Impacts of white-tailed deer on forest health in the Pine Barrens on Long Island

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Abstract - Excessive browsing due to the overpopulation of white-tailed deer (*Odocoileus virginianus*) has had impacts to forest health throughout the eastern United States, including the Long Island Pine Barrens Region. Pine Barrens are a unique ecological system characterized by dry, nutrient poor soils and the presence of pitch pines (*Pinus rigida*), oaks (*Quercus sp*.), scrub oak (*Quercus ilicifolia*), blueberries (*Vaccinium sp*.), and huckleberries (*Gaylussacia sp*.). In this ecosystem, white-tailed deer have impacted the size and abundance of tree seedlings and saplings, as well as the abundance of understory species. For this project, we collected data from pre-established forest health monitoring plots and deer exclosures as a continuation of a long-term assessment of pine barrens health within Brookhaven National Laboratory (BNL). Throughout our project, we assessed four deer exclosures and their associated forest health plots, where we looked at canopy closure, understory plants and their abundances, tree seedlings, and saplings within the plot. In doing this we found that short shrub and sapling abundances within plots differed inside and outside deer exclosures. These results suggest that different plants may react differently to the effects of deer browse. These differences may have also occurred due to varying environmental conditions other than deer, such as light or soils. Over time, BNL will be able to use our data to look farther into how, how long, or if a forest can be naturally restored to its historic composition after the exclusion of deer. This experience has allowed us to become acquainted with new field techniques and equipment, as well as to work in a habitat that we haven't had the chance to work in before.

Introduction

White-tailed deer (*Odocoileus virginianus*) are often selective browsers, but as resources become scarce they will eat anything available to them (Halls 1984). In recent decades, Long Island, New York has been plagued by an overpopulation of deer (U.S. Department of Energy 2013). As local populations increase past carrying capacities, forest health is negatively affected by over-browsing of low shrubs, trees, and herbaceous plant species, which can prevent regeneration (Boulanger *et. al.* 2015; Tanentzap *et al.* 2009). Throughout the United States, these populations are managed through the implementation of birth control, hunting regulations, culling, and the creation of deer exclosures (Alverson *et al.* 1988). On Long Island, specifically at Brookhaven National Laboratory (BNL), the deer population is managed by culling and by monitoring deer exclosures to track forest health (Timothy Green, Brookhaven National Laboratory, personal communication; U.S. Department of Energy 2013). However, management at the lab has only begun within the past year, and effects may not become apparent for several years.

For our project, we focused on changes in plant community in 4 pre-established deer exclosures compared with their paired plots throughout BNL from June to August 2015. Deer exclosures were established in the summers of 2011 and 2012, three of the paired plots were established in 2005 and 2006, and the remaining paired plot was established in 2015. Our objective was to compare vegetation diversity, growth, and abundance between deer-excluded and non-excluded areas in the Long Island Pine Barrens. The data collected will serve as part of a long-term study monitoring how long, or even if forest recovery will take place after the exclusion of white-tailed deer.

Methods

Study Site

BNL is a national research laboratory that sits on 5,265 acres of land in Upton, NY in Suffolk County, Long Island. In 1917, the land was cleared for the creation of Camp Upton, a United States Army base that served to house troops during both World Wars (Brookhaven National Lab). In the time between the World Wars it remained untouched as Upton National Forest. In 1947, Camp Upton became Brookhaven National Lab, dedicated to research on atomic energy (Brookhaven National Laboratory).

Currently, BNL is part of the 102,500 acres of protected pine barrens forest in Long Island. BNL forms the center of the Central Pine Barrens, one of only three pine barrens systems in the world. Its forests are characterized by pitch pine (*Pinus rigida*), oak species (*Quercus spp*.), and an understory consisting of scrub oak (*Quercus ilicifolia*) and various heath species such as blueberries (*Vaccinium spp*.) and huckleberries (*Gaylussacia spp*.). (Natural Resource Management Plan for Brookhaven National Laboratory Citation)

Four deer exclosures and their associated paired forest health plots were monitored to compare vegetation communities both affected by and excluded from white-tailed deer (Figure 1). Plots surveyed were located in oak-pine, pitch pine, and coastal oak forest types. Dominant plants found throughout plots included pitch pine, white oak (*Quercus alba*), scarlet oak (*Quercus coccinea*), scrub oak, black huckleberry (*Gaylussacia baccata*), late lowbush blueberry (*Vaccinium pallidum*), and early lowbush blueberry (*Vaccinium angustifolium*).

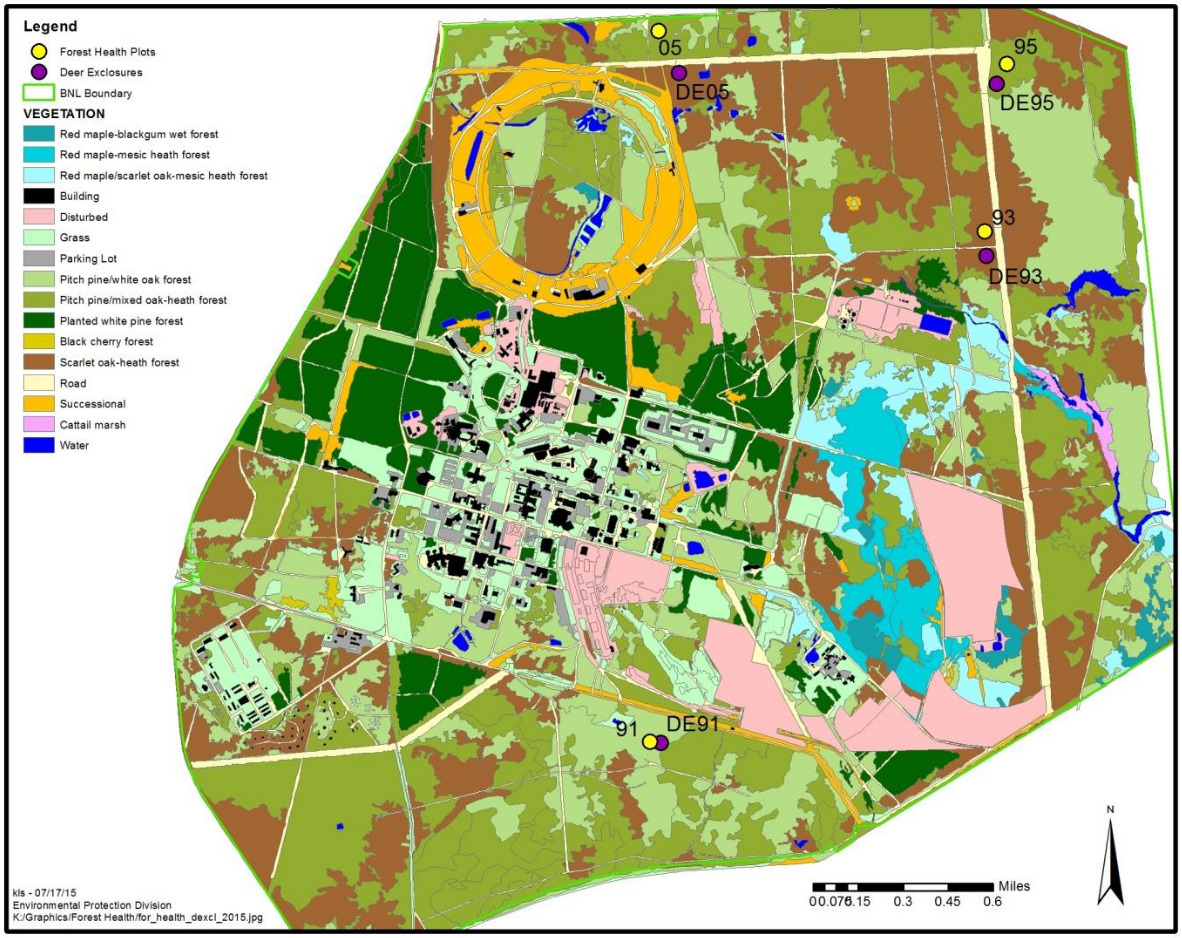

Figure 1: Deer exclosures and their associated forest health plots, monitored June-July 2015 at Brookhaven National Laboratory

Forest Health Monitoring Protocols

To establish plots within BNL, coordinates were chosen randomly using ArcGIS. Within each 16 x 25 meter plot, all flora and fauna species were recorded, photographs were taken, strata cover and height were recorded, and ten transects were run along the 16 meter edge (Foundation for Ecological Research in the Northeast, 2007). Starting points on each transect were randomly chosen, and from there, a 2 meter tent pole was used to record all adjacent plant species at each additional meter along transects. Litter and duff samples were taken at four locations along transects, and canopy cover type (pitch pine and/or hardwood) was also noted.

After the borders of the plot had been marked and established, a large, live, and healthy tree in the immediate area surrounding the plot was spray painted and marked as a witness tree. Four belt transects were constructed within each plot to collect data on seedling and sapling growth. Live trees, dead trees, and downed logs greater than 10-centimeters DBH were also identified and measured for each plot.

Statistical Analyses

Unpaired t-tests were performed to test the significance between sapling abundance and heath species abundance within deer exclosures and their paired plots (GraphPad 2015).

Results

We recorded vegetative data in four deer exclosures and their associated forest health plots throughout BNL. Species richness for each plot was recorded and was found to be insignificant between deer exclosures and paired plots (p-value = 0.7522, t = 0.3169). Differences in abundances between *G. baccata, V. pallidum, V. angustifolium,* and saplings in the deer exclosures and paired plots were also compared. Within these plots, we found that *G. baccata* abundance in deer exclosures (11.4 ± 4.58 stems per transect, mean ± SD) versus paired plots (8.95 ± 4.7 stems transect, mean ± SD) was significant (p-value = 0.0206, t = 2.36) (Figure 2). We found that of all plots surveyed, 56% of *G. baccata* was located within deer exclosures. Of the *V. pallidum* found within monitored plots, only 39% was located within deer exclosures. These results were also significant (p-value = 0.0029, t = 3.07), showing that *V. pallidum* was less abundant in deer exclosures (5.53 ± 4.12 stems per transect, mean ± SD) than in paired plots (8.95 ± 4.7 stems per transect, mean ± SD) (Figure 3). *V. angustifolium* did not have any significant differences (p-value = 0.3004, t = 1.0425) in abundance between deer exclosures

(2.48 ± 2.7 stems per transect, mean ± SD) and paired plots (3.08 ± 2.44 stems per transect, mean ± SD) (Figure 3).

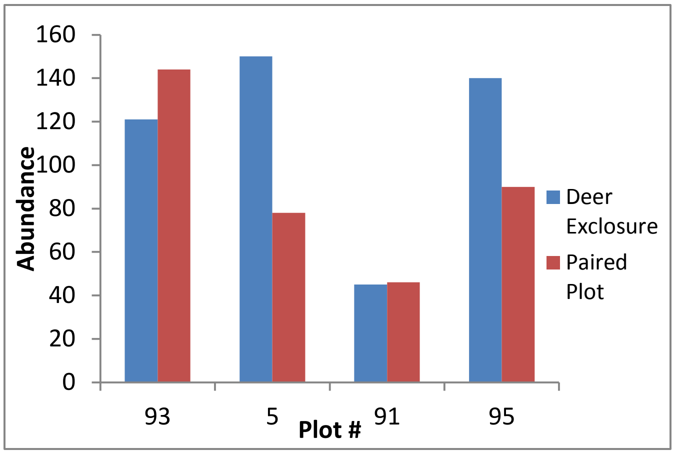

Figure 2: Black huckleberry (*Gaylussacia baccata)* abundance in deer exclosures versus paired plots at Brookhaven National Laboratory, NY. Data collected June-July 2015.

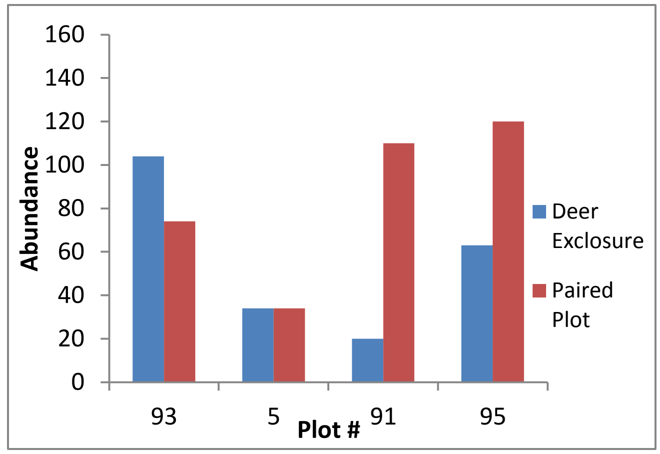

Figure 3: Late lowbush blueberry (*Vaccinium pallidum)* abundance in deer exclosures versus paired plots at Brookhaven National Laboratory, NY. Data collected June-July 2015.

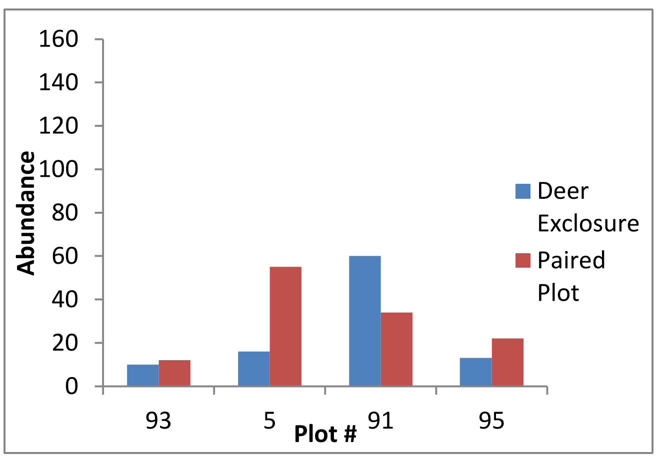

Figure 4: Early lowbush blueberry (*Vaccinium angustifolium)* abundance in deer exclosures versus paired plots at Brookhaven National Laboratory, NY. Data collected June-July 2015.

Sapling abundances between deer exclosures and paired plots were also compared. Based on our statistical analyses, we found that deer exclosures (4.25 ± 3.7 stems per belt transect, mean ± SD) had significantly more saplings than paired plots (1.44 ± 2.68 stems per belt transect, mean ± SD) (p-value = 0.0197, t = 2.46) (Figure 5).

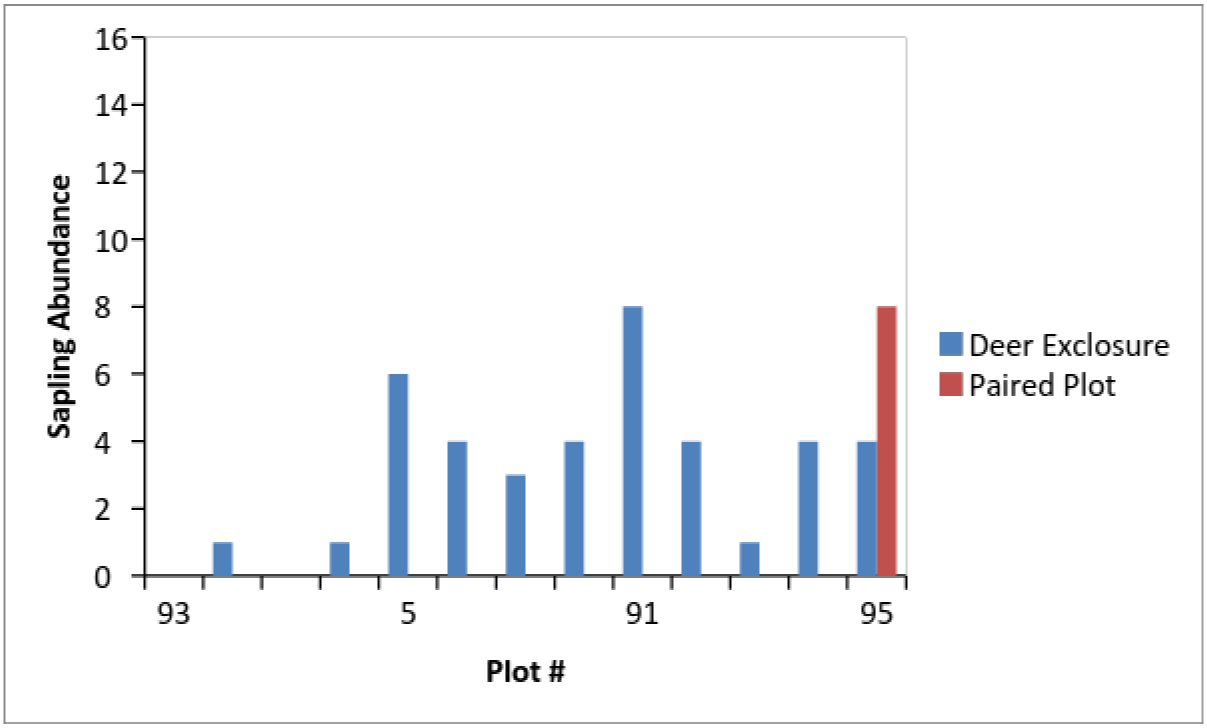

Figure 5: Sapling abundances per belt transect in deer exclosures versus paired plots at Brookhaven National Lab, NY. Data collected June-July 2015.

Discussion

There were no notable differences in species richness between deer exclosures and their paired plots. This finding can be backed by Pekin *et al.* (2015), who found that grazing by ungulates effects plant dominance within an area, but not necessarily the diversity within that area. Within our plots, plant species richness differed by four species at most between deer exclosures and paired plots. While white-tailed deer can affect species composition through selective feeding (Boulanger *et al.* 2015), the large population of deer present at BNL forces individuals to be less selective in their food choices and to consume a broader range of vegetation found throughout the site. While species richness remained similar throughout plots, differences in plant species abundance did arise between them; most notably *G. baccata* and *V. pallidum*. BNL has had problems with overpopulations of deer over 20 year, and unfortunately a lot of damage may have already been done. However, there is no record of baseline forest health data from before the explosion of the white-tailed deer population, and thus we do not know the full extent of the impacts they have had on the forest. Deer may reduce local seed sources, diminishing the seedbank needed for the future regeneration of palatable plants (Tanentzap *et al*. 2009). Species richness within plots may not have been significant because exclosures have only been up for three years. Three years may not been enough time to allow for adequate regeneration of plants heavily affected by deer. However, deer browse of new growth may have exhausted the seedbank prior to the construction of exclosures, resulting in an insignificant difference in species richness.

Based on our results, *G. baccata* showed the greatest abundance in paired plots versus deer exclosures. This information is supported by the findings of Rawinski (2008) which state that forest floors are typically composed of unpalatable food sources for white-tailed deer, such as *G. baccata.* A study by Reiners (1967) states that *Gaylussacia sp.* is generally more abundant than *Vaccinium sp.* in the Pine Barrens on Long Island. However, when it came to the deer exclosures, *V. pallidum* was much more prevalent than *G. baccata*. Strained resources due to high population sizes at the Lab could cause deer to feed on *G. baccata*. *G. baccata* generally grows taller than *Vaccinium sp*., and could shade out the *Vaccinium*. If deer are browsing *G. baccata* outside of the deer exclosures, they may be lessening competition between these species, resulting in an increased abundance of *Vaccinium sp*. outside of the exclosures (Reiners, 1967). In 2009, Mudrak and colleagues found that 36% of plant species in their study showed inconsistent change between deer exclosures and paired plots. This information suggests that different species have different responses to the presence of deer (Mudrak, 2009). This information could also suggest factors such as light or soils could be influencing plant abundances (Reiners, 1967). *V. angustifolium* showed no significant changes in abundance between the deer exclosures or the paired plots. *V. angustifolium* had the lowest mean stems present in both deer exclosures and paired plots as compared to *V. pallidum* and *G. baccata.* This information is also supported by Reiners (1967), who claimed *V. angustifolium* had the lowest biomass out of the three heath species in the previously mentioned study.

When it came to sapling abundance, deer exclosures had significantly higher abundances than paired plots. Similarly, in a study done by Tanentzap *et al.* (2009), exclosures contained greater sapling densities than control plots, even after four decades of deer management. In a study done by McGarvey *et al.* (2013), sapling abundance was reduced outside the deer exclosures due to deer browse; a fact further supporting our results. Long-term deer browse can reduce woody plant regeneration and a plant's ability to grow above the browse line (2 meters). If deer browsing on saplings continues at similar rates in the future, saplings will not be able to grow past the browse line and the forest will have a greater chance of diminishing as the overstory trees senesce (Gubanyi *et al.*, 2008; Griggs *et al.*, 2006). In the future, browse-tolerant species may be the only ones that can successfully regenerate (Griggs *et al.*, 2006).

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