







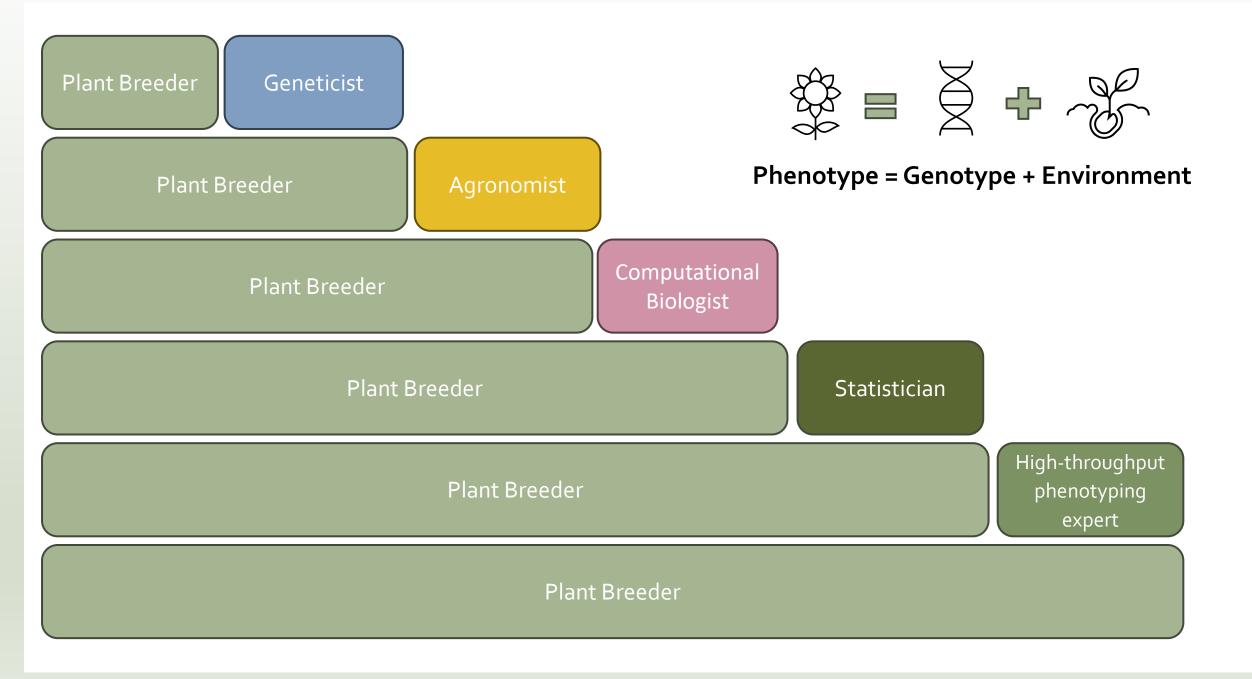


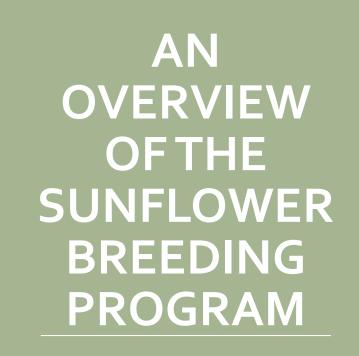


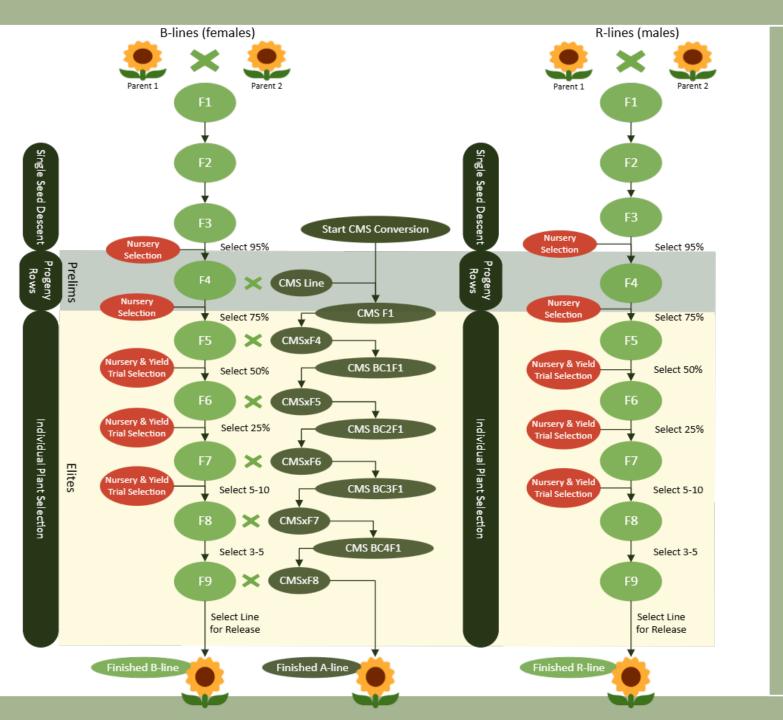
Ashley C. Barstow North Dakota State University

Dr. Brent Hulke



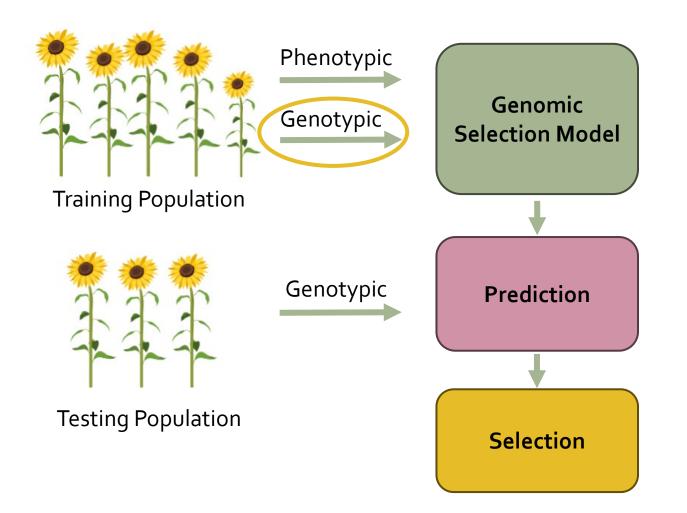






Modified from Brady Koehler

### A FASTER STRATEGY FOR PLANT BREEDING: GENOMIC SELECTION



# Objectives:

1. Develop a set of genomic markers in sunflower suitable for future genomic prediction efforts.

2.Identify haplotype structures within the sunflower genome using multiple different populations from the USDA sunflower breeding program.

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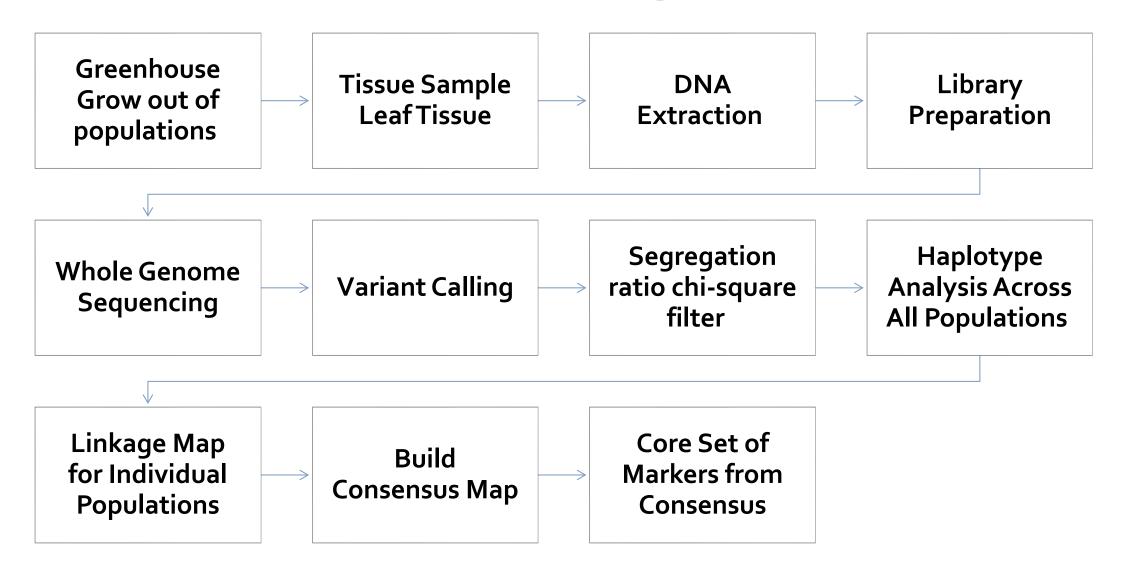
1. Develop a set of genomic markers in sunflower suitable for future genomic prediction efforts.

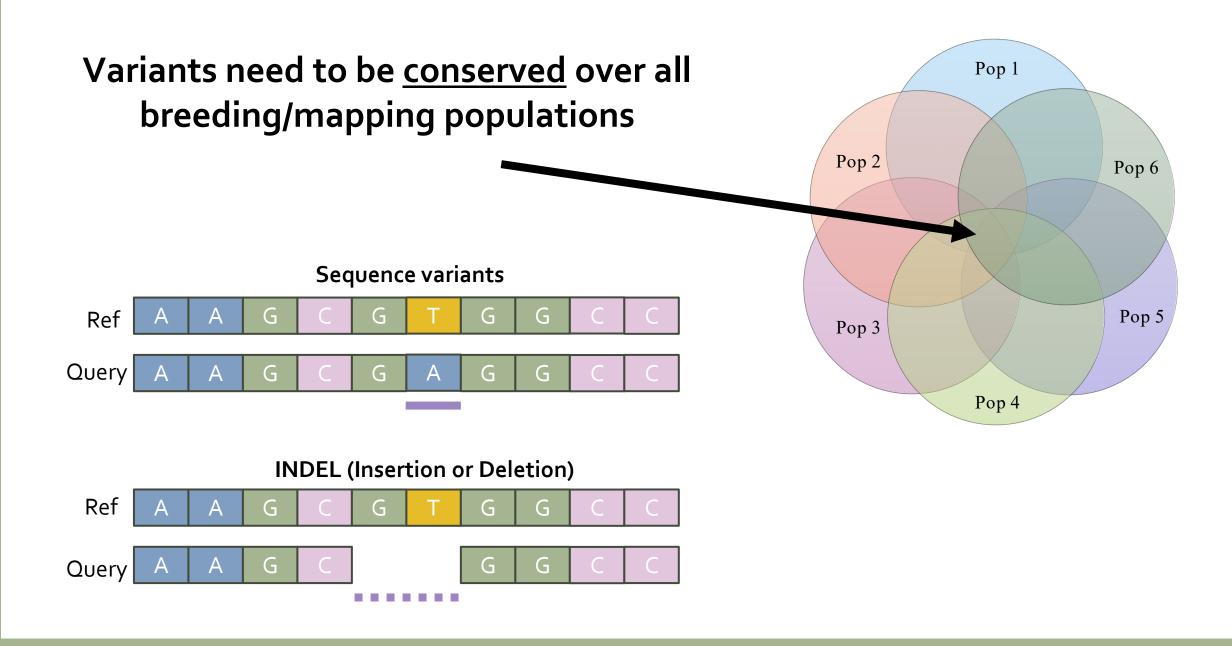
2.Identify haplotype structures within the sunflower genome using multiple different populations from the USDA sunflower breeding program.

### Agronomically important traits and utility for future genomic studies

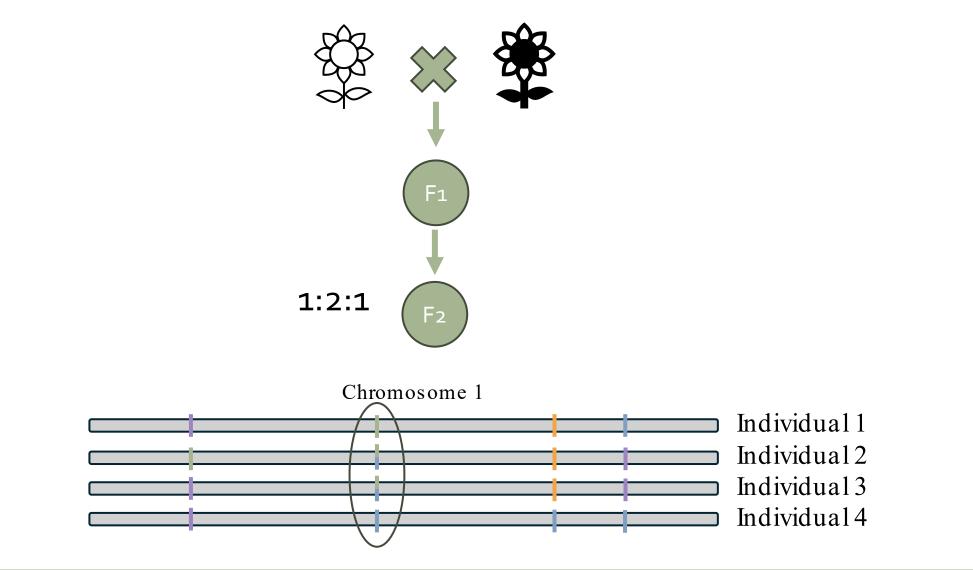
Pedigree	Population Type	B-line/ R-line	Oil	Disease Resistance	Other	Entries
16_1852/16_1410	F4	B-line	НО	Sclerotinia, Phomopsis	Drought, Herbicide Resistance (IMI)	76
HA 482/HA 487	F4	B-line	НО	Sclerotinia, Phomopsis	Herbicide Resistance (IMI)	33
RHA 474/R101dmr/6/RHA 344/NID HO// NS-H-924/4/RHA 418/RHA 419/3/RO12- 13//RHA 274/PRS5/5/RHA 475/RHA 464	F4	R-line	НО	Sclerotinia, Downy Mildew, Rust	Herbicide Resistance (IMI)	45
RHA 476/IS 3401	F4	R-line	НО		Early Maturity	61
RHA 478/16_1570	F4	R-line	НО	Sclerotinia, Phomopsis	Herbicide Resistance (IMI)	70
RHA 483/RHA 479	F4	R-line	НО	Sclerotinia, Phomopsis	Herbicide Resistance (IMI)	28
RHA 483/RHA 480	F4	R-line	НО	Sclerotinia <b>,</b> Phomopsis	Herbicide Resistance (IMI)	47
RHA 485/4/RHA 473/3/RHA 462//PET- 1gammarays/6116	F4	R-line	НО	Sclerotinia		33
RHA 484//RHA 472/R101dmr	F4	R-line	HO	Sclerotinia, Downy Mildew, Rust	Herbicide Resistance (IMI)	56
RHA 485/RHA 476	F4	R-line	НО	Phomopsis	High Oil, Early Maturity	101
RHA 486/RHA 476	F4	R-line	HO	Sclerotinia, Phomopsis, Downy Mildew	Early Maturity	50
RHA 476/687	F4	R-line	НО		Early Maturity	72
HA 456/HA 434	F6 Nectar Mapping	B-line				191
HA 467/Pl170415	F7-9 pericarp Mapping	B-line				159
Total						1022

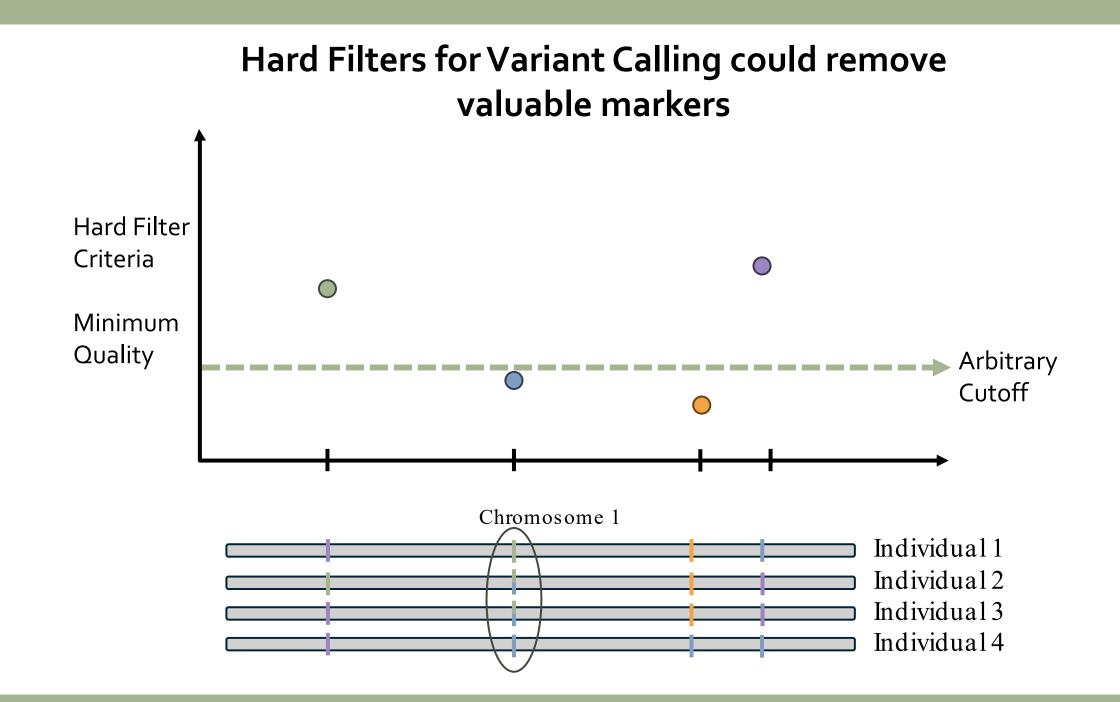
### Methodology





#### Fundamental Mendelian Ratios can be used to find Reproducible and Reliable Markers





#### Case Study: Redo mapping without hard filters

### Genetic mapping of a pollinator preference trait: Nectar volume in sunflower (*Helianthus annuus* L.)



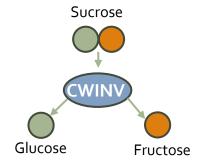


Brent S. Hulke<sup>2\*†</sup>

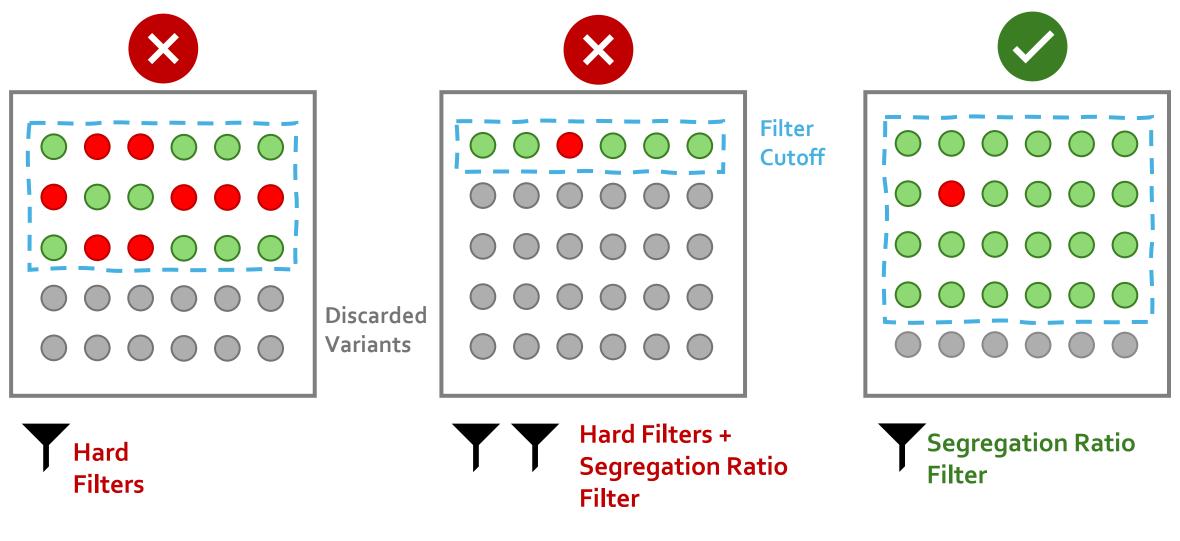
<sup>1</sup> Department of Plant Sciences, North Dakota State University, Fargo, ND, United States

<sup>2</sup> Sunflower and Plant Biology Research Unit, Edward T. Schafer Agricultural Research Center, United States Department of Agriculture (USDA)-Agricultural Research Service, Fargo, ND, United States

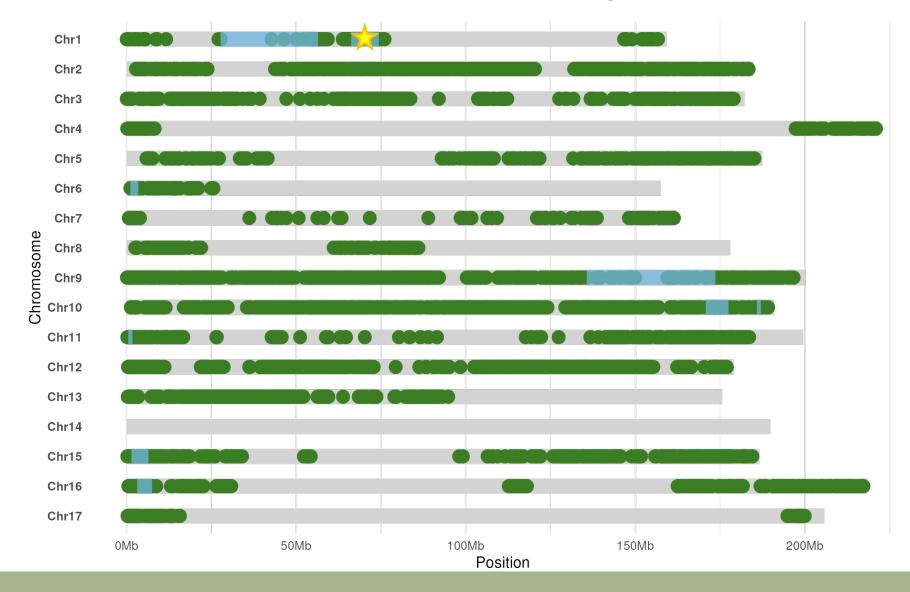
<sup>3</sup> Ecology and Evolutionary Biology Department, University of Colorado, Boulder, CO, United States



Achi-square filtering strategy based on segregation ratio retained a **larger** number of valid markers with better genome coverage.

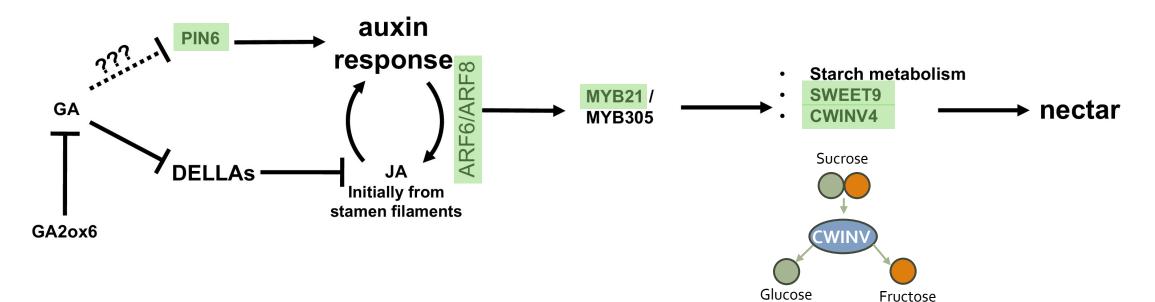


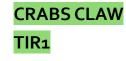
# More candidate regions with nectar-related genes were discovered because of genetic map **improvements**.



#### **Model of Floral Nectary Regulation**



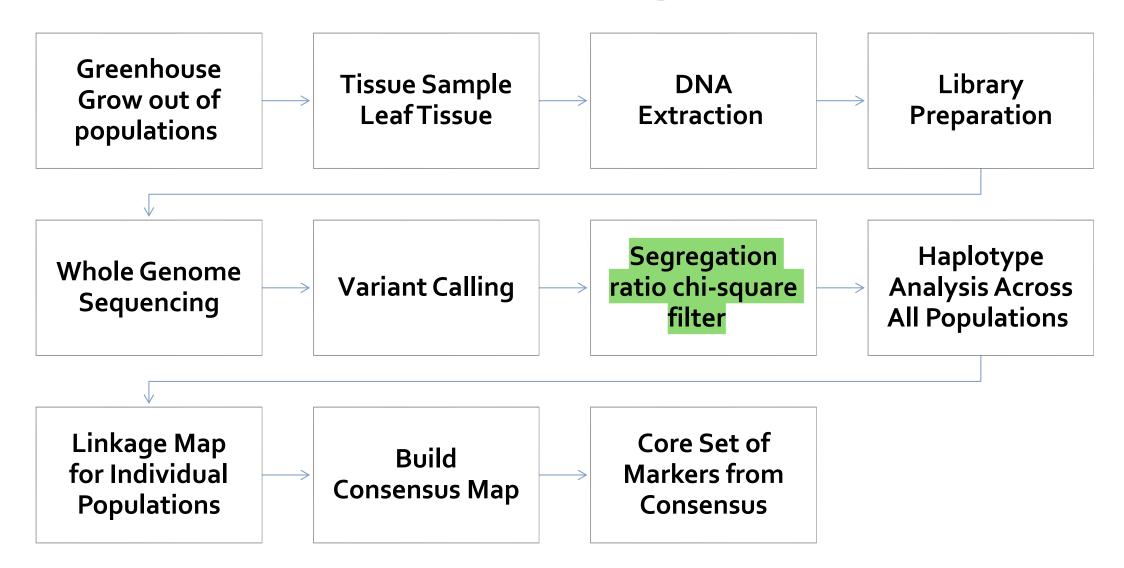




Transcription factor needed for nectary development (Bowman & Smyth, 1999) Auxin receptor that mediates auxin-regulated transcription (Schmitt et al., 2018)

(Roy et al., 2017)

### Methodology





New Results

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#### Variant filters using segregation information improve mapping of nectarproduction genes in sunflower (*Helianthus annuus* L.)

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 Brian C. Smart, 
 Kyle G. Keepers, 
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 Nolan C. Kane, 
 Brent S. Hulke

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This article is a preprint and has not been certified by peer review [what does this mean?].

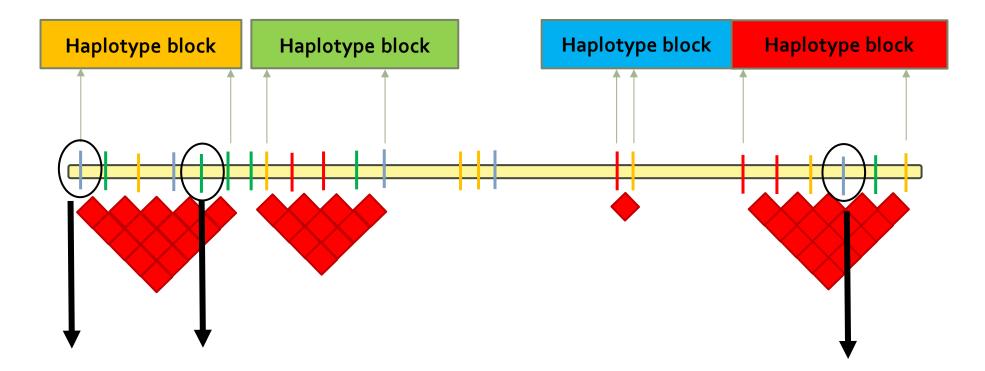


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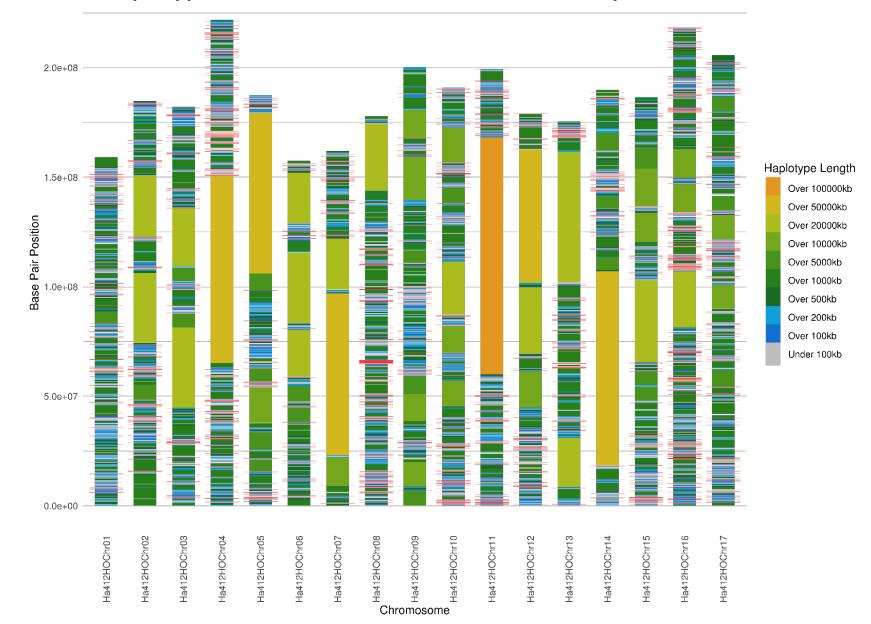
2.Identify haplotype structures within the sunflower genome using multiple different populations from the USDA sunflower breeding program.

### Haplotype Block discovery to reduce marker numbers and improve genomic selection accuracy



These variants are in strong LD with the rest of the markers in the block and can be used to characterize the genetic diversity of the entire block to reduce the marker set needed for future genomic work.

#### Haplotype Blocks across all Chromosomes and Populations



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  Brian Smart, NDSU, Fargo, ND
  James McNellie, USDA-ARS, Fargo, ND
  Brady Koehler, USDA-ARS Fargo, ND
  Kyle Keepers, University of Colorado Boulder
  Zachary Marcus, University of Colorado Boulder
  - All other graduate students and interns

### **QUESTIONS?**









