GENETICS AND BIOCHEMICAL VARIATION OF U.S. *AILANTHUS ALTISSIMA* POPULATIONS: A PRELIMINARY DISUCUSSION OF A RESEARCH PLAN

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Abstract

Ailanthus altissima (tree-of-heaven, TOH) is an increasing component of NE forests. A member of the tropical family Simaroubaceae, TOH was first imported from China in the late 1700s and has since expanded to most of the lower 48 states (Hu 1979). Although TOH is considered an urban weed, it is appearing with increasing frequency in native forests where it may interfere with native tree regeneration. Greer has documented TOH in small and large gaps and along service roads and skid rows in a near urban forest (Kanawha State Forest) in West Virginia; the largest individuals occurring in closed canopy in skid rows. Several important timber tree species (e.g., oaks and walnut) also favor disturbed habitats, or rely on some form of disturbance to complete their life cycle. Thus, TOH may compete for similar regeneration spaces in forests that are highly fragmented, especially those located near populated areas. Oaks already suffer from regeneration failure in forests that have a suppressed disturbance regime (Parker et al. 1985, Aldrich et al. submitted). As TOH continues to invade North American forests (Huebner 2003), there are reasons to anticipate increasingly detrimental effects on native forests and commercially important timber species.

The novel chemistry of TOH is thought to contribute to its invasiveness. Published research indicates a toxic effect against other plants (allelopathy), rodents, and microbes, all of which could impact forest regeneration (Heisey 1990, 1996). Published works suggest that quassinoid triterpenes, primarily ailanthone, are responsible for much of the toxicity of this species (Kubota et al. 1996, De Feo et al. 2003, Okunade et al. 2003). A study by Greer and colleagues found reduced understory biodiversity beneath TOH canopies compared to native canopies. A series of germination experiments by Greer demonstrated that TOH toxicity, in leaves and surrounding soil, is greater on a per gram basis in juveniles (2 yrs old or less) than in older age-classes and that minor injury to TOH induces an increase in phytotoxin production.

Little is known about naturalized genetic or biochemical variation in U.S. populations of TOH (Feret 1985, Feret and Bryant 1974, Feret et al. 1974). There has been considerable pharmaceutical prospecting in *Ailanthus* in search of cures for AIDS, cancer, and a variety of other ailments (Ogura et al. 1997, Chang and Woo 2003). Despite the attention given to *A. altissima* and ailanthone, there are no studies that have attempted to document regional variation in ailanthone. Many invasive plants experience an “ecological release” upon entering new habitat because their natural enemy herbivores are left behind. If the post-introduction range expansion has been rapid, as appears to be the case, the species may be lacking in genetic and biochemical variation, especially if the introductions involved relatively few founding events. Moreover, reductions in herbivore pressures might relax the production of a metabolically costly toxin, yielding uniformly low levels of ailanthone outside of China. Alternatively, *A. altissima* may be both genetically and biochemically variable. The species is a polyploidy with 2N=80 and changes in chromosome number may be fueling an adaptive radiation into its new habitat. Adaptations to local environments might involve development of ecotypes that vary in toxicity and invasiveness. Genetic variation in TOH might differ significantly between Eastern and Western sides of the continental divide. TOH colonization of the Eastern U.S. may have resulted from very few, perhaps only one, founding event. If so, much of TOH’s genetic variation may have been purged, producing a problematic though genetically benign species in the Eastern U.S. Alternatively, many founding events are believed to have occurred in the Western U.S. from Chinese immigrants, establishing populations with greater genetic diversity.

We are collecting seeds from 10-12 sites across the U.S. along an East-West transect, with focused sampling from WV and the midwest. We will use molecular genetic methods to characterize patterns of diversity in the chloroplast genome, and cytogenetic methods to characterize karyotypic variation in the nuclear genome across the range. We also will quantify variation in levels of toxic compounds through chemical assays and bioassays on plants, microbes and rodents. Some rodent species are known to eat TOH whereas others avoid it (Ostfeld et al. 1997), and such a difference might influence patterns of seedling establishment in forests.

Our research should prove useful as a foundation in basic TOH biology that may aid efforts to manage and control its spread. Knowledge of the underlying patterns of variation will allow identification of diversity hotspots that could be targeted for elimination. Patterns of genetic variation also can be used to evaluate past episodes of migration and future threats of spread and gene pool change.

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