Managing and characterizing complex traits, including quantitative traits

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UC Davis – Plant Breeding Center

Consolidate and update graduate plant breeding curriculum – include field based content/experience

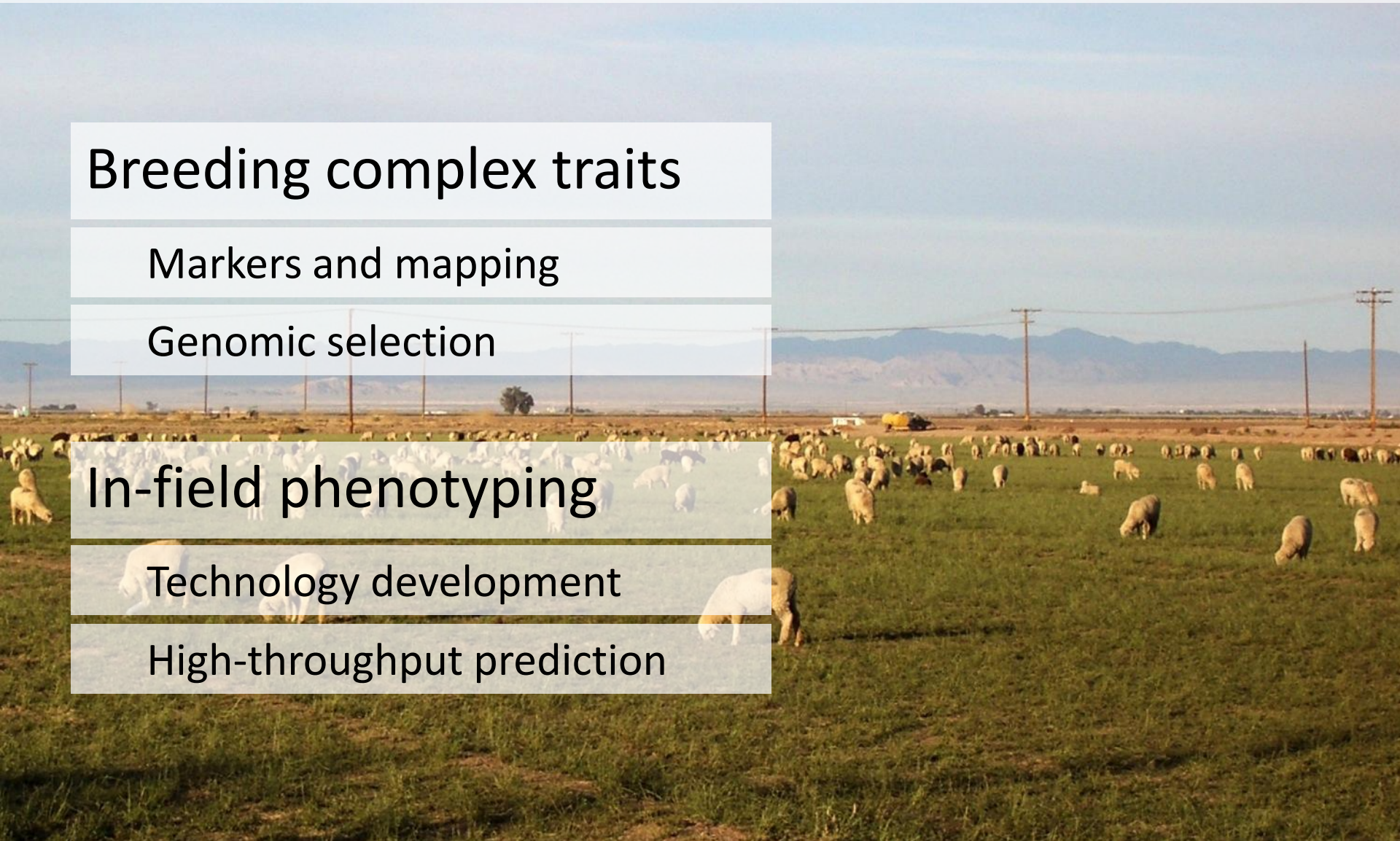
Involve industry/commodity partners in educational programs through internships, assistantships, class visits, guest lectures….

Develop post-graduate school educational programs, coordinating with Seed Central and Plant Breeding Academy

Promote hiring of more plant breeding faculty and staff with field-based expertise

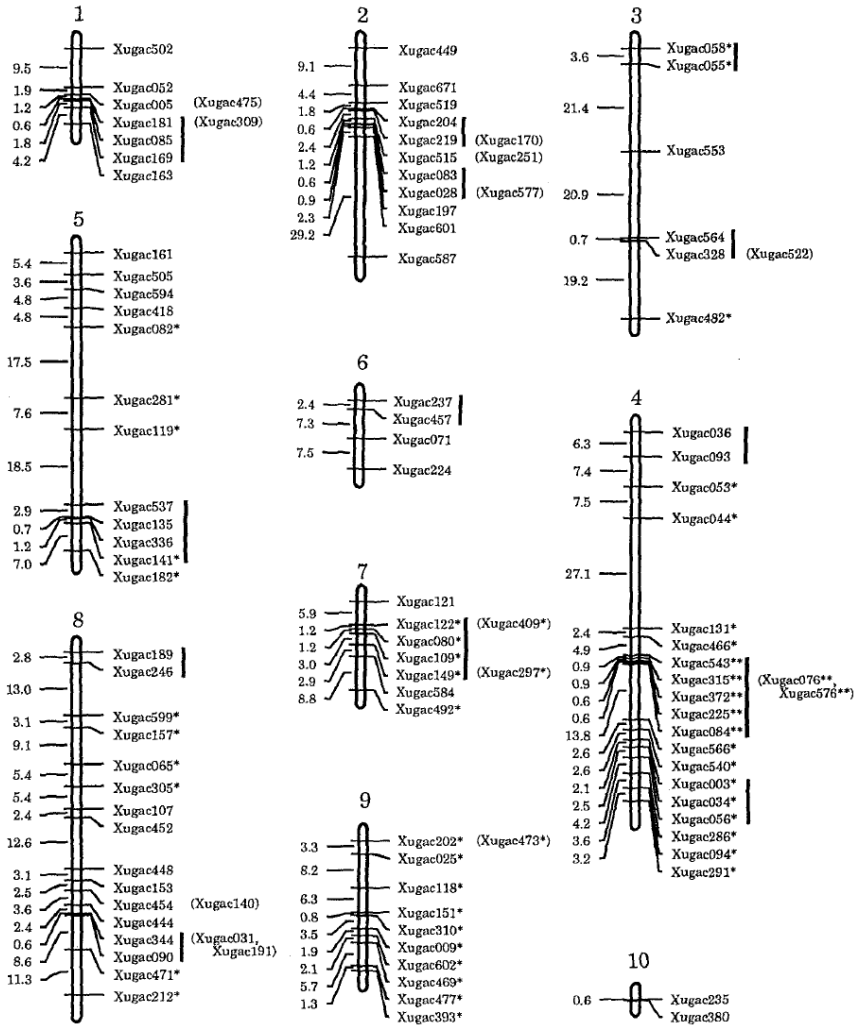
Develop useful technologies, germplasm and cultivars and actively license for commercialization

Outline



- Breeding complex traits
  - Markers and mapping
  - Genomic selection
- In-field phenotyping
  - Technology development
  - High-throughput prediction

21 years of markers and maps



Development of an RFLP map in diploid alfalfa

E. Charles Brummer [1]*, Joseph H. Bouton [1], and Gary Kochert [2]

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Theor Appl Genet (1993) 86:329–332

108 markers – 10 LG – 1 year

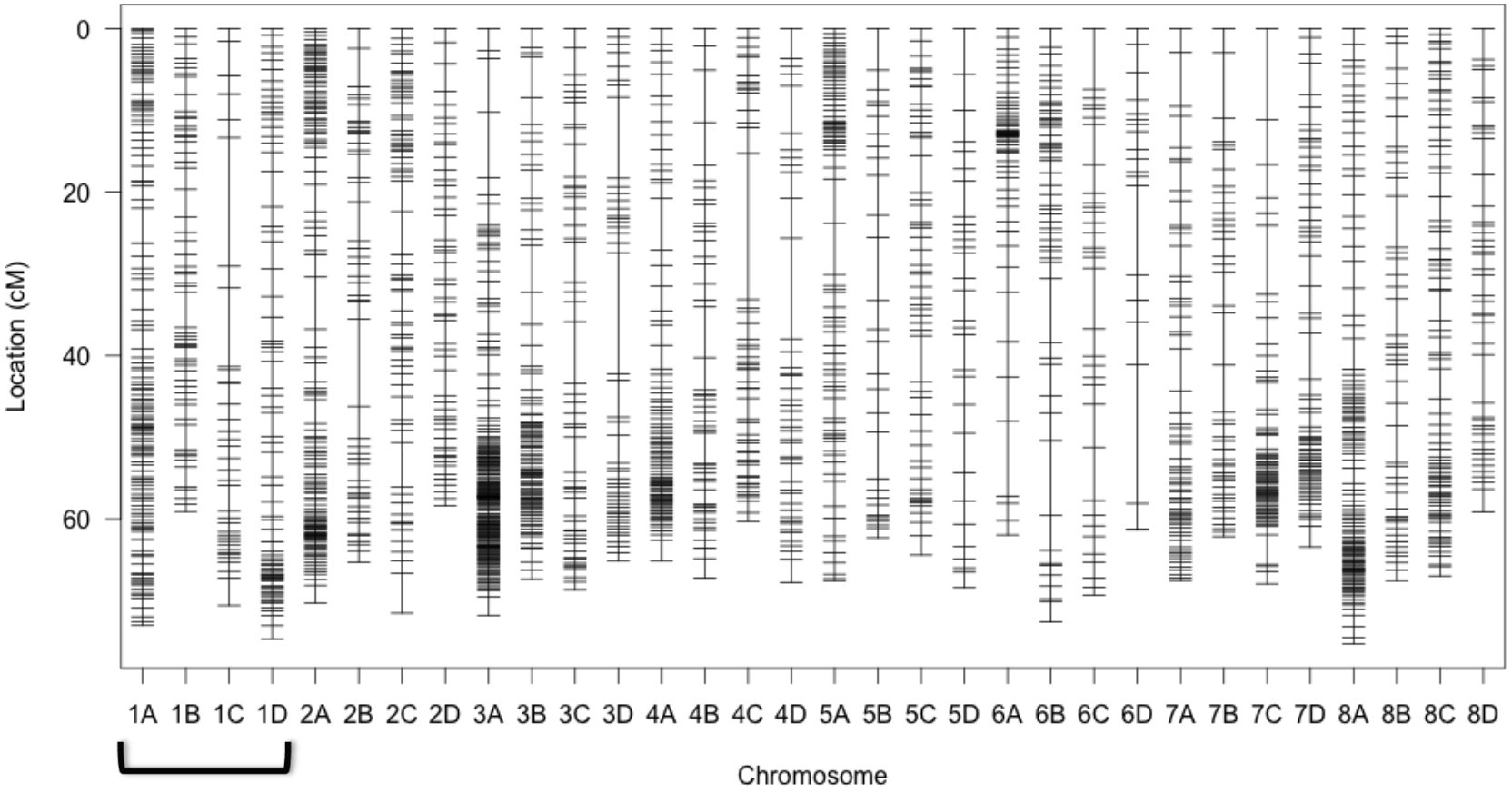
Have markers contributed to cultivar advances?

Forage cultivars developed using markers

Markers are no longer limiting

Genotyping-by-sequencing to generate saturated map in a month

Bioinformatics-intensive to manipulate sequence data

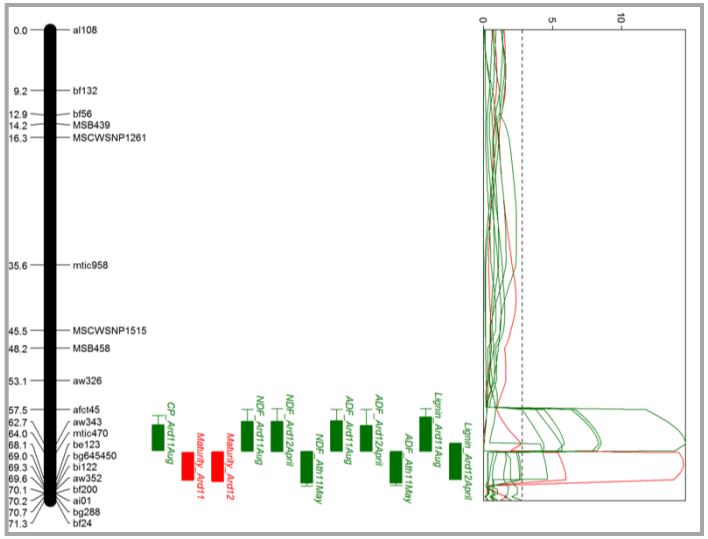


4 haplotypes per chromosome

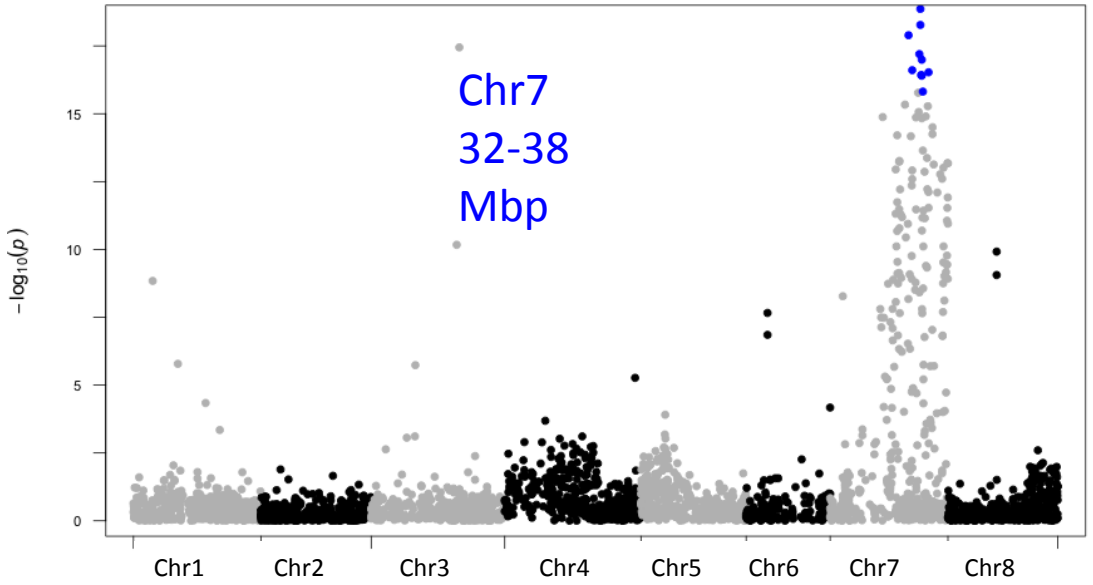
(Li et al., *Manuscript in preparation*)

Flowering time in alfalfa

CC78 SSR markers



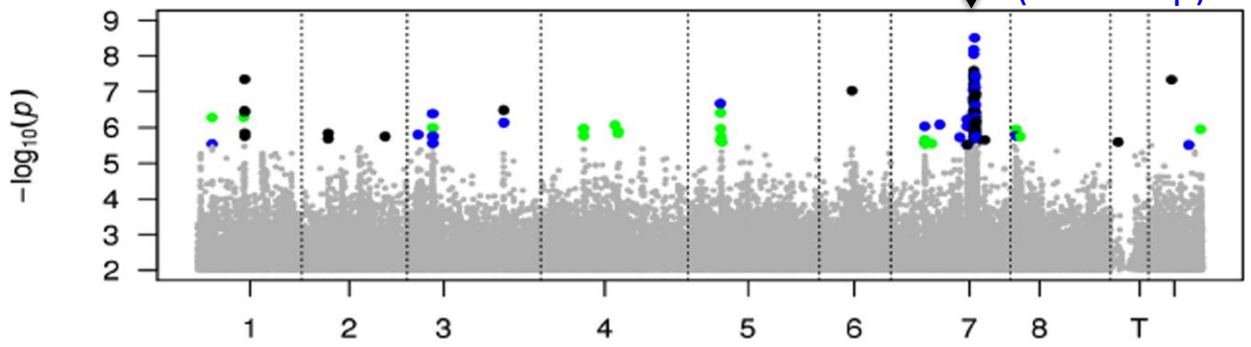
CC78 GBS SNPs



Aligned to *Medicago* whole genome sequence

A flowering time gene on chr7 in *M.truncatula*

MtFD
(34.3 Mbp)



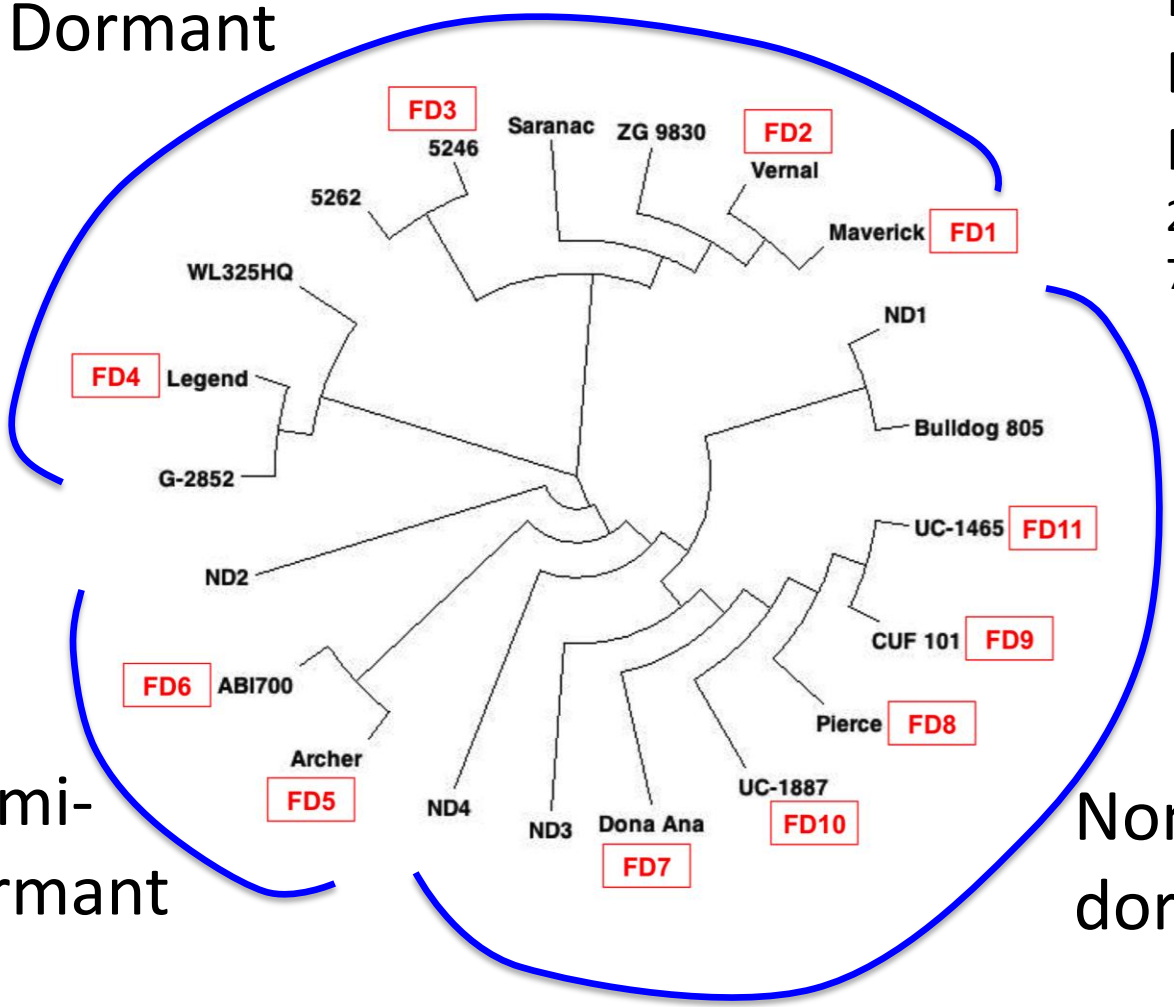
(Stanton-Geddes et al., 2013)

Fall dormancy in alfalfa

- Robust field-based protocol gives reliable results
- Based on well-defined check cultivars

Cultivated alfalfa germplasm structured by fall dormancy

Dormant



Fall Dormancy Breeding Germplasm Population

21 breeding populations

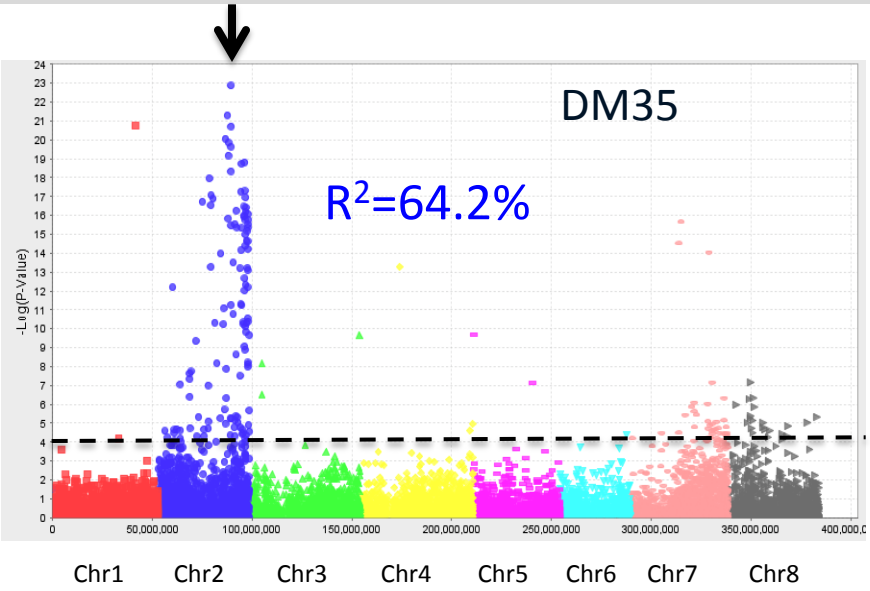
7500 Infinium SNP loci

Semi-dormant

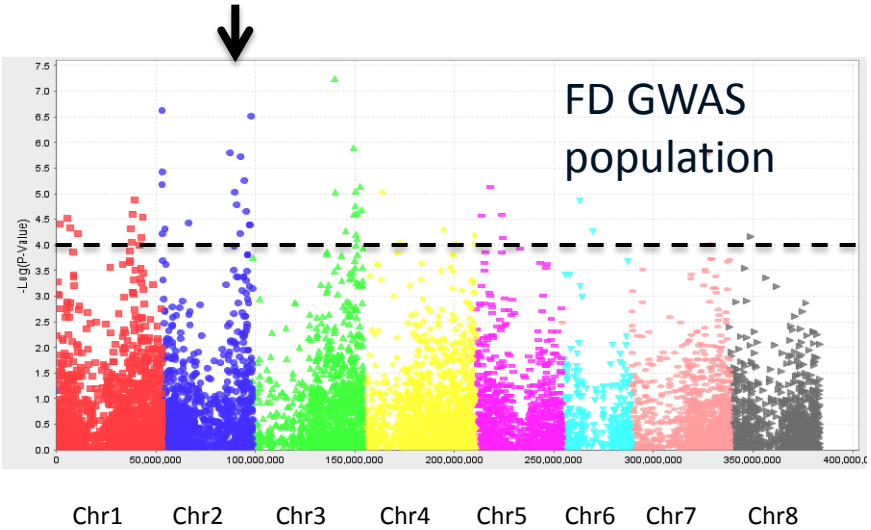
Non-dormant

(Li et al., 2014 *PlosOne*)

Autumn dormancy mapping

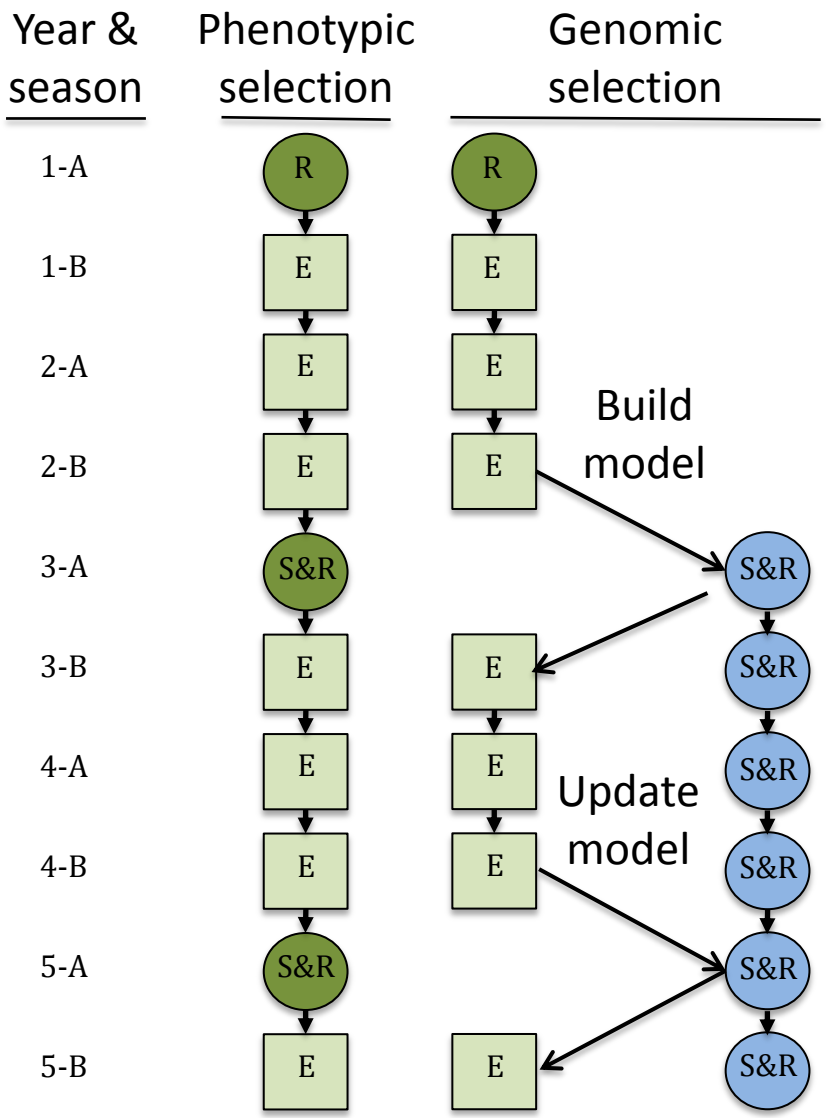


Bi-parental population



Breeding germplasm population

Predicting phenotypes with markers



Measure phenotypes on a plant population

Generate genome-wide markers and compute the effect of each marker on the trait

Select based on the sum of these affects across all markers – the Genome Estimated Breeding Value

Li & Brummer, 2012, Agronomy 2:40

Alfalfa Genomic Selection

Predict yield based on marker breeding values

NECS breeding population – Clonal selection

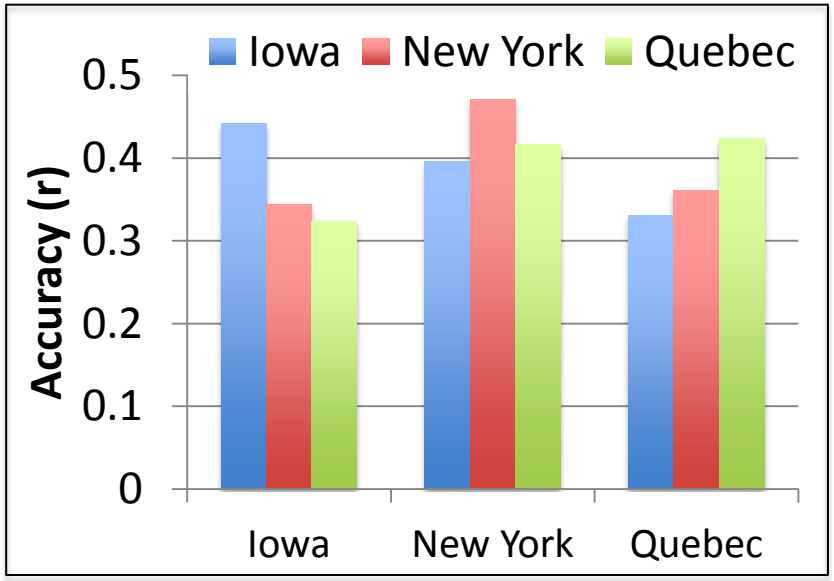
2 cycles, ~200 genotypes/cycle, 3-5 yield environments/cycle

GBS (Elshire protocol)
96-plex on Hi-Seq 2000
~2 million reads/genotype
rrBLUP (Endelman)

Li, Wei, Acharya, Viands, Hansen, Claessens, Brummer – unpub.

Accuracy (r) within locations

	Iowa	New York	Quebec
Cycle 0	0.44	0.49	0.43
Cycle 1	-	0.38	0.62
C0 – C1	**-**	**0.44**	**0.14**



Location cross-validation – Cycle 0

Markers for disease/insect resistance

Effective greenhouse (phenotypic) screen

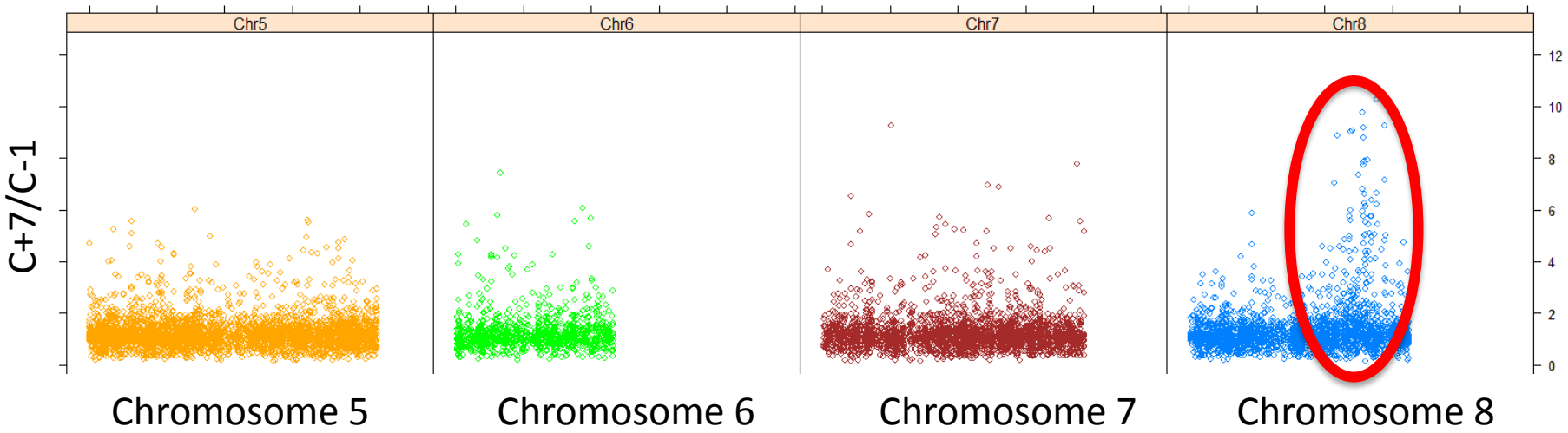
Marker confirmation during breeding program

Tracking allele frequency changes

Whitefly resistance – Larry Teuber (UCD)

GBS using ~100 bulked genotypes of C-1, C+4 and C+7

>55,000 SNP loci with >100 reads/pop; mapped to *Medicago*



Confirmed by SNP markers on individual genotypes (Monteros)

Waiting for phenotypic data….

High-throughput phenotyper
(Jesse Poland, USDA-ARS, Manhattan, KS)

COLORADO: Canopy spectral reflectance (CSR) measured with a Jaz spectroradiometer

CSR measures the amount of light reflected from the plant canopy at many wavelengths

High Throughput Phenotyping (HTP)

Geo-referenced data collection

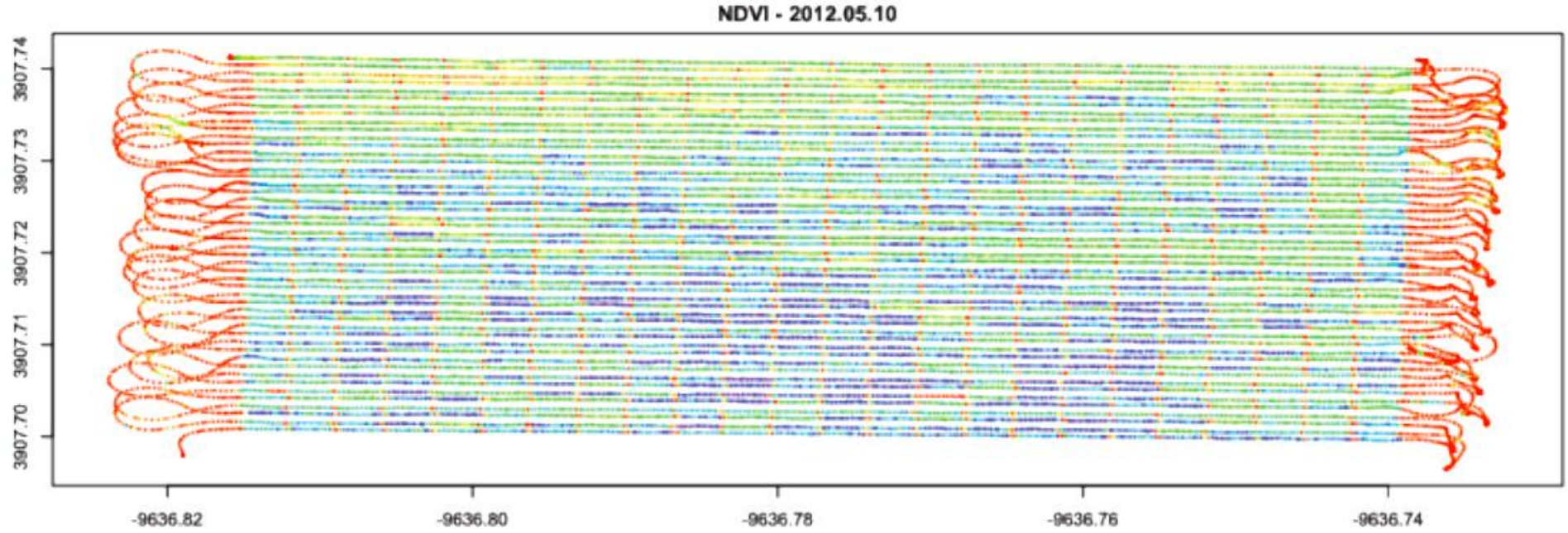
Non-destructive measurements

Fast, repeatable

Assuming good calibrations

Wheat breeding nursery, Jesse Poland, USDA-ARS, Manhattan, KS, USA

Possible Uses in Breeding



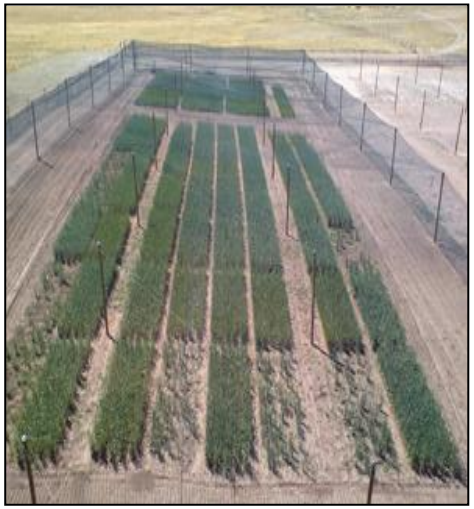
Wheat breeding nursery, Jesse Poland, USDA-ARS, Manhattan

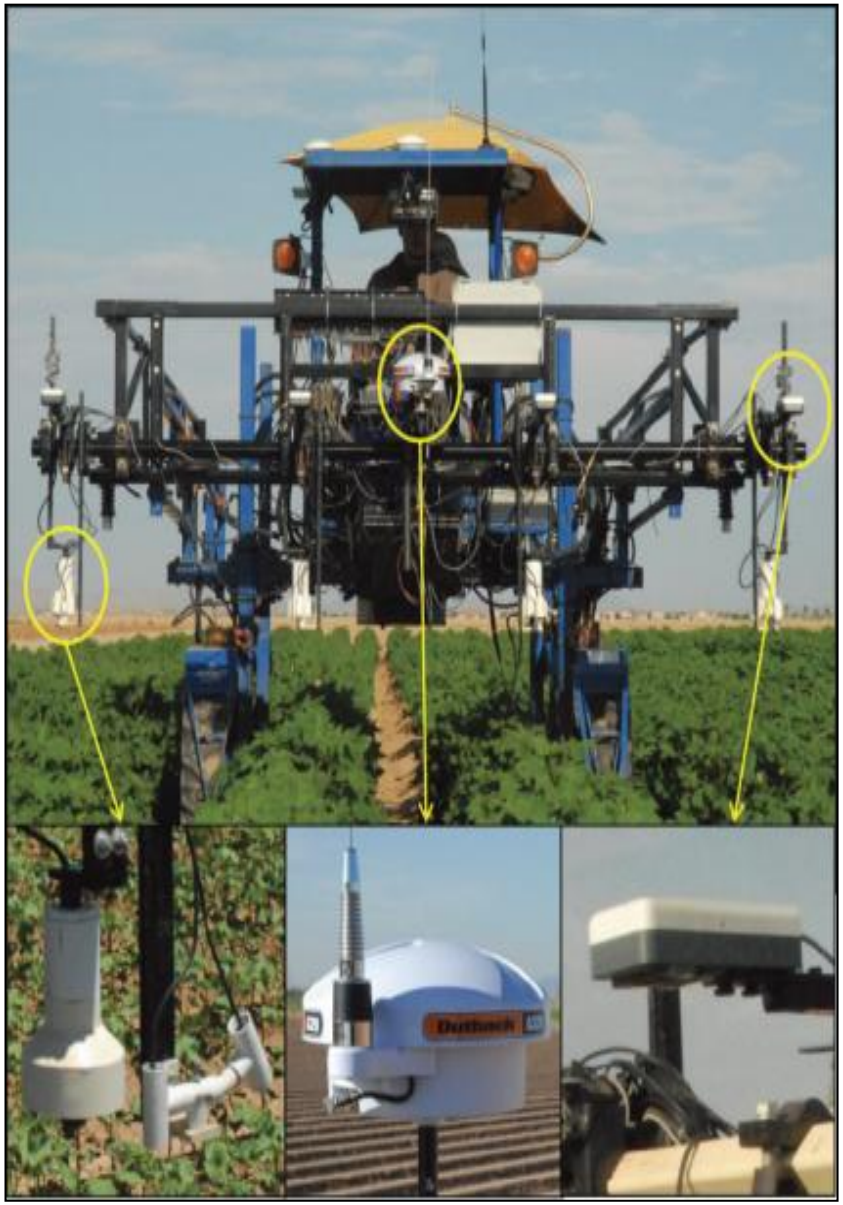
Predict yield before harvest

Measure water, nutrient status

Collect data at more locations than possible with typical trait measurements

High Throughput Phenotyping Platforms





UCD participants in HTP

- CAES
  - M. Gilbert (crop physiology), J. Ross-Ibarra (genomics), P. Gepts (genomics/breeding), C. Brummer (Plant Breeding Center), A. Walker (grape breeding), R. Hijmans (geospatial analysis)
- CES
  - S. Vougioukas (actuators, sensors and control systems), M. Delwiche (biosensors, electr instrum), Computer Sci: (data processing, large datasets, telematics)
- New positions being requested from university

Summary

High-throughput genotyping – available now

High-throughput phenotyping – predict phenotypes

- area of interest in many crops
- many questions – how well do sensors predict desired traits

Data handling

- informatics to manipulate raw sequence or phenotype data
- data processing/analysis power
- data storage and retrieval