mortality results from indirect long-term growth reductions rather than from runaway xylem embolism.

Surveys of wheat viruses in the Texas Panhandle

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The Texas Panhandle produces about half of the state's annual hard red winter wheat crop and diseases caused by viruses are some of the major production problems in the region. Wheat production in this region is dual purpose (grain and grazing) and virus diseases impact both production categories. Routinely encountered viruses are Wheat Streak Mosaic Virus (WSMV), Wheat Mosaic Virus (WMoV) and Barley Yellow Dwarf Virus (BYDV). WSMV and WMoV are vectored by the wheat curl mite, *Aceria tosichella* Keifer, while BYDV is vectored by several species of aphids. To determine the relative incidences of these viruses, surveys were conducted in which samples were collected from 167, 72, and 33 fields in 2000, 2001, and 2002, respectively. County agents assisted in the survey by collecting 5 foliage samples from each field and submitting them to the diagnostic laboratory in Amarillo for processing. In 2006 and 2007, one sample per field was arbitrarily collected from 112 and 33 fields, respectively. In addition, in 2006, two fields were grid sampled each containing 60 sampling locations. The survey samples were collected in the spring of each year while the grid samples were collected from each field both in the fall and the spring. The samples were tested for the viruses using ELISA. In all survey samples, WSMV was the most dominant virus ranging from 6% of the samples testing positive in 2007 to 93% in 2006 followed by BYDV which ranged from 0 in 2007 to 40% in 2000. Overall, WMoV was the least encountered virus with incidences ranging from 0% in 2007 to 31% in 2006. WSMV also was the predominant virus in grid-sampled fields.

Sudden aspen decline in southwest Colorado

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Sudden aspen decline (SAD) has increased rapidly in recent years, approaching 350,000 acres in Colorado in 2007, or 13% of the aspen cover type. We investigated the severity, site/stand factors and causes associated with SAD in southwest Colorado. First, we documented landscape (GIS-DEM analyses) and stand factors (stand exams). There was a strong inverse relationship between elevation and damage, damage tended to occur on south and southwest aspects, was most severe in open stands with large trees, and regeneration was poor in damaged stands. Five biotic agents were frequently associated with mortality: *Cytospora* canker, poplar borer, bronze poplar borer, and two bark beetle. We proposed a causal hypothesis in a decline context: *Predisposing factors*: low elevations, south/west aspects, low density, stand maturity; *Inciting factors*: warm drought conditions; *Contributing factors*: secondary, biotic agents mentioned above. The second phase is a field survey with 76 plots on four National Forests. Analyses indicate: (a) Regeneration has not responded significantly to crown loss; (b) Root mortality varied from 0 to over 90% of root volume and was correlated with crown loss, and damaged plots had significantly higher volume of dead roots than healthy plots; (c) Regeneration decreased significantly as root mortality increased in damaged plots, but not in healthy plots; (d) Crown loss did not vary significantly with depth of soil mollic layer; (e) Crown loss did not vary significantly with average or oldest age of sampled codominant/dominant trees. There are significant management implications and may be loss of aspen cover type where aspen stands are declining and regeneration is inadequate. Marginal regeneration may be further compromised by such factors as amount and duration of ungulate browsing.

Post-fumigation horizontal and vertical recolonization of soil by *Verticillium dahliae*

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A lettuce field infested by *Verticillium dahliae* was fumigated in 2002 fall, and then planted with various crops in 4 different blocks from 2002 to 2006. Soil samples were collected in spring in the 4 blocks in 5-cm increments to a depth of 60-cm during 2003–2006 to determine vertical recolonization by *V. dahliae*. In two other infested fields, soil samples were collected at three sites each in an 8×8 grid (64 1×1-m quadrats) in 2004 before fumigation, and post-fumigation during 2005 through 2007 to determine the horizontal recolonization by *V. dahliae*. During both studies, strawberry was planted post-fumigation followed by various leafy vegetables or crucifers. All soil samples were assayed for *V. dahliae* microsclerotia in laboratory. Results demonstrated that some microsclerotia remained viable after fumigation, fumigation offered short term disease suppression, and recolonization of soil by *V. dahliae* was highly dependent on the subsequent crops. Density of microsclerotia declined after crops such as strawberry, radicchio, and cabbage, but increased after lettuce crops. Microsclerotium densities were greater at 5 to 15-cm depths than at greater depths. During non-host crops, density of microsclerotia declined early, more rapidly near the soil surface than at greater depths, and stabilized later. In the second study, the density of microsclerotia before fumigation followed the same patterns of disease incidence, high near the edges and progressively decreased inwards, suggesting the introduction of inoculum via contaminated equipment and personnel. Post-fumigation recolonization was greatest in areas that had the highest concentration of microsclerotia prior to fumigation.

Genetic structure of North American populations of *Phoma sclerotioides*, causal agent of brown root rot of alfalfa

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Phoma sclerotioides, causal agent of brown root rot of alfalfa, is associated with winterkill and poor spring regrowth of alfalfa and other perennial forage legumes in regions with harsh winters. Single-conidium isolates of the fungus were obtained from diseased alfalfa roots and crowns collected in western, central and eastern United States in 2004 to 2007 and central and eastern Canada in 2007. Diagnostic PCR of the isolates using previously developed *P. sclerotioides*-specific primers resulted in a single amplicon of expected size. On potato dextrose agar (PDA) and on water agar with barley, all isolates produced large pycnidia with multiple beaks, white cirri darkening to yellow with age, and unicellular, hyaline, ovoid conidia. Isolates differed in mycelial pigmentation and in production of aerial mycelium on PDA, with two or more culture types represented in each region. The internal transcribed spacer (ITS) 1, 5.8S, and ITS2 of the rDNA and intron-spanning regions coding for actin, beta tubulin, and glyceraldehyde 3-phosphate dehydrogenase were sequenced and analyzed. The multilocus sequence typing (MLST) data indicate that the isolates identified as *P. sclerotioides* are diverse, with isolates falling into two or more distinct clades in each region sampled. Clades correspond to culture types on PDA. Phylogenetic analysis of the MLST data and relative pathogenicity of representative isolates from the different clades will be presented.

Developing a fungicide resistance management guide for vegetable crops grown in the mid-Atlantic region

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In the mid-Atlantic region (NJ, MD, VA, DE, PA) of the United States approximately 90,000 ha of fresh-market and processing vegetable crops are grown each year. Over the past decade, new fungicide chemistries with specific modes-of-action have been developed for use in commercial vegetable production. Many of these new fungicides have a high-risk for fungicide resistance development. The number of fungicide chemistries available and differences in modes-of-action can make it very difficult for vegetable growers to develop and follow fungicide resistance management programs. In 2007 and 2008, using Fungicide Resistance Action Committee (FRAC) codes, we developed a fungicide resistance management guide with tables for the 30 crop groups listed in the mid-Atlantic Commercial Vegetable Production Recommendation Guide. Each FRAC table consists of all