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## Genetic Diversity of *Asclepias Tuberosa* in Iowa Prairies

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## Genetic Diversity of *Asclepias Tuberosa* in Iowa Prairies

### Abstract

Reduced population size can result in the loss of genetic diversity, which in turn can make organisms more susceptible to environmental challenges. In Iowa less than one percent of the original tallgrass prairie remains, isolated in a few remnant prairies. We are undertaking a long term project to assess the genetic variability in native prairie plants on remnant prairies in Northwest Iowa. We are testing six microsatellite sequences for butterfly milkweed (*Asclepias tuberosa*) from the Steele Prairie State Preserve, Broken Kettle Grasslands, a private prairie near Cherokee IA, a prairie restoration project on the Dordt College campus and populations from suppliers in Oklahoma and Pennsylvania. We hope to answer the following questions: A) Do nearby remnant prairies share alleles and have similar allelic diversity? B) Is there evidence for inbreeding in remnant populations? C) Is there evidence that plant populations found in local native prairies are genetically distinct from restored prairies and from those originating outside the state of Iowa? Preliminary results suggest that A) Essentially all of the alleles are found in at least 2 of the populations analyzed B) the degree of homozygosity is not higher than expected values and C) the four remnant prairie populations of butterfly milkweed that were tested show little genetic differentiation from each other but show moderate differentiation from commercial seed. The answers to these questions will help inform strategies for prairie conservation and restoration in Iowa and across the Midwest.

### Keywords

milkweeds, plant genetics, prairie conservation, Iowa

### Disciplines

Botany | Christianity | Plant Breeding and Genetics

### Comments

Poster presentation given at the 2013 Iowa Academy of Sciences Conference.

# Genetic Diversity of *Asclepias tuberosa* in Iowa Prairies

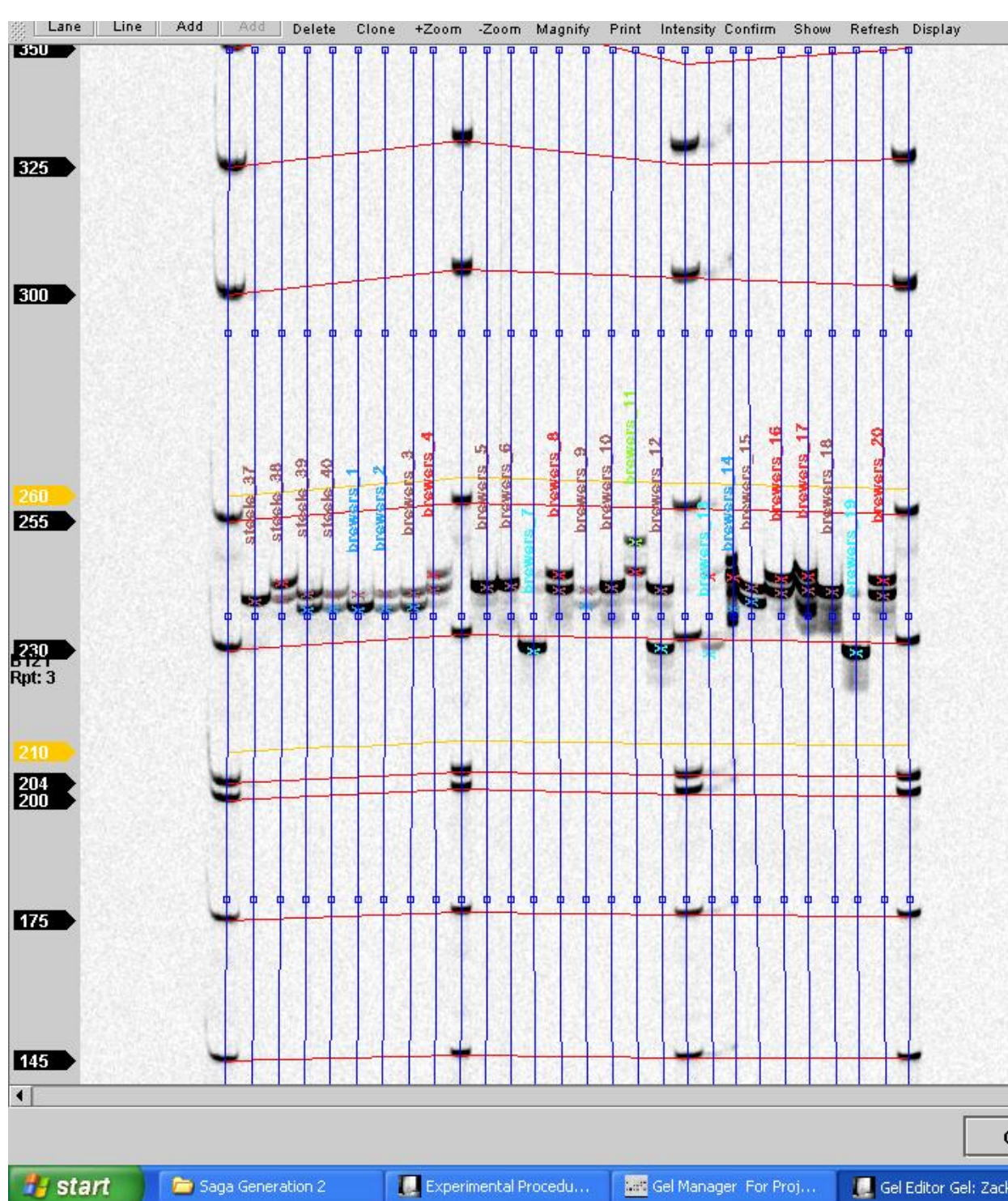
Dr. Jeffrey Ploegstra, Michelle Alkema, Kayla Graves,  
Brittany De Ruyter, Zack Petersen, Dr. Tony Jelsma  
Dordt College, Sioux Center, IA  
IAS 2013

## ABSTRACT:

Reduced population size can result in the loss of genetic diversity, which in turn can make organisms more susceptible to environmental challenges. In Iowa less than one percent of the original tallgrass prairie remains, isolated in a few remnant prairies. We are undertaking a long term project to assess the genetic variability in native prairie plants on remnant prairies in Northwest Iowa. We are testing six microsatellite sequences for butterfly milkweed (*Asclepias tuberosa*) from the Steele Prairie State Preserve, Broken Kettle Grasslands, a private prairie near Cherokee IA, a prairie restoration project on the Dordt College campus and populations from suppliers in Oklahoma and Pennsylvania. We hope to answer the following questions: A) Do nearby remnant prairies share alleles and have similar allelic diversity? B) Is there evidence for inbreeding in remnant populations? C) Is there evidence that plant populations found in local native prairies are genetically distinct from restored prairies and from those originating outside the state of Iowa? Preliminary results suggest that A) Essentially all of the alleles are found in at least 2 of the populations analyzed B) the degree of homozygosity is not higher than expected values and C) the four remnant prairie populations of butterfly milkweed that were tested show little genetic differentiation from each other but show moderate differentiation from commercial seed. The answers to these questions will help inform strategies for prairie conservation and restoration in Iowa and across the Midwest.

## BACKGROUND:

- In Iowa less than 1% of the original tallgrass Prairie remains in isolated remnants.
- Butterfly milkweed has a number of desirable characteristics for evaluating these prairies:
  - Easily identified
  - Relatively abundant
  - Available molecular markers



## Methods:

- Samples collected from:
  - Steele Prairie (remnant)
  - Brewer's Prairie (remnant)
  - Broken Kettle Prairie (remnant)
  - Freda Haffner Prairie (remnant)
  - Oklahoma seed (commercial vendor)
  - Dordt College Prairie (restoration)
- Microsatellite loci amplified using primers identified in *Asclepias syriaca*
- Samples analyzed using LI-COR 4300™
- Alleles scored using SAGA™ software
- Data analyzed using GenePop 4.0 (Raymond and Rousset, 1995; Rousset, 2008)

## Molecular Marker Results:

- The number of alleles for each locus is satisfactory
- The expected heterozygosity for each locus is also within a desirable range with the possible exception of B5

## Genetic variability per locus in *Asclepias tuberosa*

Locus	k	N	H <sub>o</sub>	H <sub>e</sub>
B2	13	162	0.7768	0.6467
B5	8	177	0.2522	0.3033
B121	10	193	0.6282	0.5770
C102	13	194	0.7253	0.6121
C109	11	201	0.7110	0.6337
C124	11	185	0.8249	0.7444

k= number of alleles, N= total number of individuals scored for a given locus, H<sub>o</sub> = the observed Heterozygosity, H<sub>e</sub>= the expected heterozygosity

### Within population Results:

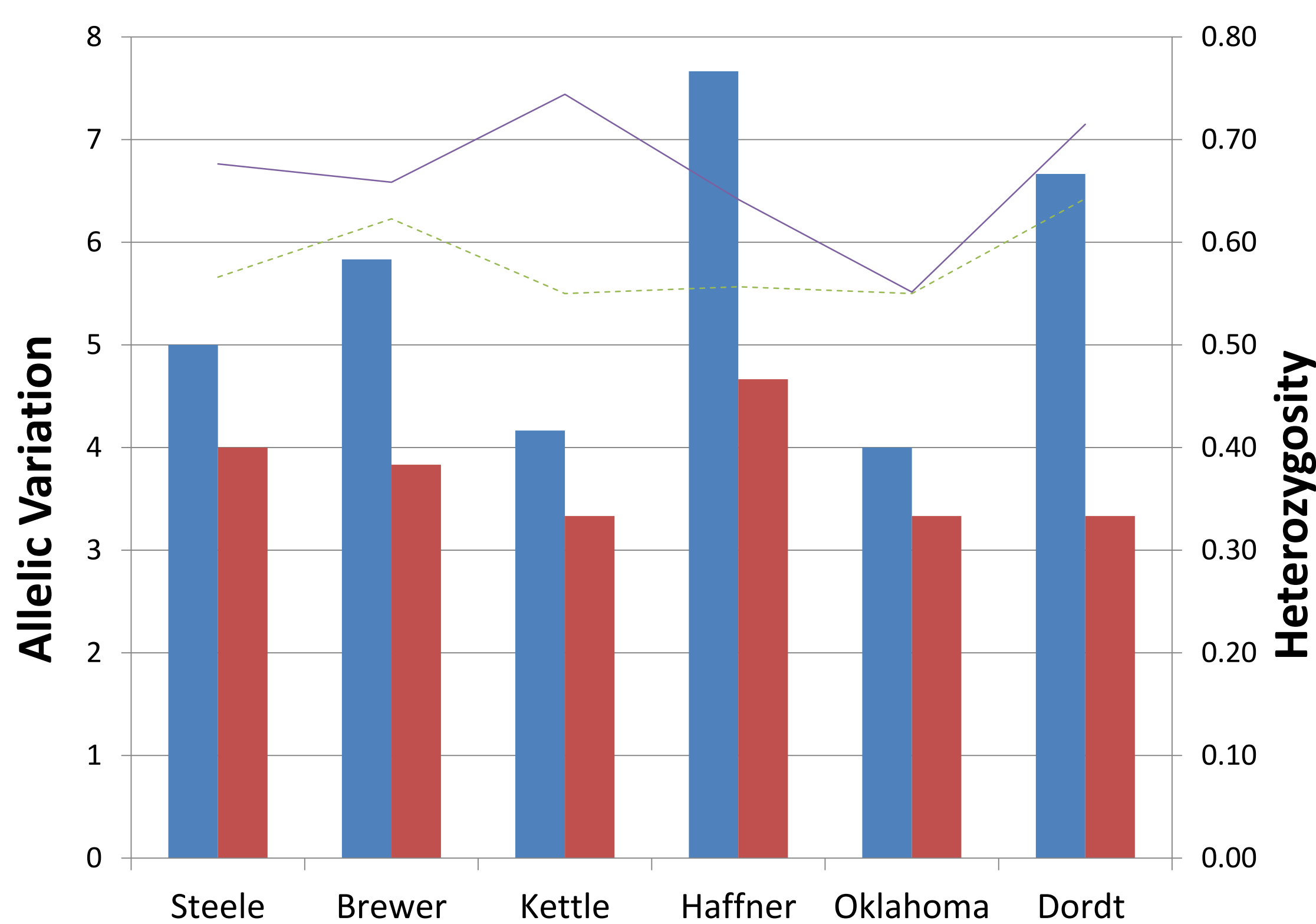
- No evidence of inbreeding
- The average number of alleles per locus is similar between our restoration and the remnant prairies

### Within population diversity indices calculated from microsatellite data

Population	# of Alleles	H <sub>e</sub>	H <sub>o</sub>	F <sub>is</sub>
Steele (40)	5.00	0.5660	0.6763	-0.1948*
Brewers (38)	5.83	0.6228	0.6585	-0.0574*
Br. Kettle (17)†	4.17	0.5500	0.7442	-0.3530*
Oklahoma (29)	4.00	0.5567	0.6417	-0.1527*
Dordt (47)	6.67	0.5501	0.5516	-0.0027*
Freda Haffner (45)	7.67	0.6425	0.7149	-0.1126*

\*No significant departure from Hardy-Weinberg equilibrium using H<sub>1</sub>= heterozygote deficit  
 † Entire population at this location

### Allele Patterns for 6 microsatellite loci



At is average number of alleles, At5% is the number of alleles with frequencies above 5%, He is the unbiased expected heterozygosity, Ho is the observed heterozygosity.

### Across Population Results:

- Similar number of alleles between large remnant prairies
- Similar allele frequencies between remnant populations
- Mean sample size: 30.8889
- Mean frequency of private alleles is low  $p(1) = 0.03585$
- Frequency of low representation alleles is high.

### Between Population Results:

- The remnant prairies show little differentiation from each other.
- The Dordt restoration and seed from a commercial vendor show moderate differentiation from the remnant prairies but not from each other.

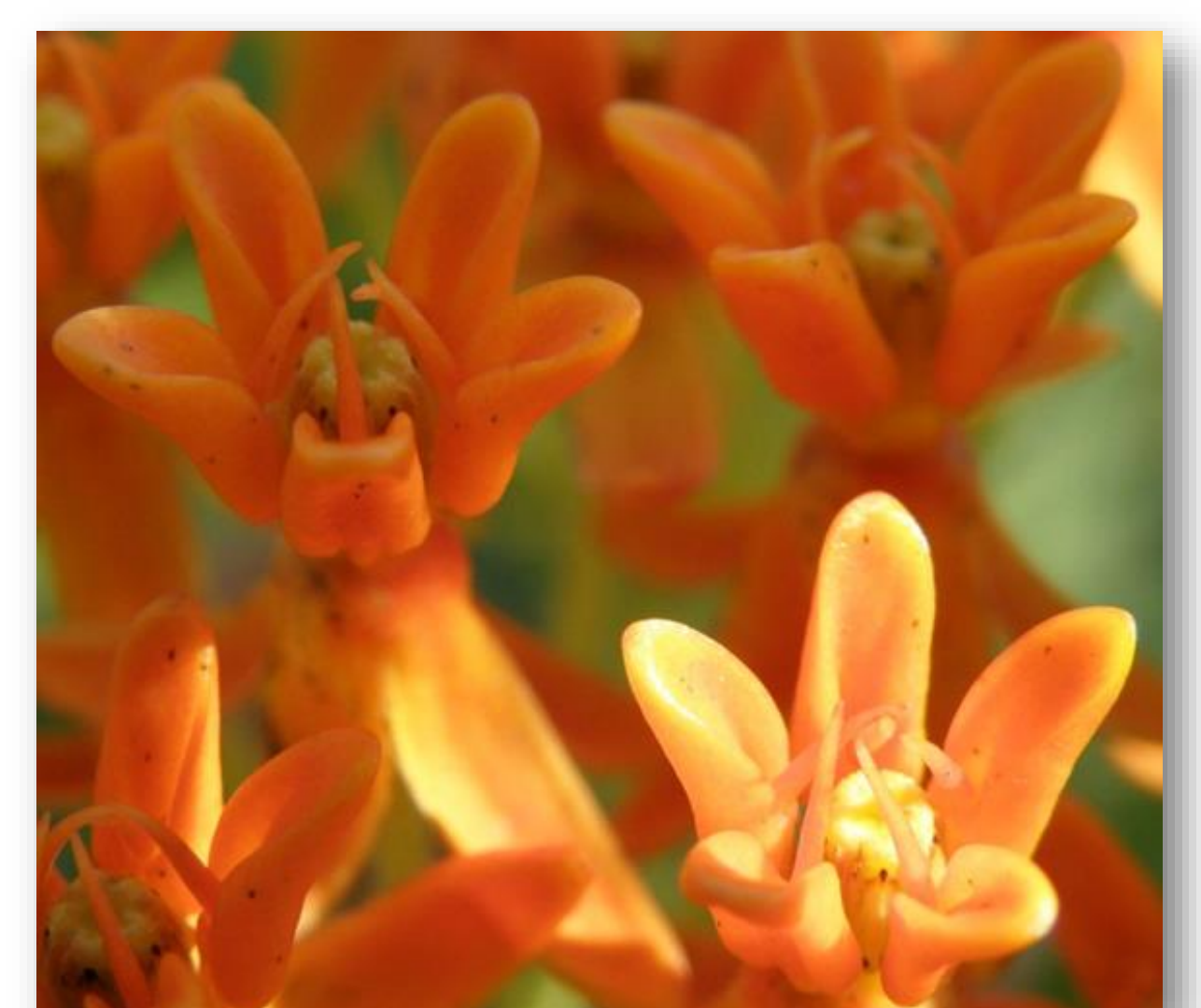
### Genetic differentiation between all pairs of populations obtained from microsatellite data

	Steele	Brewer	Br. Kettle	Fr. Haffner	Oklahoma	Dordt
Steele						
Brewer	0.03163					
Br. Kettle	0.05656	0.0339				
Fr. Haffner	0.04278	0.03308	0.07396			
Oklahoma	0.1068	0.09812	0.1041	0.1379		
Dordt	0.1122	0.07841	0.1006	0.1107	0.04387	

Blue and green color indicate little and moderate genetic differentiation respectively based on pairwise F<sub>st</sub> Estimates (Weir and Cockerham, 1984).

### Discussion:

- The markers showed appropriate characteristics for our study and performed satisfactorily.
- All prairies show healthy levels of allelic and genotypic diversity in *Asclepias tuberosa*. However, low frequency of private alleles coupled with high frequency of low representation alleles, suggests the prairies are differentiating. The differentiation of the Dordt prairie suggests that future restorations should use local seed whenever possible to preserve local alleles.
- *Asclepias tuberosa* is amenable to research but probably not the best overall indicator of genetic health for a prairie due to its pollination characteristics. Efforts are underway to investigate other species more susceptible to inbreeding depression. Breeding experiments to explore fitness effects of inbreeding in butterfly milkweed are also being pursued.



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 Significant time and energy were also contributed by Greg Beekhuizen, Ron Hall, Tyler Knobloch, Todd Nanninga and Andrea Voss in the completion of this work.