Determining the genetic underpinnings of phytochemistry and associated arthropod communities in aspen

Hilary Bultman¹,², Liza Holeski³, Pär Ingvarsson⁴, and Richard L. Lindroth²

¹Departments of Zoology and ²Entomology, University of Wisconsin-Madison; ³Department of Biological Sciences, Northern Arizona University; ⁴Department of Ecology and Environmental Science, Umeå Plant Science Center

Abstract

Community genetics research has shown that different genotypes of plants harbor analogously different arthropod communities [1]. While this pattern has been revealed in multiple plant systems, the genes underlying the pattern have not been identified. To address this void, we have established a genetic mapping population ("WisAsp") of 515 trembling aspen (Populus tremuloides) replicated genotypes to identify the genes associated with phenotypic traits (particularly secondary metabolites) that influence arthropods and arthropod community composition. Thus far, we have found substantial phenotypic variation in both condensed tannins and phenolic glycosides, two major groups of plant secondary compounds in Populus that are known to influence insects [1]. We have also found considerable variation in arthropod community composition across aspen genotypes at a nearby common garden with a subset of nine genotypes from WisAsp (PerMANOVA F = 2.02, P < 0.002). Foliar condensed tannin and phenolic glycoside levels helped explain the variation in arthropod communities (PerMANOVA F = 2.22, P < 0.002; F = 1.87, P = 0.069, respectively), indicating that plant secondary metabolites can indeed serve to structure arthropod communities (PerMANOVA F = 2.22, P < 0.002). Foliar condensed tannin and salicortin levels, which feed back to plant genetics through selection (and of the importance of secondary metabolites in structuring arthropod communities.

Key Results

1. We have found substantial variation in key anti-herbivore phytochemicals (Fig. 2) across genets in the WisAsp common garden (Fig. 3 A-C).
   - Condensed tannins vary 6-fold (foliar % dry wt)
   - Salicortin varies 13-fold (foliar % dry wt)
   - Tremulacin varies 25-fold (foliar % dry wt)

2. In a nearby common garden (with a subset of nine genets from WisAsp), we have found substantial variation in arthropod community composition across genets (Fig. 3 D; PerMANOVA F = 2.02, P < 0.002).

3. A significant portion of the variation in arthropod community composition across genets was explained by variation in both condensed tannins and tremulacin (PerMANOVA F = 2.22, P < 0.004; F = 1.87, P = 0.069, respectively), although only a small portion (1-2%) of community variation was explained by each phytochemical.

Future Directions

1. We will use association mapping with 40,000 SNP markers to identify candidate genes that underlie variation in condensed tannin, tremulacin, and salicortin levels as well as variation in foliar insect herbivore communities.
   - We will investigate whether candidate genes underlying insect herbivore community composition and phytochemical composition overlap, which would indicate the importance of secondary metabolites in structuring arthropod communities.
   - We will compare associated genetic regions to the Populus trichocarpa genome [3] to further elucidate their gene function.

2. This research will facilitate future study of insects as agents of selection in plant populations (i.e., plant genetics influence insect community composition, thus herbivory levels, which feed back to plant genetics through selection) and of the genetic bases of plant-insect interactions.

Methods

1. The WisAsp Common Garden was established in 2010 with four replicate blocks with randomized genotypes (N = 515) collected from throughout Wisconsin (Fig. 1).

2. Leaves were collected for phytochemical analyses
   - Condensed tannins + HCl-butanol spectrophotometric method [2]
   - Phenolic glycosides + ultra high pressure liquid chromatography (UHPLC) with purified reference standards

3. Visual timed insect community surveys were conducted both in July and August 2013 at a nearby common garden with a subset of WisAsp genotypes (N = 9).
   - All specimens were identified to species or morphospecies
   - Analyses → rare species were deleted for analyses and the Bray-Curtis community distance was used for PerMANOVA calculations

Acknowledgments: NSF (DGE-1256259; DEB-0841609), McIntire-Stennis (WIS01651). We would like to thank K. Keelover-Ring, N. Rubert-Nason, L. Palukis, R. Hughes, A. Stylpis, S. Lawrence, T. Jemison, and M. Landes for field and lab assistance.