

Understanding Brainworm Landscape Genomics on Grand Portage Indian Reservation to Prevent Minnesota Moose Declines

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Introduction

PROBLEM

- Moose (*Alces americanus*) experienced ~50% population declines over last decade.
- Brainworm (*Parelaphostrongylus tenuis*) infection is associated with 25-33% of deaths (Wolf et al. 2016).
- Mortality will likely remain high, barring intervention.

IMPORTANCE OF MOOSE

- Ecologically and culturally valuable to northeastern Minnesota.
- Subsistence resource for Native Americans.

STATE OF KNOWLEDGE

- White-tailed deer (*Odocoileus virginianus*) shed brainworm larvae in their feces, are natural definitive host.
- Slug and snail intermediate hosts integral to brainworm life cycle.

KNOWLEDGE GAP

- Forests could be managed to mitigate transmission, but how different forestry treatments affect transmission is unclear.

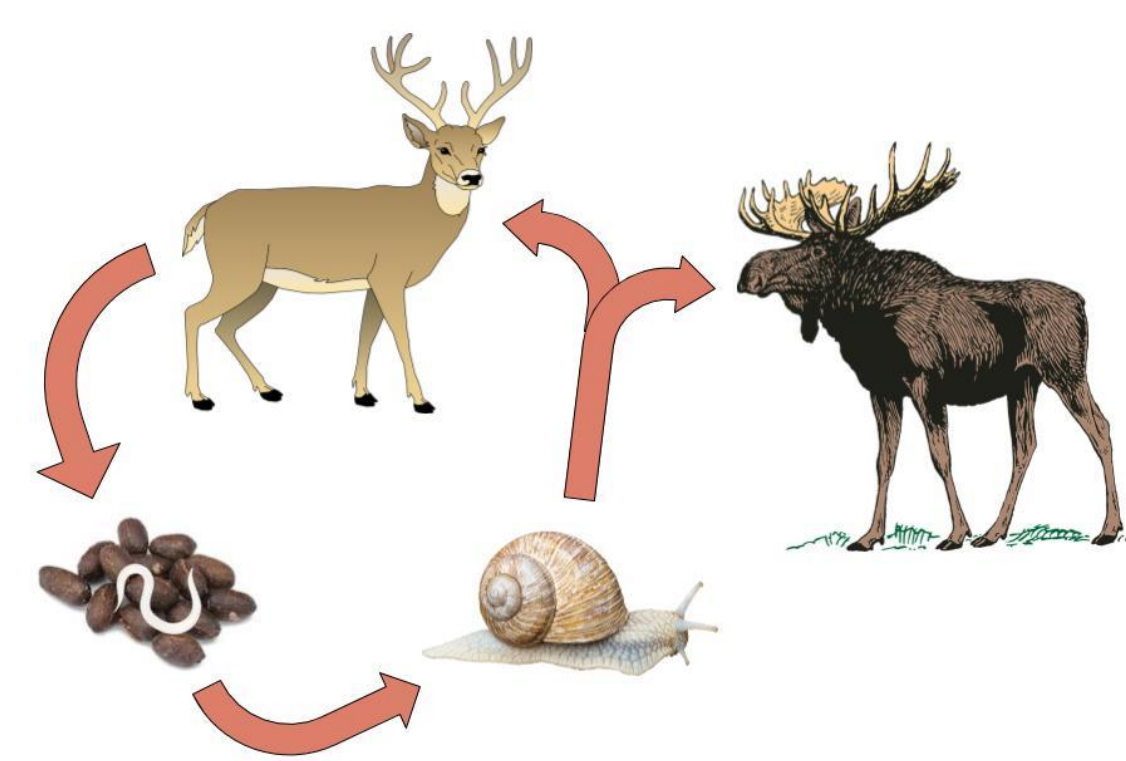


Figure 1: Visual summary of brainworm transmission cycle

Study Area

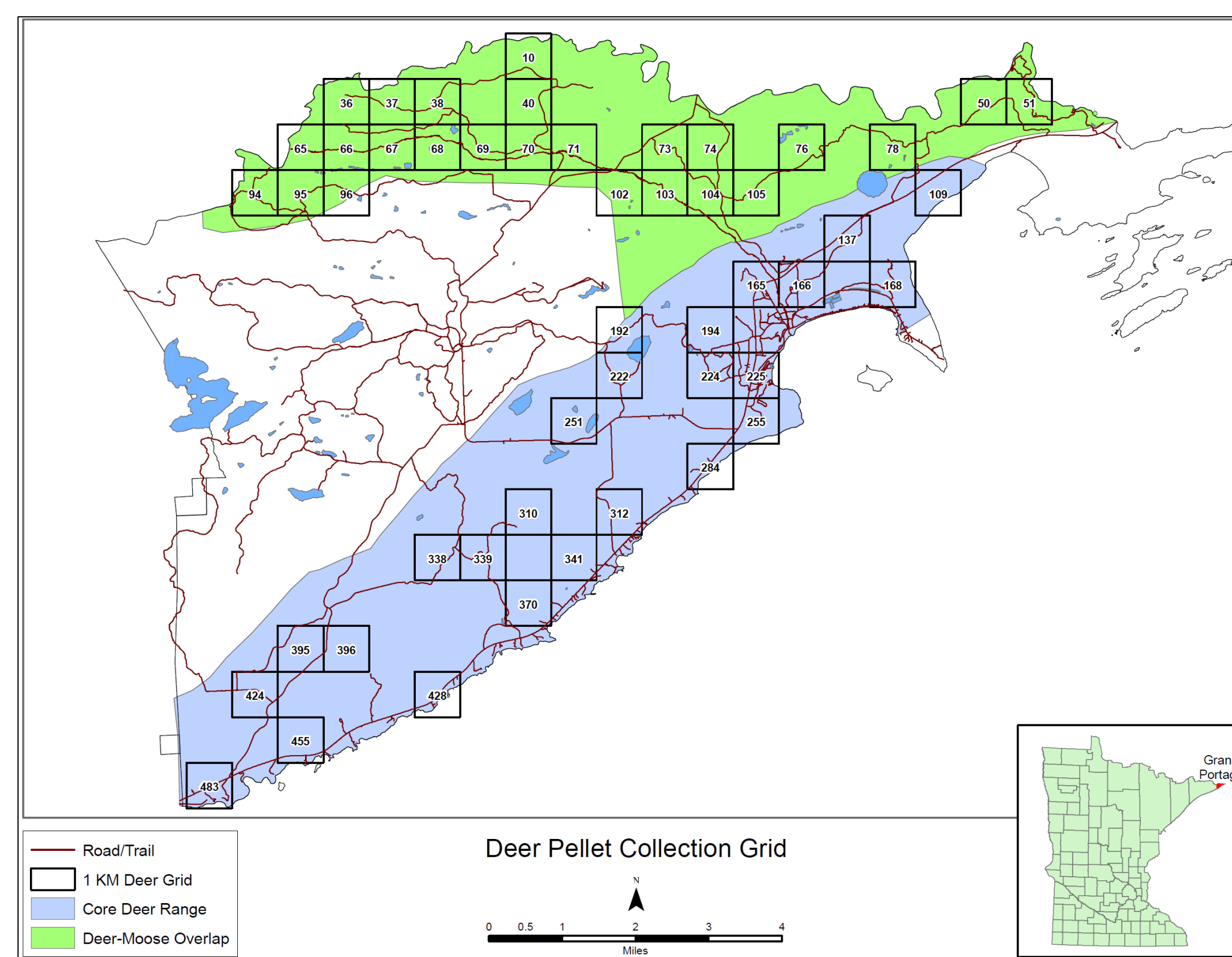


Figure 2: Study area is Grand Portage Indian Reservation in northeastern Minnesota. Outlined squares are randomly selected within each range and targeted for deer fecal collection.

Methods

FIELD SAMPLING

- Deer fecal pellets collected from deer winter range, core moose range, and deer-moose overlap range.
- Two samples from 25 1x1 km cells from each range, each year for 2 years (300 samples total).

LARVAL EXTRACTION AND RADseq

- Isolate *P. tenuis* larvae from feces using a modified Baermann flotation technique (Forrester and Lankester 1997).
- Larvae submitted to UMGC for DNA extraction and genomics work.
- Restriction site associated DNA sequencing (RADseq) allows us to build a catalog of variants for *P. tenuis*.

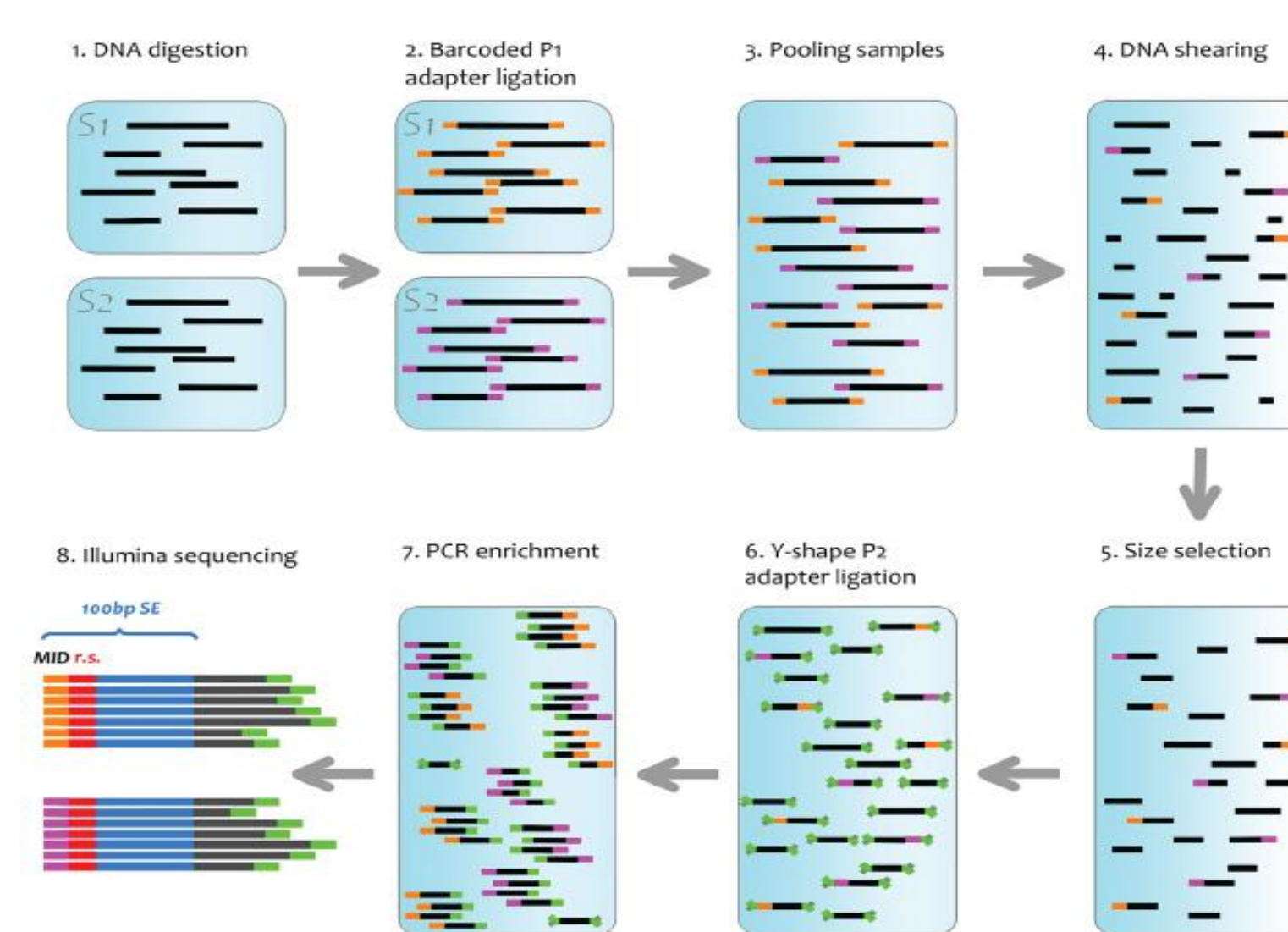


Figure 3: Summary of the steps in RADseq. Larval DNA double-digested with the enzymes PstI+MspI (targeting ~2 million reads/sample, >3000 single nucleotide polymorphisms [SNPs]).

STATISTICAL ANALYSIS

- Estimate number of populations and relative population size with Bayesian cluster analysis of the SNP dataset. Will use Structure (Pritchard et al. 2000) and SNAPP (Bryant et al. 2012) software.
- Spatial principal component analysis (sPCA) performed with the R package *adegenet* to model the spatial component of population genetic structure.

Preliminary Results

- Pilot study indicates that genetic distance of brainworm samples is similar within a single deer but different between individuals.
- Obtained 272 georeferenced deer fecal samples, 146 brainworm - positive samples (54% prevalence).
- Mean shedding rate among positive samples = 98 larvae/g feces (SD=141, max=842 larvae/g, min=0.3 larvae/g).
- DNA extraction yielded 97 samples with sufficient DNA.

Preliminary Results cont'd

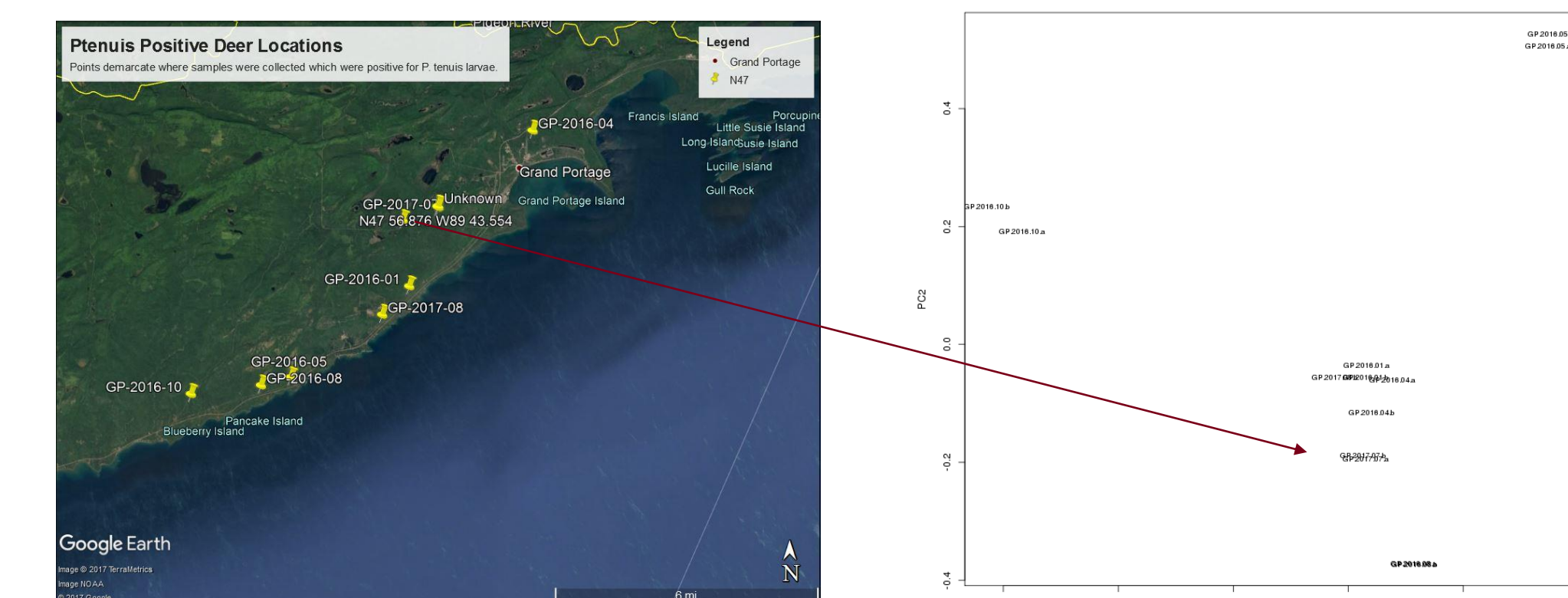


Figure 4: Georeferenced samples and sPCA plot generated by pilot study. Subsamples of brainworm larvae from a single deer cluster together; samples from different deer exhibit more genetic distance from each other.

Implications

- Knowledge of the relationship between brainworm genetic diversity and forest management practices or landscape features can be applied by forest managers across moose range to mitigate transmission to moose.
- Combined with deer movement data, will contribute to a robust, new understanding of the risk of brainworm infection on the Grand Portage Indian Reservation that can be extrapolated across northern Minnesota.
- Will provide baseline data on brainworm population structure, allowing managers to assess the efficacy of future interventions

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