Hemlock Bluffs 2018-2019 work plan – Austin M. Thomas

5-part Study Overview:

1. HEMLOCK TREE INVENTORY
2. HEMLOCK WHOLE-POPULATION GENETIC ANALYSIS
3. REPLICATE AND RE-EVALUATE 1956 HEMLOCK BLUFFS CLIMATE AND FLORISTICS SURVEY
4. LONG TERM PVA (POPULATION VIABILITY ANALYSIS) AND COMMUNITY DYNAMICS MODELING
5. HEMLOCK VEGITATIVE PROPAGATION FROM ROOTED CUTTINGS

Part 1: HEMLOCK TREE INVENTORY

1. Obtain, field verify and update Hemlock Bluffs' hemlock inventory database.
2. Tag and record new hemlock seedlings, update tree status.
3. Make inventory available to park staff to aid in ongoing hemlock population management.

Part 2: HEMLOCK WHOLE-POPULATION GENETIC ANALYSIS

1. Collect genetic material from entire population, extract and store DNA
2. Send off extracted DNA for analysis of 13 Microsatellite (STR, SSR) primers identified by Shamblin et al. 2008, Josserand et al. 2008, Amarasinghe et al. 2002, and Wellman et al. 2003 to identify clonally propagated individuals. These are the same set of primers used by Potter et al. 2012 for species wide analysis.
3. Use microsatellite analysis results to identify clonally propagated individuals from a 1990's undocumented population augmentation.
4. Use microsatellite analysis results to establish paternity where possible. Assess population level genetics (particular interest in inbreeding indicators, observed heterozygosity and Inbreeding coefficients, # of unique alleles).

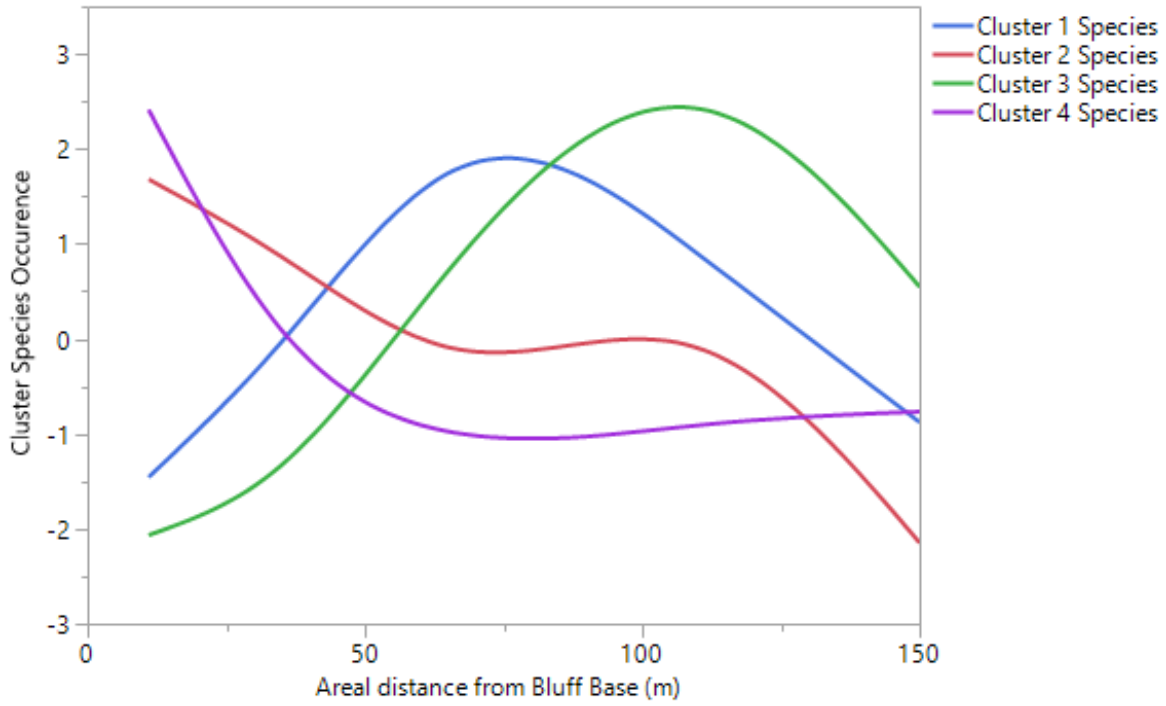
Part 3: REPLICATE AND RE-EVALUATE 1956 HEMLOCK BLUFFS CLIMATE AND FLORISTICS SURVEY

1. Digitize Oosting and Hess 1956 survey data. (completed)
2. Re-analyze 1956 survey data using modern statistical methods. (completed, see below)
3. Set-up and evaluate transects at previous locations.
4. Analyze new transect floristic data, compare to 1956 survey.
5. Purchase, set-up, and monitor climate data at historic transect points using sensors (Hobo environmental sensor units) for a 1-year period. Compare data to 1956.
6. Based on genetics (Part 2), climate data, and floristic surveys, use Environmental niche modelling, geospatial modeling, and genetic models *if possible* to assess population viability and health.

Species cluster analysis based on 1956 data:

Cluster	Members	RSquare with Own Cluster	RSquare with Next Closest	1-RSquare Ratio
1	*Panicum spp*	0.991	0.299	0.012
1	*Vaccinium tenellum*	0.966	0.238	0.045
1	*Vaccinium pallidum*	0.932	0.61	0.173
2	*Styrax rotundifolia*	0.798	0.17	0.244
2	*Styrax grandifolius*	0.893	0.197	0.134
2	*Quercus spp.*	0.95	0.236	0.065
2	*Carya spp.*	0.596	0.202	0.506
3	*Galax urceolata*	0.744	0.526	0.539
3	*Compositae*	0.725	0.105	0.307
3	*Chimaphila maculata*	0.899	0.666	0.304
3	*Gaylussacia frondosa*	0.493	0.196	0.63
3	*Acer rubrum*	0.871	0.629	0.347
3	*Quercus prinus*	0.741	0.181	0.316
4	*Athyrium asplenioides*	1	0.24	0
4	*Polystichum acrostichoides*	1	0.24	0
4	*Luzula echinata*	1	0.24	0

Interpolated species occurrence by distance from bluff base based on 1956 data:



Part 4: LONG TERM PVA (POPULATION VIABILITY ANALYSIS) AND COMMUNITY DYNAMICS MODELING

Two population models will be assessed: a matrix-based PVA and the SORTIE-ND IBM:

1. Define hemlock life-stage classes for matrix-based population modeling.
2. Determine hemlock seed production and viability for matrix model.
3. Establish long term permanent bluff observation plots according to Peet et al. 1998 CVS plot protocol (level 2 &3). Include hypsometer-based height measurements for tree species.
4. Assess plots yearly for a 10-year period, develop "Life table" according to Hartshorne 1975 for total hemlock population.
5. Assess matrix based PVA model according to Hartshorn 1975.
6. Assess CVS plot data for SORTIE-ND forest-gap analysis model to assess long-term, whole community dynamics.

Part 5: HEMLOCK VEGITATIVE PROPAGATION FROM ROOTED CUTTINGS

1. Collect cuttings from mature trees for vegetative propagation.
2. Develop and assess rooting protocols.
3. Establish rooted cuttings
4. Based on microsatellite analysis findings, select clones and planting locations on the bluff.