Field Methods

Site information and timing-

The experiment took place at the 334-hectare Great Hollow Nature Preserve in New Fairfield (Fairfield Co., Connecticut, USA) in April through July 2021. Our sampling locations include wet slopes and riparian forests along Quaker Brook which runs through the center of the property. Overstory tree composition is primarily *Acer saccarum, Betula lenta*, *Fagus grandifolia, Liriodendron tulipfera,* and *Quercus* spp. The forest understory at sections of this habitat is frequently dominated by invasive shrubs including *Berberis thunbergii, Lonicerna spp, Eunonymous alatus, Eleagnus umbellata* and *Rosa multiflora.* Native understory shrubs and understory trees include A*cer pennsylvanicum,* *Amelanchier spp., Carpinus caroliniana, Hamamelis virginiana, Lindera benzoin,* and *Viburnum spp.*

Bird exclusion setup-

Invertebrate sampling-

Lab Methods

Insect processing –

All invertebrates collected in the field were transferred immediately to 7 × 3cm plastic vials or 16 × 8cm plastic zip-top bags and preserved in a –18° C lab freezer. Afterwards, specimens collected on entire experimental branches were weighed (wet mass) on a 10^-4 g microbalance. All invertebrates were identified to taxonomic order when possible (including both Arthropoda and Mollusca). Common species (those observed > 25 times) were identified to family or superfamily when possible, and all insects in the orders Lepidoptera, Hemiptera, Hymenoptera were identified to family. True spiders (Araneae) and Opiliones were identified to family as well. Once identifications were complete, all taxonomic groups were weighed for wet mass for each individual branch sample and placed into 0.6mL and 2mL Eppendorf tubes kept in the lab freezer for later processing.

For species richness estimates, all invertebrates were classified using a morphospecies approach, at the per-branch level (modified from Clark and Seewagen, 2019). Apparently different species in an individual order or family were given numbered designations (Coleoptera-1, Coleoptera-2, or Geometridae-1, Geometridae-2, etc). All invertebrate sorting and taxonomic identification was completed from June 2021 to August 2021. Finally, for functional group analysis (e.g. major feeding guilds), we grouped all non-predatory true bugs as sucking herbivores; lepidoptera and beetles (list the families) as chewing herbivores; spiders, ants (Formicidae), and centipedes as carnivores.

Nutritional content analysis -

Nutritional content analysis required a minimum mass of 0.5g total dry biomass to complete a single extraction. Since the typical individual branch sample had 0.05 to 0.1 of wet mass alone, two strategies were employed to reach the threshold of 0.5g dry biomass. First, samples were pooled among branches and experimental replicates that were located in proximity in the field (sampled on the same days and places within the field site), but species level replication was preserved. For example, all invertebrates collected on the four *F. grandifolia* trees sampled on May 24 2021 were combined into a single sample. Second, each tree species collected was often surrounded by conspecifics, providing an opportunity for additional ‘control branches’ (unmanipulated trees) that provide similar arthropod communities at the same time points. Consequently, during the last two weeks of June (June 18 to June 30). Only branches of similar height and size to control branches in the main experiment were sampled for this supplementary insect biomass, and these branches were always sampled on the same day as the main experiment.