Population Genetic Consequences of Prairie Fragmentation

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Introduction

Habitat fragmentation reduces the size and increases the spatial isolation of plant populations. Fragmentation is predicted to cause erosion of genetic diversity and increased genetic divergence between populations.

Theoretically, the diminished size and gene pool of fragmented populations disrupts genetic equilibrium in several ways[6]:

- Creation of genetic bottlenecks
- Increased effect of random genetic drift
- Elevated likelihood of inbreeding
- Reduced gene flow between populations

These effects of fragmentation concern the conservationist because of their implications for species persistence. The resultant loss of heterozygosity and allelic richness can reduce population viability and limit a species' ability to respond to changing selection pressures.

Objective

To gauge the population genetic consequences of habitat fragmentation in prairie remnants in western Minnesota on a model prairie plant. Historically, the prairie was continuous across the sites, comprising one enormous population. The fragments we tested are the scattered remnants of the original population.

The genetic effects of fragmentation are measured by three of its consequences[6]:

- Population genetic diversity, using parameters such as allelic richness and expected heterozygosity
- Inbreeding and fitness, using observed heterozygosity.
- Interpopulation genetic divergence, using F_{st} and Hardy-Weinberg equilibria.

Study Species

Figure 1: *Echinacea angustifolia*

Narrow-leaved purple coneflower, *Echinacea angustifolia* (Asteraceae).

Our study species is a common plant native to the tallgrass prairie and plains of North America.

E. angustifolia is a model prairie species. It is long-lived, pollinated by native pollinators, and it prohibits self-fertilization and fertilization by close relatives.[5]

Method

- 18 Plant samples were obtained from *E. angustifolia* at each of 9 remnant prairie populations.
- DNA was extracted using the Qiagen extraction kit.
- 9 microsatellite loci were amplified using PCR with 9 fluorescently labeled primer pairs.
- Genotype information was obtained using the Beckman-Coulter CEQ 8000.
- Results were analyzed using the population genetics statistical programs, FSTAT[2] and SPAGEDI[3].
- To determine the presence of unique genetic clusters, we used STRUCTURE[4] to compare the 4 populations with the highest F_{st} values. Staffenson, a prairie preserve with almost 3000 flowering individuals per year, was included in the simulation as a population presumed to have maintained the genetic character of the pre-fragmentiation prairie.

Data and Analysis

Interpopulation Genetic Variation

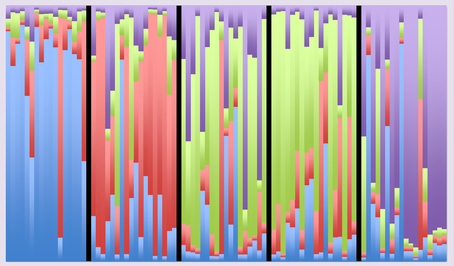
	East Riley	KJ's	Landfill	Nessman	NW of Landfill	Railroad Crossing	Steven's Approach	Staffenson
Aanenson	0.058	0.062	0.040	0.111	0.087	0.044	**0.118**	0.064
East Riley		0.092	0.039	0.082	0.088	0.064	**0.121**	0.055
KJ's			0.040	0.080	0.081	0.052	**0.151**	0.081
Landfill				0.013	0.016	0.027	0.065	0.043
Nessman					0.041	0.046	**0.128**	0.110
NW of Landfill						0.039	0.072	0.046
Railroad Crossing							0.053	0.045
Steven's Approach								0.046

Table 1: Matrix of pairwise F_{st} (ANOVA Approach) generated with SPAGEDI.

The population at Steven's Approach was observed to have moderate-to-high F_{st} values for all pairwise comparisons. With STRUCTURE, we tested the divergence of Steven's Approach,

Nessman, KJ's, and East Riley against the Staffenson preserve.

Figure 2: STRUCTURE population assignments.



STRUCTURE uses a Bayesian algorithm to introduce population structure within a group of individuals. The software attempts to assign population groupings that, as far as possible, are not in genetic disequilibrium.[1] The results of the STRUCTURE simulation performed on our samples are illustrated above. Each column in the chart represents one individual. The likelihood of its assignment to each of the introduced genetic clusters is represented by its color.

Results and Discussion

The genetic character of an entire population is ascertained from the chart by noting the predominant color among all the individuals in a population. The visibly unique coloration of each population indicates the emergence of distinct, genetically homogeneous populations among the fragment populations we tested. These results imply that, since fragmentation, the remnant populations have diverged genetically. Below, STRUCTURE'S likelihood of population assignment is visualized on a map of the study site.

Figure 3 (right) demonstrates the genetic divergence of the tested populations. The vastly different color proportions of Steven's Approach, KJ's, and Nessman from the Staffenson preserve suggest that these geographic populations do not belong to a single genetic population, as they likely once had. This genetic divergence may be the result of either or both of two processes:

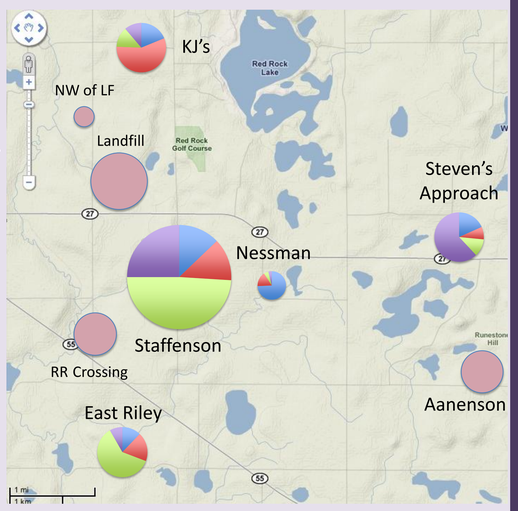


Figure 3: Map of study site by genetic population

- Genetic drift – fragmentation created minute populations within which random mutations would have larger-than-normal effects on the genetic character of the population. In this case, divergence indicates a deleterious effect of fragmentation.
- Local adaptation – the structure observed is actually a magnification of spatial structure that existed in the pre-fragmentation prairie. In this case, fragmentation may actually have helped the remnant populations by decreasing the chance of outbreeding and the incorporation of non-adapted genotypes within the locally adapted subpopulations. It bears noting that this possibility is unlikely in our study because of the environmental similarities of the test sites. Local adaptation is also not implied by our observation of genetic divergence because microsatellites are typically neutral markers of genetic identity.

Our findings implicate a need for reexamination of the genetic condition of habitat fragments and for conservation efforts that address issues of genetic divergence.

References and Acknowledgements

1. Evanno, G., et al. (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology, **14**, 2611-2620*
2. Goudet, J. FSTAT (Version 2.9.3.2, 2002) A computer program that estimates and tests gene diversities and differential statistics
3. Hardy, O. and Vekemans, X. SPAGEDI (Version 1.2, 2007) A computer program for spatial analysis of genetic diversity.
4. Falush, D. and Pritchard, J. STRUCTURE (Version 2.2, 2007) A computer program for inference of population structure
5. Wagenius, S. (2006) Scale dependence of reproductive failure in fragmented *Echinacea po*pulations. *Ecology*, **87(4)**, 931-941
6. Young, A., et al. (1996) The population genetic consequences of habitat fragmentation for plants. *Tree*, **11(10)**, 413-418

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