CHANGES IN ROOT ARCHITECTURE CAUSED BY *MELOIDOGYNE INCOGNITA* AND *THIELAVIOPSIS BASICOLA* AND THEIR INTERACTION ON COTTON Jianbing Ma J. Jaraba Terry L. Kirkpatrick University of Arkansas, Southwest Research and Extension Center Hope, AR Craig S. Rothrock Dept. of Plant Pathology, University of Arkansas Fayetteville, AR

<u>Abstract</u>

Roots are vital for the acquisition of water and minerals from the soil and to anchor plants. *Meloidogyne incognita*, the root-knot nematode, and *Thielaviopsis basicola*, a fungus that causes black root rot, are important soilborne pathogens on cotton in Arkansas and can interact in a synergistic manner increasing disease losses. Both pathogens cause distinct symptoms on affected roots. This study characterized the changes in seedling root architecture caused by these pathogens individually and in combination. Cotton was planted in soil either not infested or infested with each of these pathogens or with both pathogens, and placed in controlled environmental chambers for six weeks. Root system morphology was evaluated using morphometric and topological assessment methodologies by scanning intact root systems and using the WinRhizo software. Infection of cotton seedlings by M. incognita, T. basicola, or both pathogens resulted in smaller root systems. Changes in root system morphological and topological parameters by these pathogens included reductions in root system magnitude (the number of exterior links that feed into the root system), altitude (the longest individual path length from one exterior link to the shoot base) and total exterior path length (P_e) (the sum of all path lengths from all exterior links to the base) compared to healthy root systems. The total number of root links was also reduced, resulting in less root surface area. The branching structure of diseased root systems was decreased as well. Damage from both pathogens was greater than with either pathogen alone. Analysis of topological parameters to evaluate the architecture of diseased cotton seedlings should enable the quantitative assessment of the effect of root pathogens and also provides a fresh panorama to estimate the impact of these diseases on season-long cotton development and disease losses.