

Determining the Basis for Emerald Ash Borer Resistance in Asian Ash

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Goals:

The objectives of this study are to compare metabolomic and transcriptomic profiles of North American and Asian ash species in order to determine what makes the Asian ash species resistant to emerald ash borer, while leaving the North American species susceptible.

Statement of Problem:

At present, North American ash species (genus *Fraxinus*) are under attack by emerald ash borer (*Agrilus planipennis* Fairmaire; Coleoptera: Buprestidae), an aggressive invasive species of insect native to eastern Asia. Interestingly, native Asian ash species are comparatively resistant to this phloem-feeding insect. Most researchers currently working on emerald ash borer are focused on improving detection, monitoring, biological control, and eradication methods in an attempt to protect our population of North American ashes against the advancing infestation front. To date, however, little work has been done to determine why our North American ash species are so markedly different from the Asian ash species, in terms of susceptibility to emerald ash borer. We must determine if the difference in resistance level between the North American and Asian ash species is due to radically different metabolites produced by one species but not by another. This is vital information if we have any intention of saving our North American ashes from otherwise certain annihilation (and the subsequent detrimental effect on the hardwood industry).

Current Activities:

This research project is being undertaken using two main approaches. The first, transcriptomic analysis, will involve characterizing the ash transcriptome (set of all transcripts, or RNAs, in an organism at a given time), as well as making an ash microarray chip and having ash ESTs sequenced—two tools that do not currently exist for ash trees. This is the current focus of the project. The transcriptomic work outlined here is imperative, as an ash microarray chip and ash EST sequences will be useful for research on a much wider scale than only within the scope of this project.

Metabolomic analysis is the other approach we are taking to this project. Studying the ash metabolome will allow us to identify metabolites that play an important role in providing ash trees with resistance to emerald ash borer. This knowledge will be useful in the future, for example, for engineering ash trees with elevated resistance to emerald ash borer.

Finally, we plan to integrate the data we generate on the transcriptome and metabolome levels. Characterization of the transcriptomic and metabolomic profiles of ash trees under attack by emerald ash borer will provide us with a key tool for identifying infested trees prior to the appearance of symptoms (not generally seen until one to three years after infestation); this will greatly aid efforts to stem the spread of emerald ash borer.