

Brassica carinata crop improvement & molecular tools for improving crop performance

Germplasm screening

- Germplasm collection and diversity
- What has been done in the US to date, plans for future

Genetic diversity analysis of *B. carinata* collection

- Genotyping by SSR, genotype by sequencing (GBS)
- Population structure

Molecular tools for breeding

- Nested Association Mapping (NAM) project underway
- Traits of interest in *carinata* breeding
- Phenotyping of lines

B. carinata Germplasm Collection

- Agrisoma collection: > **600** accessions and breeding lines from eight sources
- AAFC breeding material



Carinata diversity



Carinata diversity



US Carinata germplasm screening

- *Most lines that have been yield tested in US have been subset of advanced yield trial lines (origin: AAFC breeding program)*
- *Agrisoma has/is developing diverse inbred lines that can also be screened in various geographies*

Montana

- Havre, Moccasin, Huntley: 2012 (5 to 25 entries), 2013 (5 entries)

North Dakota

- Minot, Drake 2012 (25 entries); Minot 2013 (5 entries)

South Dakota

- Bison, Dakota Lakes, Wall 2012 (5 entries); 2013 (5 entries)
- 2014 – 30 entry trial at 3 sites (AAFC + Agrisoma breeding lines)

Florida

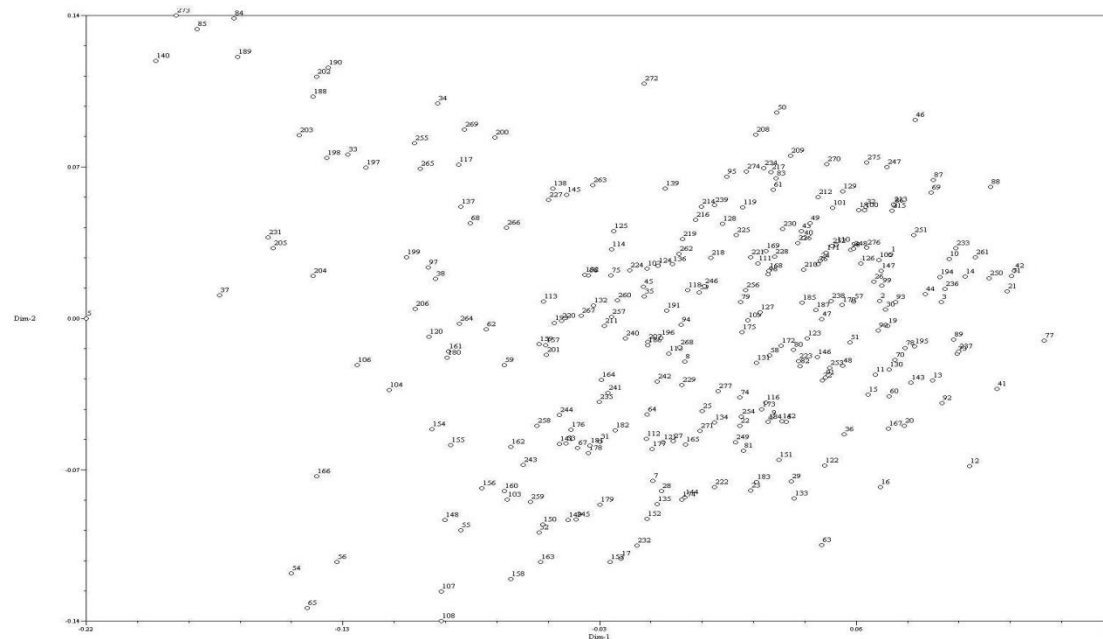
- Quincy, Winter 2012-13 (6 entries)
- Winter 2013-14 (40 entry trial, AAFC + Agrisoma breeding lines)

Discussion on germplasm screening?

Assessing population structure and similarity among lines

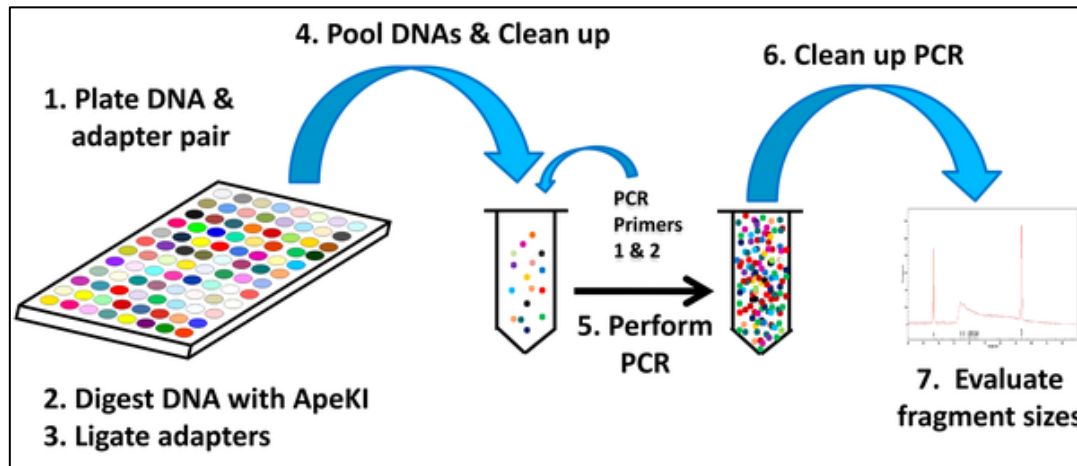
- 277 lines analyzed using 76 SSR markers (approx. equal # B and C genome markers)

PCA DICE Genetic diversity analysis

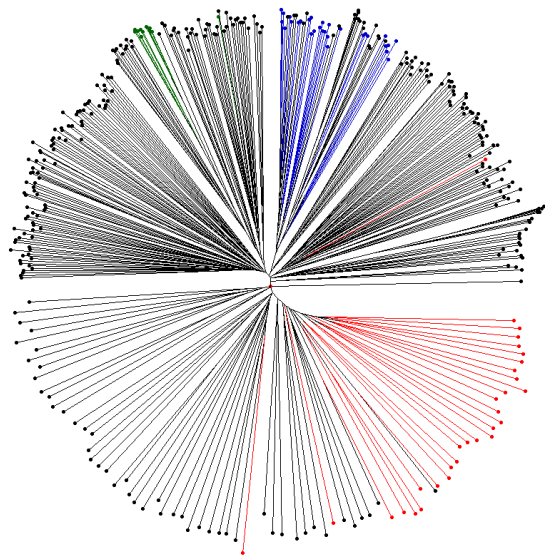
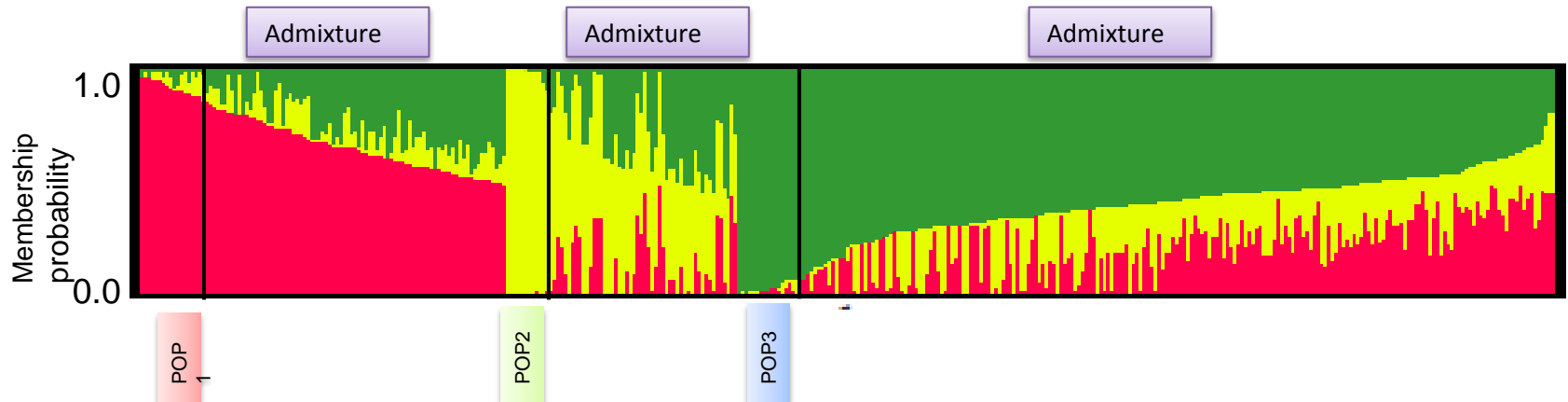


Genotyping of *B. carinata* collection

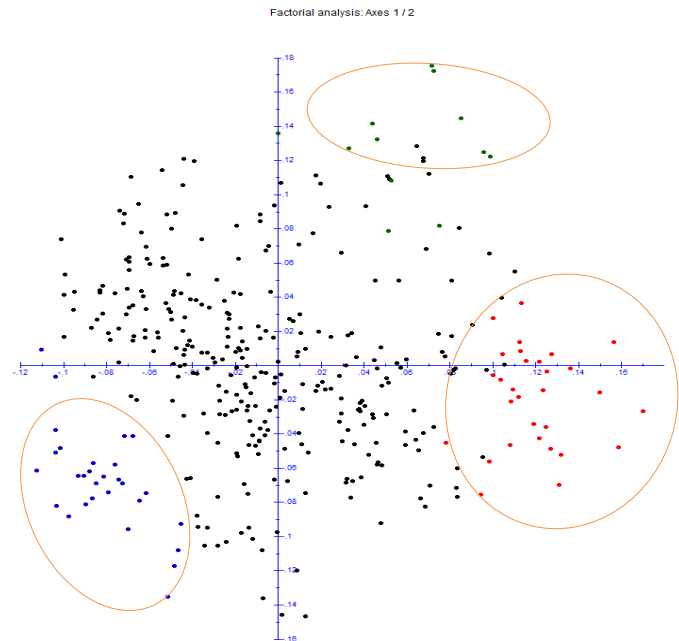
- Genotyping by sequencing of close to 500 lines
- Aligned sequence data to diploid A and B genomes (available at time)
- Identified 71,000 raw SNPs
- Selected 6,046 SNP loci
 - minor allele frequency (0.05), less than 30% missing data, read depth ≤ 4



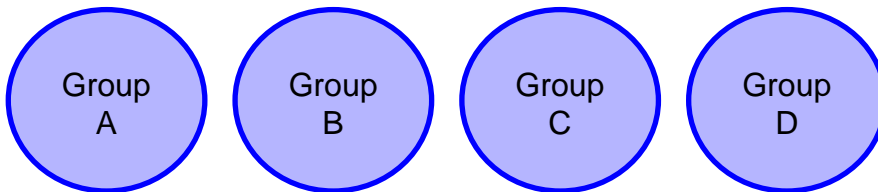
Assessing population structure and similarity among lines



- Pop 1
- Pop 2
- Pop 3
- Admixture



Practical uses and application

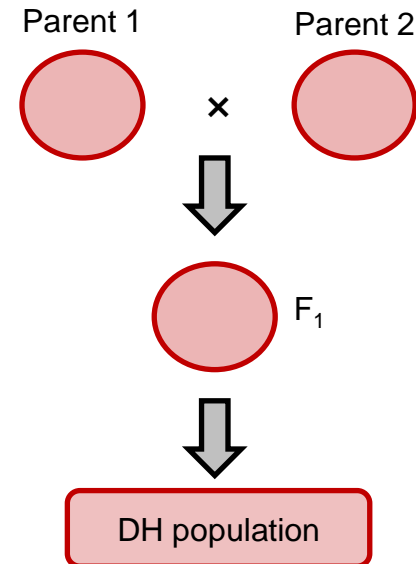


Hybrid development: Initial grouping of accessions and lines for combining ability analysis; will be valuable for identifying patterns of high general and specific combining ability

Decisions on A- and R-line development

Marker discovery: Use information to identify and/or develop markers linked to alleles of interest

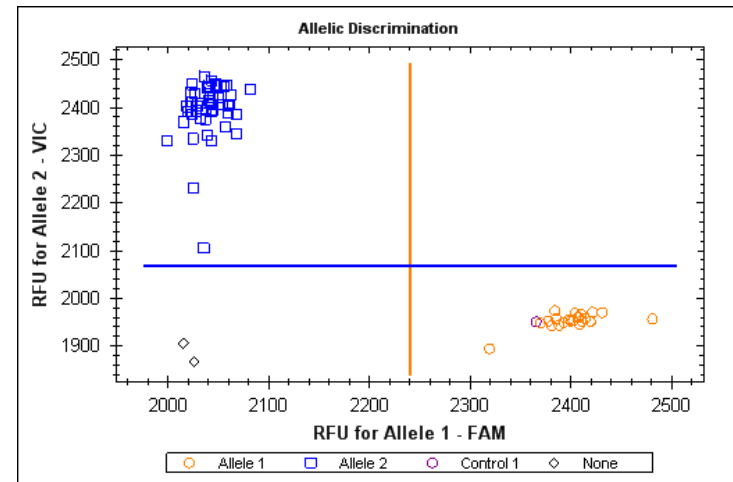
Criteria for choosing parents in cross for DH production:
Phenotypic, Agronomic, **Genetic**
data to be used in decision-making process



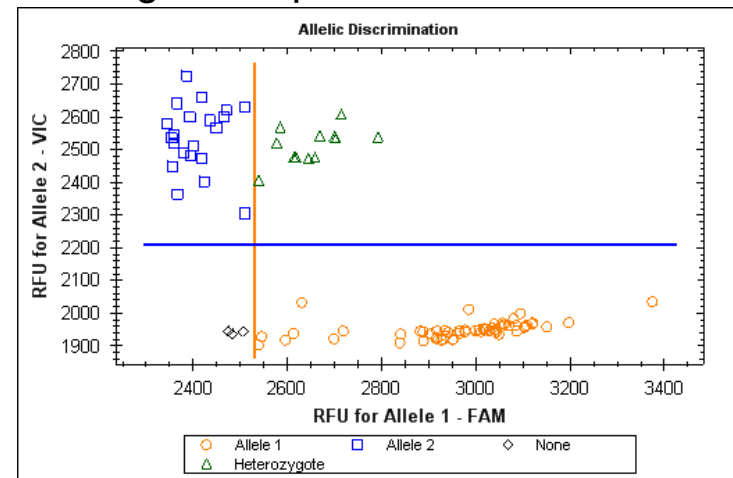
Marker Development

- Assessing population structure and relationships among lines
- Currently re-sequencing 20 *B. carinata* lines for SNP development using the new genome sequence
 - potential Illumina or Affymetrix SNP array
- Developed approximately 350 singleplex Kaspar SNP markers mapped across the genome

BcCtg13840-p369 – mapped to B3



BcCtg13840-p369 – 96 accessions



B. carinata NAM population in development

- High allele richness – **50 founder lines**
- High mapping resolution – **2500 RILS**
- Repeated phenotyping possible
- High statistical power
 - every allele represented many times
- Confounding effect of unlinked genes (false positive) lessened
 - all lines half of background one parent
- Lower impact of genetic heterogeneity
- Crossing to common adapted parent



Marker discovery for *B. carinata* germplasm improvement

Phenotyping of NAM lines

- 2014, 2015 – Phenotyping of 50 founder lines + common adapted parent
- 2016, 2017 – Phenotyping of NAM population lines – locations?

Traits of interest

- Seed oil content
- Earlier maturity
- Yield related components: TKW, seeds per pod, etc.
- Glucosinolate reduction – low GSL
- Frost/cold tolerance
- Plant architecture characteristics
- Etc.

Discussion on marker discovery

- Interest/opportunities?