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THE EFFECT OF DEER BROWSE ON *ACHYRANTHES JAPONICA*

by

Nicholas Richard Seaton

B.S., Southern Illinois University, 2013

A Thesis

Submitted in Partial Fulfillment of the Requirements for the
Master of Science Degree

School of Biological Sciences
in the Graduate School
Southern Illinois University Carbondale
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THESIS APPROVAL

THE EFFECT OF DEER BROWSE ON *ACHYRANTHES JAPONICA*

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Nicholas Richard Seaton

A Thesis Submitted in Partial
Fulfillment of the Requirements
for the Degree of
Master of Science
in the field of Plant Biology

Approved by:

Dr. David Gibson, Chair

Dr. Loretta Battaglia

Dr. Eric Schauber

Graduate School
Southern Illinois University Carbondale
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AN ABSTRACT OF THE THESIS OF

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TITLE: THE EFFECT OF DEER BROWSE ON *ACHYRANTHES JAPONICA*

MAJOR PROFESSOR: Dr. David Gibson

Plants respond in many ways to damage. These responses vary between sites depending on the severity and duration of the incident. One common form of damage in the forest understory is herbivory or browse. White tailed deer (*Odocoileus virginianus*) have been observed to change the dominant species of forests by selectively browsing palatable species in the understory. These changes in species dominance can lead to unwanted consequences, sometimes resulting in a proliferation of weedy or invasive plants or a reduction in performance and competitive abilities based on morphological traits. Understanding the changes that occur to undesirable species after deer browse can help land managers in their prioritization of sites for land management and understand the driving forces behind a species' success or failure.

Using deer exclosure plots, this study looks at the effects of white-tailed deer on *Achyranthes japonica*, an herbaceous invasive species in the Ohio River floodplain of Illinois and surrounding states. White tailed deer have been observed to browse *A. japonica* throughout the invaders range, but little is known about the plant's response. Deer browse data were collected in the summer of 2018 from May to August. Estimated deer densities among six study sites ranged from 8 to 22 deer per km². Plants that were browsed during the growing season were morphologically different to those that were not browsed. Browsed plants were 11.5 ± 0.1 cm shorter ($F_{1,218}=11.658$; $p<0.001$) on average and produced 0.33 ± 0.09 fewer nodes ($F_{1,216}=4.045$; $p<0.05$). Browsed plants also produced 2.7 ± 0.32 fewer flowering spikes and were

similar in length to those of un-browsed plants. Deer browse reduced the value of some measured variables at some but not all sites but had little to no impact on the length of browsed *Achyranthes japonica* flowering spikes.

These morphological differences showed significant variation between sites. Floristic Quality Indices of the herbaceous plant communities ($\bar{Y} = 3.5$) ranged from 3.2 to 3.9 among study sites. This study shows that site conditions can impact the response of *A. japonica* growth as it continues to invade across its current introduced range and that the species is adaptive and grows along-side other similar weedy species such as *Microstegium vimineum* and *Parthenocissus quinquefolia*.

Keywords: *Achyranthes japonica*, *Odocoileus virginianus*, herbivory, browse, deer density, site quality

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CHAPTER 1

INTRODUCTION

WHITE TAILED DEER AND HERBIVORY RESPONSE

White tailed deer (*Odocoileus virginianus*) henceforth deer, are the most abundant ruminant ungulates in North America (Rooney, 2001). Deer populations across North America have fluctuated over time with pre-European (1500-1800) numbers estimated at approximately 24-33 million (McCabe & McCabe, 1997). Unregulated commercial hunting reduced deer populations to near extinction in the early 20th century. Stricter regulations, specifically the Lacey Act were later enforced to prosecute those that practiced unsustainable hunting and moved deer from state to state (Hewitt, 2011). Three fluctuations in deer populations occurred from 1500 to 1900 resulting in deer numbers nearly cut in half to approximately 15 million deer (Dostaler et al., 2011 ; McCabe & McCabe, 1997). Timber harvesting and silvicultural practices benefiting deer indirectly led to damage on agricultural crops from browsing and the reduction of timber stand quality by excessive over-browsing of desirable plants. As a result, land management has shifted from land manipulation for the benefit of deer, to population management of deer herds (Côté, Rooney, Tremblay, Dussault, & Waller, 2004). The current deer population levels in the United States are estimated at approximately 28.5 million, with approximately one third of the population, or about 10 million deer, in the Midwest (Hewitt, 2011).

Deer are generalist consumers and are considered "keystone herbivores", altering plant populations as they travel (Waller & Alverson, 1997). Being a generalist herbivore does not necessarily mean that preference is high for all plant species in the forest understory. Individual

deer are more prone to eat foods that were consumed early in their lives (Provenza, 1995) choosing larger plants over smaller ones (Augustine & Frelich, 1998).

As deer browse, they choose desirable species based off of their sense of smell, which can reveal potential plant toxins that may upset digestion (Averill, Mortensen, Smithwick, & Post, 2016). This type of selection is known as Euphagia (Provenza, 1995). In a cafeteria-style study conducted on captive deer in Quebec, the primary determinant of browse was the crude protein content found within the eight plants chosen for the study (Dostaler, Ouellet, Therrien, & Côté, 2011). Other studies have noted phylogenetic similarities between both browsed and unbrowsed plant species, indicating similar palatable qualities or flavors within closely related species (Agrawal, 2000).

Plants can respond to damage in numerous ways. The severity and duration of an incident can have lasting effects (Doak, 1992) . Plants that are browsed may display signs of either tolerance or resistance to the damage that has occurred (Augustine & McNaughton, 1998; Augustine & Frelich, 1998). At risk native plant populations that have not adapted to increased browse can be reduced in size by up to fifty percent (Augustine & Frelich, 1998). Previous studies have shown the ability of deer suppress woody species and alter species dominance (Bressette, Beck, & Beauchamp, 2012; Habeck & Schultz, 2015; Peebles-Spencer, Haffey, & Gorchov, 2018)

A review comparing thirteen deer exclosure studies found that overabundant populations had a negative effect on woodland structure reducing richness and diversity in both the tree and shrub layer and altering viability and dispersal rates of some species (Gill & Beardall, 2001). These measurable changes in community composition have been reported at densities as low as 4 deer/km² (William S. Alverson, 1988) However, some plant communities have higher or lower

deer browse densities where damage may be noticed depending on their tolerance to browse (Côté et al., 2004). A type of mutualism referred to as overcompensation is thought to be a response mechanism by plants resulting in the increased fitness of browsed individuals (Agrawal, 2000). A review on the impacts of deer overabundance included recommendations to improve the quality of research for future studies. Previous studies have failed to determine the local deer densities at their study sites, making it difficult to understand plant damage by herbivores being studied because the severity of browse is hard to determine at such a small scale (Côté et al., 2004; Habeck & Schultz, 2015). In addition, gradients of deer densities across multiple forest types will help to improve research (Habeck & Schultz, 2015). The size of a plant population can also determine the likelihood of long-term damage along with local browsing pressure (Bressette et al., 2012; Doak, 1992). In some cases, unpalatable species can have an advantage over palatable ones (Heckel, Bourg, McShea, & Kalisz, 2010; Knight, Dunn, Smith, Davis, & Kalisz, 2009). A study in New Jersey and Pennsylvania reported that the avoidance of deer increased the percent cover of three invasive species (Eschtruth & Battles, 2009). The increased cover was due to the preference of native species over less palatable invaders. Unpalatable native species however may still be at risk of trampling by deer as they move through an area (Heckel, Bourg, McShea, & Kalisz, 2010).

INVASIVE SPECIES

It is estimated that invasive species cause 120 billion dollars in damage annually in the United States. There are an approximated 25,000 nonindigenous species in the U.S. that have established and can cause various degrees of damage and instability (Pimentel, Zuniga, & Morrison, 2005). The ecological damage of invasion can be significant and have lasting effects.

The homogenization of species across the globe from invasions will result in species extinctions and a significant decrease in diversity (Rosenzweig, 2001).

The field of invasion ecology was formed after the publication of Elton's book on invasive species in 1958. Many terms have been used to describe the status of a foreign species. This plethora of terms may lead to confusion due to the use of undefined terminology and the use of unregulated synonyms. The term invasive indicates that a plant or animal is non-indigenous and is currently expanding within its introduced range across multiple habitats. Exotic species that are not termed invasive are non-native but have stayed confined to the artificial habitats that they occupy and do not invade natural ecosystems. In both cases these species may have been accidentally, or intentionally introduced (PySek, 1995).

Determining the driving mechanism of invasion is difficult. The enemy release hypothesis states that if a non-native plant is able to escape its predators it can establish itself in a new range uninhibited by any of the common processes affecting native communities (Keane & Crawley, 2002). Other ecologists have proposed the idea that invaders become successful through the use of “novel weapons” (Callaway & Ridenour, 2004) which may allow non-native species to outcompete native ones. Multiple paradigms have been accepted for biological invasions (Richardson, Allsopp, D'Antonio, Milton, & Rejmánek, 2000; Williamson & Fitter, 1996). Within these paradigms there are built in barriers or checkpoints that invaders must overcome if they are to succeed within a new territory. The barriers are, in their simplest form, introduction, establishment and propagation.

If established, and allowed to proliferate, unattended invaders can significantly alter the forest understory (Gilliam, 2007). The time between introduction to invasion referred to as “lag time”, varies from species to species (Ellstrand & Shirenbeck, 2004). It may take years for a

species to begin to show signs of invasion, as the population has not grown to levels that impede ecological function. Invasive species offer unique experimentation scenarios in which interactions are occurring for the first time in their histories. A study testing the enemy release hypothesis for invasiveness found that exotics experienced less insect damage than native congeners (Carpenter & Cappuccino, 2005). A meta-analysis also found that invaders were larger and more reproductively viable under lower levels of deer herbivory in their introduced ranges (Hawkes, 2007).

STUDY SPECIES

Achyranthes japonica (miq.) Nakai, (Amaranthaceae) commonly known as Japanese Chaff Flower is of growing concern throughout its introduced range in North America. Native to eastern Asia, it was first discovered in 1981 in Martin County, KY along the banks of the Tug Fork River within the Big Sandy watershed (Medley, Bryan, MacGregor, & Thieret, 1985) and has since expanded its range throughout the Ohio River flood plain (Evans & Taylor, 2011; Vincent & Cusick, 1998) and more recently within the Mississippi River flood plain. Though found in Kentucky, *Achyranthes japonica* was not recorded in Illinois as of 1981 (Henry & Scott, 1981). First identification of the species was at Chestnut Hills Nature Preserve off the banks of the Ohio river in the early-2000's. *Achyranthes japonica* spread approximately 560 km in fifteen years from its original source location in Kentucky after its initial discovery (Evans & Taylor, 2011). It is thought that seeds were dispersed by railroad cars and deposited in the Tug Fork River, forming the original source population (Medley et al., 1985).

The form that Medley discovered is believed to be *Achyranthes japonica* var. *hachijoensis*, which is the maritime variety. *Achyranthes japonica* is a perennial, herbaceous species that can grow 1.5-3 meters tall (Evans, 2010; Medley et al., 1985; Schwartz, Gibson, &

Young, 2016a), Leaves are simple with entire margins, acuminate tips and are oppositely arranged. The nodes have a red coloration and plants produce small flowers in spikes. Each flower produces a seed with a subulate spinose bracteole, which allows it to attach to fur and clothing (Medley et al., 1985).

Achyranthes japonica has multiple interactions with local fauna. Modes of seed dispersal include native animals, pets, humans and water that pass through infestations and carry seeds to new locations (Evans & Taylor, 2011; Medley et al., 1985; Vincent & Cusick, 1998). A study in Korea found that seeds were carried on bird feathers from one location to another suggesting epizoochory as an important dispersal mechanism (Choi, Nam, & Chae, 2010). In one extreme case on a Pacific island, a single stem of *A. japonica* had killed fourteen storm petrels by entanglement (Arcilla, Choi, Ozaki, & Lepczyk, 2015). Within its native range, Macaques have been noted to consume *A. japonica* leaves as a food source (Huffman & Andrew, 2012). Another study reported that a pathogenic fungus, *Cercospora achyranthis*, caused decreased growth within the *Achyranthes* genus (Groenewald, Groenewald, & Crous, 2005; J. Z. Groenewald et al., 2013). A species of Lepidoptera, *Lasioptera achyranthii*, produces galls on *A. japonica* plants and feeds on leaves after emergence (Yamazaki & Sugiura, 2003).

A study conducted in Southern Illinois comparing the competitive abilities of four species within the Amaranthaceae family including *A. japonica*, *Amaranthus palmeri*, *Amaranthus tuberculatus* and the state threatened *Iresine rhizomatosa* found that the overall invasive tendencies of a species and not their individual life histories were the determining factors of competition (Schwartz, 2015). In the same study, *A. japonica* performed similarly to two agricultural invasives, *Amaranthus palmeri* and *Amaranthus tuberculatus*, causing concern for its spread into crop fields and the potential loss of crop yield (Schwartz, 2015). A projection model

used to predict future spread indicated that *A. japonica* had high fecundity and showed positive population growth whereas the endangered *Iresine rhizomatosa* displayed negative population growth and was projected to continue its decline (Schwartz, Gibson, & Young, 2015, 2016b). The functional trait measured, e.g., height, from the source population of *A. japonica* were greatest when compared to areas that were infested as the plant has moved westward (Neal, 2018).

OBJECTIVE OF STUDY

The objective of this study was to determine the effects of deer browse on *Achyranthes japonica*. Previous research on this species have noted deer browse as a form of damage on populations of *A. japonica* but have not specifically studied their effects (Smith, 2013).

Understanding the relationship new invaders have with local fauna and the disturbance of animal browsing can help assist in their management. Deer densities may have positive or negative effects on populations throughout southern Illinois. Deer could either reduce *A. japonica* growth or aid in its proliferation throughout the region. Site-specific characteristics such as soil and moisture may also act to alter the response of browsed individuals as well.

PREDICTIONS AND ANTICIPATED RESULTS

It is anticipated that there will be a response from deer herbivory on *Achyranthes* plants throughout the growing season. Plants that are browsed are expected to have a decrease in fecundity. *Achyranthes japonica* density and deer densities may be correlated. Sites that have the highest deer densities are also expected to have *A. japonica* plants that are browsed more frequently. Having multiple sites across representative forest types will better identify the changes that occur to the species across the region, as *Achyranthes japonica* may perform better

in one forested type over another after being browsed as has been observed before (Neal, 2018; Schwartz, 2015; Smith, 2013).

QUESTIONS AND HYPOTHESES

Q₁: What morphological responses occur in *Achyranthes japonica* individuals after deer browsing?

H₁: Browsed *Achyranthes japonica* individuals will be shorter, have decreased fecundity, and display greater degrees of branching.

Q₂: What is the effect of site quality on the response of *Achyranthes japonica* individuals to deer browsing?

H₂: Based off the Floristic Quality Assessment Program (FQA) (Freeman, Masters, and Packard, 2016), higher quality sites will produce larger plants on average than lower quality sites.

Q₃: What is the effect of deer density on browsing preference for native plants compared to *Achyranthes japonica* plants?

H₃: *Achyranthes japonica* plants will be browsed more frequently than native species at higher deer densities.

CHAPTER 2

METHODOLOGY

Six sites were selected for this study based on the presence of *A. japonica* growing on the property in a sufficiently large population to establish twenty 3 x 3-meter plots. Each site was categorized by the natural division that it represented to establish a relationship between site characteristics and the performance of *A. japonica*. Forest categories were determined following previously identified cover types within the Shawnee forest (Olson, 2004). Maps of each property are in the Appendix.

1. Chestnut Hills Nature Preserve IDNR: mesic upland forest 1 - Pope County

Located in Pope County within the Coastal Plain division and the Cretaceous Hills natural division, Chestnut Hills Nature Preserve comprises 86 hectares of protected land characterized by its geology which dates to the Cretaceous period. These formations are home to rare plant and animal communities and previously harbored one of the few populations of American chestnut *Castanea dentata* (Marshall) in Illinois prior to the chestnut blight. The site has a southeastern aspect with highly eroded soils composed of silt loam. The dominant overstory species are red oak *Quercus rubra* (L), beech *Fagus grandifolia* (Ehrh.) and sugar maples *Acer Saccharum* (Marshall). *Achyranthes japonica* is scattered extensively throughout the site. Chestnut Hills NP is occasionally managed with prescribed fire by the IDNR. Previous management to eradicate the population of *A. japonica* included herbicide treatments along the outer boundaries, but no interior work has been completed to eradicate the population to date. A previous study analyzed the *A.japonica* population at Chestnut Hills NP for performance and growth throughout the growing season (Neal, 2018). Schwartz (2016a) found the survivorship and fecundity of *A.japonica* individuals to be variable in a comparative study between two

populations. In the study, *A. japonica* density was 53% greater at Chestnut Hills NP compared to the other site in the study, Limekiln Springs. *A. japonica* plants at Chestnut Hills Nature Preserve had lower fecundity compared to those from other sites.

2. Dixon Springs Agricultural Center: mesic upland forest 2- Pope County

Located in Pope County within the Shawnee Hills division and the lesser Shawnee hills natural division, Dixon Springs Agricultural Center is a large-scale outdoor research facility run and maintained by the University of Illinois. The site, approximately 2,064 hectares, does not display a dominant aspect and is composed of silt loams which are occasionally flooded.

Dominant overstory species include planted white pine, *Pinus strobus* (L.) green ash *Fraxinus pennsylvanica* (Marshall), sugar maple *Acer saccharum* (Marshall), and box elder *Acer negundo* (L.). The *P. strobus* population was planted in 1979 as part of a spacing study with trees planted in rows that differ in spacings. Although it was maintained during the research, further management has not occurred since the early 1990's. The *A. japonica* population is found within this pine planting.

3. Limekiln Springs FWS: wet-mesic floodplain forest 1- Pulaski County

Located in Pulaski County within the coastal plain's division and the bottomlands natural division Limekiln springs is managed by the U.S. Fish and Wildlife Service as part of the 6,070-hectare area known as the Cache River National Wildlife refuge. The bottomland woods do not display a dominant aspect and are composed primarily of silt loams, which occasionally flood. Dominant species include white oak *Quercus alba* (L.), red maple *Acer rubrum* (L.) *Fraxinus* species and *Acer negundo*. *Achyranthes japonica* is scattered throughout the area and is being managed with herbicide on an annual basis.

4. Mallard Road FWS: wet-mesic floodplain forest 2- Pulaski County

Located in Pulaski County within the coastal plain's division and the bottomlands natural division the Mallard road site is managed by the US Fish and Wildlife Service as part of the 6,070-hectare area known as the Cache River National Wildlife Refuge. The site does not have a dominant aspect and is primarily composed of silty clay loams, which occasionally flood.

Dominant species include *Q. alba*, *A. rubrum*, *Fraxinus* species and *A. negundo*. Herbicide has been used in efforts to remove the population of *A. japonica* from the site.

5. Mchutchinson Property: dry-mesic upland forest 1- Jackson County

Located in Jackson County within the Shawnee hills division and the greater Shawnee hills natural division this 16-hectare site is privately owned and managed. The property has a western aspect and is composed primarily of silt loam soils. *Achyranthes japonica* is found scattered throughout the property and no management to date has been conducted to remove the populations. Dominant tree species include *Quercus alba*, *Carya ovata*, and *C. tomentosa* along with *Acer saccharum*, and *Acer negundo*. Personal observations of deer browsing on the stems of *A. japonica* have been confirmed by the landowner.

6. Nawrot Property: dry-mesic-upland forest 2- Union County

Located in northern Union County on the border with Jackson County within the Shawnee hills division and the greater Shawnee hills natural division, this 8-hectare site is privately owned and managed. The property has a dominant western aspect and is composed primarily of silt loam. There are numerous rock outcroppings on the property with dominant species including *Quercus rubra*, *Q. alba* and *Carya ovata* (Miller) and *C. tomentosa* (Lam.) Nutt. A timber harvest occurred approximately ten years ago, and *A. japonica* is scattered throughout in large patches both inside and out of the harvested area. No previous management

to date has been conducted to remove the population, however, plots were placed to ensure that natural plant communities were best represented.

Experimental Design

Plots were flagged prior to the growing season using the previous year's growth to determine where *A. japonica* plants would likely regrow. Ten 3x3m enclosure plots, and ten 3x3m open plots were placed within known populations at each site during the early spring of 2017. Placement was made to ensure that enclosure plots and open plots were not directly adjacent to one another. Treatment assignments were determined using a random number generator. A 15 cm gap was left from the ground to the caging to ensure that small animals including squirrels, rabbits, mice and woodchucks had continued access, but deer, turkey, bobcats and other large animals did not.

There is a height to size relationship with caging and enclosures (VerCauteren, Lavelle, & Hygnstrom, 2006). As the size of the area increases, the height of the fencing should also increase to ensure protection from deer jumping over. Areas less than 5m² can be protected with caging as short as 1m (Hewitt, 2011). During the data collection period there were no reported cases of deer jumping over the established enclosures or browsing any *A. japonica* plants inside the enclosures. Fencing enclosures were made from 14-gauge welded wire fencing that was 1.9 m tall. At each site, the population of *A. japonica* was mapped. Remote sensing data were collected from the center of each plot using ESRI's collector program (ESRI, 2018). After installation of the plots, data were collected three times throughout the growing season between June 1, 2017 and September 30, 2017.

To determine deer densities, distance sampling was used with a transect counting deer pellets throughout the population of *A. japonica* at each site (C. W. Anderson et al., 2013). Pellet

surveys were conducted once throughout the data collection timeframe and computed in the distance package version 0.9.8 (Miller, 2019) in R Studio Version 3.4.3. Using the Floristic Quality Assessment Program (FQA) (Freyman, Masters, & Packard, 2016) average conservation coefficients were measured for each site using data collected from two separate floristic surveys during the growing season. These data were used to determine site quality based on the plants presently growing.

Sampling/Data Collection

Within each plot, the percent cover of *A. japonica* and other plant species were visually determined using the modified Daubenmire scale (Abrams & Hulbert, 1987). This scale ranges from 1-7 (Table 1). These data were collected during the 2017 growing season from all twenty plots at each site. To ensure consistency, only the author's Daubenmire scale estimations were used in the final readings. The *Vascular Flora of Illinois* (Mohlenbrock, 2013) was used to identify plants to the species level in the field. All plant species present were identified in both open and closed plots twice throughout the season to capture early and late emerging species. Any unknown species were collected from outside of the plots and pressed for later identification.

To categorize the most common and widespread species, the plant communities that were present at each site in >25% of the plots and were $\geq 10\%$ total cover were extracted from the total species list at each site and globally. Cover estimates were recorded from the central 2 m² of the plots to avoid plant interference from the fencing.

Table 1: The modified Daubenmire scale (Abrams & Hulbert 1987) used to record the percent cover of each species present within each plot. The number used on the scale is in column one and the corresponding range that the number relates to is in column two. The midpoint of each range (column three) was used in subsequent analyses.

Category	Range (%)	Midpoint (%)
1	0-1	.5
2	1-5	2.5
3	5-25	15
4	25-50	37.5
5	50-75	67.5
6	75-95	80
7	95-100	97.5

In each enclosed plot, five *A. japonica* plants were randomly chosen and tagged with aluminum tags that allowed for a permanent record of the plant and plot number to be included with identification information. Plants near the edge of the fencing were not tagged to avoid interference from the fencing. On each tag, the plot number, plant number and month was written and loosely wrapped around the base of the stem of each plant to avoid any interference with growth. The height of each tagged plant was recorded in centimeters. The number of nodes and degrees of branching were recorded for each tagged plant. Degrees of branching were only recorded at the last measurement by following the outermost branch and counting the number of

degrees to the main stem for each plant (Whitney, 1976). After flowering had begun all the flowering spikes on tagged plants were counted and then measured in centimeters at each succeeding measurement.

Within each open plot, five *A. japonica* plants were tagged following the same protocol. In addition, plants that were browsed were tagged throughout the season as the browse occurred. These browsed plants were tagged in all open plots up to a maximum of 20 browsed plants per plot. The phenological state (new expanding leaves, young fully expanded leaves, mature leaves, mix of green and senescing leaves, mostly senescing or senescent leaves) of each tagged plant was recorded monthly throughout the study in accordance with protocols established in (Cornelissen et al., 2003). All additional browse on species other than that of *A. japonica* was noted and the phenology of the browsed plants were recorded in accordance to the same phenological criteria. Spherical crown densiometer (concave model C) (Forestry Suppliers, Jackson, MS) readings were taken once at each plot following the methods recommended in Jennings, Brown, and Sheil (1999) and from the directions on the back of the densiometer.

Statistical Analyses

Using the statistical program (R . Core Team, 2017) a linear mixed effects model was used with the lmer package (Bates, Mächler, Bolker, & Walker, 2015). Plots were nested within site to create a unique identifier for the analysis. The fixed effects used in the model were month, treatment, and site. The dependent variables of the browsed *A.japonica* plants were measured throughout the season and included height, number of nodes and flower spikes, length of flower spikes, and degrees of branching. Fecundity and degrees of branching were analyzed using a one-way ANOVA, as these measurements were only collected once.

Each species present in the plots was recorded and the species by site matrix ordinated using the R statistical program with the vegan package (Oksanen et al., 2017). The pairwise ADONIS package (Martinez, 2017) was used to determine if community composition differed between treatments across sites and collection periods. Using the vegan package in R (Oksanen et al., 2017; R . Core Team, 2017) Daubenmire readings were transformed to display their midpoints (Table 1) and ordinated in a Non-Metric Dimensional Scaling (NMDS). Significant vectors were fit using the vegan package to the ordination using the “envfit” function. Environmental data collected were overhead canopy cover, number of species per plot, and number of browsed *A. japonica* plants per plot. An environmental matrix was included in the analysis and significant vectors were added to the ordination. A correlation matrix was used to test for interactions between the measured variables.

Site quality was determined by recording the plant taxa that were present at a site, while also determining deer population density. Deer population density was estimated using the Distance package in R (Miller, 2019). Three models were fit using the perpendicular distance to a transect run through the area infested with *Acyranthes japonica*. FQA values were determined using the universal FQA calculator (Freyman et al., 2016). The FQA calculator uses conservation coefficients to determine site quality based on the current herbaceous layer. The scale ranges from 1-10. A plant lower on the scale is less conservative than a plant higher on the scale. A site with a low average conservation coefficient is considered to contain species that are either weedy, or adapted to anthropogenic disturbances (Taft, Wilhelm, Ladd, & Masters, 1997).

CHAPTER 3

RESULTS

I. Morphological

During the summer of 2017, morphological data were collected three times from each of the six sites. Collection dates occurred in June, July and August (Table 2). Statistical results from these collections are presented on Table 3. A total of 1,048 individual plants were tagged and measured throughout the growing season. Of these tagged plants, 448 were browsed.

Table 2: Data collection dates during the summer of 2017 at each site. Collections were made approximately one month apart from each other. *Collections at Mallard road were made on May 29, 2017. When analyzing these data, the month of May was coded as June to pair with the other sites.

Site	June Collection Date	July Collection Date	August Collection Date
Chestnut	7	20	26
Dixon Springs	29	21	27
Limekiln Springs	20	23	10
Mallard Road	*May (29)	3	19
Mchutchinson	31	25	15
Nawrot	27	27	18

Table 3: The F, DF, and P values showing the effect of deer browse on each variable. Results were calculated using the R statistical program with the lmerTest, lme4 packages. Height and number of nodes were measured during each collection period. Number of flower spikes, length of flower spikes, and degrees of branching were measured only once throughout the growing season during the last collection in August.

Height				Nodes			
	DF	F.value	Pr(<F)		DF	F.value	Pr(<F)
Month	2	135.559	<0.0001	Month	2	275.883	<0.0001
Treatment	1	23.323	<0.0001	Treatment	1	1.832	0.1790
Site	5	14.536	<0.0001	Site	5	11.267	<0.0001
Month:Treatment	2	.751	0.4734	Month:Treatment	2	0.661	0.517
Month:Site	10	4.937	<0.0001	Month:Site	10	3.809	<0.0001
Treatment:Site	5	3.078	0.0127	Treatment:Site	5	4.646	<0.0001
Residuals	145	-	-	Residuals	145	-	-
Number of Flower Spikes				Length of Flower Spikes			
Site	5	9.783	<0.0001	Site	5	9.020	<0.0001
Treatment	1	0.171	.680	Treatment	1	1.410	0.239
Treatment: Site	5	4.201	.002	Treatment: Site	5	1.685	0.149
Residuals	76	-	-	Residuals	76	-	-
Degrees of Branching							
	DF	F.value	Pr(<F)				
Site	5	2.778	0.0231				
Treatment	1	1.522	0.2210				
Treatment: Site	5	2.274	0.0551				
Residuals	76	-	-				

Height

The mean (\bar{Y}) height of the plants was $74.9 \text{ cm} \pm 0.1$ in the exclosure plots and 63.3 ± 0.1 cm in the open plots. Analyses of the data from each site are presented in Table 3 with treatment averages in Table 4. There was a significant interaction between site and treatment, ($F_{(5, 97)} = 3.078$; $p < 0.001$, fig. 1), along with month and site ($F_{(10, 153)} = 4.937$; $p < 0.001$) (fig. 2). Plants in the open plots at Dixon Springs were significantly shorter than plants in the closed plots (Fig 1). The Tukey pairwise test for the month to site interaction (Fig.2) indicate significant differences in growth from June to August at Chestnut Hills, Limekiln Springs, and Mchutchinson. June through August growth was different at these sites.

Table 4: Average height of plants from each site between open and closed plots.

Site	Exclosure Mean Height (cm)	Exclosure SE \pm	Open Mean Height (cm)	Open SE \pm
Chestnut	55.2	0.1	54.2	0.1
Dixon Springs	88.9	0.1	67.7	0.1
Limekiln Springs	61.7	0.1	65.1	0.1
Mallard Road	77.4	0.1	62.6	0.1
Mchutchinson	62.9	0.1	51.9	0.1
Nawrot	102.5	0.1	78.2	0.1

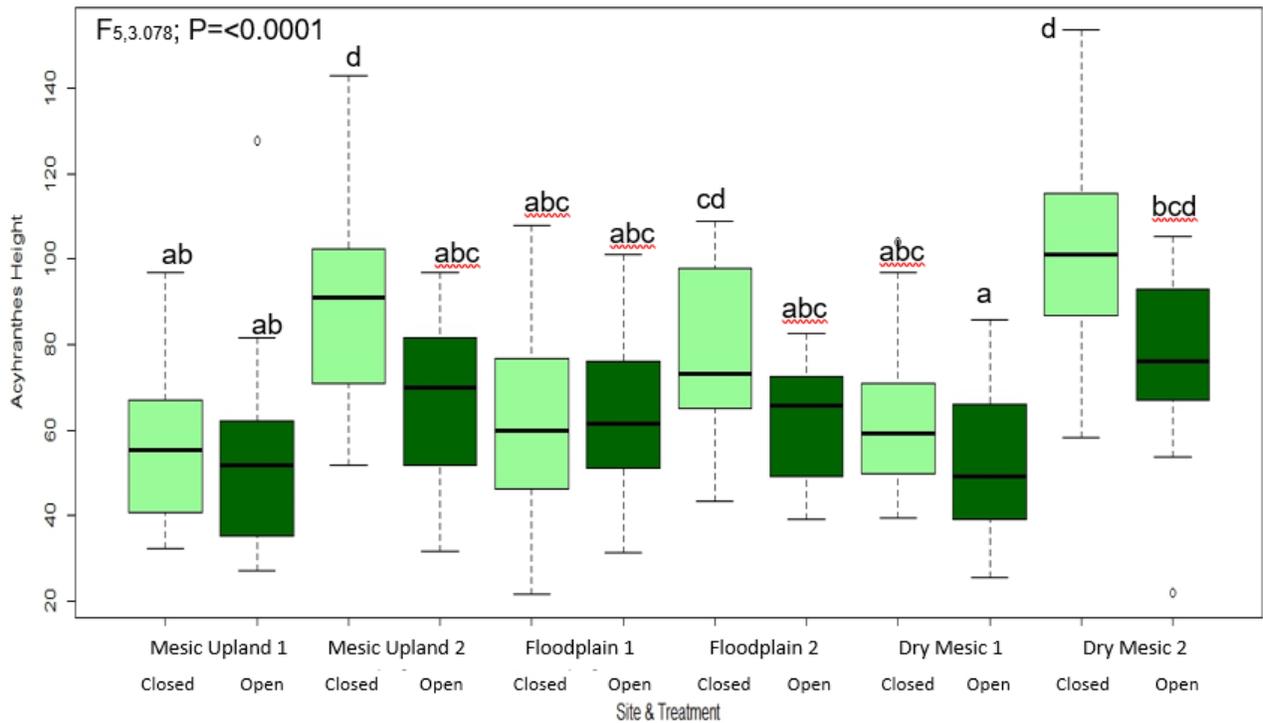


Fig. 1: The height of *Achyranthes japonica* plants in open and closed plots at each site represented by forest type. Treatment plots are labeled as either “Closed” or “Open”. Mean values sharing the same letter(s) are not significantly different (Tukey’s test). These box and whisker plots present the means of each site (black line) for height only.

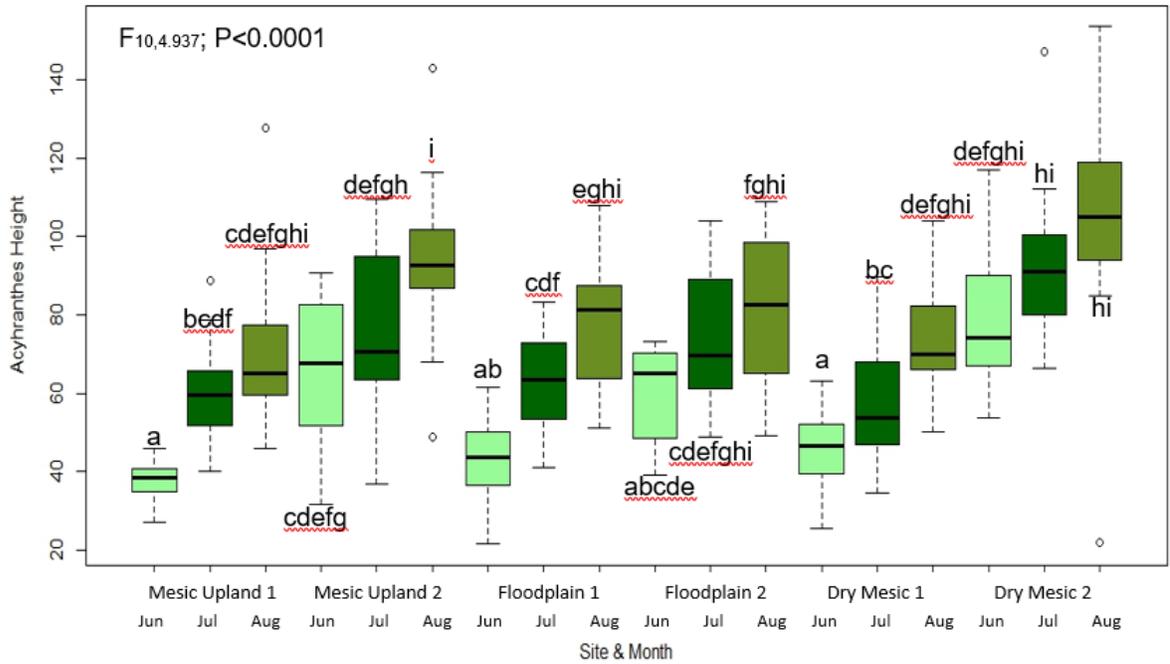


Fig. 2: The height of *Achyranthes japonica* plants between site and the months of June, July and August of 2017. Collection periods are labeled as either “Jun”, “Jul” or “Aug” under each site. Mean values sharing the same letter(s) are not significantly different (Tukey’s test). Box and whisker plots present the means of each site (black line) for height only.

Number of Nodes

There was an interaction between treatment and site variables ($F_{5,95}=4.646; p<0.001$), and month and site ($F_{10,152} = 3.809; p<0.001$) on the number of nodes per plant. The mean (\bar{Y}) number of nodes per plant was 15.33 ± 0.08 in the enclosure plots and was 15.04 ± 0.09 in the open plots. There were significantly fewer nodes on plants in the open plots compared with the closed plots at Dixon Springs where plants in the open plots had $13.5 \pm .08$ nodes, and plants in the enclosure plots had 19.6 ± 0.07 nodes (Fig.3). The direction of difference between open and

enclosed plots was inconsistent among sites. Over the three survey periods, the number of nodes per plant increased each month but the amount of increase varied among sites (Fig 4).

Table 5: Average (± 1 SE) number of nodes on each plant in open and closed plots at each site.

Site	Exclosure Mean Number of Nodes	Exclosure SE \pm	Open Mean Number of Nodes	Open SE \pm
Chestnut	11.4	0.1	12.7	0.1
Dixon Springs	19.6	0.1	13.45	0.1
Limekiln Springs	12.3	0.1	17.1	0.1
Mallard Road	13.6	0.1	12.1	0.1
Mchutchinson	12.5	0.1	13.4	0.1
Nawrot	22.6	0.1	21.3	0.1

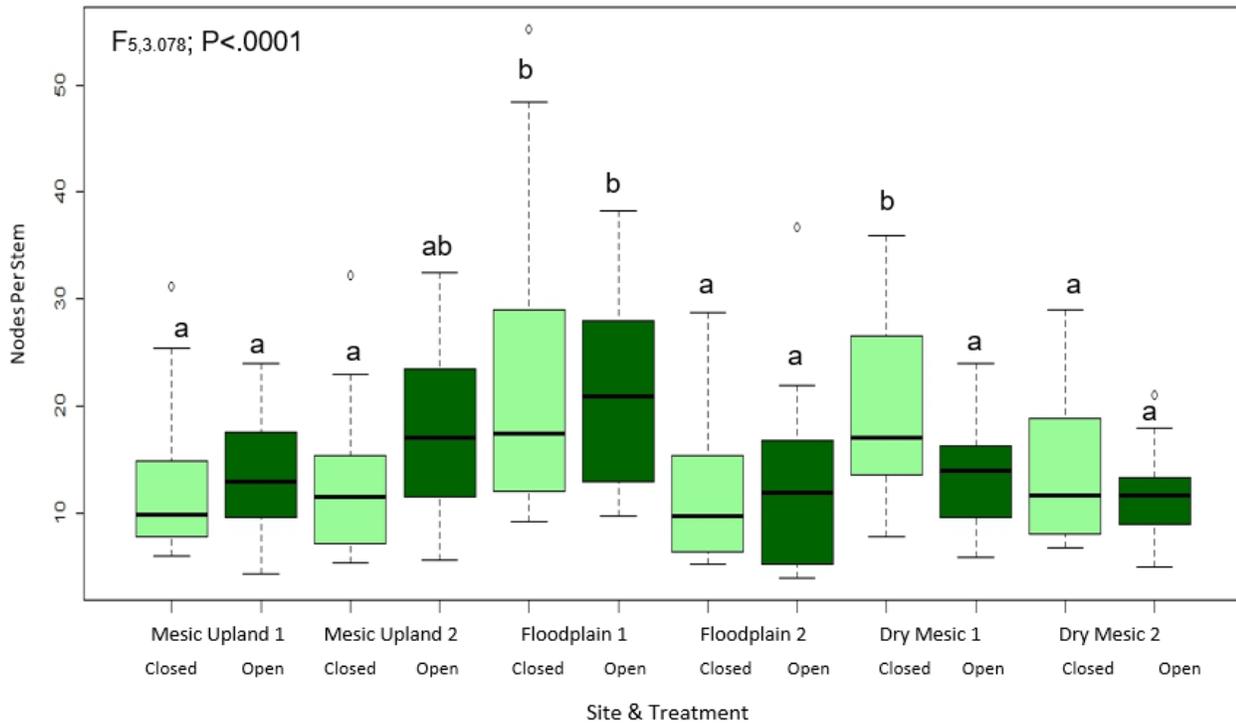


Fig. 3. The number of nodes on *Achyranthes japonica* plants in open and closed plots at each site represented by forest type. Treatment plots are labeled as either “Closed” or “Open”. Mean values sharing the same letter(s) are not significantly different (Tukey’s test) box and whisker plots present the means of each site (black line) for height only.

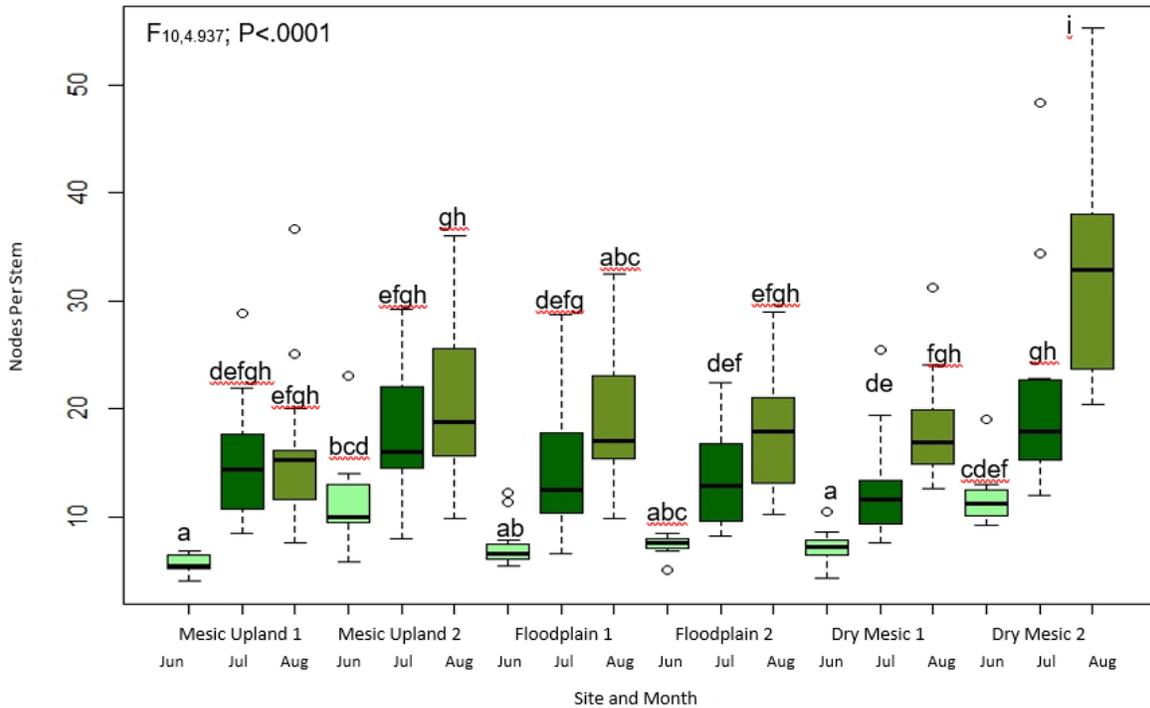


Fig. 4: The number of nodes on *Achyranthes japonica* plants between site during the months of June, July and August of 2017. Collection periods are labeled as either “Jun”, “Jul” or “Aug” along under each site. Mean values sharing the same letter(s) are not significantly different (Tukey’s test) box and whisker plots present the means of each site (black line) for the number of nodes only.

Number of Flower Spikes

There was a significant interaction between treatment and site on the number of flower spikes per plant ($F_{5, 18}=4.201; p<0.01$) (Table 3). This was the only significant interaction. The average number of flower spikes in the enclosure plots was 19.58 ± 0.25 , and 16.90 ± 0.32 in the open plots (Table 6). Despite the significant interaction, the Tukey analyses show differences among sites, but none between treatments (fig.5). Both number of nodes and number of flower

spikes show the same pattern of higher numbers in open plots at most sites, but lower in open plots in the dry mesic sites.

Table 6: Average number of flowering spikes on each plant in open and closed plots at each site along with standard errors.

Site	Exclosure Mean Number of Flower Spikes	Exclosure SE \pm	Open Mean Number of Flower Spikes	Open SE \pm
Chestnut	7.34	0.1	15.04	0.3
Dixon Springs	26.86	0.3	13.46	0.3
Limekiln Springs	18.34	0.3	24.69	0.3
Mallard Road	24.24	0.3	7.78	0.4
Mchutchinson	10.77	0.3	12.58	0.3
Nawrot	29.94	0.3	27.55	0.3

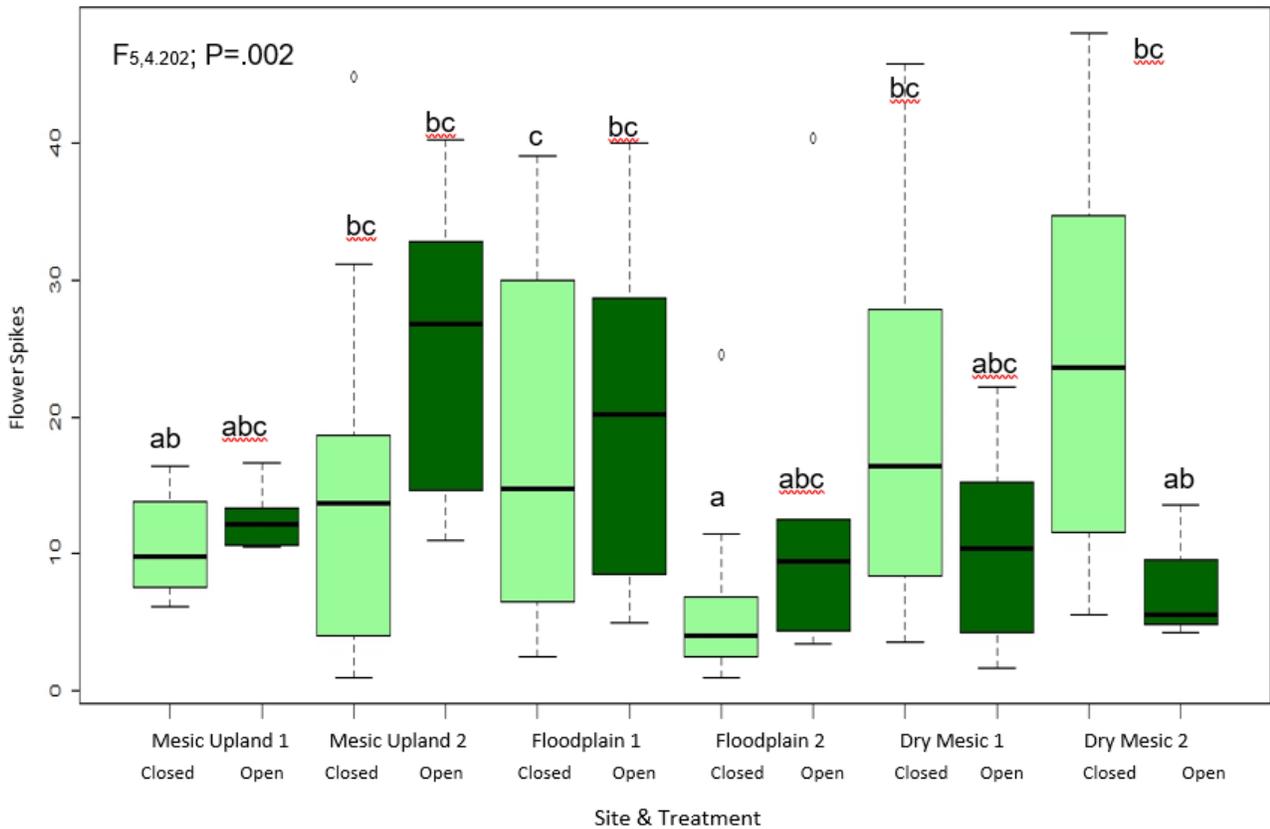


Fig. 5: The number of flower spikes on *Achyranthes japonica* plants in open and closed plots at each site represented by forest type. Treatment plots are labeled as either “Closed” or “Open”. Mean values sharing the same letter(s) are not significantly different (Tukey’s test) box and whisker plots present the means of each site (black line) for number of spikes only.

Length of Flower Spikes

There was a significant site effect on flower spike length ($F_{5,9.5}=9.020$; $p<0.0001$) (fig.6). The Tukey test indicates that that length of the flowering spikes produced from site to site varies significantly. The length of the flowering spikes on *A. japonica* at Chestnut were shorter than those on plants at Limekiln, Nawrot, and Dixon Springs.

Table 7: Average length of flowering spikes at each site along with standard errors. Calculations were conducted using the R statistical program (Appendix A). The site with the plants with the longest flowering spikes was Nawrot's property ($11.31 \pm .2955$ cm). The plants with the shortest flowering spikes were at Mallard Road measuring $5.53 \pm .2041$ cm.

Site	Mean Length of Flower Spikes (cm)	SE \pm
Chestnut	5.72	0.3
Dixon Springs	9.32	0.3
Limekiln Springs	9.64	0.2
Mallard Road	5.53	0.2
Mchutchinson	6.59	0.2
Nawrot	11.31	0.3

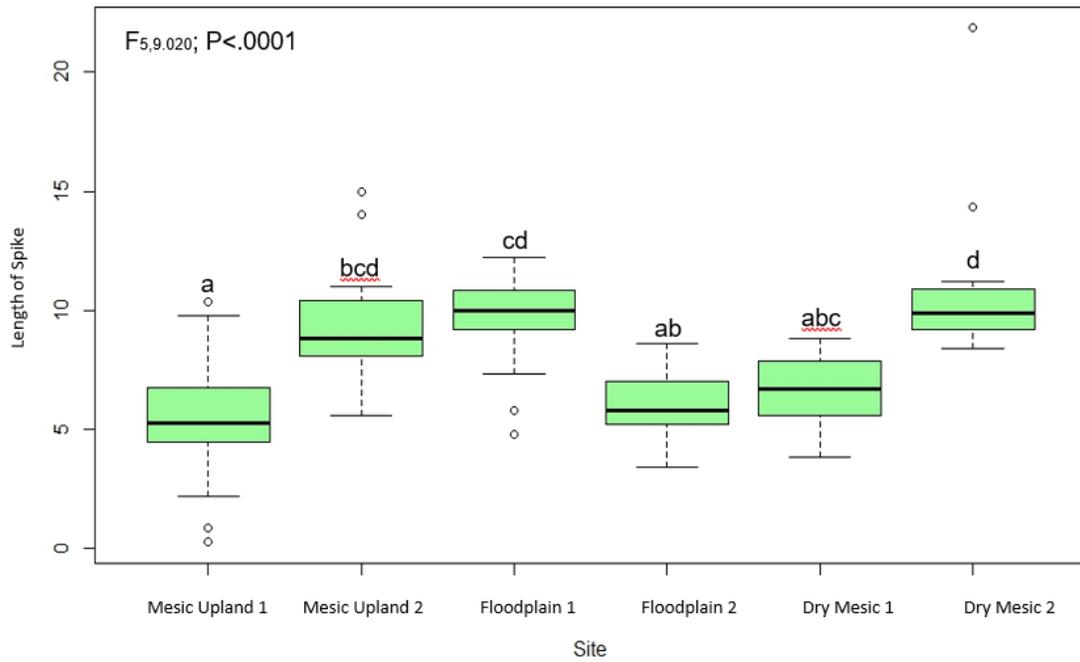


Fig. 6: The average length of flower spikes on *Achyranthes japonica* plants across each forest type. Mean values sharing the same letter(s) are not significantly different (Tukey's test) box and whisker plots present the means of each site (black line) for spike length only.

Degrees of Branching

There was a significant site effect on the degrees of branching ($F_{5,2.69}=2.778$; $p<0.05$) (fig.7), but no main effect or interaction with treatment. The Tukey analysis indicates that the plants at the Nawrot property had significantly more degrees of branching (5.7 ± 0.2) than plants at the Dixon Springs site (4.5 ± 0.2). The degrees of branching of the plants at the four other sites were not significantly different from each other or from plants at the Nawrot or Dixon Springs. Table 8: Average degrees of branching at each site along with standard errors. Calculations were conducted using the R statistical program (Appendix A). The site with the longest flowering spikes were at Nawrot's property measuring $11.31 \pm .2955$ cm. The plants with the shortest flowering spikes were at Mallard Road measuring $5.53 \pm .2041$ cm.

Site	Mean Degrees of Branching	SE \pm
Chestnut	4.95	0.1
Dixon Springs	4.54	0.2
Limekiln Springs	4.91	0.2
Mallard Road	4.60	0.2
Mchutchinson	4.92	0.2
Nawrot	5.70	0.2

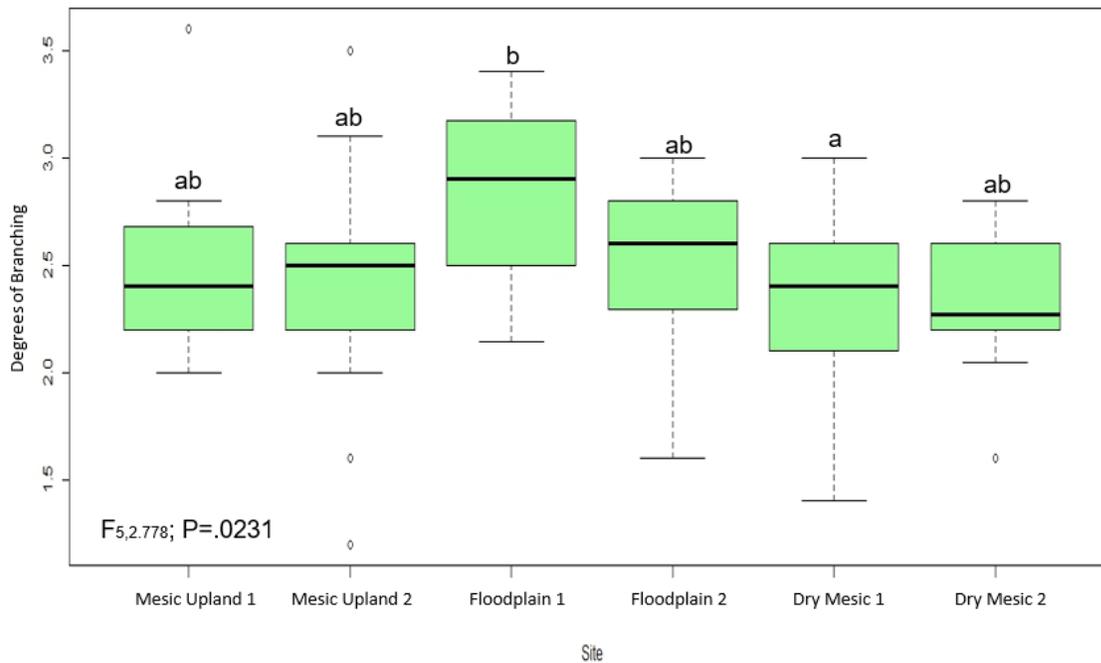


Fig. 7: The degrees of branching of *Achyranthes japonica* plants at each site. Mean values sharing the same letter(s) are not significantly different (Tukey's test) box and whisker plots present the means of each site (black line) for degrees of branching only.

II. Community data results

The community dataset had 119 observations and 136 variables, or species. *Achyranthes japonica* was found in each plot by design, at $74.1\% \pm 7.0$ cover in 100% of the plots (n=119). There were nine other species that occurred within > 25% the plots at 10.0% or more on the Daubenmire scale (Table 9). Japanese stilt grass (*Microstegium vimineum*) (Trin.) was the second most common species at $25.75\% \pm 5.07$ and found in $44.53\% \pm 7.60$ of the plots (n =53). Ten species were found to occur at greater than 25% of plots at over 10% cover. *Pilea pumilla* (L.) was the fifth most common species found to occur in the study.

Table 9: Global species cover from all the plots combined. Species are listed if they have occurred in greater than twenty five percent of the plots at greater than or equal to ten percent cover across all sites. Species names are presented with the first two letters of the genus and first two letters of the species names. ACJA is *Achyranthes japonica*, CARA is *Campsis radicans*, FRAM is *Fraxinus americana*, IMLU is *impatiens lutea*, MIVI is *Microstegium vimineum*, PAQU is *Parthenocissus quinquefolia*, PEPE is *Persicaria pennsylvanica*, PIPU is *Pilea pumilla*, VIOL is *viola species*. A key to each species name is provided in Appendix C.

Species	Global Cover					
	Code	(%)	SE ±	Frequency (%)	SE ±	Frequency (#)
ACJA		74.09	6.9	100	7.6	119
MIVI		25.75	5.1	44.53	6.7	53
PAQU		13.2	3.6	44.53	6.7	53
PEPE		23.05	4.8	42.01	6.5	50
PIPU		14.13	3.8	38.65	6.2	46
ELCAN		26.05	5.1	37.81	6.2	45
IMLU		30.32	5.5	32.77	5.7	39
FRAM		20.5	4.5	29.41	5.4	35
VIOL		14.14	3.8	26.89	5.2	32
CARA		18.75	4.3	25.21	5.0	30

Using the same criteria as the global view of the community dataset (Table 9), species at each site were separated to retain those that occurred in twenty-five percent of the plots at greater than or equal to ten percent cover using the Daubenmire scale. These tables are presented in the following pages.

Table10: The 19 species that occurred in at least twenty five percent of plots and had greater than ten percent cover at Chestnut. Species codes are in Appendix C.

CHESTNUT				
Species Code	Average Cover (%)	SE \pm	Frequency (%)	SE \pm
ACJA	87.50	8.3	100	7.3
CARA	12.50	3.5	25	4.7
CRCA	10.23	3.2	55	2.9
FRAM	26.90	5.2	80	5.8
GAAP	16.07	4.0	35	3.4
GACI	10.00	3.2	25	4.7
LOJA	11.94	3.5	45	1.4
MIVI	10.00	3.2	25	4.7
PAPE	11.56	3.4	40	2.6
PAQU	15.57	3.9	65	4.3
PEPE	16.25	4.0	40	2.6
PHLE	11.07	3.3	35	3.4
PIPU	17.34	4.2	80	5.8
POSY	20.41	4.5	30	4.1
POPE	27.5	5.2	25	4.7
POLY	17.22	4.2	45	1.4
TORA	14.58	3.8	60	3.6
ULAM	17.00	4.1	25	4.7
ULAL	10.45	3.2	55	2.9

Table 11: The 9 species that occurred in at least twenty five percent of plots and had greater than ten percent cover at Dixon Springs. Species codes can be found in appendix C.

DIXON SPRINGS				
Species Code	Average Cover (%)	SE \pm	Frequency (%)	SE \pm
ACJA	73.12	7.1	100	6.4
AGAL	14.55	2.9	85	5.1
ECAN	16.81	2.5	55	2.1
LOMA	13.21	3.2	35	4.9
MIVI	30.13	2.6	90	5.5
PAQU	14.68	2.9	40	4.4
PHAM	20.00	1.8	45	3.8
POLY	12.50	3.3	55	2.1
RUOC	14.58	2.9	30	5.4

Table 12: The 15 species that occurred in at least twenty five percent of plots and had greater than ten percent cover at Limekiln Springs. Species codes can be located in appendix C.

LIMEKILN SPRINGS

Species Code	Average Cover (%)	SE \pm	Frequency (%)	SE \pm
ACJA	70.00	6.9	100	7.2
ECAN	31.50	3.1	75	5.2
CARA	26.81	2.2	55	2.7
VIOL	26.13	5.1	55	7.4
PEPE	25.76	1.9	65	4.1
CELA	25.35	1.9	35	3.6
URDI	25.00	5.0	55	7.4
AGPE	17.85	2.0	35	3.6
PIPU	16.66	2.3	45	1.7
TORA	16.25	3.0	30	3.6
SOLCA	12.85	3.0	35	3.6
ACSA	10.41	3.4	30	4.2
TECA	10.31	3.4	40	2.8
FACO	10.00	3.5	25	4.8
ACNE	4.06	4.2	40	2.8

Table 13: The 15 species that occurred in at least twenty five percent of plots and had greater than ten percent cover at Mallard Road. Species codes can be located in appendix C.

MALLARD ROAD				
Species Code	Average Cover (%)	SE \pm	Frequency (%)	SE \pm
ACJA	66.71	6.4	100	6.9
ECAN	23.83	1.2	78	5.1
URDI	23.33	1.4	78	5.1
IMLU	41.53	6.4	68	8.3
MIVI	27.08	1.3	63	3.3
AGPE	16.59	2.9	57	2.3
CARA	16.11	4.0	47	6.9
CRCA	15.83	3.1	47	2.2
EOFO	20.00	2.3	42	3.1
PEPE	11.56	3.7	42	3.1
PIPU	11.56	3.7	42	3.1
VEAL	38.57	3.6	36	3.9
CALU	28.50	1.8	26	5.1
PAQU	28.50	1.8	26	5.1
TECA	10.00	3.9	26	5.1

Table 14: The 7 species that occurred in at least twenty five percent of plots and had greater than ten percent cover at Mchutchinson. Species codes can be located in appendix C.

MCHUTCHINSON				
Species Code	Average Cover (%)	SE \pm	Frequency (%)	SE \pm
ACJA	86.75	7.4	100	6.12
IMLU	31.88	0.8	60	1.5
LOJA	10.41	4.7	30	5.7
PAQU	6.96	2.6	70	8.4
PEPE	45.27	3.6	45	4.1
SYOR	24.33	2.9	75	3.6
CAMCB	22.27	4.7	55	7.4

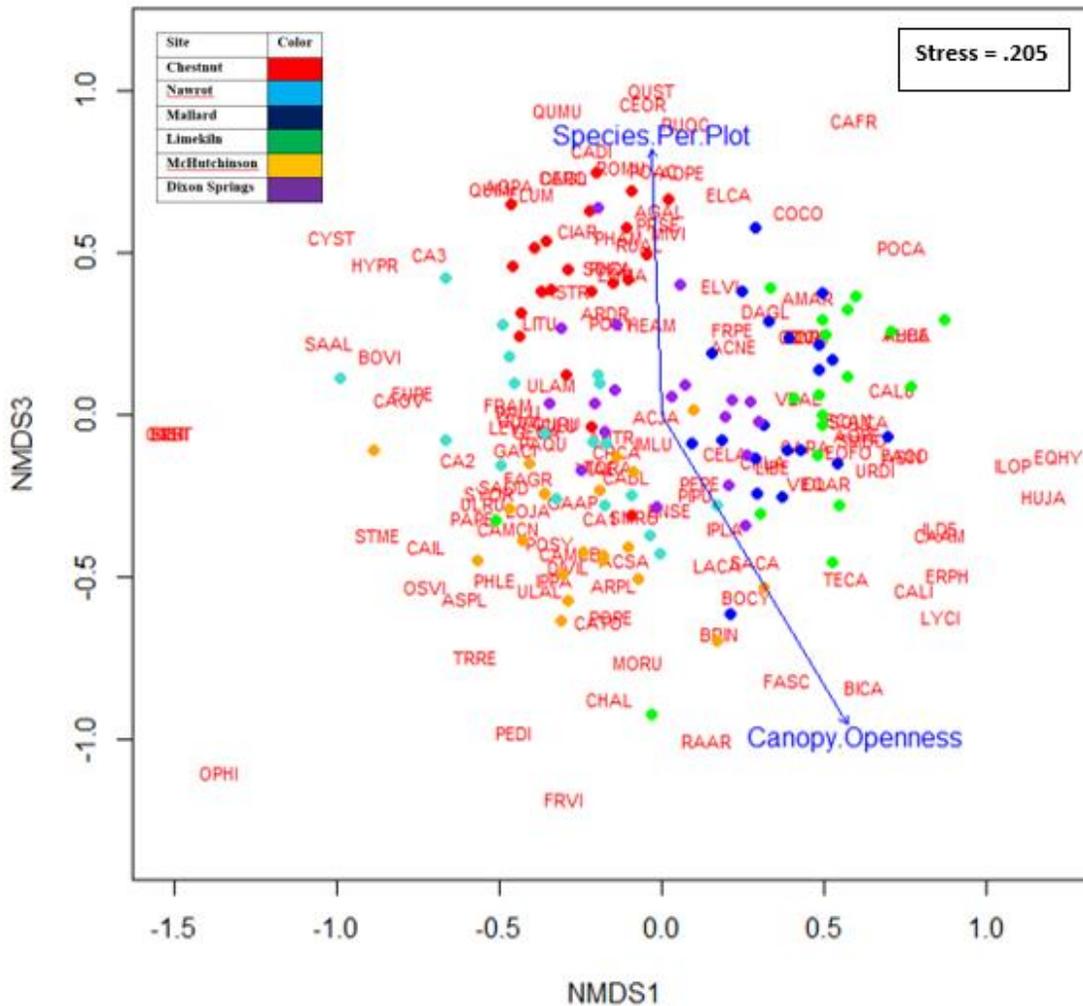


Figure 8: NMDS with Axes (1-3) with all the species that occurred more than once throughout the collection period. Species names are displayed using a four-letter code (Appendix 2) based upon the first two letters of the genus and species, respectively. Significant vectors are displayed in blue with “species per plot” and “Cover.value” (=canopy openness). Sites are displayed with colored points. Chestnut Hills Nature Preserve is displayed in red, Nawrot is light blue, Mallard Road is dark blue, Limekiln Springs is green, Mchutchinson is orange and Dixon Spring Agricultural Center is purple. Each site and their associated color are identified in the legend on the figure.

Table 15: The two species that occurred in at least twenty five percent of plots and had greater than ten percent cover at Nawrot. Species codes can be located in appendix C.

NAWROT

Species Code	Average Cover (%)	SE ±	Frequency (%)	SE ±
ACJA	57.3	4.30	100	3.5
MIVI	20.4	4.30	75	8.7

Table 16: The X, Y, r², and Pr (<r) values from vectors that were fit with the community dataset with singleton species removed. Significant vectors were fitted to the ordination.

Vector	X	Y	r ²	Pr (<r)
Browse Per Plot	0.72	0.69	0.02	0.759
Canopy Openness	0.51	-0.86	0.08	0.006
Species Per Plot	-0.04	0.99	0.66	0.001

Within the vegetation dataset 45 species only occurred once. These species were omitted from the analysis. After removing these “singleton” species from the dataset, there were 119 observations, or plots and 91 variables, or species from the previous 136 species. A two-dimensional NMDS ordination (stress= 0.205 was retained for interpretation along with significant vectors (Figure 8 & Table 16). Overhead canopy cover was fit as a significant environmental variable (r²=0.08Pr<.006) along with the number of species per plot (r²=0.66, Pr<.001).

A permanova analysis was used to test for significant relationships between the species present, treatment and site. Site was significant (F_{5, 8.40} = 6.3862; p<0.001) along with a marginal site by treatment interaction (F_{5, 1.30} = 0.9631; p<0.0621). The pairwise comparisons between site and treatment indicate Chestnut (F_{19, 2.06} = 0.103; p<0.026) and Mchutchinson (F_{19, 1.89} = 0.095;

p<0.057) have a significant and marginally significant treatment effects, respectively between open and closed plots. These effects are likely driven by the occurrence of two more species in the open plots at both sites. Deer density estimates ranged from 8.1 to 18.0 deer per km² (11.7 ± .06) (Table 17).

Table 17: Deer density, Mean FQA Value and canopy cover estimates for the six sites surveyed in this study. Site Quality indices (FQA) values that were determined using the universal site FQA calculator. FQA values can range from (1-10) with scales ranging from 1-3, 4-6, 7-9 and 10.

Site	Deer Density / km ²	Mean CC Value	Canopy Openness (%)
Chestnut	18.00	3.9	8.138
Mchutchinson	12.50	3.4	8.502
Nawrot	12.50	3.5	14.196
Limekiln Springs	10.70	3.2	11.18
Dixon Springs	8.90	3.7	5.421
Mallard Road	8.07	3.6	9.841

Using the Universal Floristic Quality Assessment (FQA) assessment program (Freyman et al., 2016) on universalfqa.org website, all the species that were found at each site within each plot were analyzed. These floristic values range from 3.2 to 3.9 (Table 17). Floristic Quality Indices and deer densities were positively correlated with each other (Fig 9). The higher the floristic quality of the site, the more deer were present. Most of the plant size variables were positively correlated, but none of them were significantly correlated with FQI or DD (Fig 9).

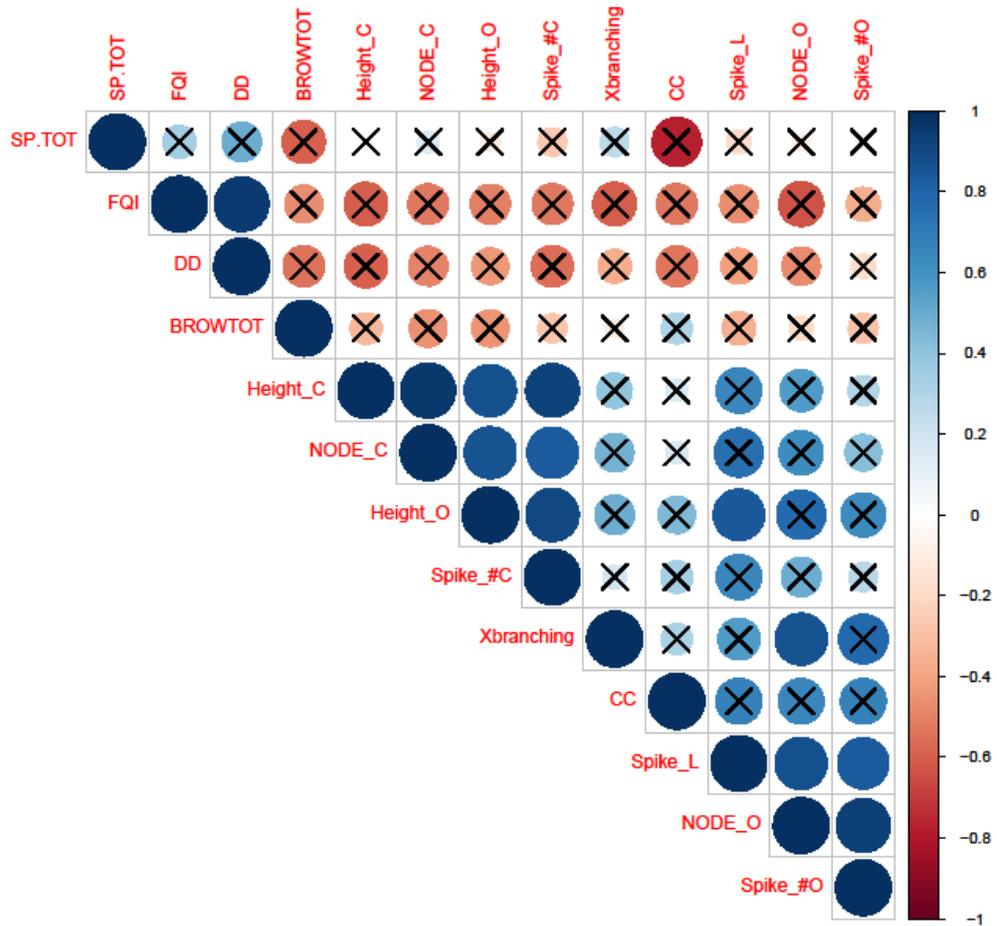


Fig 9: Correlation matrix comparing all measured variables. All nonsignificant correlations ($p > 0.05$) have an “X” otop of them. Positive correlations are blue and negative correlations are red.

SP. TOT – Species total

DD – Deer density

FQI – Floristic quality index

BROWTOT – Total number of browsed plants in a plot

Height_C – Height of plants in a closed plot

NODE_C – Number of nodes on plants in a closed plot

Height_O - Height of plants in an open plot

Spike_#C – Number of spikes on plants in a closed plot

Xbranching – Degrees of branching

CC – Canopy cover

Spike_L – Spike Length

NODE_ O – Number of nodes on plants in an open plot

Spike_#O – Number of spikes on plants in an open plot

CHAPTER 4

DISCUSSION & RECOMMENDATIONS

Q₁: What morphological responses occur in *Achyranthes japonica* individuals after deer browsing?

H₁: Browsed *Achyranthes japonica* individuals will be shorter, have decreased fecundity, and display greater degrees of branching.

Height, number of nodes and number of flowering spikes produced were the morphological variables of *A. japonica* that were significantly affected by deer browse, although often inconsistently (Table 3). However, several of these measures showed highly inconsistent effects from browsing. A study measuring the effects of clipping on *A. japonica* (Smith, 2013) speculated that *A. japonica* plants were palatable to deer but recommended additional information from a more thorough study. In my study, H₁ was only partially supported by the results. Browsed plants were shorter (Fig. 1), produced fewer nodes (Fig. 3) and had fewer flowering spikes (Fig. 5) at some sites, but higher at some other sites. It is worth mentioning that there were more nodes and flowering spikes at other sites. The length of the flowering spikes was not significantly shorter after browse but overall, fewer spikes were produced. This change in spikes produced could have an impact on total number of seeds produced. An island study measuring the response of the herbaceous species *Plectritis congesta* (Lindl.) to browse found that browsed plants were shorter and produced morphologically variable seeds depending on the presence or absence of deer (Skaiven & Arcese, 2017). In the study, plants growing without deer were larger and produced fruits with wings. Those growing in the presence of deer were shorter and did not have wings on their fruits. Although the shape and size of the seeds were not measured in this study, the average length of flowering spikes were altered (Table 6). A study measuring the effect of deer browse on the invasive shrub *Lonicera maackii*, measured a

decrease in cover and change in architecture of browsed individuals. Plants that were excluded from deer were larger and showed an increase in basal area (Peebles-Spencer et al., 2018).

A study in southern Illinois found a difference between *A. japonica* fecundity during drought and flood years at wet and dry sites (Schwartz, 2015). In that study, the length of the flowering spikes were variable among sites during drought years and produced the most viable seeds at the dryer site in both cases. Neal (2018) also recommended managing the largest *Achyranthes japonica* plants first, as they had the greatest potential for spread by producing the greatest number of flowering spikes, and hence seed. Site was a significant variable determining the growth response of *A. japonica* plants in previous studies (Neal, 2018; Schwartz et al., 2016a; Smith, 2013). My findings are consistent with these studies and height and length of flowering spikes are positively correlated. The site with the tallest plants were at Nawrot (Table 4) and these plants also had the largest number of flowering spikes (Table 6). There were no treatment effects on fecundity or degrees of branching within sites, but there were among sites. Variability in growth among sites is consistent with other studies where *A. japonica* plants were measured. This variability is referred to as adaptive phenotypic plasticity, or the ability of a species to adjust its phenotype under site specific conditions. This variability could also be the result of higher plasticity found within the species at a site compared with plants of the same species across their native range that may increase fitness across its invasive range (Anderson, Wagner, Rushworth, Prasad, & Mitchell-Olds, 2014). This quality would be in comparison with species that are specialists, and those that are generalists.

Q₂: What is the effect of site quality on the response of *Achyranthes japonica* individuals to deer browsing?

H₂: Higher quality sites will produce larger plants on average than lower quality sites.

To get an estimated value for site quality and address H₂, the FQA generator was used (Freyman et al., 2016). The average conservation coefficient among the studied sites was relatively low (Table 18), indicating that many of the species currently growing are adapted to disturbance or anthropogenic alterations (Taft et al., 1997). In other words, the sites that *A. japonica* is invading are disturbed. Chestnut Hills is a designated Nature Preserve that has already been recognized for its unique features and species diversity. This site had the greatest number of species present (Fig 8), highest deer density, and highest mean CC value (Table 17). Browsed *A. japonica* from this site were shorter (Fig.1) and produced fewer spikes (Fig.5) than plants at the other sites. The site with the lowest number of species and largest *A. japonica* grew at Nawrot which showed signs of previous disturbance.

Although *A. japonica* successfully overcame barriers to invasion, sites with the greatest diversity may better resist its spread. The biologic resistance theory (Elton, 1958) states that with greater species present, fewer species can establish. At Nawrot, where the largest and most productive plants grew, there were only two species that occurred in large amounts i.e., the exotics *M. vimineum* and *A. japonica* (Table 15). *Microstegium vimineum* is similar in its adaptable characteristics to *A. japonica* and can easily establish in many habitats (Gibson, Spyreas, & Benedict, 2002). Blossey & Gorchov (2017) noted that the presence of invasive species is symptomatic of high deer populations or a combination of multiple stressors compounding each other. The initial invasion of a species is the sign of serious unnoticed alterations that may have already taken place.

Q₃: What is the effect of deer density on browsing preference for native plants compared to *Achyranthes japonica* plants?

H₃: *Achyranthes japonica* plants will be browsed more frequently than native species at higher deer densities.

Each site contained weedy species with low conservation coefficients more consistent with high levels of disturbance. The second most common plant found throughout the study was the exotic C3 grass *Microstegium vimineum* which tends to occur in disturbed areas and is a threat to the Shawnee National Forest. Similar to this study, Neal (2018) found that *Pilea pumila* and *Microstegium vimineum* were present throughout the invaded areas at each site in his study. *Achyranthes japonica* was found at high densities within each plot, however there were still many native species present in each of the plots at various densities (Appendix C). Heckel & Kalisz (2017) used trillium species *Trillium grandiflorum* and *T. erectum* (Liliaceae) as indicators of deer browse impact because of their conservative nature and palatability. In their study, morphological characteristics were recorded and placed into a “deer impact index”. At the sites that had the lowest deer densities, the trillium plants in the study had larger leaves, a greater average number of flowering stems and fewer browsed stems compared with sites with higher deer densities. In my study, trillium species were not found. This lack of trillium species at my sites may be due to the browsing of palatable species past disturbance or site history. Deer densities as low as 3-10 deer / km² have been reported to impact plant communities. The lowest reported density estimate in this study was 8.07 deer/km² and the highest was 18.00 deer/km². Deer browsing behavior would favor palatable species and those with the greatest nutritional content. Subindividual variability, like phenotypic plasticity can help to spread species to new locations (Herrera, 2017). This type of adaptive behavior can help to explain the variation among sites but not among treatments.

RECOMMENDATIONS

Because of its unpredictable nature and prolific spread, future studies should continue to focus on the management and control of *A. japonica*. Areas to focus research with browse should measure crude protein of plants and other nutrients at different invaded sites compared to native species present. Future work should also continue to use the enclosure plots and sites that were established in this study, to document the changes that may continue to take place in the community in the absence of deer.

A. japonica can be browsed by deer or clipped mechanically without affecting its ability to reproduce. After reaching three to four nodes, clipped plants have shown the ability to regrow within the same season (Smith, 2013). It is at this stage in growth that perennial status is reached, and individuals can re-sprout the following year.

In order to control current and established populations of *A. japonica*, herbicide can be a useful tool. In a controlled experiment, the herbicide triclopyr was found to be the most effective herbicide to manage infestations requiring the least amount of active ingredient (Smith, 2013). While controlling populations of *A. japonica* it is most effective to target small to intermediate sized plants, as this will have the greatest effect on growth and provide the greatest control (Schwartz et al., 2016a). Integrated pest management (IPM) includes multiple tools for management of invasive species. The use of fire has been shown to be effective at reducing recruitment of *A. japonica* (Garrie, 2018). After one growing season however, the plants were able to fill in the gap rather quickly. Pairing the use of fire and chemical control can help to control areas where *A. japonica* has invaded and the two control methods are appropriate.

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APPENDIX A

R SCRIPT FOR LINEAR MIXED EFFECTS, REPEATED MEASURES ANALYSES AND TUKEY TESTS

Raw data are archived at: <https://figshare.com/s/4e267a3af4bf58c6a170>

```
library(car)
library(ggplot2)
library(nlme)
library(phia)

ACJAMeasure<- read.csv("Acjameasure.csv",header=TRUE, row.names=1, sep=",")
print(ACJAMeasure)

# get the dimension of the community object (rows x columns)
dim(ACJAMeasure)

#look at row names
rownames(ACJAMeasure)

#column names
(colnames(ACJAMeasure))
colclasses=c("factor", "factor", "factor", "factor", "factor", "factor", "factor", "factor", "factor", "factor", "numeric", "numeric")

#CM
ACJAMeasure<- read.csv("Acjameasure.csv",header=TRUE, row.names=1, sep=",")
aovcm <-aov(cmb~Month*Site*Treatment+Error(Plot),data=ACJAMeasure)
print(summary(aovcm))

#Lmer test
library(lmerTest)
library(lme4)
ACJAMeasure<- read.csv("Acjameasure.csv",header=TRUE, row.names=1, sep=",")
# The "1" in (1|Plot) indicates the repeated measures
# fixed effects are month, treatment and site
# random effects are cm, and plot
lmercm<-lmer(log(cmb)~Month*Treatment*Site+(1|Plot),data=ACJAMeasure)
print(summary(lmercm))
lmertcm<-lmerTest::anova(lmercm)
print(lmertcm)
rand(lmercm)

#Means
```

```

with(ACJAmearure,tapply(cm, list(Site, Treatment), mean, na.rm=TRUE))

#Means
with(ACJAmearure,tapply(cmb, list(Site, Treatment), mean, na.rm=TRUE))

#Standard Deviation
with(ACJAmearure,tapply(cm, list(Site, Treatment), sd, na.rm=TRUE))

#Standard Deviation
with(ACJAmearure,tapply(cmb, list(Site, Treatment), sd, na.rm=TRUE))

#Lsmeans
#Treatment to Site
library(lsmearns)
library(multcomp)
library(multcompView)
leastsquare=lsmearns(lmercm,pairwise~Treatment*Site) ####Tukey-adjusted comparisone
#leastsquare = lsmearns(model, pairwise~Site)
CLD <- cld(leastsquare,
           alph..=0.05,
           Lettere= lettere, #### Use lower-case lettere for .group
           adjust. = "tukey")####. Tukey-adjusted comparisone
CLD
#Lsmeans
#Treatment to Site
library(lsmearns)
library(multcomp)
library(multcompView)
leastsquare=lsmearns(lmercm,pairwise~Month*Site) ####Tukey-adjusted comparisone
#leastsquare = lsmearns(model, pairwise~Site)
CLD <- cld(leastsquare,
           alph..=0.05,
           Lettere= lettere, #### Use lower-case lettere for .group
           adjust. = "tukey")####. Tukey-adjusted comparisone
CLD

#normality
with(ACJAmearure,{
  hist(cmb)
  qqnorm(cmb)
  qqline(cmb)})
with(ACJAmearure,{ shapiro.test(cmb)
})

#Log Transform
with(ACJAmearure,{

```

```

hist(log(cmb))
qqnorm(log(cmb))
qqline(log(cmb))})
with(ACJAmeasure,{ shapiro.test(log(cmb))})

#Simple box plot CM transforms to true NRI value

boxplot((cmb) ~ Treatment*Site,
  data = ACJAmeasure, notch=FALSE, col=(c("palegreen","darkgreen")),
  xlab = "Site & Treatment",
  ylab = "Acyhranthes Height")

boxplot((cmb) ~ Month*Site,
  data = ACJAmeasure, notch=FALSE, col=(c("palegreen","darkgreen","olivedrab")),
  xlab = "Site & Month",
  ylab = "Acyhranthes Height")

#Nodes
ACJAmeasure<- read.csv("Acjameasure.csv",header=TRUE, row.names=1, sep=",")
aovnodesperstem <-
aov(nodesperstemb~Month*Site*Treatment+Error(Plot),data=ACJAmeasure)
print(summary(aovnodesperstem))

#Lmer test
library(lmerTest)
library(lme4)
ACJAmeasure<- read.csv("Acjameasure.csv",header=TRUE, row.names=1, sep=",")
# The "1" in (1|Plot) indicates the repeated measures
# fixed effects are month, treatment and site
# random effects are nodesperstem, and plot
lmernodes<-lmer(log(nodesperstemb)~Month*Treatment*Site+(1|Plot),data=ACJAmeasure)
print(summary(lmernodes))
lmernodes<-lmerTest::anova(lmernodes)
print(lmernodes)
rand(lmernodes)

#Means
with(ACJAmeasure,tapply(nodesperstem, list(Site, Treatment), mean, na.rm=TRUE))

#Means
with(ACJAmeasure,tapply(nodesperstemb, list(Site, Treatment), mean, na.rm=TRUE))

#Standard Deviation
with(ACJAmeasure,tapply(nodesperstem, list(Site, Treatment), sd, na.rm=TRUE))

#Standard Deviation

```

```

with(ACJAMeasure,tapply(nodesperstemb, list(Site, Treatment), sd, na.rm=TRUE))

#lsmeans
#Treatment to Site
library(lsmeans)
library(multcomp)
library(multcompView)
leastsquare=lsmeans(lmernodes,pairwise~Treatment*Site) ###Tukey-adjusted comparisons
#leastsquare = lsmeans(model, pairwise ~Site)
CLD<- cld(leastsquare,
          alph..=0.05,
          Letters= letters, ### Use lower-case letters for .group
          adjust. = "tukey")###. Tukey-adjusted comparisons
CLD

#lsmeans
#Month to Site
library(lsmeans)
leastsquare=lsmeans(lmernodes,pairwise~Month*Site) ###Tukey-adjusted comparisons
#leastsquare = lsmeans(model, pairwise ~Site)
CLD<- cld(leastsquare,
          alph..=0.05,
          Letters= letters, ### Use lower-case letters for .group
          adjust. = "tukey")###. Tukey-adjusted comparisons
CLD

#lsmeans
#Month to Site
library(lsmeans)
leastsquare=lsmeans(lmernodes,pairwise~Treatment*Site) ###Tukey-adjusted comparisons
#leastsquare = lsmeans(model, pairwise ~Site)
CLD<- cld(leastsquare,
          alph..=0.05,
          Letters= letters, ### Use lower-case letters for .group
          adjust. = "tukey")###. Tukey-adjusted comparisons
CLD
Plot(CLD)
#Normality
with(ACJAMeasure,{
  hist(nodesperstemb)
  qqnorm(nodesperstemb)
  qqline(nodesperstemb)})
with(ACJAMeasure,{shapiro.test(nodesperstemb)})

#Log Transform
with(ACJAMeasure,{

```

```

hist(log(nodesperstemb))
qqnorm(log(nodesperstemb))
qqline(log(nodesperstemb)))
with(ACJAmesure,{ shapiro.test(log(nodesperstemb))})

#Simple box plot nodesperstem transforms to true NRI value
boxplot((nodesperstemb) ~ Treatment*Site,
        data = ACJAmesure, notch=FALSE, col=(c("palegreen","darkgreen")),
        xlab = "Site & Treatment",
        ylab = "nodesperstem")

boxplot((nodesperstemb) ~ Month*Site,
        data = ACJAmesure, notch=FALSE, col=(c("palegreen","darkgreen","olivedrab")),
        xlab = "Site & Month",
        ylab = "nodesperstem")

#Spikes
ACJAmesureA<- read.csv("August.csv",header=TRUE, row.names=1, sep=",")
aovflowerspikes <-aov(log(flowerspikesb)~Site*Treatment+Error(Plot),data=ACJAmesureA)
print(summary(aovflowerspikes))

#Means
with(ACJAmesureA,tapply(flowerspikes, list(Site, Treatment), mean, na.rm=TRUE))

#Means
with(ACJAmesureA,tapply(flowerspikesb, list(Site, Treatment), mean, na.rm=TRUE))

#Standard Deviation
with(ACJAmesureA,tapply(flowerspikes, list(Site, Treatment), sd, na.rm=TRUE))

#Standard Deviation
with(ACJAmesureA,tapply(flowerspikesb, list(Site, Treatment), sd, na.rm=TRUE))

#lsmeans flower spikes and site
library(lsmeans)
library(multcomp)
library(multcompView)
leastsquare=lsmeans(aovflowerspikes,pairwise~Site*Treatment) ###Tukey-adjusted
comparisons
#leastsquare = lsmeans(model, pairwise ~Site)
CLD<- cld(leastsquare,
        alph.=0.05,
        Letters= letters, ### Use lower-case letters for .group
        adjust. = "tukey")###. Tukey-adjusted comparisons
CLD

```

```

#Normality
with(ACJAmesureA,{
  hist(flowerspikesb)
  qqnorm(flowerspikesb)
  qqline(flowerspikesb)})
with(ACJAmesureA,{ shapiro.test(flowerspikesb)})

with(ACJAmesureA,{
  hist(log(flowerspikesb))
  qqnorm(log(flowerspikesb))
  qqline(log(flowerspikesb))})
with(ACJAmesureA,{ shapiro.test(log(flowerspikesb))})

#Simple box plot flowerspikes transforms to true NRI value

boxplot((flowerspikesb) ~Treatment*Site,
  data = ACJAmesure, notch=FALSE, col=(c("palegreen","darkgreen")),
  xlab = "Site & Treatment",
  ylab = "flowerspikes")

#Spike length
ACJAmesureA<- read.csv("August.csv",header=TRUE, row.names=1, sep=",")
aovlengthspike <-aov(log(lengthspikeb)~Site*Treatment+Error(Plot),data=ACJAmesureA)
print(summary(aovlengthspike))

#Means
with(ACJAmesureA,tapply(lengthspike, list(Site, Treatment), mean, na.rm=TRUE))

#Means
with(ACJAmesureA,tapply(lengthspikeb, list(Site, Treatment), mean, na.rm=TRUE))

#Standard Deviation
with(ACJAmesureA,tapply(lengthspike, list(Site, Treatment), sd, na.rm=TRUE))

#Standard Deviation
with(ACJAmesureA,tapply(lengthspikeb, list(Site, Treatment), sd, na.rm=TRUE))

library(lsmmeans)
leastsquare=lsmmeans(aovlengthspike,pairwise~Site) ###Tukey-adjusted comparisons
#leastsquare = lsmmeans(model, pairwise ~Site)
CLD<- cld(leastsquare,
  alph.=0.05,
  Letters= letters, ### Use lower-case letters for .group
  adjust. = "tukey")###. Tukey-adjusted comparisons
CLD

```

```

#Normality
with(ACJAmesureA,{
  hist(lengthspikeb)
  qqnorm(lengthspikeb)
  qqline(lengthspikeb)})
with(ACJAmesureA,{ shapiro.test(lengthspikeb)})

with(ACJAmesureA,{
  hist(log(lengthspikeb))
  qqnorm(log(lengthspikeb))
  qqline(log(lengthspikeb))})
with(ACJAmesureA,{ shapiro.test(log(lengthspikeb))})

#Simple box plot lengthspike transforms to true NRI value

boxplot((lengthspikeb) ~ Site,
  data = ACJAmesureA, notch=FALSE, col=(c("palegreen")),
  xlab = "Site",
  ylab = "lengthspike")

#Branching
ACJAmesureA<- read.csv("August.csv",header=TRUE, row.names=1, sep=",")
aovx <-aov(Xb~Site*Treatment+Error(Plot),data=ACJAmesureA)
print(summary(aovx))

library(lsmmeans)
leastsquare=lsmmeans(aovx,pairwise~Site) ###Tukey-adjusted comparisons
#leastsquare = lsmmeans(model, pairwise ~Site)
CLD<- cld(leastsquare,
  alph.=0.05,
  Letters= letters, ### Use lower-case letters for .group
  adjust. = "tukey")###. Tukey-adjusted comparisons
CLD

#normality
with(ACJAmesureA,{
  hist(Xb)
  qqnorm(Xb)
  qqline(Xb)})
with(ACJAmesureA,{ shapiro.test(X)})

with(ACJAmesureA,{
  hist(log(Xb))
  qqnorm(log(Xb))
  qqline(log(Xb))})
with(ACJAmesureA,{ shapiro.test(log(Xb))})

```

```
#Simple box plot X transforms to true NRI value

boxplot((Xb) ~ Site,
        data = ACJAmesure, notch=FALSE, col=(c("palegreen")),
        xlab = "Site",
        ylab = "X")
#Means
with(ACJAmesureA,tapply(X, list(Site, Treatment), mean, na.rm=TRUE))

#Means
with(ACJAmesureA,tapply(Xb, list(Site, Treatment), mean, na.rm=TRUE))

#Standard Deviation
with(ACJAmesureA,tapply(X, list(Site, Treatment), sd, na.rm=TRUE))

#Standard Deviation
with(ACJAmesureA,tapply(Xb, list(Site, Treatment), sd, na.rm=TRUE))
```

APPENDIX B

R-SCRIPT FOR COMMUNITY DATA

```
library(depth)
library(grid)
library(ggplot2)
library(vegan)
library(abind)
library(circular)
library(MASS)

#Read in Data
#Community Data
comm.matrix<-read.csv("VegAnalysis.csv",header=TRUE, row.names=1)
class(comm.matrix)
head(comm.matrix)
veg1<- comm.matrix
colnames(comm.matrix)
rownames(comm.matrix)

#Environmental Data
env.matrix<-read.csv("environmentalcover.csv", header=TRUE,row.names=1) #,na.rm=true)
class(env.matrix)
head(env.matrix)
env2<-(env.matrix)
colnames(env.matrix)
rownames(env.matrix)

#NMDS Graph with 2 dimensions and Colored Points With ACJA
comm.matrix<-read.csv("VegAnalysis.csv",header=TRUE, row.names=1)
ord<- metaMDS(comm.matrix, distance = "bray", k = 3, trymax = 100)
names(ord)
print(ord$stress)

#AXES 1-2
ordiplot(ord, choices = c(1,2), type="t", display=c("species"))
points(ord$points[1:21,], col= "red", pch =19, asp=1)
points(ord$points[22:40,], col= "turquoise", pch =19, asp=1)
points(ord$points[41:60,], col= "blue", pch =19, asp=1)
points(ord$points[61:80,], col= "green", pch =19, asp=1)
points(ord$points[81:100,], col= "orange", pch =19, asp=1)
points(ord$points[101:119,], col= "purple", pch =19, asp=1)
ord.fit<-envfit(ord~Browse.Per.Plot,data=env.matrix,perm=999)
ord.fit
ord.fit<-envfit(ord~Cover.value,data=env.matrix,perm=999)
```

```
ord.fit
plot(ord.fit)
ord.fit<-envfit(ord~Species.Per.Plot,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
```

```
#AXES 1-3
```

```
ordiplot(ord, choices = c(1,3), type="t", display=c("species"))
points(ord$points[1:21,], col= "red", pch =19, asp=1)
points(ord$points[22:40,], col= "turquoise", pch =19, asp=1)
points(ord$points[41:60,], col= "blue", pch =19, asp=1)
points(ord$points[61:80,], col= "green", pch =19, asp=1)
points(ord$points[81:100,], col= "orange", pch =19, asp=1)
points(ord$points[101:119,], col= "purple", pch =19, asp=1)
ord.fit<-envfit(ord~Browse.Per.Plot,data=env.matrix,perm=999)
ord.fit
ord.fit<-envfit(ord~Cover.value,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
ord.fit<-envfit(ord~Species.Per.Plot,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
```

```
#AXES 2-3
```

```
ordiplot(ord, choices = c(2,3), type="t", display=c("species"))
points(ord$points[1:21,], col= "red", pch =19, asp=1)
points(ord$points[22:40,], col= "turquoise", pch =19, asp=1)
points(ord$points[41:60,], col= "blue", pch =19, asp=1)
points(ord$points[61:80,], col= "green", pch =19, asp=1)
points(ord$points[81:100,], col= "orange", pch =19, asp=1)
points(ord$points[101:119,], col= "purple", pch =19, asp=1)
ord.fit<-envfit(ord~Browse.Per.Plot,data=env.matrix,perm=999)
ord.fit
ord.fit<-envfit(ord~Cover.value,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
ord.fit<-envfit(ord~Species.Per.Plot,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
```

```
#NMDS Graph with 3 dimensions and Colored Points Without ACJA and Without Singles
```

```
#Remove Singletons
```

```
comm.matrixnoacja<-read.csv("VegAnalysis.csv",header=TRUE, row.names=1)
comm.matrixnoacja <- veg1[,colSums(comm.matrixnoacja<1)<1,drop=FALSE]
```

```
#Remove ACJA from dataset
```

```

comm.matrixnoacja = subset(comm.matrixnoacja, select = -c(ACJA))
comm.matrixnoacja<-wisconsin(comm.matrixnoacja)
ord<- metaMDS(comm.matrixnoacja, distance = "bray", k = 3, trymax = 100)
names(ord)
print(ord$stress)

```

#AXES 1-2

```

ordiplot(ord, choices = c(1,2), type="t", display=c("species"))
ord.fit<-envfit(ord~Browse.Per.Plot,data=env.matrix,perm=999)
ord.fit
ord.fit<-envfit(ord~Cover.value,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
ord.fit<-envfit(ord~Species.Per.Plot,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
points(ord$points[1:21,], col= "red", pch =19, asp=1)
points(ord$points[22:40,], col= "turquoise", pch =19, asp=1)
points(ord$points[41:60,], col= "blue", pch =19, asp=1)
points(ord$points[61:80,], col= "green", pch =19, asp=1)
points(ord$points[81:100,], col= "orange", pch =19, asp=1)
points(ord$points[101:119,], col= "purple", pch =19, asp=1)

```

#AXES 1-3

```

ordiplot(ord, choices = c(1,3), type="t", display=c("species"))
ord.fit<-envfit(ord~Browse.Per.Plot,data=env.matrix,perm=999)
ord.fit
ord.fit<-envfit(ord~Cover.value,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
ord.fit<-envfit(ord~Species.Per.Plot,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
points(ord$points[1:21,], col= "red", pch =19, asp=1)
points(ord$points[22:40,], col= "turquoise", pch =19, asp=1)
points(ord$points[41:60,], col= "blue", pch =19, asp=1)
points(ord$points[61:80,], col= "green", pch =19, asp=1)
points(ord$points[81:100,], col= "orange", pch =19, asp=1)
points(ord$points[101:119,], col= "purple", pch =19, asp=1)

```

#AXES 2-3

```

ordiplot(ord, choices = c(2,3), type="t", display=c("species"))
ord.fit<-envfit(ord~Browse.Per.Plot,data=env.matrix,perm=999)
ord.fit
ord.fit<-envfit(ord~Cover.value,data=env.matrix,perm=999)
ord.fit

```

```

plot(ord.fit)
ord.fit<-envfit(ord~Species.Per.Plot,data=env.matrix,perm=999)
ord.fit
plot(ord.fit)
points(ord$points[1:21,], col= "red", pch =19, asp=1)
points(ord$points[22:40,], col= "turquoise", pch =19, asp=1)
points(ord$points[41:60,], col= "blue", pch =19, asp=1)
points(ord$points[61:80,], col= "green", pch =19, asp=1)
points(ord$points[81:100,], col= "orange", pch =19, asp=1)
points(ord$points[101:119,], col= "purple", pch =19, asp=1)

#ADONIS
#transform catagorical vars to factors
env2$Treatment <- factor(env2$Treatment)
#Remove Singletons
comm.matrix <- veg1[,colSums(comm.matrix<1)<1,drop=FALSE]

#use the first one to report on
adonis (comm.matrix ~ Sites*Treatment, method="bray", strata = env2$Sites, data=env.matrix,
permutations=9999)

#make sure to remove singletons
adonis (comm.matrix ~ Sites*Treatment, method="bray", data=env.matrix, permutations=9999)
adonis (comm.matrix~Cover.value*Treatment*Sites, method="bray", strata = env2$Site,
data=env2, permutations=9999)

#pairwise distances among groups using betadisper (=permdisp)
dis <- vegdist(veg1, method="bray") #calculate Bray distances
mod <- with(env2, betadisper(dis, Sites))
boxplot(mod)
TukeyHSD(mod)

#Pairwise ADONIS
pairwise.adonis()
library(devtools)
library(pairwiseAdonis)
install_github("pmartinezarbizu/pairwiseAdonis/pairwiseAdonis")
comm.matrix <-read.csv("VegAnalysis.csv", header=TRUE,row.names=1)
env2$SiteTreat <- paste(env2$Site,'_',env2$Treatment) #create concated variable for
HERBT*SEEDT interaction in the dataset env
pairwise.adonis(comm.matrix[2:120],factors=env2$SiteTreat,sim.function =
'vegdist',sim.method = 'bray',p.adjust.m='bonferroni')

```

APPENDIX C

LIST OF SPECIES CODES AND ASSOCIATED NAMES

ACNE	<i>Acer negundo</i>
ACSA	<i>Acer saccharum</i>
ACJA	<i>Achyranthes japonica</i>
ADPE	<i>Adiantum pedatum</i>
AGAL	<i>Ageratina altissima</i>
AGPA	<i>Agrimonia parviflora</i>
AGPE	<i>Agrostis perennans</i>
ALCA	<i>Allium canadensis</i>
ARDR	<i>Arisaema dracontium</i>
AMAR	<i>Ambrosia artemisiifolia</i>
ARTR	<i>Arisaema triphyllum</i>
ARPL	<i>Arnoglossum plantagineum</i>
ASIN	<i>Asclepias incarnata</i>
ASTR	<i>Asimina triloba</i>
ASPL	<i>Asplenium platyneuron</i>
BLHI	<i>Blephilia hirsuta</i>
BICA	<i>Bidens canadensis</i>
BOCY	<i>Boehmeria cylindrica</i>
BOVI	<i>Botrychium virginianum</i>
BRIN	<i>Bromus inermis</i>
CAAM	<i>Campanulastrum americanum</i>
CARA	<i>Campsis radicans</i>
CA1	<i>Carex 1</i>
CA2	<i>Carex 2</i>
CA3	<i>Carex 3</i>
CABL	<i>Carex blanda</i>
CAFR	<i>Carex frankii</i>
CAGL	<i>Carex glaucoidea</i>
CALU	<i>Carex lupulina</i>
CAIL	<i>Carya illinoensis</i>
CEOR	<i>Celastris orbiculatus</i>
CAOV	<i>Carya ovata</i>
CATO	<i>Carya tomentosa</i>
CELA	<i>Celtis laevigata</i>
CHLA	<i>Chasmanthium latifolium</i>
CHAL	<i>Chenopodium album</i>
CILU	<i>Cicciaea lutetiana</i>

CIAR	<i>Cirsium arvense</i>
COCO	<i>Commelina communis</i>
COCA	<i>Conyza canadensis</i>
CYST	<i>Cyperus strigosus</i>
CRCA	<i>Cryptotaenia canadensis</i>
DAGL	<i>Dactylis glomerata</i>
DERO	<i>Desmodium rotundifolium</i>
DIVIL	<i>Dioscorea villosa</i>
DIVI	<i>Diospyros virginiana</i>
ELUM	<i>Eleagnus umbellata</i>
ELCA	<i>Elephantopus carolina</i>
ELVI	<i>Elymus virginiana</i>
ECAN	<i>Elymus canadensis</i>
ENSE	<i>Endodeca serpentaria</i>
EQAR	<i>Equisetum arvense</i>
EQHY	<i>Equisetum hyemale</i>
ERHI	<i>Erichtites heiracifolia</i>
ERPH	<i>Erigeron philadelphicus</i>
EOFO	<i>Eunoymus fortunii</i>
EUPE	<i>Eupatorium perfoliatum</i>
FAGR	<i>Fagus grandifolia</i>
FASC	<i>Fallopia scandens</i>
FRVI	<i>Fragaria virginiana</i>
FACO	<i>Fallopia convovulus</i>
FRAM	<i>Fraxinus americana</i>
FRPE	<i>Fraxinus pennsylvanica</i>
GAAP	<i>Galium aparine</i>
GACI	<i>Galium circaezans</i>
HEAM	<i>Heuchera americana</i>
GECA	<i>Geum canadensis</i>
HUJA	<i>Humulus japonica</i>
HYPR	<i>Hypericum prolificum</i>
ILDE	<i>Ilex decidua</i>
ILOP	<i>Ilex opaca</i>
IMLU	<i>Impatiens lutea</i>
IPLA	<i>Ipomea lacunosa</i>
IPPA	<i>Ipomea pandurata</i>
LACA	<i>Laportea canadensis</i>
LIBE	<i>Lindera benzoin</i>

LITU	<i>Liriodendron tulipifera</i>
LEVI	<i>Leersia virginica</i>
LOJA	<i>Lonicera japonica</i>
LOMA	<i>Lonicera maackii</i>
LYCI	<i>Lysimachia ciliata</i>
MIVI	<i>Microstegium vimineum</i>
MORU	<i>Morus rubra</i>
OPHI	<i>Ophioglossum</i>
OSVI	<i>Ostrya virginiana</i>
OXST	<i>Oxalis stricta</i>
PAPE	<i>Parietaria pennsylvanica</i>
PAQU	<i>Parthenocissus quinquefolia</i>
PALU	<i>Passiflora lutea</i>
PEDI	<i>Penstemon digitalis</i>
PEPE	<i>Persicaria pensylvanica</i>
PHHE	<i>Phaegopteris hexagonoptera</i>
PHDI	<i>Phlox divaricata</i>
PHLE	<i>Phyrma leptostachya</i>
PHAM	<i>Phytolacca americana</i>
PIPU	<i>Pilea pumilla</i>
POSY	<i>Poa sylvestris</i>
POPE	<i>Podophyllum peltatum</i>
POLY	<i>Polygonum</i>
POCA	<i>Polymonia canadensis</i>
POAC	<i>Polystichum acrosticoides</i>
PRSE	<i>Prunus serotina</i>
QUAL	<i>Quercus alba</i>
QUIM	<i>Quercus imbricaria</i>
QUMU	<i>Quercus muehlenbergii</i>
QURU	<i>Quercus rubra</i>
QUST	<i>Quercus stellata</i>
RAAR	<i>Ranunculus arborvitus</i>
ROMU	<i>Rosa multiflora</i>
RUAL	<i>Rubus allegheniensis</i>
RUOC	<i>Rubus occidentalis</i>
SACA	<i>Sambucus canadensis</i>
SAOD	<i>Sanicula odorata</i>
SAAL	<i>Sassafras albidum</i>
SIST	<i>Silene stellata</i>

SMBO	<i>Smilax bona-nox</i>
SMRO	<i>Smilax rotundifolia</i>
SOCA	<i>Solanum carolinense</i>
SOLCA	<i>Solidago caesia</i>
SORI	<i>Solidago rigida</i>
STME	<i>Stellaria media</i>
SYOR	<i>Symphoricarpos orbiculatus</i>
TECA	<i>Teucrium canadense</i>
TORA	<i>Toxicodendron radicans</i>
TRRE	<i>Trifolium repens</i>
ULAM	<i>Ulmus americana</i>
ULAL	<i>Ulmus alata</i>
ULRU	<i>Ulmus rubra</i>
CADI	<i>Carex Dixon</i>
CALI	<i>Carex Limekiln</i>
CAMCB	<i>Carex Mchutchinson (broad)</i>
CAMCN	<i>Carex Mchutchinson (narrow)</i>
URDI	<i>Urtica dioica</i>
VEAL	<i>Verbesina alternifolia</i>
VIOL	<i>Viola sp.</i>
VIAE	<i>Vitis aestivalis</i>

APPENDIX D

R-SCRIPT FOR DEER DENSITY ESTIMATES

```
library(devtools)
install_github("DistanceDevelopment/Distance")
library(Distance)
library(gdata)
library(mrds)
library(knitr)

Deerplots <- read.csv("DeerdistR.csv")
names(Deerplots) <- c("Region.Label","Area","Sample.Label","Effort","distance")
head(Deerplots)

#half normal key function
halfnorm.deer<-(ds(Deerplots,key="hn",adjustment="cos",mono="strict",convert.units=0.0001))
par(mfrow=c(1,2))
plot(halfnorm.deer,main="Deerplots, Half Normal detection function")
fit.test<-ddf.gof(halfnorm.deer$ddf)
par(mfrow=c(1,2))
#Density Estimates
kable(halfnorm.deer$dht$individuals$summary,format="markdown")
kable(halfnorm.deer$dht$individuals$D,format="markdown")

#uniform key function
unifo.deer<-(ds(Deerplots,key = "unif", adjustment =
"cos",mono="strict",convert.units=0.0001))
par(mfrow=c(1,2))
plot(unifo.deer,main="Deerplots, Uniform detection function")
fit.test<-ddf.gof(unifo.deer$ddf)
par(mfrow=c(1,1))
#Density Estimates
kable(unifo.deer$dht$individuals$summary,format="markdown")
kable(unifo.deer$dht$individuals$D,format="markdown")

#hazard key function
hazard.deer<-(ds(Deerplots,key="hr",adjustment = "poly",convert.units = 0.0001))
par(mfrow=c(1,2))
plot(hazard.deer,main="Deerplots,Hazard detection function")
fit.test<-ddf.gof(hazard.deer$ddf)
par(mfrow=c(1,1))
#Density Estimates
kable(hazard.deer$dht$individuals$summary,format="markdown")
kable(hazard.deer$dht$individuals$D,format="markdown")
```

APPENDIX E

R-SCRIPT FOR CORRELATION MATRIX

```
install.packages("corrplot")
library(corrplot)

Correlation <- read.csv("Correlation.csv")
names(Correlation) <- c("BROWTOT","SP.TOT","FQI", "DD", "CC", "Height_O"
"Height_C", "NODE_O", "NODE_C","Spike_#O",
"Spike_#C","Xbranching","Spike_L")
head(Correlation)

#This is the correlation matrix testing for interactions with ACJA plants FQI, Deer Density,
canopy,
#Bring in the matrix
mcor<-cor(Correlation)

#Print mcor and round to two digits
round(mcor,digits = 2)
print(mcor)
corrplot(mcor)

#Label with coefficients
col<-colorRampPalette(c("#BB4444","#EE9988","#FFFFFF","#77AADD","#4477AA"))
corrplot(mcor,method="shade",shade.col=NA,tl.col="black",tl.srt=45,
col=col(200),addCoef.col="black",addcolorlabel="no",order="AOE")

# matrix of the p-value of the correlation
p.mat <- cor.mtest(Correlation)$p
print(p.mat[, 1:13])

# Specialized the insignificant value according to the significant level
corrplot(mcor, type = "upper", order = "hclust",
p.mat = p.mat, sig.level = 0.05)

#Pvalue displayed
corrplot(mcor, p.mat = p.mat, insig = "label_sig", pch.col = "white",
pch = "p<.05", pch.cex = .5, order = "AOE")
```

VITA

Graduate School
Southern Illinois University

Nicholas Richard Seaton

Nickseaton567@gmail.com

Southern Illinois University Carbondale
Bachelor of Science, Forestry, December 2013

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