Appendix A

Sampling Design and Protocols for
A Rapid Assessment Forest Vegetation Monitoring Program

For the Project

**Developing And Testing A Rapid Assessment Protocol For Monitoring Vegetation
Response To Deer Population Reduction In DMAP Areas On State Forest Lands**

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OBJECTIVES

The Deer Management Assistance Program (DMAP) has been applied on state forests to areas that are thousands of acres in size and the response of vegetation to deer population reduction needs to be assessed on these large areas. The proposal funded by DCNR is to design a rapid assessment technique that can be used over large areas as cost-effectively as possible. The purpose of this project is to develop a vegetation survey protocol and test the protocol on state forests enrolled in the Pennsylvania Game Commission's (PGC) DMAP to assess advanced regeneration of tree species and presence of competitive species of tree seedlings and saplings. In addition, the protocol will measure the condition of other herbaceous plant species that are indicators of the intensity of deer browsing.

SAMPLING DESIGN

The sampling design will be based on a two-stage design with systematic sampling from a random starting point. At the first stage, a systematic sample from a random starting point of n primary units will be selected. From the ith selected primary unit a systematic sample of m_i secondary units will be selected, for $i = 1, \ldots, n$.

Treating the systematic sample with a random starting point as a simple random sample (Thompson 1992), the mean y-value for the ith primary unit in the sample is

$$\hat{\bar{y}}_i = \frac{1}{m_i} \sum_{j=1}^{m_i} y_{ij}$$

Then, because systematic random sampling is used at the first stage, an unbiased estimator of the population mean is

$$\hat{\bar{y}} = \frac{1}{n} \sum_{i=1}^{n} \hat{\bar{y}}_i \quad .$$

The estimated variance of $\hat{\bar{y}}$ is

$$\hat{v}\text{ar}(\hat{\bar{y}}) = \frac{s_u^2}{n} + \frac{1}{n} \sum_{i=1}^{n} \frac{s_i^2}{m_i}$$

where

$$s_u^2 = \frac{1}{n-1} \sum_{i=1}^{n} \left(\hat{\bar{y}}_i - \hat{\bar{y}} \right)^2 \qquad \text{and} \qquad s_i^2 = \frac{1}{m_i - 1} \sum_{j=1}^{m_i} \left(y_{ij} - \hat{\bar{y}}_i \right)^2$$

are the variance terms for the primary and secondary sampling stages, respectively. However, if I end up sampling every primary sampling unit, the finite population correction (fpc $= 1 - \dfrac{n}{N}$, where n is the actual number of primary sampling units sampled and N is the total number of primary sampling units) causes the first term of the variance formula to go to zero:

$$\hat{\mathrm{var}}(\hat{\bar{y}}) = \left(1 - \frac{n}{N}\right)\frac{s_u^2}{n} + \frac{1}{n}\sum_{i=1}^{n}\frac{s_i^2}{m_i}$$

I am ignoring the fpc in the formula for the secondary sampling units because the proportion of the area sampled will be extremely small and treating the secondary sampling units as if from an infinite sampling frame is acceptable (Cochran 1977).

The above formulas can be used to estimate such parameters as mean basal area, mean stem density, mean height, etc. For presence-absence data the following formulas will be used to estimate the proportion of plots in which the species of interest is present ($y_{ij} = 1$ if present, 0 otherwise; $p_i = a_i/m$ is the proportion of plots with the species present in the subsample from the ith primary sampling unit):

$$s_1^2 = \frac{1}{n-1}\sum_{i=1}^{n}(p_i - \bar{p}) \quad \text{and} \quad s_2^2 = \frac{m}{n(m-1)}\sum_{i=1}^{n}p_i q_i$$

where $\bar{p} = \sum p_i / n$ and

$$\hat{\mathrm{var}}(\bar{p}) = (1 - f)\frac{s_1^2}{n} + \frac{s_2^2}{n}.$$

Again, if all primary sampling units are visited then the first term in the variance formula goes to zero.

SAMPLING FRAME and SAMPLING UNITS

The sampling frame consists of 11 DMAP areas identified by Merlin Benner (email dated 16 February 2006). These are DMAP areas 18, 29, 44, 54, 55, 99, 266, 370, 543, 704, and 931 (Table 1) and encompass approximately 500 square miles.

This summer six technicians (3 teams of 2 people) will be conducting the data collection. These three teams are available for about 14 weeks (not including time for training). To most efficiently collect data I anticipate these teams working four 10-hour days in the hopes that, on average, each team will collect data on 2 primary sampling units per day. Consequently, I expect to be able to sample approximately 336 primary sampling units over the course of the summer (3 teams x 2 sampling units/day x 4 days/week x 14 weeks = 336 sampling units visited).

However, 20-30 primary sampling units will be re-visited during the course of the summer to evaluate the effect of pheological changes in vegetation on data collection. For example, timing of flowering may affect detectability of some species. Thus, by conducting revisits I hope to be able to incorporate detectability into the parameter estimation.

Given that the total area sampled is approximately 500 square miles, and I anticipate being able to visit 336 sampling units, I have defined the primary sampling unit to be one square mile in area. These primary sampling units will be defined by using a GIS to randomly place a grid of points over each DMAP area. Each primary sampling unit will be a rectangle approximately 980 m by 1470 m.

Within each primary sampling unit will be a rectangular transect (see Figure 1). This transect path will be 900 m long and 600 m wide (3,000 m total length, just under 2 miles). Along this transect, every 300 m, will be a secondary sampling point. There will be 10 secondary sampling points within each primary sampling point.

Table 1. Deer Management Assistance Program (DMAP) areas on DCNR lands selected for sampling.

DMAP	Acres	Km^2	Miles^2	No. primary sampling units[a]	No. secondary sampling units[a]	Description
18	23,398	9,034	36.6	37	370	Moshannon SF and Parker Dam SP
29	15,008	5,795	23.5	23	230	Susquehannock SF – Denton Hill
44	77,672	29,989	121.4	121	1,210	Tioga SF
54	4,045	1,562	6.3	6	60	Elk SF – Dents Run
55	13,969	5,393	21.8	22	220	Bald Eagle SF – Paddy Mtn
99	10,556	4,076	16.5	16	160	Tuscarora SF – Fowlers Hollow
266	5,906	2,280	9.2	9	90	Delaware SF – Promised Land East of Rte 390
370	13,414	5,179	21.0	21	210	Wyoming SF
543	3,502	1,352	5.5	6	60	Michaux SF
704	25,499	9,845	39.8	40	400	Sproul SF – Rte 144
931	6,250	2,413	9.8	10	100	Gallitzin SF
TOTAL	199,219	76,919	311.3	311	3,110	

[a] These numbers are estimates. The exact number of primary sampling units will depend upon the configuration of each DMAP area and the random placement of the sampling grid overlaid in the GIS. This, in turn, will affect how many secondary sampling units will be visited.
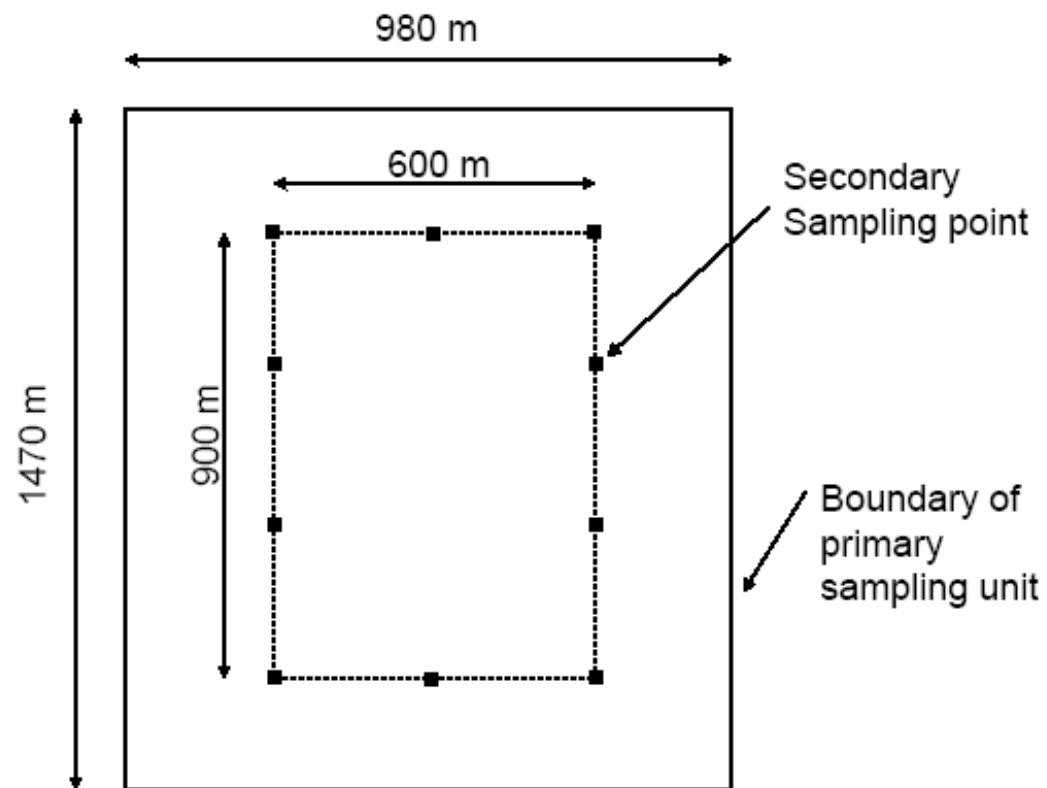
Figure 1. Boundary of primary sampling unit (1 sq. mile) and location of secondary sampling points along the 3,000 m transect within each primary sampling unit.

SECONDARY SAMPLING POINTS

Secondary sampling points that fall on roads or trails will be moved 5 m from trails or 10 m from the edge of the road. General site characteristics will be obtained from the GIS (aspect, topographic position, etc.) or recorded by technicians (moisture [xeric, mesic, hydric], presence of recent fire, logging, etc.).

At each secondary sampling point a prism plot will be used to estimate basal area (20 BAF prism corrected for slope). Tallies will be by species and diameter. Trees will be defined as having dbh >10 cm.

In addition, there will be two 1.5-m radius plots and a single 1.5 m x 40 m plot (see Figure 2). One of the circular plots will be centered on the secondary sampling point and the rectangular plot will be oriented in the direction of the transect (see Figure 1).

The 1.5-m radius plots will be used to collect tree regeneration and herbaceous species data. A tally of tree seedlings >30 cm and <150 cm tall, by species will be collected. Also, the presence of deer browsing on each seedling will be recorded. I have decided to collect data on this height class because Latham et al. (2005) noted, "Typically, tree seedlings of species that deer prefer fail to grow over 1 foot tall if subjected to heavy browsing in uncut or partially cut stands." In addition, I have excluded smaller seedlings (<30 cm) because they can be extremely time consuming to enumerate, may be difficult to identify correctly, and their abundance may reflect a good mast year rather than changes in deer browsing pressure. However, I will record the presence of species of seedlings <30 cm tall.

At these same 1.5-m radius plots I will tally *Trillium* spp., Indian Cucumber, Canada Mayflower, and Jack-in-the-Pulpit. Also, the percent of Canada mayflower that are flowering/fruited will be recorded and the height of the tallest specimen of *Trillium* spp., Indian Cucumber, Canada Mayflower, and Jack-in-the-Pulpit will be recorded.

Percent ground cover of ferns, Rubus spp., grasses, and forbs will be recorded at each 1.5-m radius plot sampling point. However, this will be estimated over a 3.5-m radius plot (1/100 acre)

The rectangular 1.5 m x 40 m plots will be used to tally shrubs and saplings (>1.5 m tall and <10 cm dbh) by species. Also, within this plot the presence of *Viburnum* spp. shrubs (esp. hobblebush), greenbrier, and elderberry. Most of the time these species will be captured in the shrub/sapling tally, but not necessarily, which is why presence data will be collected.
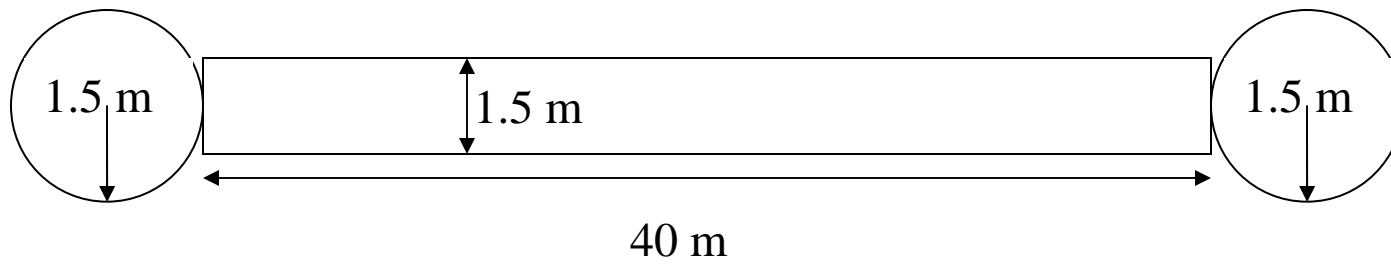
Figure 2. Layout of 1.5-m radius plots for measuring seedling and herbaceous vegetation and 1.5 m x 40 m plot for measuring stem density of shrubs and saplings and presence of specific shrub and herbaceous species.

JUSTIFICATION OF SAMPLING DESIGN AND PROTOCOLS

This sampling protocol was designed with the intention of being able to cover extensive areas quickly. I have incorporated in these protocols the recommendations of Latham et al. (2005:138) for indicator species for monitoring deer browsing and the ecological measures used by the Quality Hunting Ecology Demonstration Areas (Anacker et al. 2003). Finally, the protocols outlined here incorporate ideas generated at a meeting of DCNR, USFS, PSU, and PGC staff on 9 September 2005.

As a comparison of the measures estimable by this protocol and the Kinzua Quality Deer Cooperative (KQDC), the following table provides a comparison between these two protocols. Although not a complete comparison, it does address the most important measures of both protocols.

	Provided by	
Measure	KQDC	Rapid Assessment
Tree basal area by species with dbh	Yes	Yes
Stem density of saplings and shrubs (>1.5 m tall and <10 cm dbh) by species	Yes	Yes
Stem density of seedlings 0.3 – 1.5 m tall by species	Yes	Yes
Presence of browsing by species	Yes	Yes
Presence of seedlings, by species, <30 cm tall	Yes	Yes
Classification and tally of seedlings by height (1, 30, 100 cm)	Yes	No
Density of Indian Cucumber (1)	Yes	Yes
Density of Jack-in-the-Pulpit (2)	Yes	Yes
Average height of *Trillium* spp. (3)	Yes	Yes
Average height of (1) and (2)	Yes	No
Average height of tallest (1), (2), (3)	Yes	Yes
Presence of (1), (2), and (3)	Yes	Yes
Reproductive status of *Trillium* spp.	Yes	No
Species richness of herbaceous species	Yes	No
Percent of Canada mayflower flowering/fruited	Yes	Yes
Density of Canada mayflower	Yes	Yes
Presence-absence of the following species:		
Greenbrier	Yes	Yes
Viburnum shrubs (incl. Hobblebush)	Yes	Yes
Elderberry	Yes	Yes

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