

## **Ecosystem consequences of feedbacks between herbivore guilds and plant genetic variation**

Rapid rates of species extinction and homogenization of the world's biota have initiated a focus in ecology on how biodiversity mediates ecosystem processes<sup>1</sup>. To date, much of this research has focused on the role of primary producer diversity<sup>2</sup>, though diversity in other trophic groups is also likely to be important<sup>3</sup>. Recent studies have shown that particular herbivore feeding guilds can have dramatic consequences for ecosystems by reducing primary productivity and altering decomposition rates<sup>4</sup>. Even though herbivores can drive ecosystem processes, no studies have examined the effects of multiple, potentially interacting, herbivore guilds on terrestrial ecosystems. Understanding these interactions is critical because the effects of herbivores, as in other trophic levels<sup>3</sup>, can be non-additive<sup>5</sup>.

Genetic variation within a plant's species can alter ecosystem processes either directly<sup>6</sup> or indirectly through its effects on resident insect communities<sup>7</sup>. In oaks, intraspecific genetic diversity mediates litter chemistry and decomposition<sup>8</sup>. In cottonwoods, intraspecific genetic variation can account for nearly 60% of the variation in arthropod diversity<sup>9</sup>. One potential mechanism by which genetic diversity in plants may indirectly influence ecosystem processes is through its effects on dominant herbivores<sup>9</sup>. However, most of this work has focused on only individual herbivore species. My research extends this hypothesis by examining how genetic variation in hostplants may mediate the interactive effects of multiple herbivore guilds on ecosystems by driving the structure of herbivore communities.

My dissertation research will rigorously test two novel and inter-related hypotheses:

***Hypothesis 1:*** Diversity of insect herbivore guilds increases rates of nutrient cycling and decomposition by altering primary productivity and plant architecture.

***Hypothesis 2:*** Population genetic diversity of hostplants alters herbivore guild diversity and mediates herbivore effects on ecosystem processes.

**Methods:** My fieldwork will be conducted over a 3-year period in an old-field ecosystem in east Tennessee. I will focus on the effects of herbivorous insects on *Solidago canadensis* (tall goldenrod). Three herbivore species, representing three different guilds, dominate both the abundance and biomass of the well-known community of ~130 arthropod species that occur on *S. canadensis*: a leaf-chewing beetle (*Trirhabda* sp.), a xylem-tapping spittlebug (*Philaenus spumarius*), and a bunch-galling midge (*Rhopalomyia solidaginis*)<sup>10</sup>. Each of these species is individually known to alter *Solidago* biomass<sup>11</sup>. The bunch galls alone attack an average 50% of all *Solidago* stems at my field site (Crutsinger unpublished data 2004).

*Solidago* genotype can determine the preference, performance, and distribution of its insect herbivore species<sup>12</sup>, including dominant herbivores that can affect other insects. **Because *Solidago* is well studied, easily manipulated and its genotype is known to influence susceptibility to herbivory, this is an ideal system in which to examine how diversity of herbivorous insect guilds and plant genotypes mediate ecosystem processes.**

***Hypothesis 1:*** To test how diversity of herbivore guilds influences ecosystem processes, I will establish a field experiment with goldenrods planted in a field array. Each plant will be subjected randomly to one of 8 treatment combinations: no insects (to serve as a control), galls only, leaf beetles only, spittlebugs only, galls + spittlebugs, galls + leaf beetles, spittlebugs + leaf beetles, and galls + spittlebugs + leaf beetles. Each treatment will have 8 replicates. Table 1 provides a brief summary of the methods I will use to test how diversity in herbivore guilds directly and indirectly affects ecosystem processes. I will analyze the results using an MANOVA, followed by univariate ANOVA's as necessary.

*Hypothesis 2:* To test how genetic variation within plant populations mediates herbivore effects on ecosystem processes, I will establish a common garden experiment consisting of 10 different goldenrod

| TABLE 1                |                         |                                       |                            |
|------------------------|-------------------------|---------------------------------------|----------------------------|
| 1<br>Ecosystem process | 2<br>Response variables | 3<br>Methods                          | 4<br>Measurement Intervals |
| NPP                    | Root production         | In-growth bags                        | Every two months           |
|                        | Plant biomass           | Harvesting                            | End of growing season      |
| Microclimate           | Leaf Area               | PAR sensors                           | Monthly                    |
|                        | Soil Moisture           | TDR probes                            | Weekly                     |
|                        | Soil temperature        | Hobo temp. sensors                    | Hourly                     |
| Nutrient cycling       | Nitrogen availability   | Nitrogen resin bags, C:N autoanalyzer | Every two months           |
|                        | Litter production       | Litter traps                          | Monthly                    |
| Decomposition          | Decomposition rates     | Decomp. bags                          | Six months                 |

genotypes planted from field-collected rhizomes following the techniques of Anderson *et al.* (1989)<sup>14</sup>. Genotypes will be selected based on the observed density of galls in the late fall with resistant genotypes (< 10% stems galled) and susceptible genotypes (>50% stems galled). I will establish 24 1 m × 1 m field plots of 3 resistance genotypes (n=8), 3 susceptible genotypes (n=8), and mixed plots of all six genotypes (n=8). I will record herbivore colonization of common garden plots and measure ecosystem processes (see table 1). I will then repeat the factorial experiment from *Hypothesis 1* (see above), but also add plant genotype as an additional treatment for a total of 12 treatments with 5 replicates. I will analyze the results using an MANOVA.

### **Importance of this research**

Though plant species diversity and composition are potential drivers of ecosystem processes, the importance of herbivore guild diversity to ecosystem processes has been overlooked<sup>2</sup>. Chronic herbivory by various insect guilds can cause large economic losses in forest and grassland ecosystems, and particular species can affect community composition and structure<sup>15,16</sup>. If diversity of herbivore guilds or plant genetic diversity can mediate these effects, whether positively or negatively, my results will have large economical and ecological implications. Because tall goldenrod is a dominant plant throughout old agricultural fields and meadows in North America and an invasive species in Europe<sup>17</sup>, my research will have implications across many landscapes. In conclusion, my research will also greatly increase our general understanding of the feedbacks among species to communities and ecosystem processes.

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