Pollen Donor Diversity in a Fragmented, Prairie Perennial Population

Diedre F. Reitz[1], Jacob J. Friedman[2], and Jennifer L. Ison[3,4]

1) Carleton College, 2) Yeshiva University, 3) University of Illinois at Chicago, 4) Chicago Botanic Garden

Introduction

Habitat fragmentation occurs when a large, continuous population is broken into several, smaller populations. Fragmentation can lead to loss of genetic diversity within a population as a result of inbreeding and alter community dynamics. Due to recent agricultural and urban development, the tallgrass prairie has become one of the most fragmented ecosystems in the world.

Given their sessile nature, the interactions plants have with their pollinators are essential to their reproduction. Flowering phenology and synchrony may aggravate the constrictions placed on pollen flow by habitat fragmentation. Studying influences on pollen movement within fragmented populations is essential to understanding how genetic diversity and population vitality can be maintained.

Flowering phenology—the time, synchrony, duration, and intensity of flowering—likely plays a major role in determining the diversity of pollen donors. Plants which flower synchronously (i.e. shed pollen at the same time) are more likely to exchange pollen. Thus, the more plants that are flowering at a given time, the more possible pollen donors a plant has. Peak flowering plants, however, may not have the most varied pollen donors because they are likely to flower synchronously with near neighbors. Large displays of pollen across a small area may influence pollinators and cause the flower to be pollinated by several near, simultaneously flowering plants.

Objective

To examine the effects of flowering phenology on the gene flow and diversity of pollen donors in common prairie perennial.

Study Species & Site

Echinacea angustifolia

- Generalist pollinators
- No specialized seed dispersal
- Individuals flower on average 9 days
- Self-incompatible
- Uniovular

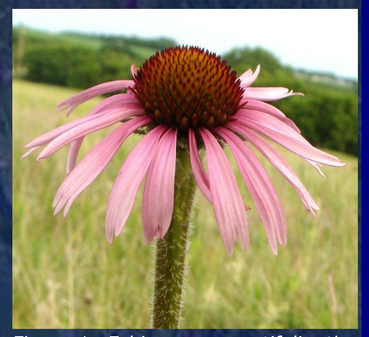

Figure 1: *Echinacea angustifolia*, the narrow-leaf purple cone flower

Site

- Western Minnesota in an experimental plot
- Plants for the experimental plot were collected from remnant prairie populations within 5 km of the plot

Experimental Design

- 224 flowering plants which represent pollen donors (paternal plants)
- 30 maternal plants, from which 900 seeds were collected
- Seeds were germinated and grown until leaf samples could be collected
- DNA extractions were performed using the Qiagen DNeasy Plant Mini Kit and the DNA was amplified with a fluorescently-labeled primer
- Parental plants and offspring were genotyped and analyzed using 9 microsatellite primers screened on a Beckman Coulter CEQ 8000.
- Paternity was assigned using Cervus 3.0.3 (Kalinowski et al. 2007) with 90% strict confidence intervals
- Correlated paternity was estimated using POLDISP (Robledo-Arnuncio et al 2007).

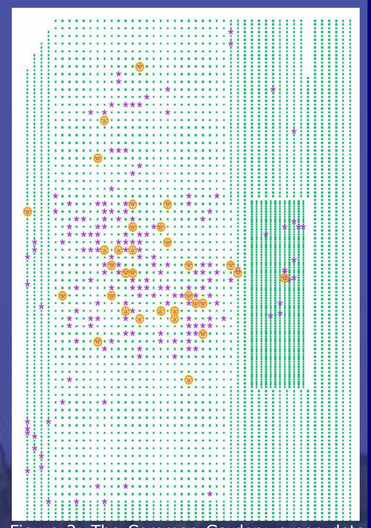

Figure 2: The Common Garden; green dots are basal plants and purple stars are flowering. The maternal plants are circled in orange.

Figures

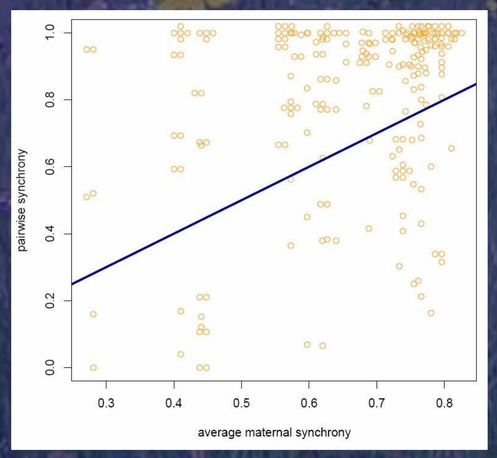

Figure 3: The pair-wise (i.e. maternal plant to paternal plants) synchrony versus the average synchrony of the maternal plants to all the other plants in the Common Garden. Most of the points fall above the line, indicating that the pair-wise synchrony is higher than the average synchrony for the maternal plant to the rest of the population.

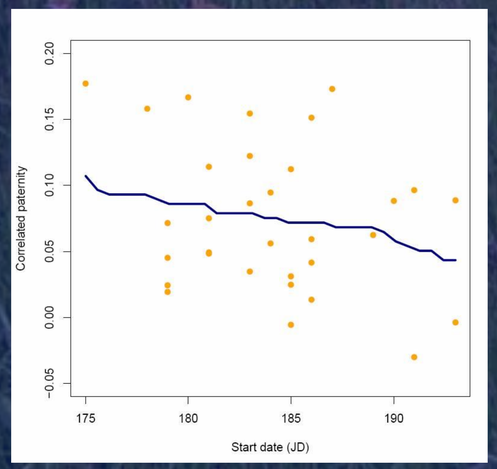

Figure 4: The correlated paternity within progeny arrays versus the beginning date of flowering for the maternal plant. A value of 0.5 indicates that all the offspring had the same paternal plant. Relatedness of offspring decreases (i.e. number of pollen donors increases) as start date for flowering becomes later.

Results

- Paternity was assigned to 320 offspring, and of those 5 represented pollen flow from outside the experimental common garden . This leads to an estimated gene flow rate of 1.6%

Figure 5: Offspring plants which were analyzed to assess pollen donor diversity.

- Pair-wise synchrony between crossing plants was significantly higher than average synchrony of the maternal plant to all other plants in the common garden (2 sample t-test; $p < 0.01$; Figure 3).
- Pair-wise synchrony average is 0.80, and maternal plant synchrony average to all plants in the common garden is 0.66.
- The start date of the maternal plant significantly predicted the correlated paternity of the plant's offspring (glm $P<0.01$; Figure 4).
- Plants that started earlier had lower pollen donor diversity than later flowering plants.

Conclusions & Implications

- Gene flow was relatively high indicating that fragmented populations may still be exchanging genetic material.
- Most gene flow events (4 of 5) occurred early in the flowering season demonstrating that flowering phenology can be an important factor in keeping populations from differentiating.
- Nearby plants may become isolated from each other if they do not flower synchronously.
- Pollen donor diversity significantly increases as the flowering season continues.
- Indicates that plants of concern need to be monitored for an extended period of time to ensure that genetic diversity is such that the species' sustainability is possible.
- Further fragmentation could lead to the elimination of species and disrupt vital, community interactions.
- Ex situ seed harvesting is important to conservation where population fragmentation limits pollen flow.

References & Acknowledgements

Kalinowski, ST, Taper, ML & Marshall, TC (2007) Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. *Molecular Ecology* 16: 1099-1006.
Robledo-Arnuncio JJ, Austerlitz F, Smouse PE (2007) POLDISP: a software package for indirect estimation of contemporary pollen dispersal. *Molecular Ecology Notes 7: 763-766.*
Our thanks to: M.V. Ashley, J. Fant, D. Feng, K. Fieldheim, S. Monroe, E. Rosenthal, and S. Wagenius, and the Echinacea field crew 2005
Funding: Royal Botanic Garden-Kew at Wakehurst Place. Millennium Seed Bank Project Research Grant