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Vegetation Community Monitoring at Tallgrass Prairie National Preserve, Kansas

2002 - 2010

Natural Resource Report NPS/HTLN/NRDS—2011/146

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Introduction

Vegetation community monitoring of core sites has been ongoing in the western upland pastures since 2002. Initially known as the Spring Hill Ranch area and continuously grazed for beef production for over 120 years, Tallgrass Prairie National Preserve (TAPR) is over 10,000 acres of unplowed tallgrass prairie in the Flint Hills physiognomic province of Kansas. This report summarizes findings from eight years of vegetation community monitoring efforts by the Heartland Inventory and Monitoring Network.

Methods

Data collection

The Heartland Inventory and Monitoring Network (HTLN) implemented monitoring of core sites at TAPR in 2002 to provide analysis and to assess future change in the upland pastures (see James et al, 2009 for detailed information on monitoring protocol). Monitoring of core sites occurred annually from 2002 to 2008 and again in 2010. Core monitoring sites (n = 30) are located in four western upland pastures (Fig. 1).

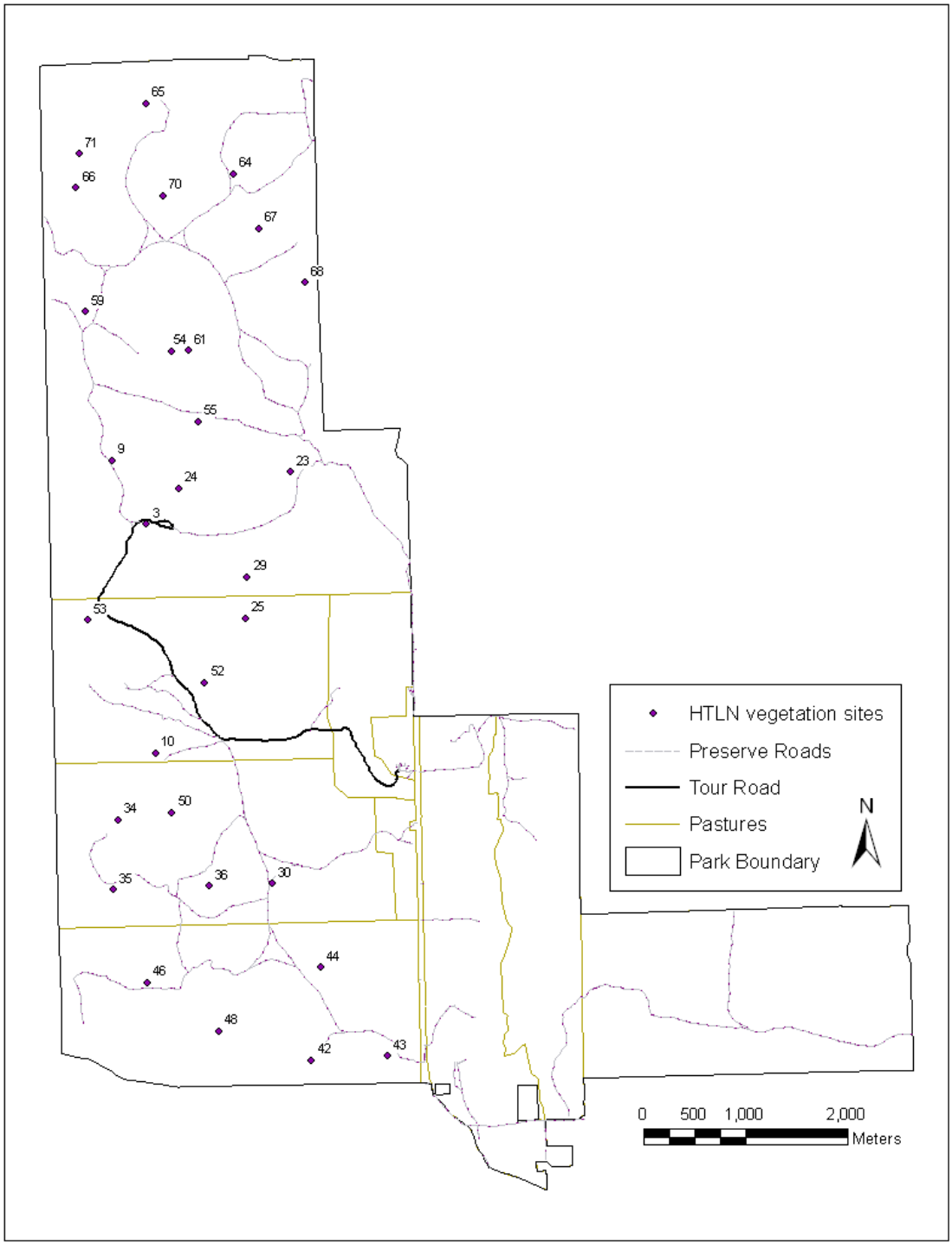

Figure 1. Location of Heartland Inventory and Monitoring Network core vegetation monitoring sites (n=30) at Tallgrass Prairie National Preserve, Kansas.

All sites are monitored according to the revised 2009 protocol and are comprised of two parallel transects each containing five nested sample plots (Fig. 2). Species composition and foliar cover estimates are collected from each plot and values are summarized to the individual site.

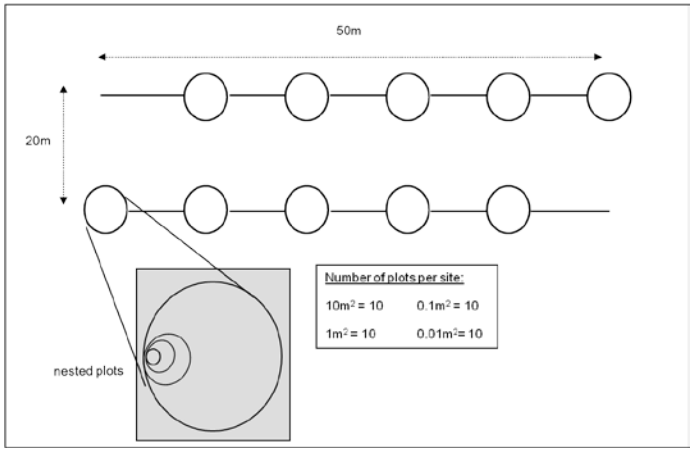

Figure 2. Heartland Inventory and Monitoring Network vegetation community sample design showing transects and plots including nested plots.

Individual species percent foliar cover is calculated for each site. Foliar cover serves as an estimate of abundance for herbaceous species. Cover class intervals are converted to median values to estimate percent cover for each herbaceous and shrub species. Mean percent cover is then calculated as the species percent cover for a site, averaged for all ten plots within the site.

Data Summary and Analysis

Data collected from all plots within a site are summarized by species to the site level. Mean site values along with a measure of among site variability (± 1 standard error of the mean) are presented for the community. Foliar cover estimates collected for each species within a plot are the basis of field data used in all subsequent analysis.

Prairie community diversity

Three measures of diversity were calculated among all sites within the upland prairie. Alpha diversity (i.e., site level diversity) was calculated as the average species richness per site; gamma diversity (i.e., community level diversity) was estimated as the total number of species across all sites (McCune and Grace 2002). Each measure of diversity was summarized for the upland prairie. Beta diversity, as a measure of the heterogeneity in the data, was calculated as (Whittaker 1972):

$$\beta_w = (S_c / S) - 1$$

where:

β_w = beta diversity,
S_c = the number of species in the prairie,
S = the average species richness in the sample sites.

As a rule of thumb, values of $\beta_w < 1$ are rather low and $\beta_w > 5$ are considered high beta diversity (McCune and Grace 2002). If $\beta_w = 0$, then all species are found within each site. The one is subtracted to make zero beta diversity correspond to zero variation in species presence. While

this measure does not have any formal units, the result could be thought of in approximate units as the "number of distinct communities" (McCune and Grace 2002).

Prairie species diversity

For each site within the community, species richness (S) along with the effective number of species derived from both Shannon diversity index (Shannon number or H_e) and Simpson's diversity index (Simpson's number or D_e) was calculated. Foliar cover estimates for each species in a site are used to determine each measure of species diversity in PC-ORD (McCune and Medford 1999).

Initial plant diversity for each site was calculated using the Shannon diversity index:

$$H' = -\sum_{i=1}^{n} p_i \ln p_i$$

where p*i* is the relative cover of species *i* (Shannon 1948). Simpson's index of diversity for an infinite population (D) was calculated by site (McCune and Grace 2002). It is the likelihood that two randomly chosen individuals from a site would dbe different species and emphasizes common species (McCune and Grace 2002). It is calculated by site using the complement of Simpson's original index of dominance:

$$\text{Simpson's index} = 1 - \sum_{i}^{n} p_i^2$$

Shannon and Simpson's index values were converted into effective number of species for each community (H_e and D_e, respectively). This allowed for both diversity measures to be compared directly to species richness of the sites (S) within and among sample years based on counts of distinct species in the community (Joust 2006). Shannon index was converted into effective number of species (H_e) using the following formula:

$$H_e = \exp^{(H)}$$

where H was the Shannon index value. The effective number of species based on Simpson's index (D_e) was the inverse of the index value or:

$$D_e = 1/(1-D)$$

where D was the Simpson's index value.

As S, H_e and D_e approach the same number, species begin to be equally abundant in the prairie while large differences in the number of species between each measure reflect an increasing number of less abundant species and decreasing number of more abundant species. See Jost (2006) and James and Rowell (2009) for a complete explanation and implementation of species diversity measures, respectively.

Prairie guild abundance
Species are grouped into functional guilds and foliar cover estimates are presented at the guild level for the prairie. For each guild, foliar cover is totaled for each plot and then a mean site value is calculated from all ten plots. Guilds are first divided among native and nonnative groups and then among grasses, forbs, sedges/rushes, ferns and woody species within each group.

Results

Originally, 18 core sites were designated to be sampled annually with additional secondary sites to be sampled at different intervals. As changes in the 2009 HTLN vegetation community monitoring protocol were implemented, an additional set of core sites were assigned from previously sampled secondary sites. This change brought the sample size of all core sites in 2010 up to 30. For all prior sample years, the sample size reflects the number of the 30 core sites sampled at that time (Table 1).

Annual total species richness in the western upland pastures varied from 132 to 157 species during the monitoring period (gamma diversity, Table 1). Mean site species richness (alpha diversity, Table 1) differed by as much as 13.6 species among the eight sample years. Although both alpha and gamma diversity measures were highest in 2007, beta diversity was greatest in 2010.

Table 1. Alpha, beta and gamma diversity for the upland prairie by sample year. N is the number of monitoring sites sampled that year.

N	Year	Alpha	Beta	Gamma
19	2002	51.9	1.5	132
19	2003	62.7	1.3	144
19	2004	64.8	1.2	140
20	2005	58.3	1.5	147
25	2006	59.2	1.6	153
24	2007	65.5	1.4	157
23	2008	61.7	1.5	153
30	2010	56.3	1.8	156

The HTLN sites were characterized by a larger number of species that were represented by a few individuals and/or low foliar cover (species richness, Fig. 3), and a small number of species that occurred frequently in large abundance (Shannon and Simpson number, Fig. 3). This was consistent with the distribution patterns of species within a native prairie (Collins and Glenn. 1991).

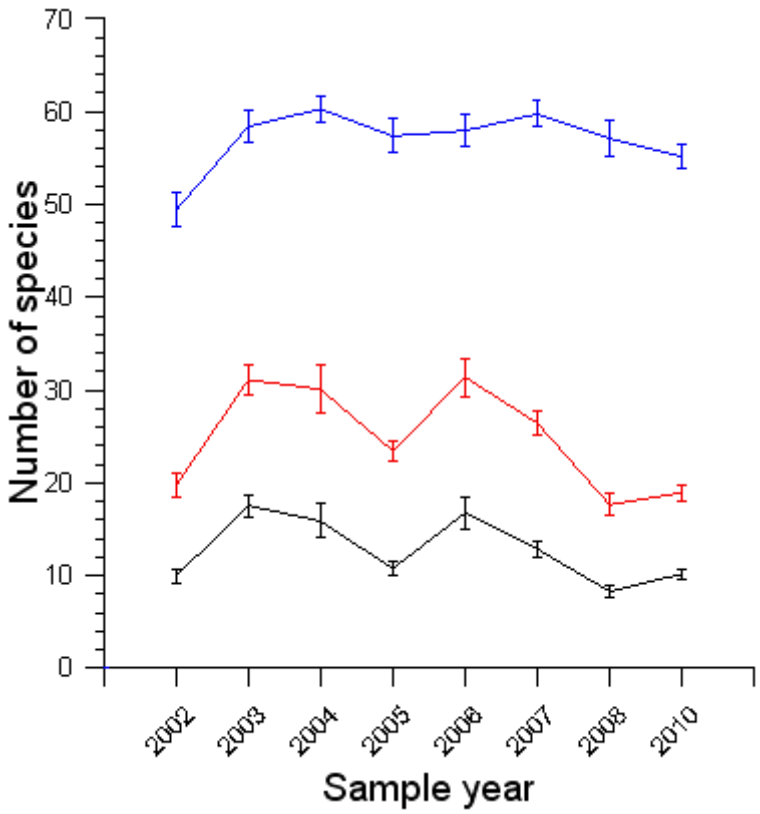

Figure 3. Mean number of species within a site as measured by species richness (blue) and effective number of species for two diversity measures (Shannon number, red; and Simpson's number, black) for core sites. Error bars are ± 1 standard error of the mean.

Native forb and grass guilds occurred in greatest abundance during all eight sample years (Fig. 4). All other plant guilds did not exceed mean foliar cover estimates over five percent during any sample year.

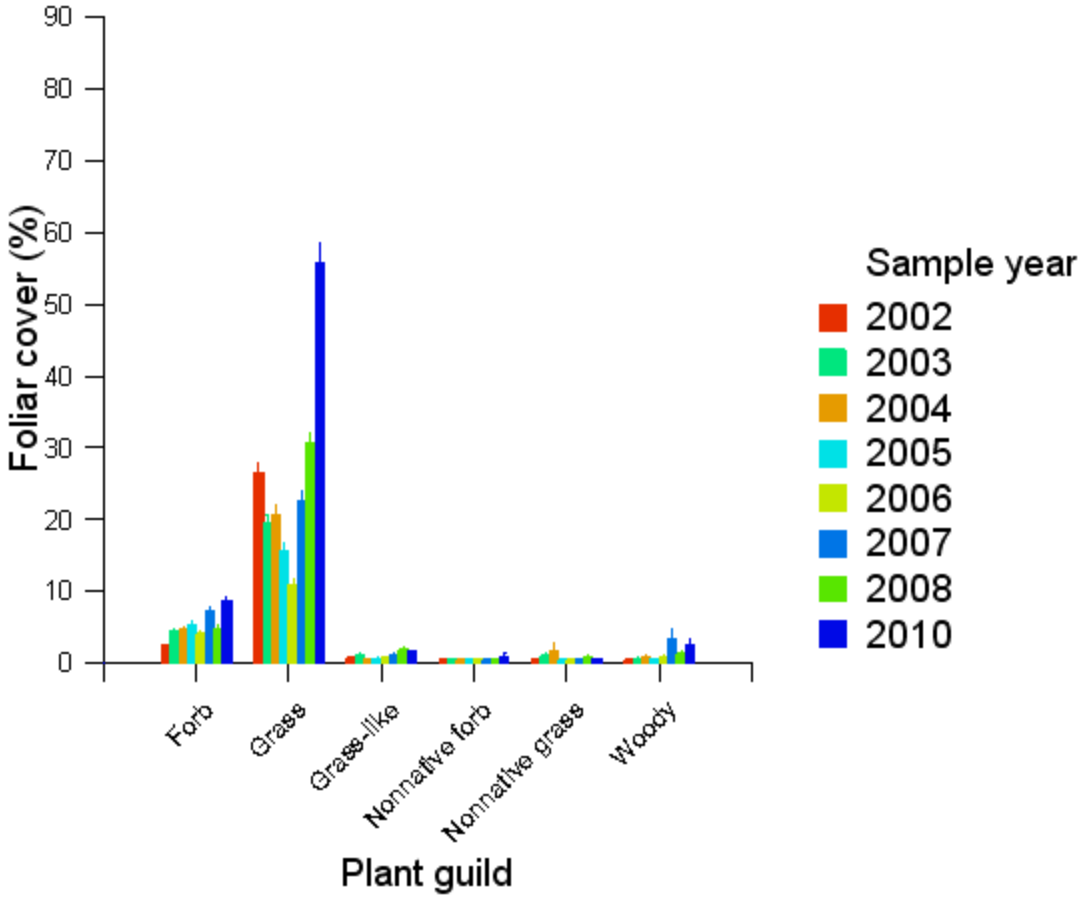

Figure 4. Mean foliar cover (± 1 standard error of the mean) for plant guilds in the western upland pastures.

Summary

Diversity measures and guild abundance derived from HTLN core sites across eight years reflect composition and structure of a functioning tallgrass prairie community. Beta diversity values throughout the monitoring period can be interpreted to indicate that all sites belong to the same broader upland tallgrass community.

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