Advances in breeding at USDA

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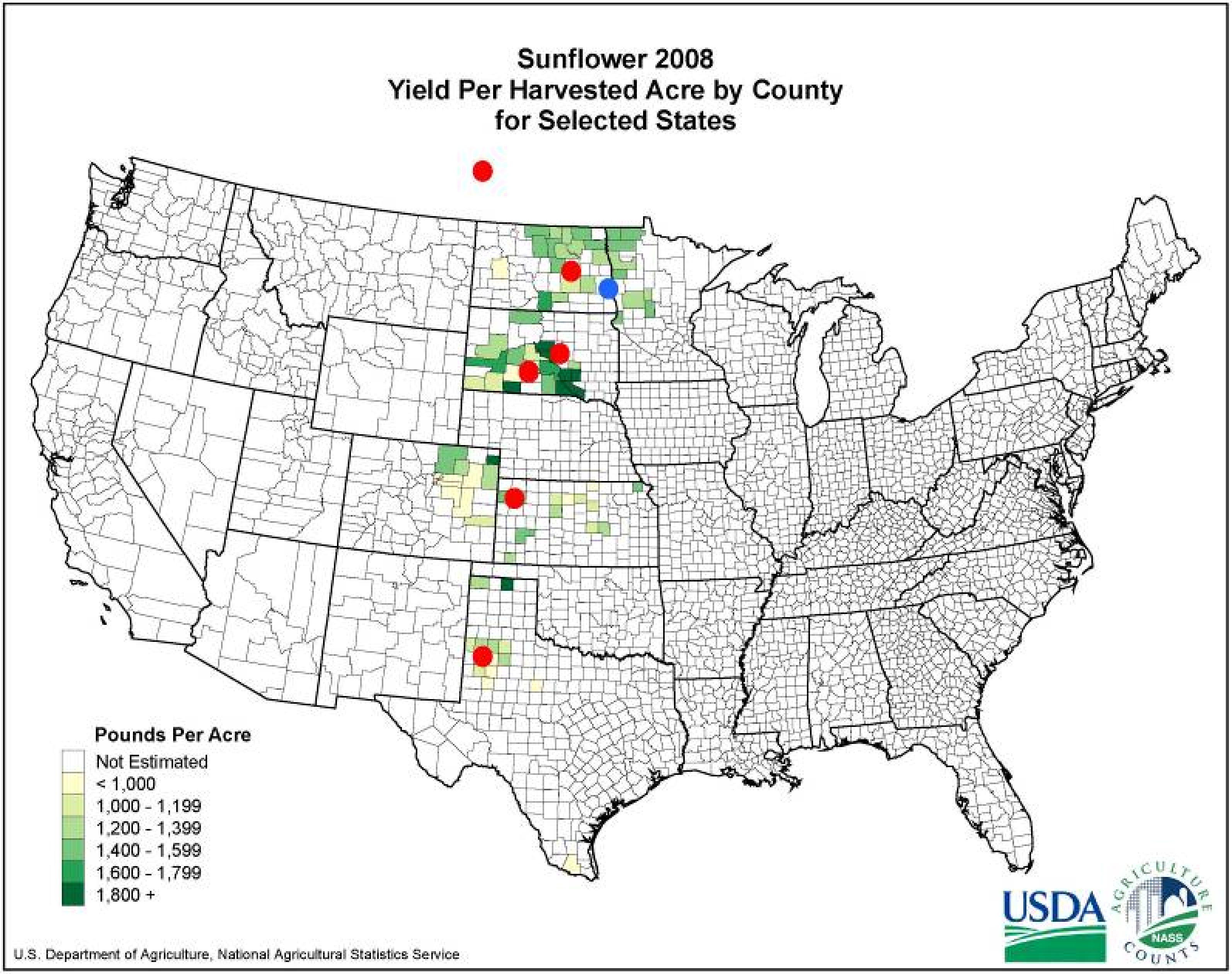
List of traits studied

- Work is mostly in oilseed with some ventures into confection
- Disease resistance
  - Sclerotinia resistance
  - Downy mildew resistance – mostly stacking with Sclerotinia and other traits
  - Rust resistance stacked with Sclerotinia resistance
  - Early work on Verticillium resistance (pending results from Sam Markell and associates on VCGs)

List of traits studied

- Insect resistance (now in winter nursery)
  - Banded sunflower moth resistance
  - Red sunflower seed weevil resistance
  - Sunflower moth resistance
  - Stem weevil resistance
- Low Saturated fat
- Diversification of sunflower germplasm
- Perennial sunflower as a bird trap crop

Testcross Yield Trial Sites, USDA-ARS, 2010



New Releases

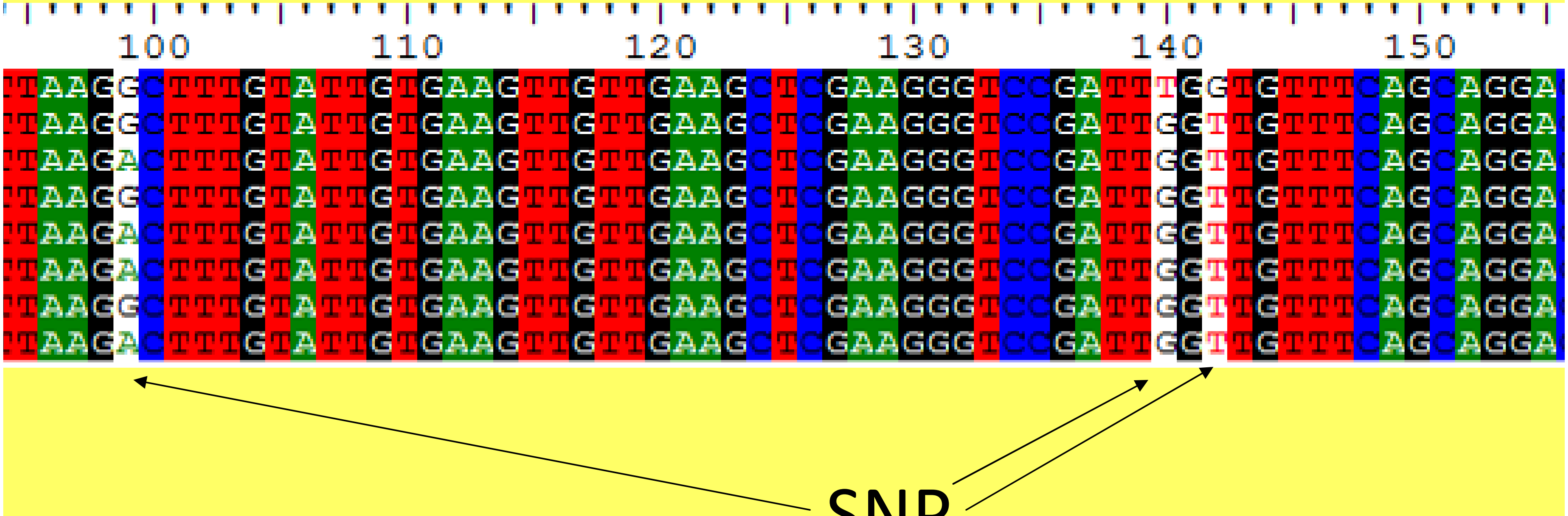
- Still in the process of looking over multiple year data set, increasing seed in Chile
- Releases may include lines with Sclerotinia resistance, HO, Phomopsis resistance, and IMI (old gene)

SNP markers

- Much progress in 1 year.
- Data set for 10,000 SNPs should be available shortly.
- First project: Sclerotinia stalk rot resistance using AM (association mapping) approach
- Development of a unified BeadXpress assay for key traits?

SNP example

Arabidopsis thaliana EIN2 (Ethylene Insensitive 2) homologus gene sequences in cultivated *Helianthus annuus* lines



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    100       110       120       130       140       150
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TAAGGCTTTGTATTGTGAAGTTGTTGAAGCTCGAAGGGTCCGATTGGTTGTTTCAGCAGGA
TAAGACTTTGTATTGTGAAGTTGTTGAAGCTCGAAGGGTCCGATTGGTTGTTTCAGCAGGA
TAAGGCTTTGTATTGTGAAGTTGTTGAAGCTCGAAGGGTCCGATTGGTTGTTTCAGCAGGA
TAAGACTTTGTATTGTGAAGTTGTTGAAGCTCGAAGGGTCCGATTGGTTGTTTCAGCAGGA
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TAAGGCTTTGTATTGTGAAGTTGTTGAAGCTCGAAGGGTCCGATTGGTTGTTTCAGCAGGA
TAAGACTTTGTATTGTGAAGTTGTTGAAGCTCGAAGGGTCCGATTGGTTGTTTCAGCAGGA
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SNP

Trait Bead Assay

- I propose we develop a “trait bead” which includes SNPs that are significantly associated with traits of interest
  - Use in marker assisted breeding
  - Allow us to study the breeding value of individual plants before going to the field
  - Breeding value assessment depends on the type of trait of interest
  - Multiples of 48 markers allowed in a single test

Traits of interest

- Single gene
  - Disease resistance
    - Downy mildew
    - Sunflower rust
    - Verticillium wilt
  - Herbicide resistance
  - High oleic
  - Insect resistance???

- Many genes
  - Disease resistance
    - Phomopsis
    - Sclerotinia stalk rot
    - Sclerotinia head rot
  - Insect resistance???
  - Yield
  - Oil content
  - Confection v. Oilseed

Single gene traits and Many gene (quantitative) traits require different applications of SNP technology

Single genes and SNPs

- Breeder's assumptions:
  - Complete heritability: presence/absence in direct test of a trait (like GC test for HO)
  - A marker would provide information on a plant months before a progeny test is possible
- Preferred strategy: produce an F2 or F3 population of plants, analyze young plants with SNPs individually, keep homozygotes for selection for yield, oil, etc., discard others
- Allows breeder to develop a larger F2 population and conduct selection for "must haves" first.

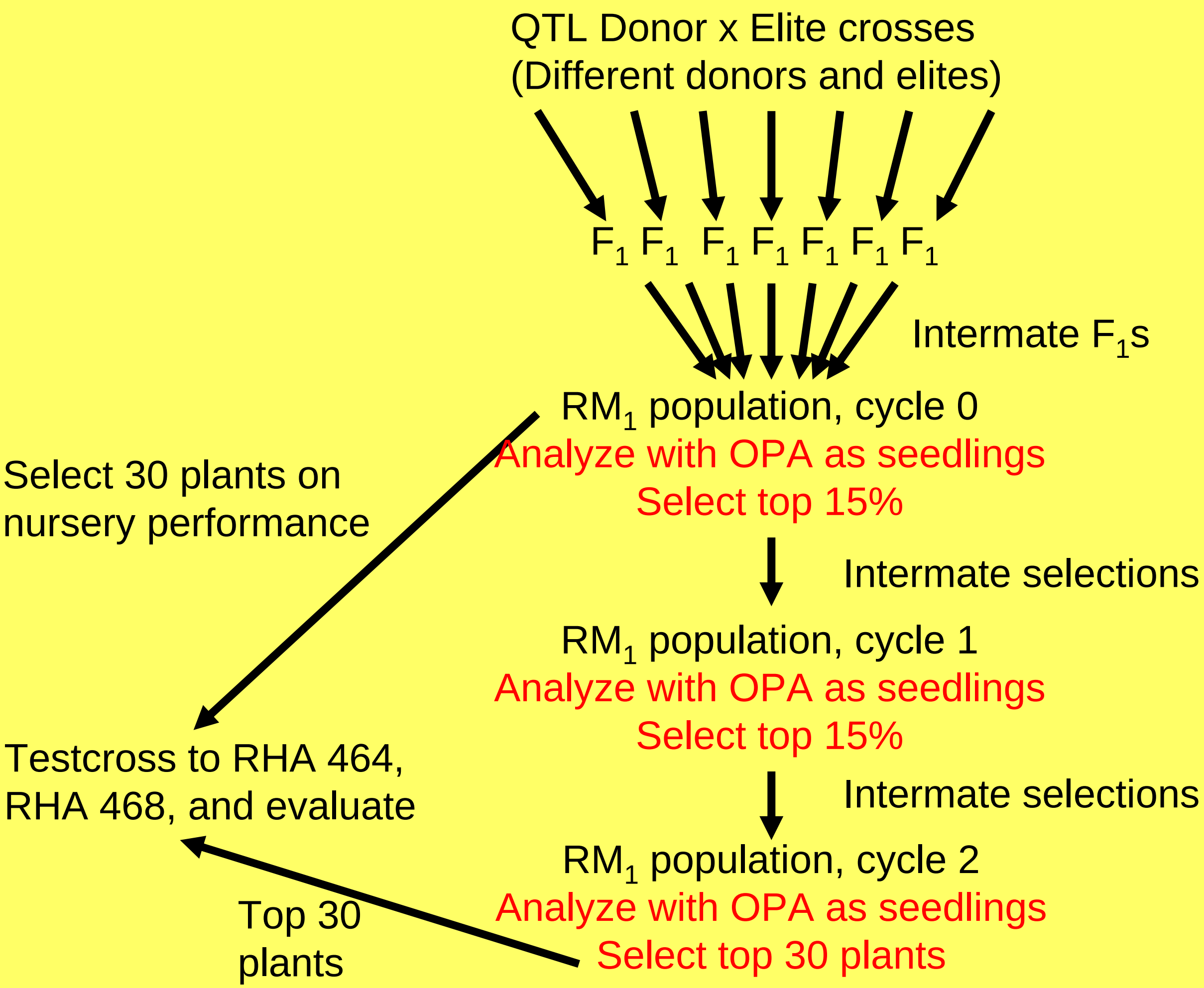
Multiple genes and SNPs

- Breeders' assumptions:
  - Trait has low to moderate heritability and unknown number of genes responsible
  - Even with markers, we still do not know every gene responsible (marker x background effects)
- Methods of using markers for selection of this trait type are diverse and not as straightforward as single genes.

Methods for multi-gene traits

- QTL introgression: put all genes in the line of interest by backcrossing. Not efficient
- Methods that increase <u>frequency</u> of QTL in lines rather than making “perfect” stack
  - Allow you to take advantage of what you don’t know
  - MARS: Use many (10-50) trait-specific markers, assign breeding values to them, genotype lines in populations and keep top “X”%
  - Genomewide selection: Use random markers (~1000), model random markers with field data, use markers to select top “X”% of populations.

MARS example - Sclerotinia



QTL Donor x Elite crosses
(Different donors and elites)

F_1 F_1 F_1 F_1 F_1 F_1 F_1

Intermate F_1s

RM_1 population, cycle 0
Analyze with OPA as seedlings
Select top 15%

Intermate selections

RM_1 population, cycle 1
Analyze with OPA as seedlings
Select top 15%

Intermate selections

RM_1 population, cycle 2
Analyze with OPA as seedlings
Select top 30 plants

Select 30 plants on
nursery performance

Top 30
plants

Testcross to RHA 464,
RHA 468, and evaluate

Table 1 in Eathington et al.

Comparison of multiple trait index values following one year of MARS and conventional selection.

Year	# of populations	Conventional selection (2 seasons)	MARS (3 seasons)		
2002	79	0.63	1.10		
2003	97	0.25	0.97		
2004	72	0.76	1.62		
All	248	0.50	1.18		

Multi-gene traits:
Guides for breeders

- Breeding for quantitative traits in plants. By Rex Bernardo. 2010 Stemma Press. www.stemmapress.com
- Eathington et al. 2007. Molecular markers in a commercial breeding program. Crop Science 47(S3) S154-S163 (part of International Plant Breeding Symposium proceedings)

Thanks!

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