

## Testing whether corridors increase gene flow and generic diversity via pollen movement

### *People involved*

Julian Resasco, John Orrock, Nolan Kane, a yet unidentified technician

### *Background*

Populations isolated on habitat fragments are often vulnerable to extinction due to having small population sizes with reduced gene flow and low genetic diversity. Corridors could offer a management strategy to mitigate these negative effects of fragmentation by connecting populations and increasing gene flow. Increasing gene flow is important because it could increase the genetic diversity and movement of adaptive alleles to inbred populations on fragments. These genetic effects are precursors for adaptive evolution to occur via genetic rescue. Genetic rescue is a process of restoring genetic diversity and adaptive alleles to reduce extinction risks in small, isolated populations like those affected by habitat fragmentation.

We propose using the SRS corridor experiment to test whether landscape connectivity via corridors can increase gene flow to and genetic diversity of isolated inbred populations via pollination using a model organism, the sunflower, *Helianthus annuus*. Our experimental landscapes are ideal because they allow us to test for the effects of connectivity while controlling for typically confounding factors and to conduct our experiments at large spatial scales that approximate those of conservation management activities. Our design is also ideal because it allows us to separate the effects of genetic rescue from those of demographic rescue that are typically confounded due to their difficulty in teasing apart in other studies.

Our questions are:

Question 1: Does connectivity (via pollinator facilitated by corridors) increase the gene flow and genetic diversity of *Helianthus annuus* populations on fragments?

Question 2: Does increased gene flow and genetic diversity lead to increased fitness of individuals under drought stress? (Greenhouse experiment not described here)

Below we describe the field portion of the study.

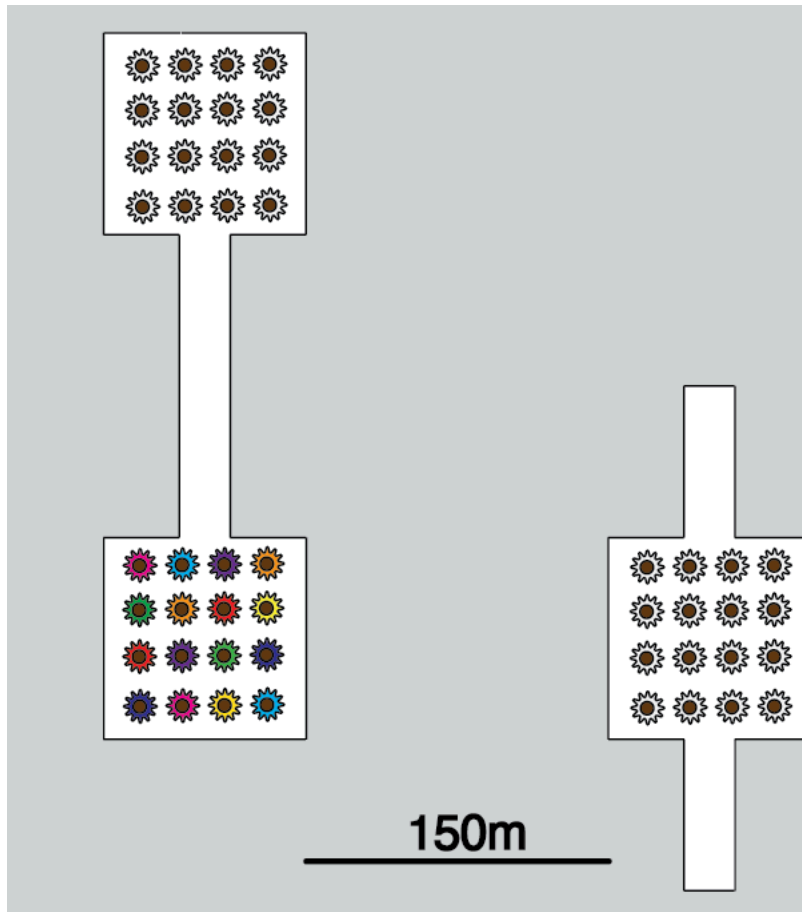


Fig. 1 – Schematic of experimental design showing 1 of the 7 blocks. Center patches (lower left) are planted by with 16 source populations of wild sunflowers from locations throughout the US (from US-NPGS; represented by rainbow colors) and will be randomly assigned to a grid pole location. Connected and one unconnected patch, C location (rectangular or winged) will each be planted with an inbred line (HA 467).

### Methods

We aim to answer these our questions using a tractable model system, the sunflower *Helianthus annuus* at the SRS Corridor Experiment in South Carolina, a state that has experienced drought during eight of the last ten years. The SRS Corridor Experiment provides an unparalleled opportunity to test for connectivity-mediated genetic effects at large scales.

### Study organism

Sunflowers are common in open sites throughout North America, southern Canada, and Mexico. Sunflowers are an ideal study organism. (1) They rely on pollinators for gene flow and reproduction. (2) They are annuals and produce many seeds, making them amenable to experiments. (3) Their genome has recently been sequenced, creating tools for mapping loci that contribute to traits like drought tolerance. (4) They are not found within our landscapes, allowing us to control pollen sources. (5) They are widespread and vary in their susceptibility to drought. Seeds are available from parts of their range that vary in climatic conditions through

USDA's National Plant Germplasm System (US-NPGS). Seeds from inbred populations are also available. (6) They are an important food crop and could help clarify the role of connectivity in changing environments for the viability of wild ancestors of domesticated crops, which has implications for food security. (7) They are native to the southeastern US.

#### *Experimental design*

We propose to plant central patches with 16 accessions obtained from the US-NPGS. These accessions originate from different locations across the United States that differ in their average annual rainfall by more than five-fold. Available accessions are in Table 1 below. We expect that due to environmental variation these populations experience in their respective parts of their range, populations will vary in their susceptibility stressful precipitation conditions. We propose to plant 2 peripheral patches, one connected and one unconnected ("C" location) with seeds of the inbred line HA 467.

We will plant 10 seeds at each grid pole location to improve the odds that a plant will grow. We will bury seeds at 2" depth. We will water seeds when they are planted. To reduce seed predation, we will spray the area with natural rodent repellent and sprinkle diatomaceous earth in the planting area. We will thin *H. annuus* seedlings to one individual (the largest) 1-2 months after planting.

Plants will be monitored throughout the summer for survival and flowering and pollinator visitation.

Flowers will be bagged in mesh bags to prevent seed dispersal and seed predation in late summer. Seed heads will then be harvested and plants will be pulled out of the ground. Seed will be taken to Colorado for genetic sequencing and green house experiments to test drought tolerance.

#### *Study timeline*

Early May – seed planting

June – August – monitoring plant growth, survival, flowering, and pollinator visitation

August – Flowers will be bagged and harvested. Plants will be pulled out of the ground.

#### *Possible impacts*

There is a possibility that *Helianthus annuus* could be introduced into the patches. We will take measures such as bagging flowers to prevent seed dispersal. We will check planting sites in subsequent years and uproot any *H. annuus* plants.

**Table 1.** Wild *Helianthus annuus* seed accessions obtained

ACCESSION	NAME	ORIGIN	NUMBER OF SEEDS I HAVE ON HAND	SOURCE DATE	COORDINATES	ANNUAL PRECIP (IN; SOURCE PRISM 1981- 2010)
PI 673289	ANN-2793	California	100	09/01/2013	36.54633000, -118.07472000	6
PI 695657	DB_1806	Arizona	50	09/12/2015	35.19566000, -114.06666000	10
PI 435534	ANN-601	Texas	100	11/03/1976	31.84555556, -102.36722222	14
PI 435542	ANN-632	Arizona	100	11/17/1976	34.25416667, -110.02916667	14
PI 468474	ANN-1194	Texas	100	09/13/1979	34.87444444, -102.28138889	18
PI 468491	ANN-1278	Oklahoma	100	09/03/1980	34.89361111, -98.36555556	30
PI 435610	ANN-823	Oklahoma	100	09/15/1977	35.08027778, -96.39888889	38
PI 468495	ANN-1282	Texas	100	09/04/1980	33.65000000, -97.38277778	38
PI 435414	ANN-357	Texas North	150	09/14/1976	33.60250000, -95.42805556	45
PI 435612	ANN-861	Carolina	100	09/22/1977	35.73305556, -81.34138889	45
PI 435616	ANN-881	Missouri	100	09/25/1977	36.91666667, -92.16666667	45
PI 613727	ANN-1114 Ames	Arkansas	100	09/08/1979	36.40111111, -93.73777778	45
PI 649853	23238	Ohio	100	10/13/1996	39.17111111, -84.49972222	45
PI 435613	ANN-874	Kentucky	100	09/23/1977	36.66666667, -86.50000000	55
PI 468445	ANN-1141	Texas	100	09/10/1979	29.84750000, -94.89055556	55
PI 664809	Eubank 2	Mississippi	100	10/01/2011	33.55210000, -91.10620000	55