

Abstract of a poster presented at the 13<sup>th</sup> SIPaV Annual Meeting that was not included in the Supplement to No. 3, 2006

**CHARACTERIZATION OF *ALTERNARIA* SPECIES GROUPS ASSOCIATED WITH DISEASE COMPLEXES OF WALNUT AND HAZELNUT.** S.G. Hong<sup>1</sup>, M. Maccaroni<sup>2</sup>, P.J. Figuli<sup>1</sup>, B.M. Pryor<sup>1</sup> and A. Belisario<sup>2</sup>. <sup>1</sup> Division of Plant Pathology, Department of Plant Sciences, University of Arizona, Tucson, AZ, 85721; <sup>2</sup> CRA, Centro di Ricerca per la Patologia Vegetale, Via C.G. Bertero 22, 00156 Rome, Italy; Fax: +39.0682070370 or +39.0686802296; E-mail: a.belisario@ispave.it

Brown apical necrosis (BAN) of English walnut and gray necrosis (GN) of hazelnut are recently described destructive diseases caused by a complex of fungi including several small-spored catenulate *Alternaria* taxa. *Alternaria* isolates recovered from diseased tissues and tested pathogenic on fruit of their respective host could be separated into three distinct morphological groups, each typified by representative *Alternaria* species: the *A. alternata* group, the *A. tenuissima* group, and the *A. arborescens* group. All three groups were represented across both hosts. Genetic relationships among these groups were evaluated with AFLP and ISSR markers, and histone gene sequence data comparison. Among the three groups morphologically differentiated, only the *A. arborescens* group was resolved as a monophyletic lineage. Monophyly was revealed in AFLP analysis as well as by shared polymorphic bases in H4 sequence analysis. ISSR data produced a slightly different grouping from AFLP data as three *A. alternata* group isolates were marginally included in the cluster of the *A. arborescens* group. The *A. alternata* and *A. tenuissima* groups failed to resolve as monophyletic lineages based on AFLP, ISSR, or H4 data sets. The inability to link pathogenicity, symptom development, or even host range to specific morphological groupings make difficult the development of diagnostic criteria and precise nomenclature for these pathogenic *Alternaria* taxa, and a robust understanding of their ecology.

