

PITCH CANKER DISEASE AS A MODEL TO DISCOVER BIOLOGICAL DRIVERS OF PITCH CANKER DISEASE IN A CHANGING CLIMATE

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Natural and agricultural ecosystems are affected by climate change through increased temperature, humidity, and unusual weather patterns. They are increasingly threatened by invasions by non-native pests and pathogens. The fungus *Fusarium circinatum* causes pitch canker disease in several pine species, leading to high economic losses in the timber industry. Favored by high temperatures and humidity, future outbreaks may become more frequent under predicted changes in environmental conditions over the next 50-100 years. A better understanding of *F. circinatum* biology is needed to inform predictions of which pathogen variants would likely cause outbreaks in future climate settings. We evaluated growth, spore production and germination among *F. circinatum* isolates cultured at various temperatures (25, 28, and 31°C). Results show significant temperature effects ($p < 0.05$) in mycelium growth and sporulation among isolates.

Disease screening experiments were performed at the USDA Resistance Screening Center (RSC) in Asheville, NC. Eight different isolates from Florida and Georgia, including those used for RSC routine screening, were tested on one resistant and two susceptible hosts. Significant differences among isolates were observed, suggesting differential host response to the isolates tested. Some of those isolates were even more virulent than those routinely used at the RSC. Incorporating these new isolates in the RSC screening protocols would aid in the selection and breeding of pitch canker-resistant material.

We also implemented spore trapping experiments in three north-Florida sites to survey spore release throughout the spring and summer of 2016, and to test if weather events trigger increased spore discharge. Though spore trapping experiments need to be followed across several growth seasons, we present preliminary trends on spore release in the environment. These experiments will be repeated throughout the growing season of 2017 to validate our results. The product of these findings will contribute as a baseline for future research on fungal diversity, spatial distribution patterns and disease prediction, aimed at mitigating adverse effects of climate change on forest health.

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