Development of Genomic Resources to Facilitate the Domestication of *Silphium integrifolium* as a Perennial Oilseed Crop

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**Introduction**

The majority of worldwide food production relies on the cultivation of annual grains. These systems present a number of challenges, including inefficient nutrient and water use, and the risk of soil erosion. Perennial agricultural systems may address these issues, but there are currently few agronomically viable perennial grain species. One solution is to domesticate new crops to fill this niche1. *Silphium integrifolium* (Michx.) is a wild member of the Asteraceae family native to prairies throughout the central United States. *S. integrifolium*, or silphium, was selected as a candidate for domestication due to relatively large seed size, drought tolerance, and agronomically favorable morphology2. Subsequent analysis has found seed oil content comparable to traditional sunflower varieties. Domestication is a complex process that historically took centuries, but leveraging modern knowledge of genetics and genomics will speed progress. Here we present the first draft linkage map for *silphium*, investigate synteny with the Helianthus annuus (annual sunflower) genome, and discuss plans to assess linkage disequilibrium in a multi-environment diversity panel that will be used for mapping putative domestication traits.

**Material & Methods**

**Linkage Map**
- Two elite individuals with different flowering habits were crossed in the summer of 2015 to generate an F1 mapping population (Fig 1).
- 77 seedlings and parent plants were genotyped using RAD-Seq GBS method2.
- SNPs were called using Stacks pipeline.
- Maps were made using JoinMap 4.1L. Groups with more than 10 makers and a LOD independence score over 7 were selected. Mapping was done using Monte Carlo regression method.
- Synteny with Helianthus annuus was investigated using BLAST.
- 380 genotypes, representing 102 half-sib families were selected from The Land Institute’s breeding nursery.
- Parental crowns were dug up and divided in the winter of 2015.
- One replication of each genotype was planted in each of the six locations in 2016, with 10% of genotypes planted replicated twice (Fig 2).

**Future Plans**
- Linkage Disequilibrium Characterization
  - 18 pairs of SNP markers identified as being between 0 and 3.7 centimorgans apart on the linkage map, and covering the range of linkage groups, were selected to assess linkage disequilibrium in the diversity panel.
  - Each plant with surviving tissue was genotyped for these markers using a KASP assay.
- LD assessment will inform genotyping decisions.
- Plants will be phenotyped for traits of interest over several years; traits will be mapped as a GWAS.
- Results & Discussion
  - Number of chromosomes could not be resolved to match 7 physical *silphium* chromosomes with current data.
  - Better linkage groups may help to clear synteny picture.
  - Several synteny regions may contain domestication QTL in *H.* annuus, including 14HA-14SI, 6HA-5SI, and 7HA-13SI.

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**References**


**Figures**

- Fig. 1. Com BREAKpoint of F2 and F1 mapping.
- Fig. 2. Map shows experiment locations. States included on map are recorded native range of *silphium*.
- Fig. 3. Silphium plant ready for harvest. Seed heads visible at the top of the plant; plant is approximately 2 meters tall.
- Fig. 4. Silphium flower in mid-bloom. Ray petals are female; each produces one seed.
- Fig. 5. Silphium stem (right) and kernels (left).

**Tables**

- Table 1: Summary of linkage groups and markers used in the linkage map.

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**Figures**

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- Fig. 5. Silphium stem (right) and kernels (left).