ABSTRACT

Of the many exotic plants occurring in the United States, the Asian grass *Microstegium vimineum* is highly invasive. A number of environmental variables seem to play a part in *Microstegium*’s invasiveness. However, the exact mechanisms that allow *M. vimineum* to outcompete native plants are not altogether known. This research used Brightfield microscopy and Automated Ribosomal Intergenic Spacer Analysis (ARISA) to investigate the role of mycorrhizae in this grass’ invasive tendencies. Mycorrhizal communities of two native plants (*Onoclea sensibilis* and *Amphicarpa bracteata*) were compared with the mycorrhizal community found in *Microstegium*. All three plants occurred as monoculture communities and mixed communities in Northern Virginia.

Brightfield microscopy identified Arbuscular Mycorrhizal fungi (AM) and Dark Septate Fungi (DSF) in all three plants. AM colonization rates were greater than 50% in all three plants in both monoculture and mixed plant communities.

Principal Coordinate Analysis (PCO) of ARISA fingerprint data identified fungal communities unique to each monoculture. When the three plants co-occurred in the mixed setting, *Microstegium* was found to maintain its unique fungal community while the two native plants were found to share their communities. A few small shifts between the communities in
the grass and the fern suggest that the invasive grass might be integrating its fungal community into the native plant community. Unlike the root samples, multivariate analysis of soil fingerprints did not identify fungal communities unique to each plant. Instead, soils showed a random distribution. Overall, the sharing of fungal communities between roots of the two natives may represent the long-standing relationship between the two natives in contrast to the recently introduced exotic grass.