Dissecting Alfalfa Dormancy Using Selection Mapping

Charlie Brummer, Gitanshu Munjal, and Scott Newell
University of California, Davis

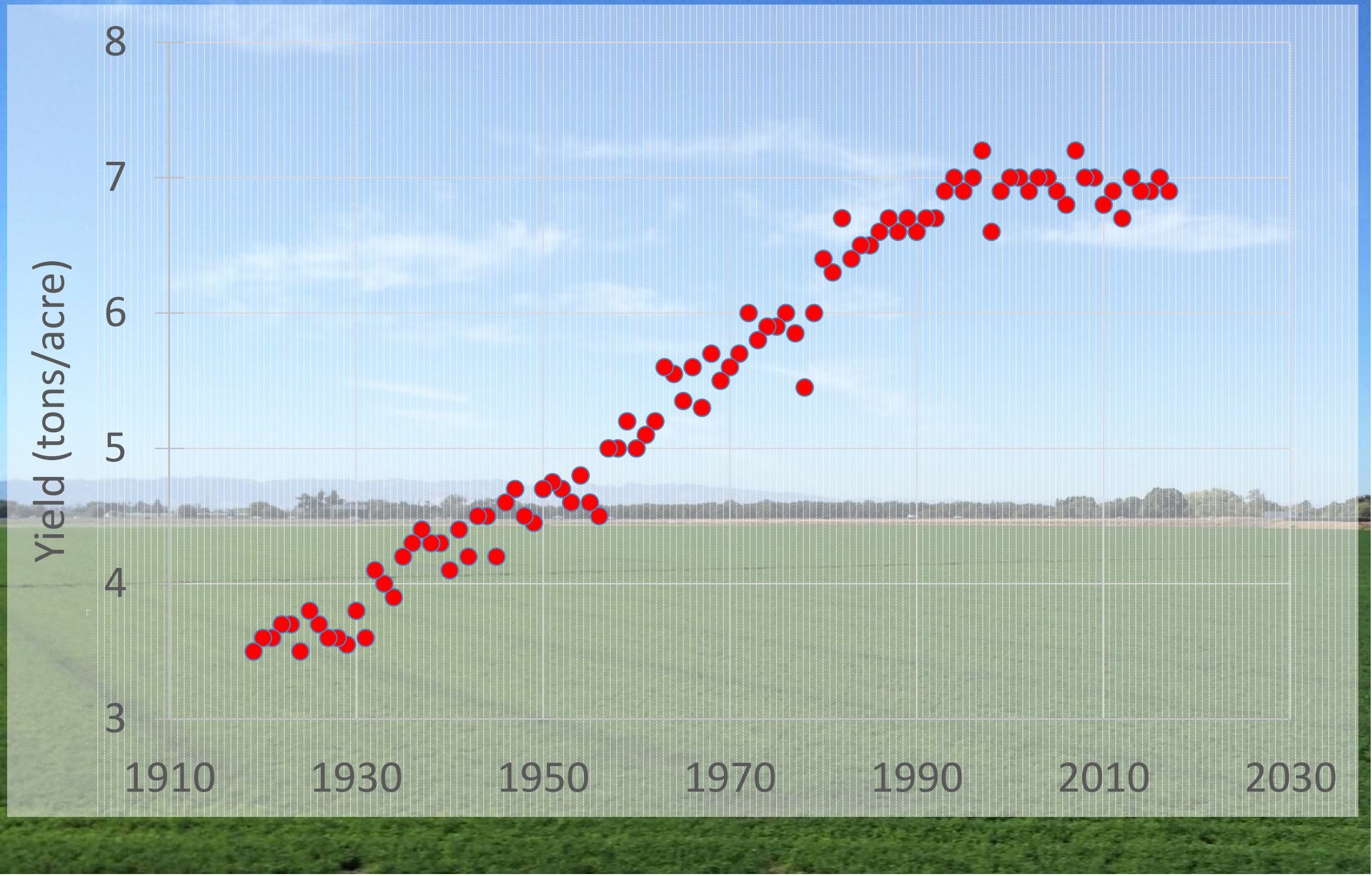
Outline

Yield and Fall Dormancy

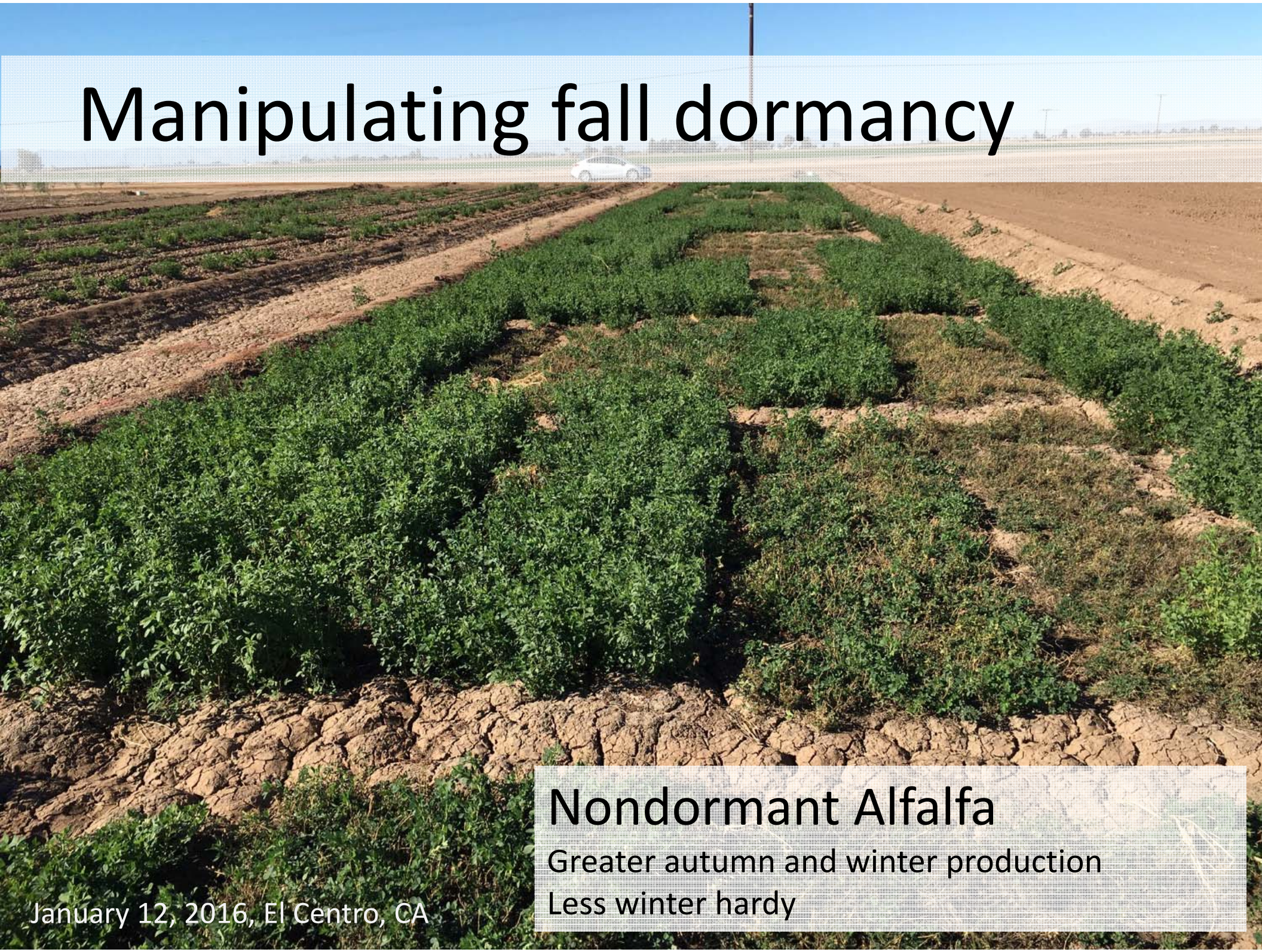
Selection Mapping

GWAS in a breeding population

California Alfalfa Yield – USDA Ag Statistics



Manipulating fall dormancy



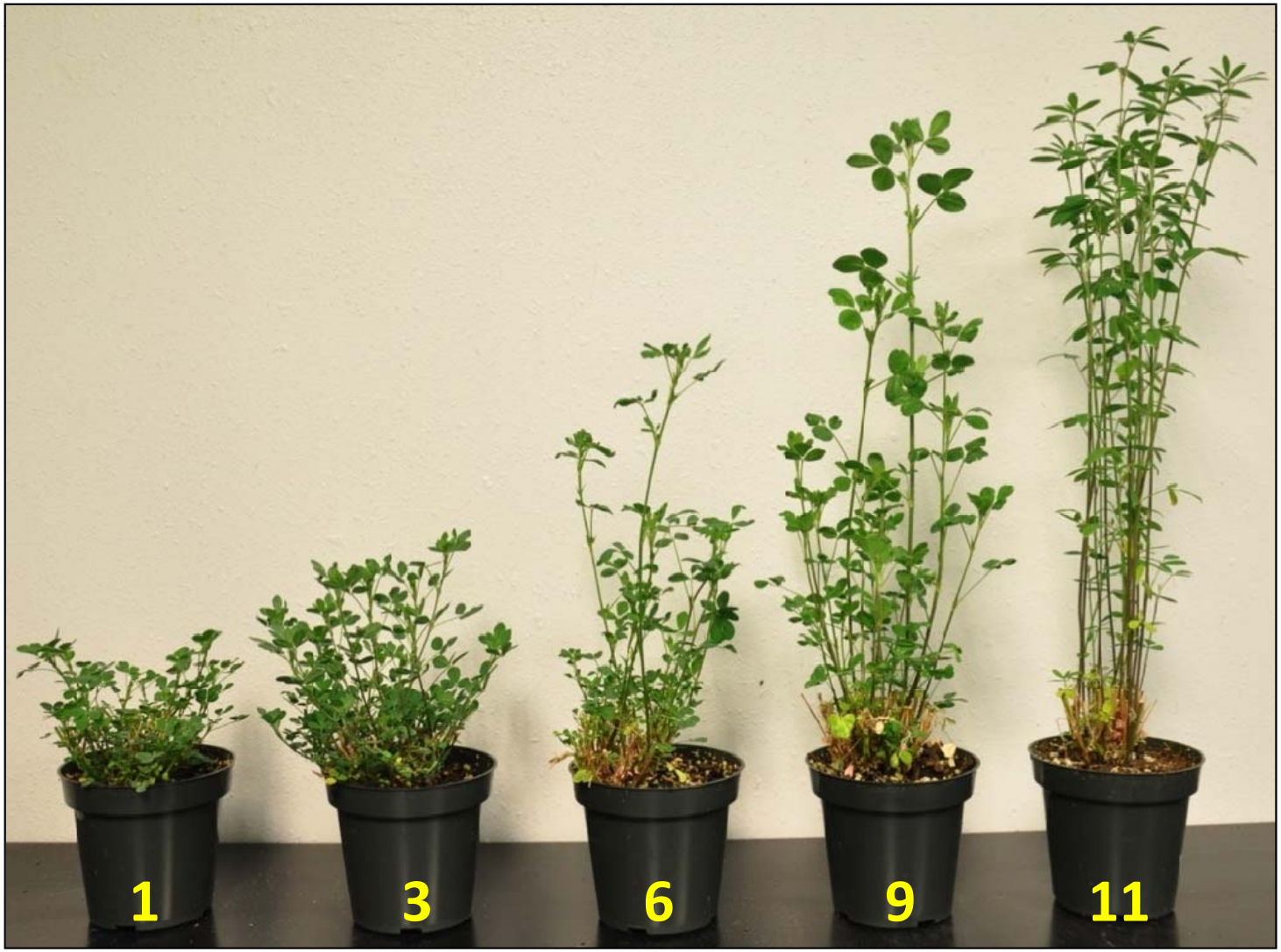
Nondormant Alfalfa

Greater autumn and winter production

Less winter hardy

January 12, 2016, El Centro, CA

Dormancy is measured by height of regrowth in autumn



Dormancy phenotype observed in five of 11 standard check cultivars when in growth chamber under decreasing temp and photoperiod

Divergent selection for fall dormancy

Larry Teuber's dormancy selections

Norseman
FD = 1

Saranac
FD = 4

Lahontan
FD = 6

Mesilla
FD = 8

CUF101
FD = 9

Wadi
FD = 11

For each cultivar

C+3 **H**

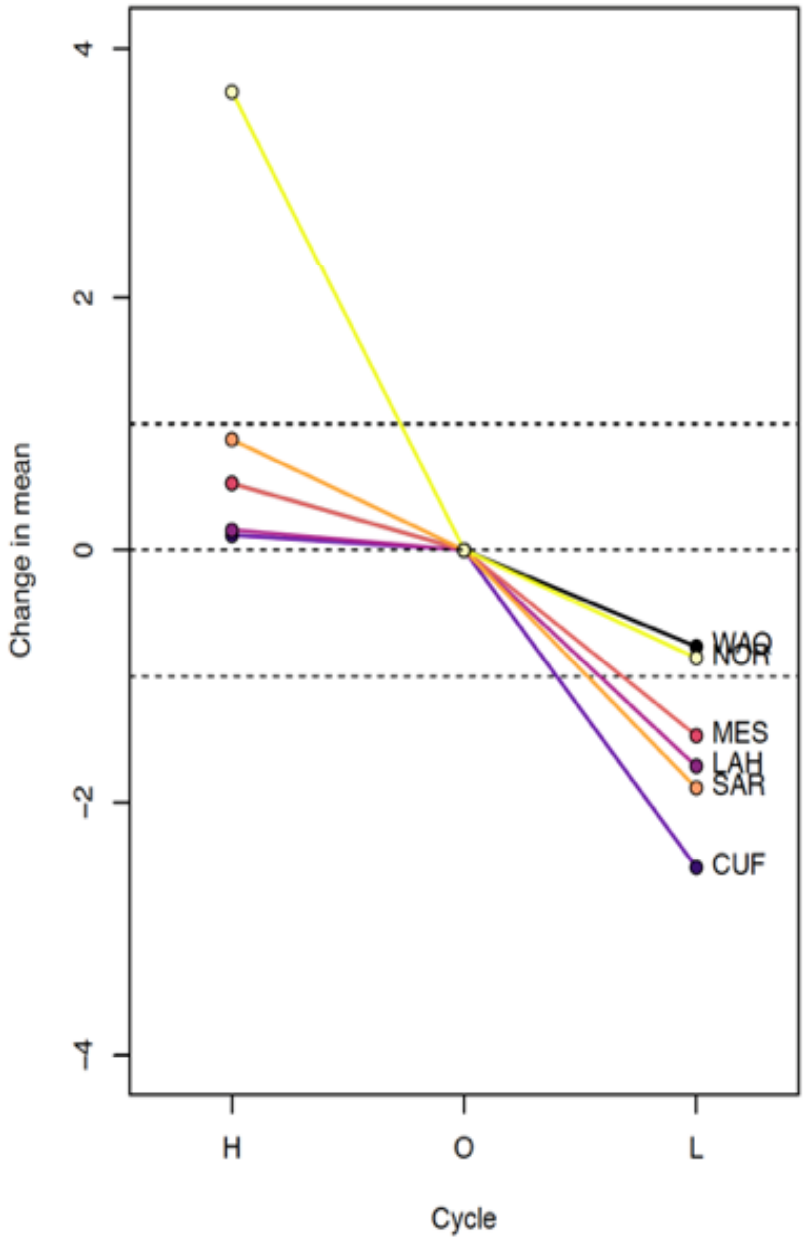
Taller in autumn

Less Dormant

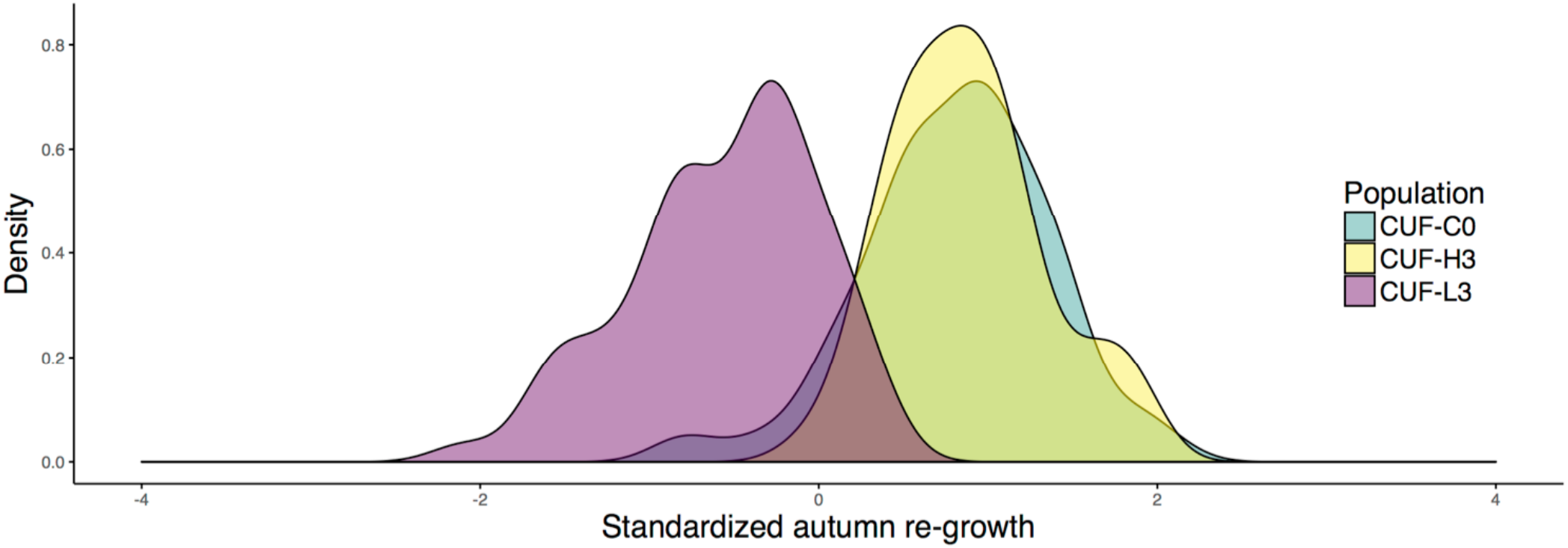
C-3 **L**

Shorter in Autumn

More Dormant



CUF101: ‘L’ selection increased dormancy



‘H’ selection did not decrease dormancy

Munjal et al., G3, 2017

GBS marker discovery and filtering

Modified GBS-SNP-CROP (BMC Bioinformatics. 2016. 17:29)

Retained marker tags that aligned to *Medicago* and/or alfalfa

~ 85,000 SNP at **≥100 reads/population**; ~17,000 alfalfa specific SNP

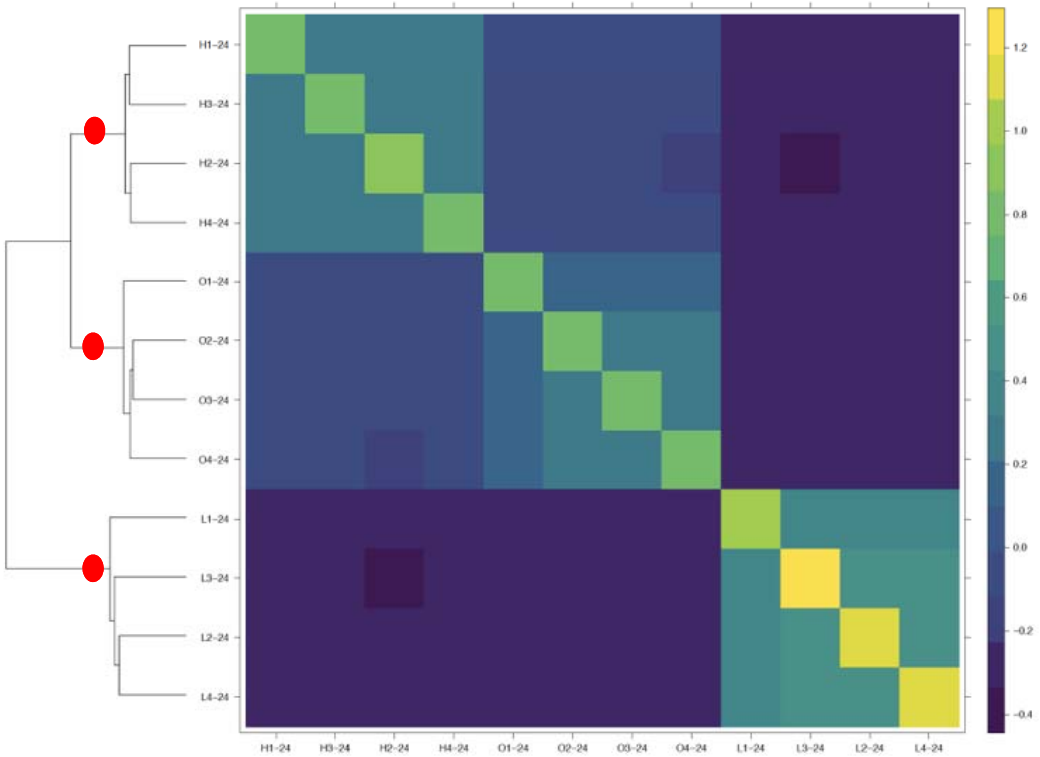
96 genotypes/population - 4 pools of 24 plants each per pop

Computed frequencies for each allele in each pool

CUF101 H

CUF101 O

CUF101 L



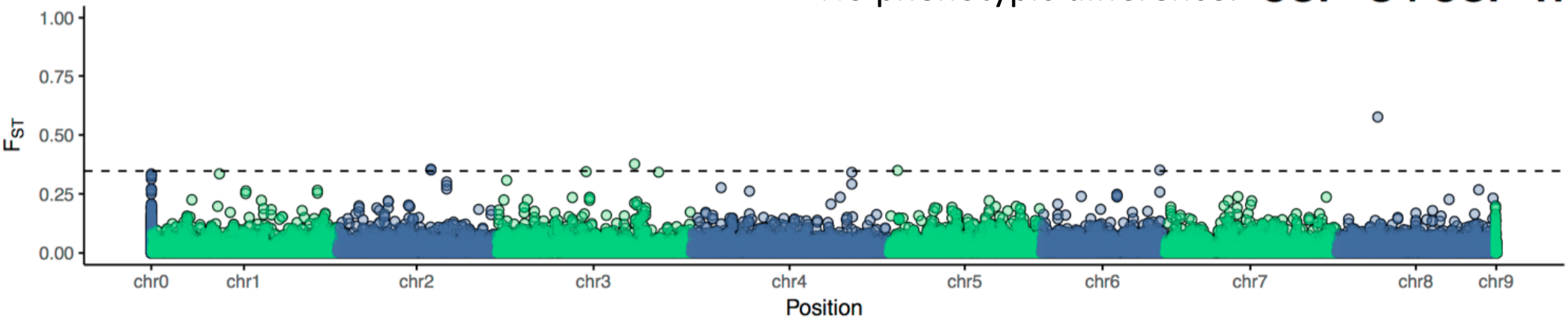
Replicate pools cluster together

The 'L' population which was phenotypically distinct was also genetically distinct

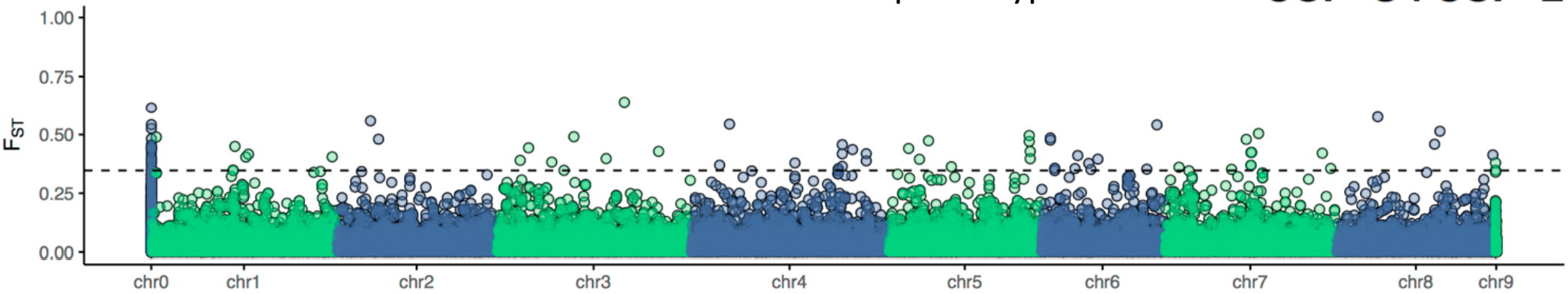
Munjal et al., G3, 2017

Loci possibly under selection – CUF101

No phenotypic difference: **CUF–O | CUF–H**



Clear phenotypic difference: **CUF–O | CUF–L**

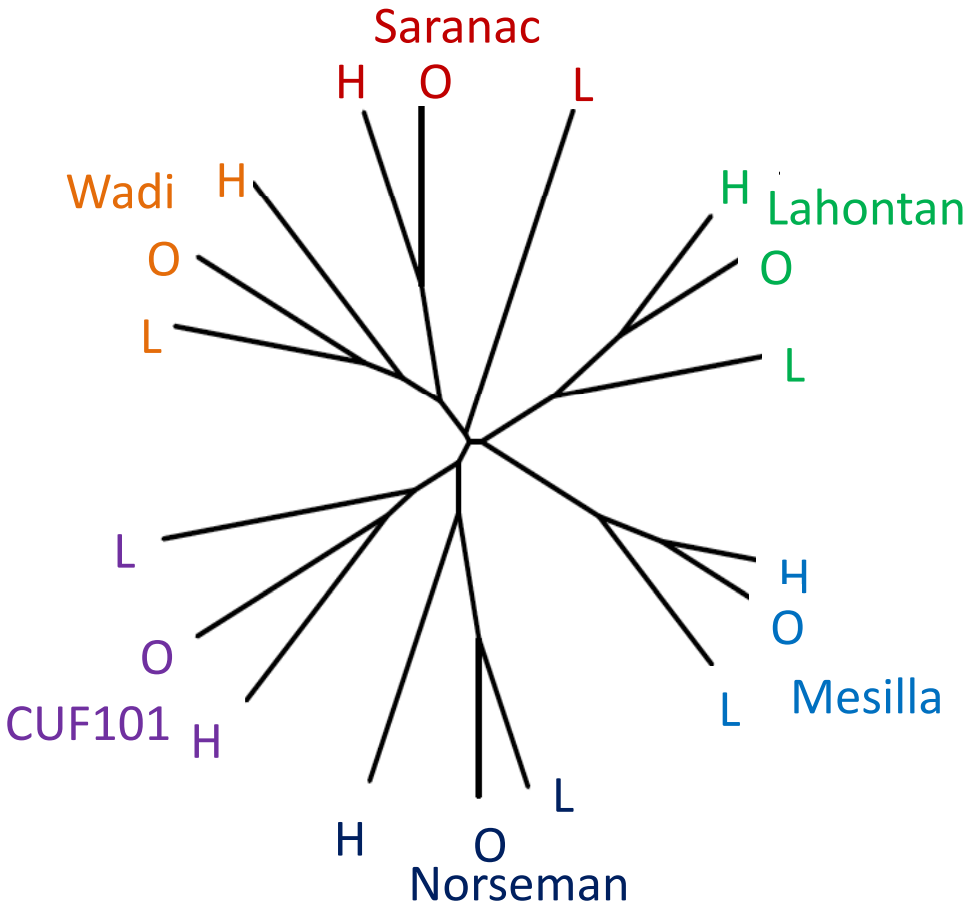


Position on *Medicago truncatula*

SNP loci that align to alfalfa scaffolds but not to *Medicago*

Munjal et al., G3, 2017

Evaluating selection across all populations



Few markers with >100 reads/population

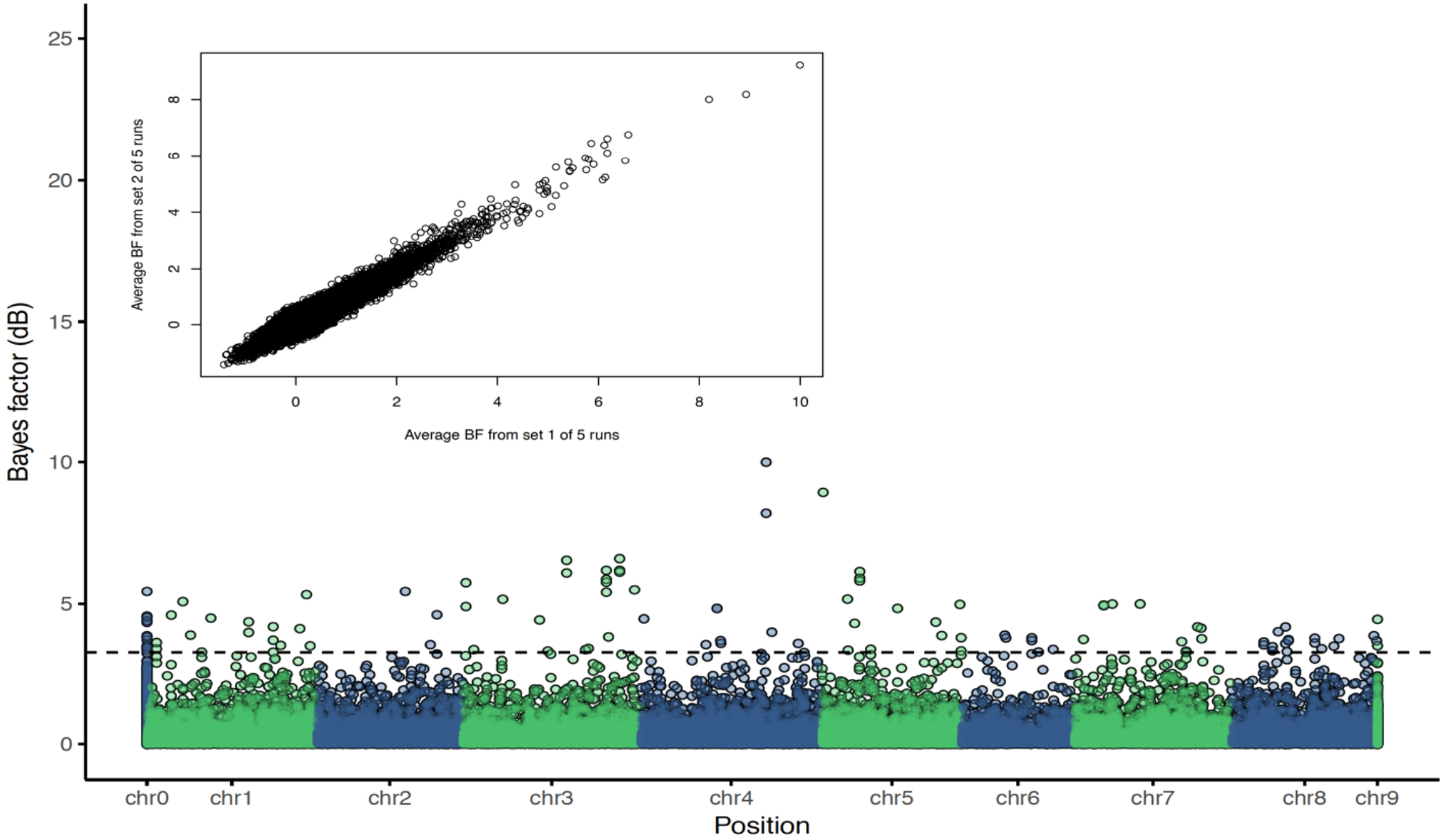
Model allele frequencies using Bayesian analysis

Account for population structure

Identify selection signature across H – O – L pops

Munjal et al., in prep.

Markers associated with dormancy across all cultivars



GWAS in a breeding population

Forage Genetics, Intl. breeding population

268 families, 2 reps

Measured fall height on all plants

Genotyped one plant per plot with GBS

Associate height with markers for chosen plant

Determining genotypes with low-read GBS data

Assigning discrete *genotype calls* to individuals for marker loci is problematic in autopolyploids

Need substantial depth to unequivocally call the heterozygote classes (AAAa, AAaa, Aaaa)

Two alternative approaches:

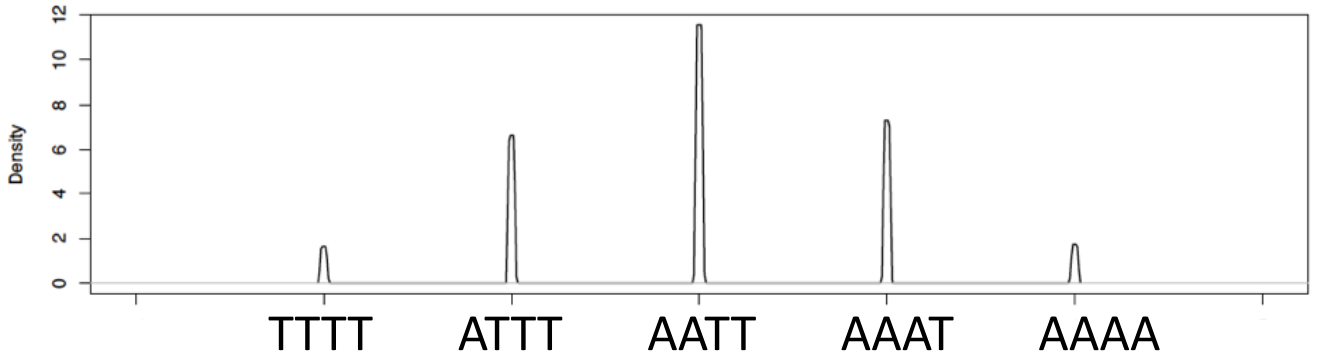
"Diploidize data – only call three genotypic classes (AAAA, heterozygotes, aaaa)

Model the uncertainty

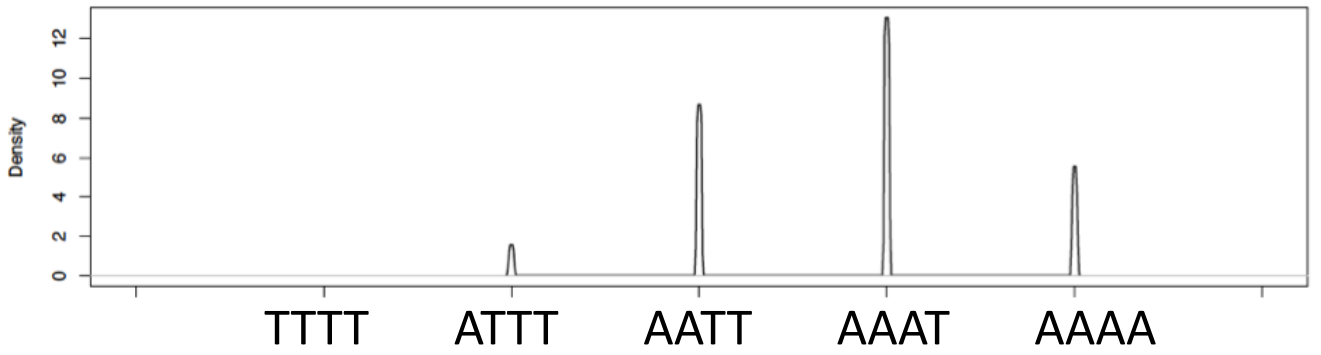
Modelling auto-tetraploid genotypes

Assume 2 alleles (A/T) with pop freq = 0.5; sampled an “AAAA” genotype

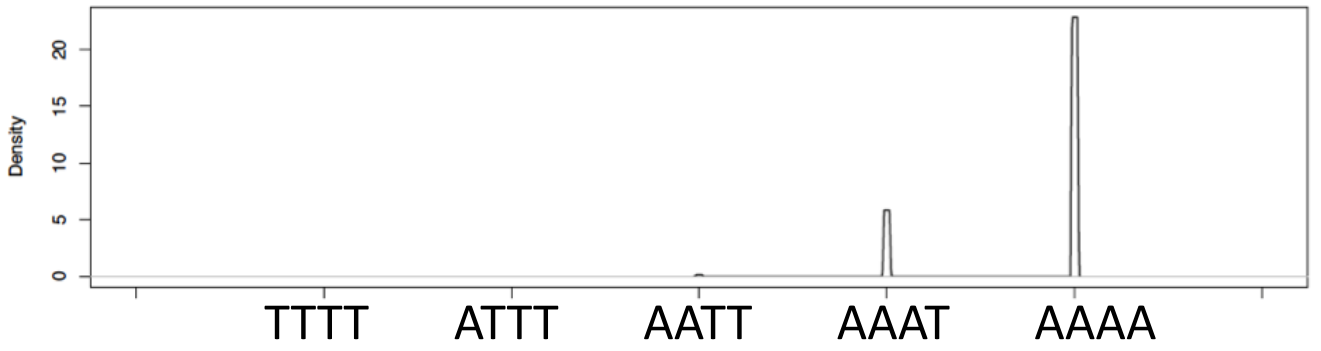
No reads



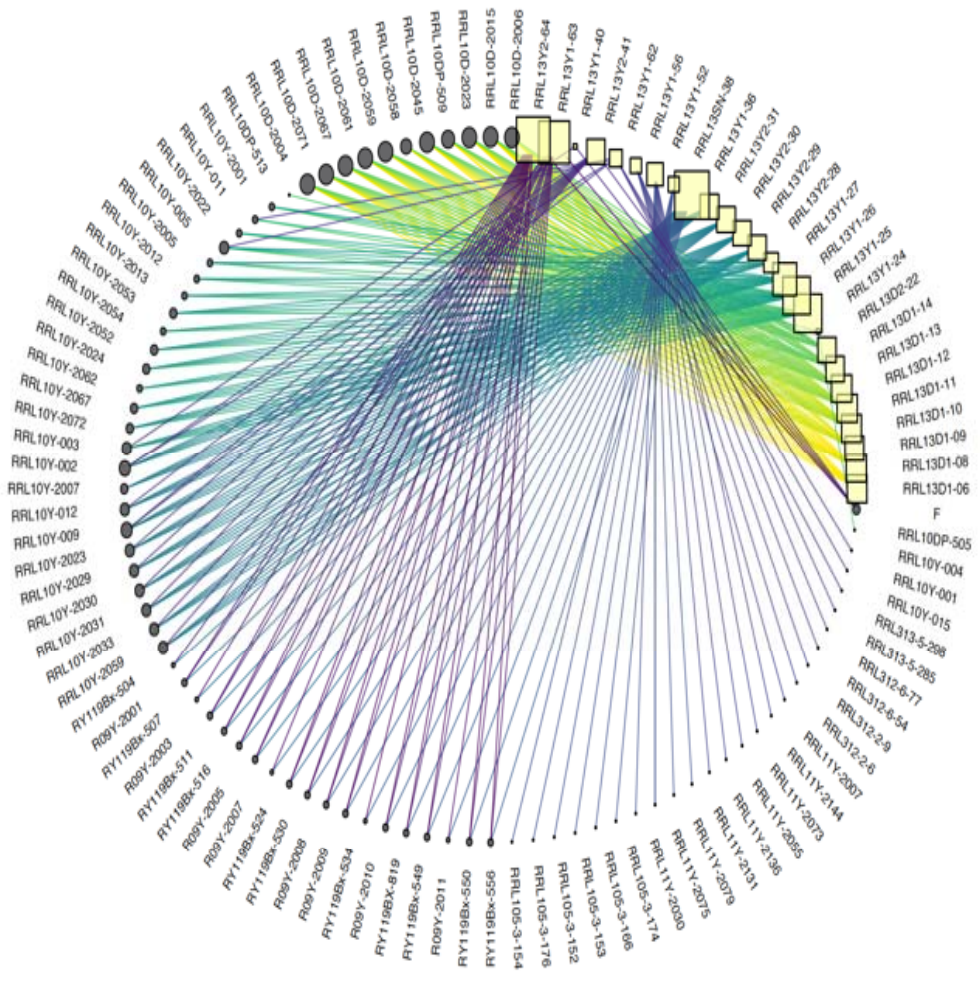
2 Reads, Both “A”



10 Reads, All “A”



GWAS with modeled genotypic data



Pedigree of FGI breeding population

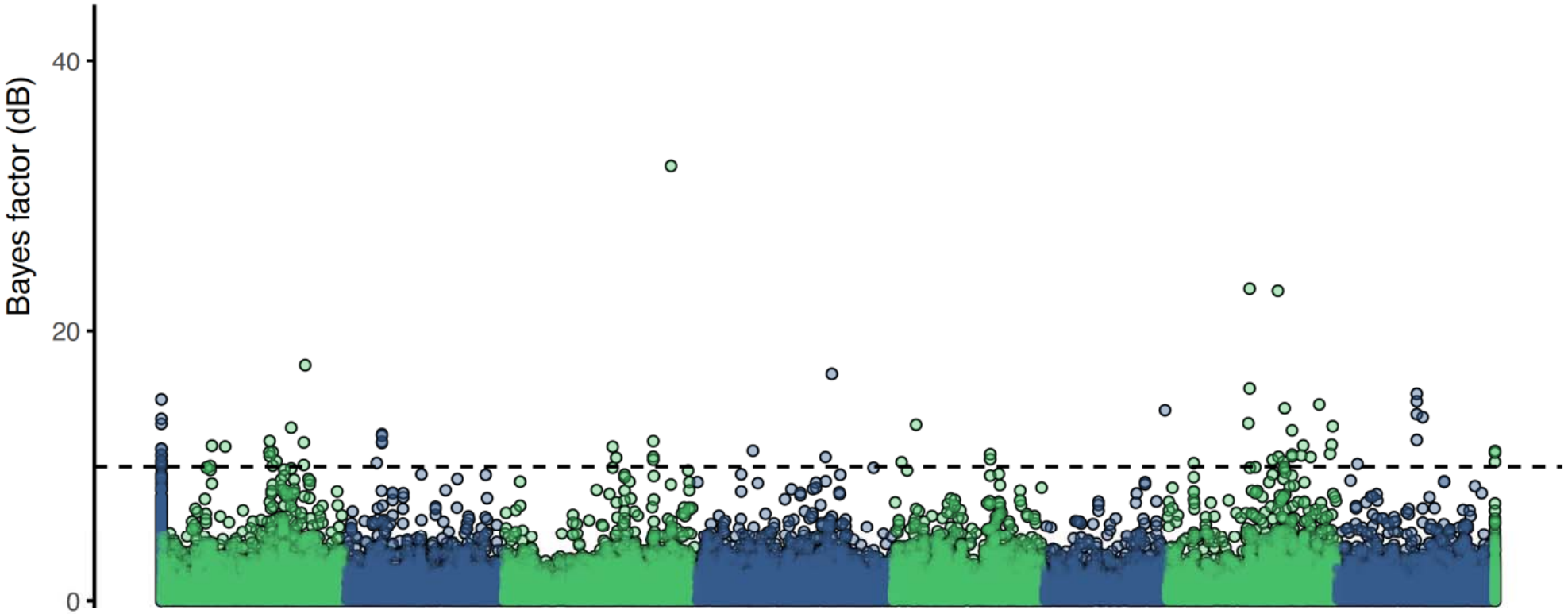
Structure related to pedigree so used a design matrix in the model

Modeled genotypes based on population allele frequency and read depth for each individual

Developed a model to find associations between markers and plant height

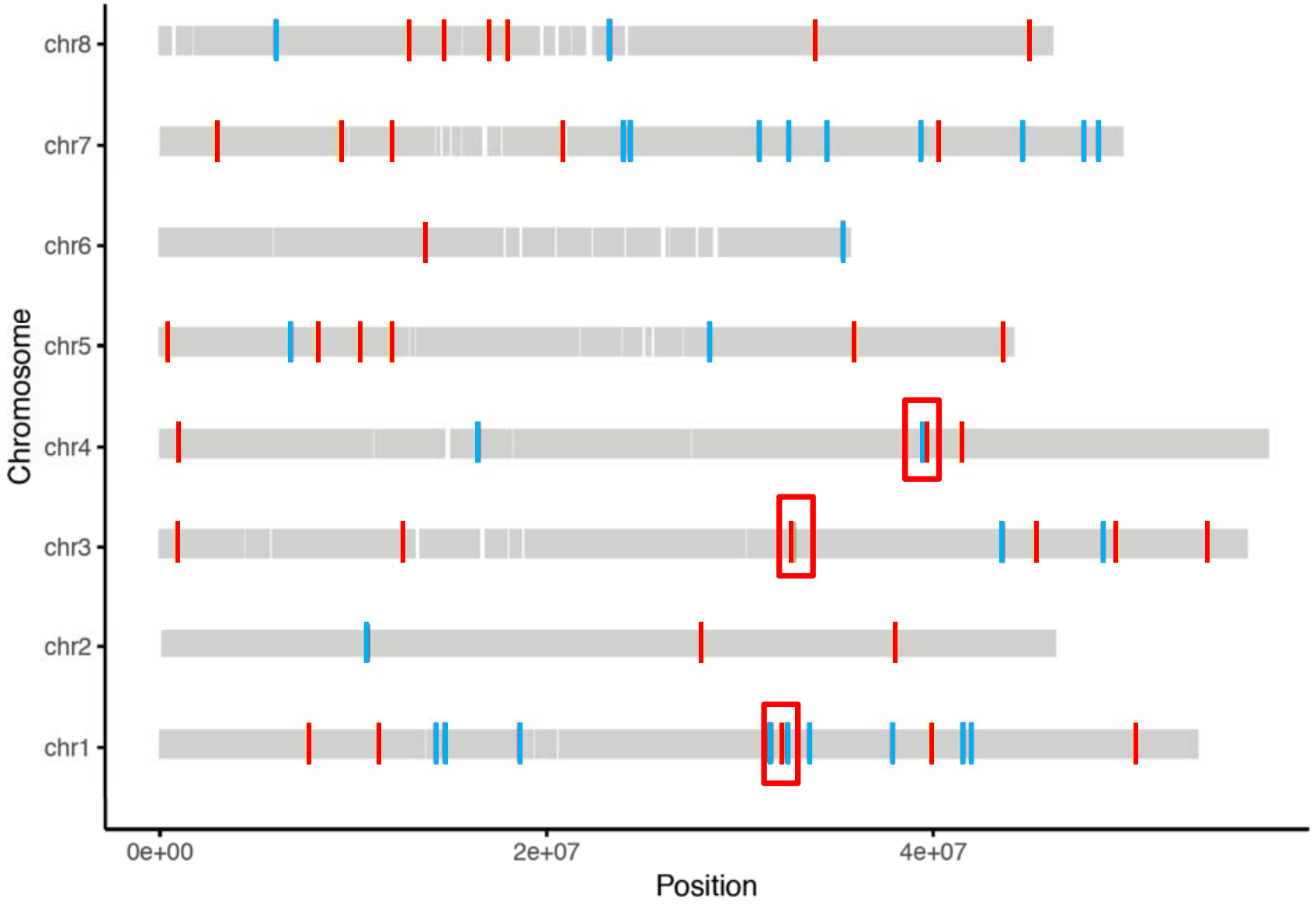
Model fitting performed with *JAGS* using *rjags* (Bayesian Graphical Models using MCMC)

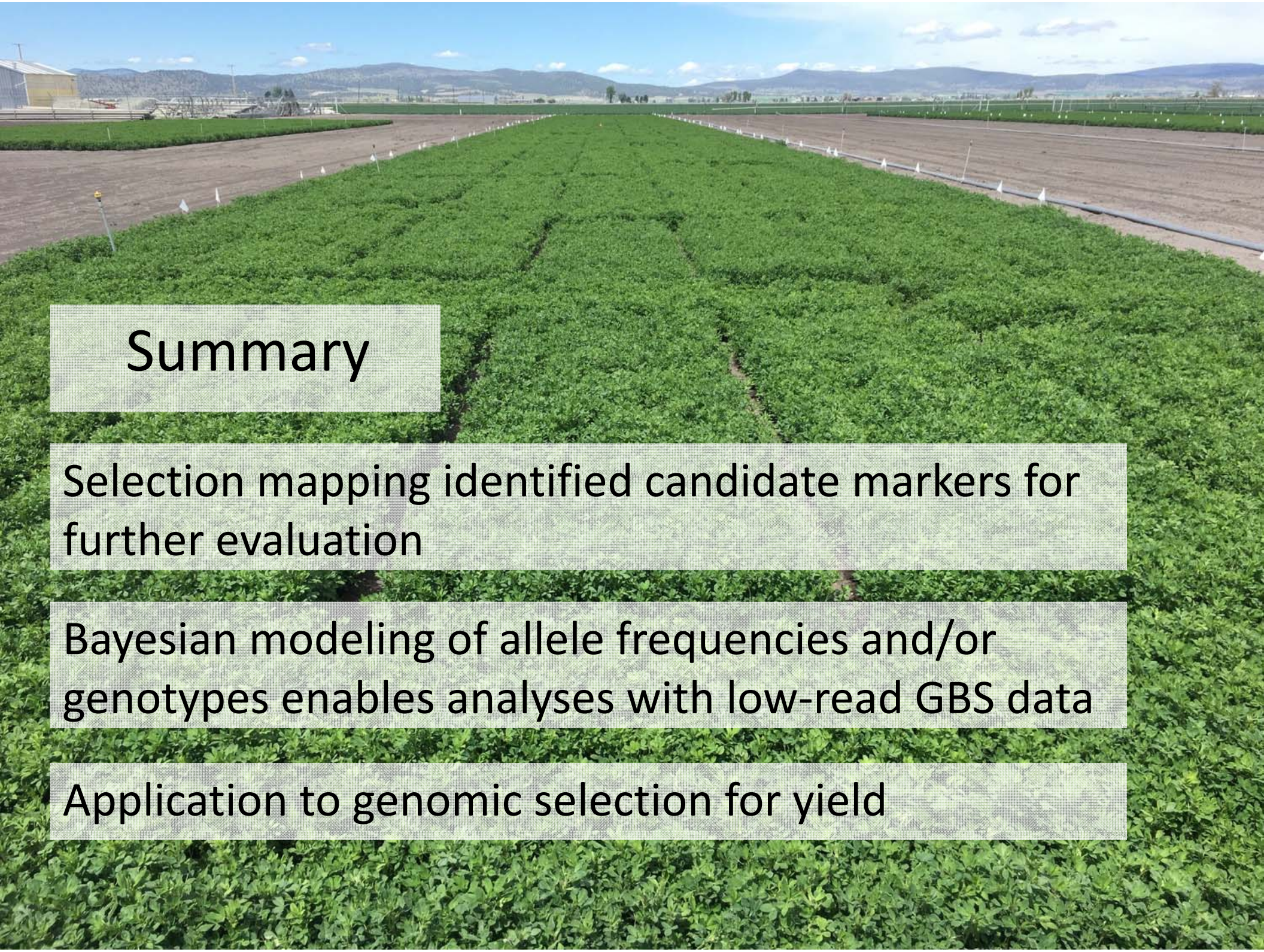
Markers associated with height



Manhattan plot of Bayes factors in dB units (10*log10(BF)). Dashed line represents an empirical cut-off implying 10:1 odds in favor of association. Mapping positions are based on alignment to the M. truncatula reference genome. The synthetic chromosomes “chr0” and “chr9” represent markers that do not align to M. truncatula chromosomes but have valid alignments to both CADL and M. truncatula scaffolds (“chr9”) or CADL scaffolds only (“chr0”).

Localization of top associated markers from GWAS (blue) and selection mapping (red)





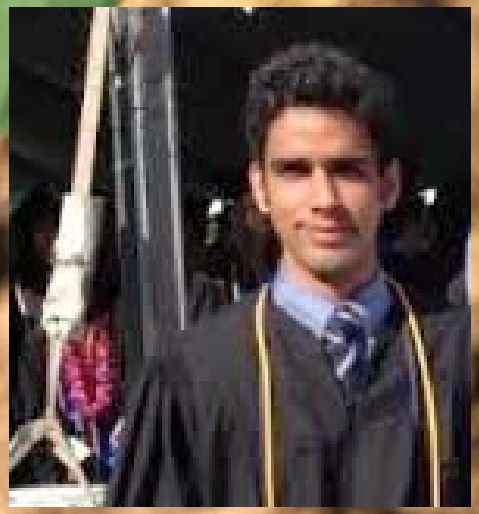
Summary

Selection mapping identified candidate markers for further evaluation

Bayesian modeling of allele frequencies and/or genotypes enables analyses with low-read GBS data

Application to genomic selection for yield

Thank you!



Gitanshu Munjal

USDA United States Department of Agriculture

National Institute of Food and Agriculture

Alfalfa and Forage Research Program (AFRP)
Agriculture and Food Research Inititiative (AFRI)

UC DAVIS UNIVERSITY OF CALIFORNIA

Alfalfa U.S. Alfalfa Farmer Research Initiative