A MEDIUM THROUGHPUT GREENHOUSE PHENOTYPING ASSAY OF *POPULUS* SPP. FOR SEPTORIA CANKER RESISTANCE

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Poplar trees are increasingly important for fiber production and as a potential feedstock for bioenergy. Septoria leaf spot and stem canker, two common diseases of hybrid poplar caused by the fungus, Septoria musiva, have limited the sustainability of commercial poplar plantations. In the north central region of the United States stem cankers have the greatest impact on hybrid poplar production as cankers weaken stems, increasing the risk of wind breakage. The best strategy for minimizing the impact of S. musiva is to plant resistant genotypes. Screening for disease resistance is challenging in terms of time and space requirements. A study was conducted to develop an increased throughput assay for greenhouse phenotyping of Septoria canker resistance in Populus spp. and their hybrids. To induce canker development a spore suspension spray of 1 x 10^6 conidia per ml was applied to the stem of each tree and incubated for 48 h in black plastic bags (incubation chambers). In the first trial the variation among incubation chambers was tested by placing 25 genotypes of hybrid poplar in each of 10 incubation chambers. The results indicated no significant differences among incubation chambers ($P = 0.1509$) whereas significant differences among genotypes ($P < 0.0001$) were detected. In the second trial we reduced the number of incubation chambers per genotype ($n = 5$) and increased the number of genotypes ($n = 59$) and were still able to detect significant differences among genotypes ($P < 0.0001$). In the third trial we increased the number of genotypes a second time ($n = 92$) and were able to detect significant differences between genotypes ($P = 0.0012$). The ability to screen large numbers of host genotypes for resistance to Septoria canker will facilitate QTL and association mapping of resistance loci in hybrid poplar.