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106. © Root colonization of several species of native grasses by *Ophiosphaerella*.
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Root colonization of several species of native grasses by *Ophiosphaerella herpotricha*

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Spring dead spot, caused by *O. herpotricha*, is the most damaging disease of turf-type bermudagrass (*Cynodon* spp.) in Oklahoma. The objective of this study was to evaluate root colonization of native grasses in the greenhouse by an isolate of *O. herpotricha* obtained from bermudagrass. Soil in pots containing established native grasses (*Buchloe dactyloides*, *Chloris cucullatta*, *Eragrostis secundiflora*, *Eragrostis trichodes*, *Sporabolus airoides*, and *Tridens strictus*) was inoculated with wheat grain infested with *O. herpotricha*. Non-inoculated pots containing the same plant species served as a control. Fourteen months after inoculation, plants appeared healthy and a sub-sample of roots from all plants was assayed on potato dextrose agar for the presence of *O. herpotricha*. The fungus was recovered from at least one plant of each species. Recovery ranged from 11 to 25% of the pots inoculated. The results of this study suggest that *O. herpotricha* may survive in the roots of native grasses for extended periods under greenhouse conditions.

Tissue repair in fusiform rust-infected loblolly and slash pines

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Healing of wounds caused by *Cronartium quercuum* f. sp. *fusiforme* is a complex process that influences the cambial tissues of the pine host. These tissues inhibit the capacity of the fungus to invade stems of loblolly and slash pines. This disruption of the cambium can result in death of stem tissues including resin canals. Herein, we describe events of tissue repair and regression of gall growth on loblolly and slash pines. We used light microscopy to measure changes in cellular traits in restoring cambial and cortical tissues to their normal state. Over 25% of the nuclei in affected clusters of cortical cells stained abnormally and the cells died. Callus cells grew inward and replaced the remaining dead tissue. Haustoria became necrotic in the clusters of dying cells. The number of tannin cells in the cortex averaged 24%. Tissue healing was evident in the formation of reaction zones

transcripts are infectious for *Nicotiana benthamiana* and *N. tabacum* protoplasts, and LIYV can be transmitted back to plants after feeding virions to the whitefly, *Bemisia tabaci*. However, improvement is needed to increase inoculation efficiency and simplicity. We constructed binary plasmid 35S-driven constructs and attempted to inoculate plants via agro-infiltration. No LIYV infection was observed from agro-infiltration using the two original 35S-driven constructs. Further attempts including co-infiltrations with different gene silencing suppressors and modifying the predicted RNA 1 5′ nucleotide sequence were done, however no whole plant infections were obtained. We also used two different ribozymes predicted to give different RNA 1 3′ termini in order to see if this might affect RNA 1 replication ability. The *Hepatitis delta virus* (HDV) ribozyme proved to be effective for yielding infectious LIYV RNA 1 transcripts in protoplasts, as judged by GFP expression of a LIYV RNA 2 defective RNA when it was co-inoculated with RNA 1. We are now constructing additional 35S-driven RNA 1 clones that contain the HDV ribozyme in attempts to develop a direct whole plant infection method.

A high throughput screen using virus-induced gene silencing in *Nicotiana benthamiana* identifies the requirement of squalene synthase for nonhost resistance

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Nonhost resistance is the most common form of disease resistance exhibited by plants against the majority of potential pathogens in nature. We used virus-induced gene silencing (VIGS) in *Nicotiana benthamiana* to identify genes involved in nonhost resistance. We individually silenced 3,000 genes by using cDNA clones from a normalized NbcDNA library. Eleven genes were identified to be involved in type I and/or type II nonhost resistances. One of them encoding squalene synthase (SQS), a key enzyme catalyzing the first enzymatic step in sterol biosynthesis, was further characterized by RNA interference (RNAi) and gene overexpression in both *N. benthamiana* and *Arabidopsis*. The transgenic *SQS* RNAi lines of *Arabidopsis* were not only susceptible to nonhost pathogens, *Pseudomonas syringae* pv. *tabaci* and *P. syringae* pv. *syringae*, but also slightly more susceptible to pathogens, *P.*