SCREENING RANGE-WIDE BLACK WALNUT SEED FAMILIES FOR THOUSAND CANKERS DISEASE (TCD) RESISTANCE AND MEASURING THE REGIONAL ADAPTABILITY OF RESISTANT SEED SOURCES

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Black walnut (*Juglans nigra*), an economically important native species in the Eastern United States is threatened by a new disease thousand cankers disease (TCD) caused by a fungus (*Geosmithia morbida*) vectored by a bark beetle (*Pityophthorus juglandis*). Both organisms originate in the Southwestern United States but have spread to become endemic throughout the Western United States and the disease was first found in the eastern native range in 2010. We challenged a range-wide collection of native black walnut (*Juglans nigra*) families, collected in 2012, to artificial stem inoculation of *Geosmithi morbida* (*Gm*) to determine the variation among regions and families of black walnut, to test the regional adaptability of any sources of resistance and to capture resistant material for future breeding and new seed orchards. In addition, we included a number of our select timber families from Indiana as an improved check-lot.

Up to 9 seedlings per family were shipped to Colorado State University (CSU) and planted in three complete blocks in the field. Families with more than 9 seedlings were planted into the common garden (CG) plots in Arkansas, Indiana, and Michigan. Each plot was planted on a 2.2 meter grid with 24 mixed families per provenance per block and 12 seedlings of three oak species (bur, northern red, and cherry bark) per block (36 trees total). Each plot was fenced to exclude deer and weeds were controlled for the first 2 years with herbicides and cultivation.

Trees were inoculated with two *Gm* strains first in 2014 the summer after planting, and then again in the summer of 2016 at CSU. Plugs of two *Gm* isolates and a sterile control were placed into live stems with a 6-mm cork-borer and the branches cut 90 days later and stored in a cooler until we could scrape off the outer bark and measure the length and width of cankers. The first year screen at CSU showed *Gm* isolate significantly affected canker size, but provenance did not. In the repeat screen of 2016, stem diameter significantly affected canker size as did family and provenance. Breeding values were used to estimate the percent difference among provenances in canker size relative to all trees in the study and we found western provenances had from -5.3 to -5.7 percent smaller *Gm* cankers while the eastern provenances had +5.5 percent to +5.8 percent larger *Gm* cankers. The center provenance had cankers midway between both western and eastern provenances (+0.3 percent). The improved walnut families, selected for increased growth and timber quality, had the most variation and as a group produced the largest cankers +6.8 percent.

First year survival was poorest for both the SW provenance and the Arkansas CG plot. HTI families survived the best in all 3 CG plots and there was no significant plot × provenance effect. Three year height growth of the provenances in the CG plots shows that the selected HTI walnut outgrew all wild provenances in Indiana, growing nearly 70 percent taller than wild CTR families.

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We had difficulties keeping deer out of the MI CG plot but were successful at eliminating deer browse in AR and IN. Thus, meaningful growth differences among the CG plots is not possible yet.

Previous studies have demonstrated variation among black walnut genotypes by this type of screening which suggests that black walnut has co-evolved with *Gm* and hence variation in resistance exists. Our results suggest that western black walnut possesses more resistance than eastern black walnut. Ranking families by State show NC, PA, and TN families produced the largest *Gm* cankers and those States were the first three where TCD was found in the East after 2010. Whether or not this is a coincidence will require further study. Finally, black walnut selected for faster growth may unwittingly reduce resistance to TCD and should be addressed by improvement programs.