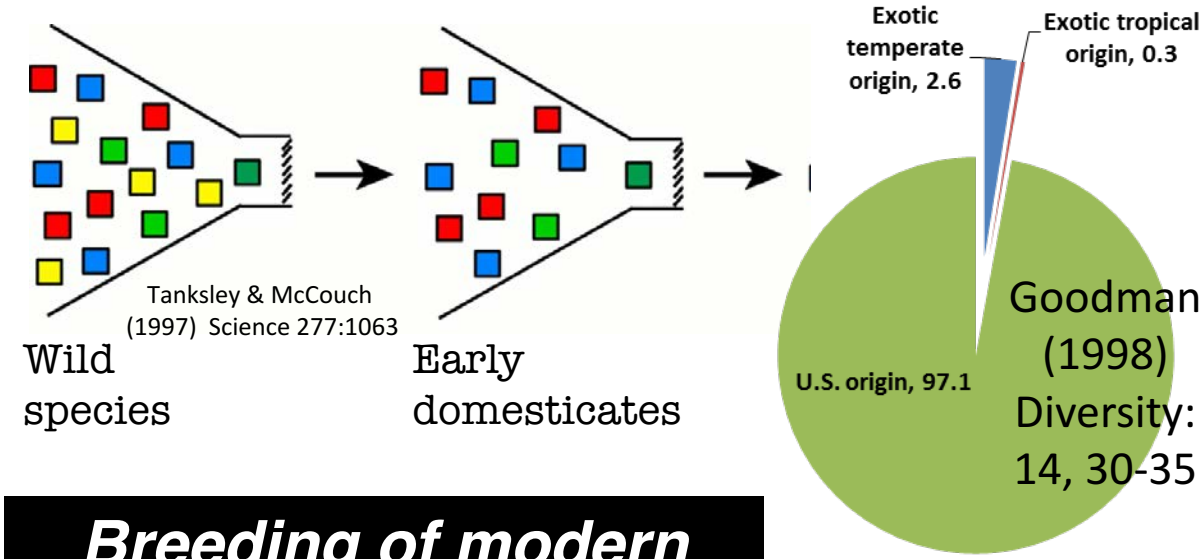
@G2F-2017

A NILAS Platform for Interrogating Tropical-Line Haplotypes in a Temperate-Adapted Hybrid Genome

Randy Wisser
University of Delaware

Variation at the intersection of genomes and environments: insights into breeding for maize adaptation

Extensive variation in maize, but adaptation and selection history restricted the U.S. Corn

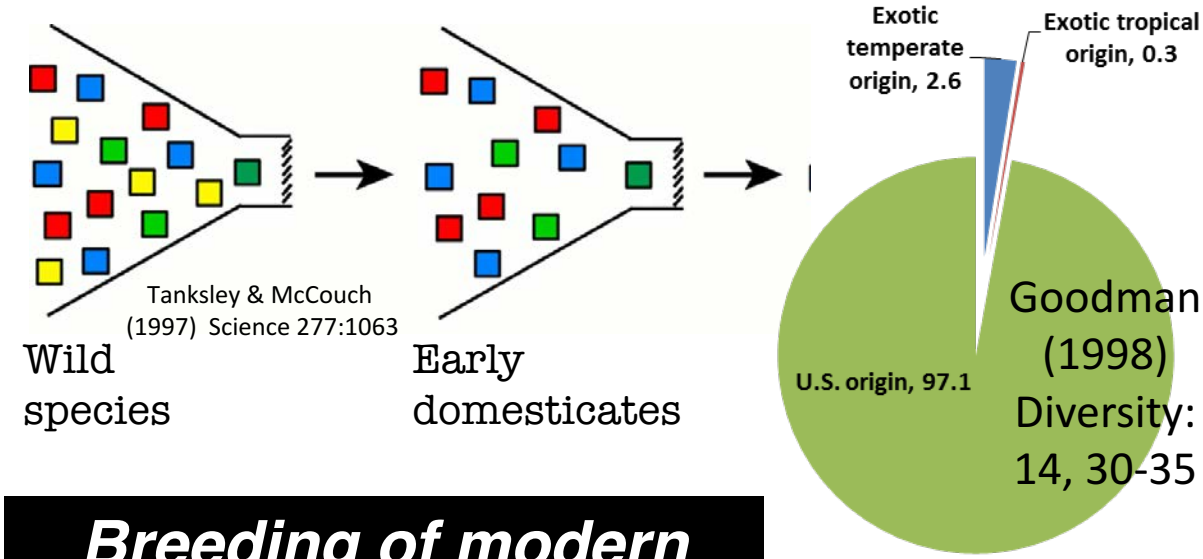


Breeding of modern varieties whittled away genetic diversity

Romay et al. (2013) Ex-PVPs – Share 45% SNPs of NPGS collection

Variation at the intersection of genomes and environments: insights into breeding for maize adaptation

Extensive variation in maize, but adaptation and selection history restricted the U.S. Corn



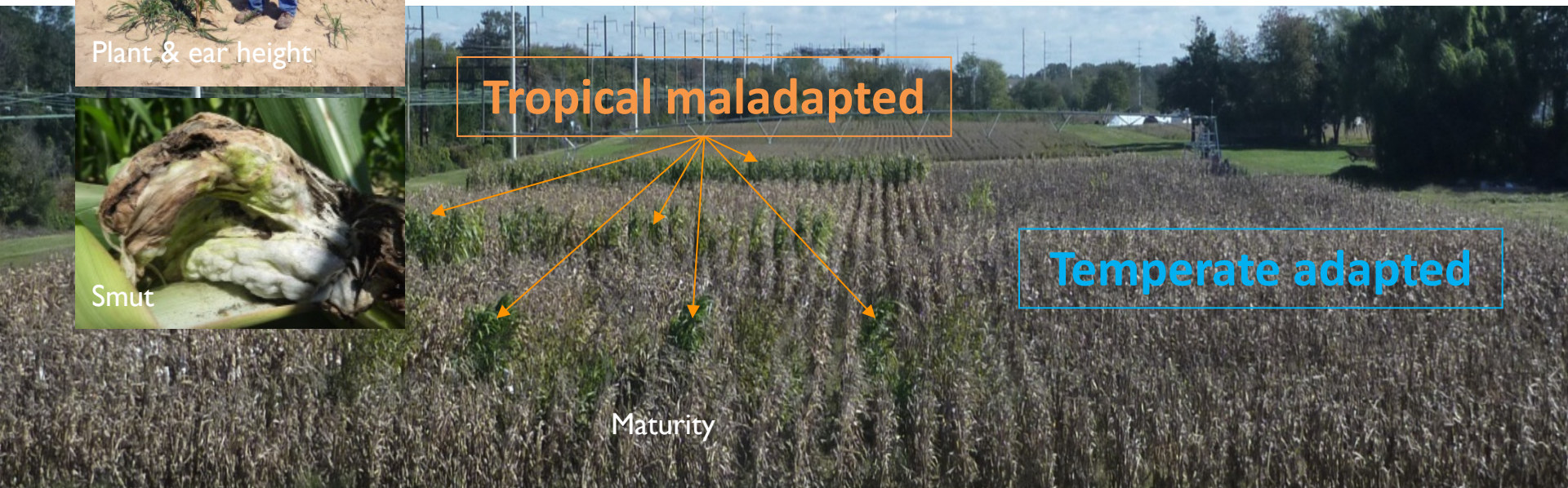
Breeding of modern varieties whittled away genetic diversity

Tropical germplasm contains favorable alleles for temperate maize production

Holland *et al*. (1995) Crop Sci. 35:767; Jines *et al*. (2007) TAG 114:659

- **Favorable Haplotypes Reside in Maladapted or Non-Elite Germplasm →**
- **Photothermally Induced "Maladaptive Syndrome:" Complex of Traits Affected by Genetics and Environment** (Teixeira *et al*. 2015 Heredity 114:229) →

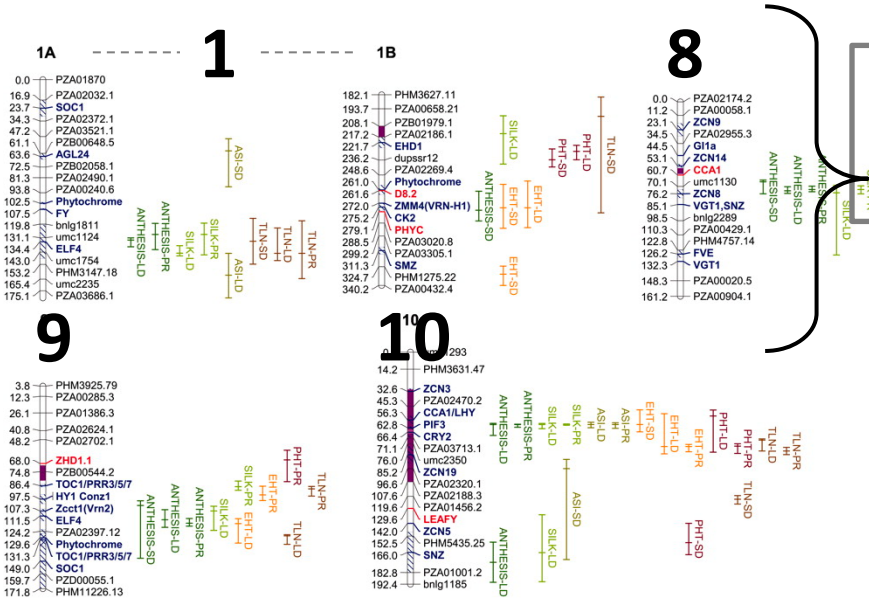
A Clinal Barrier to Diversity & Favorable Alleles



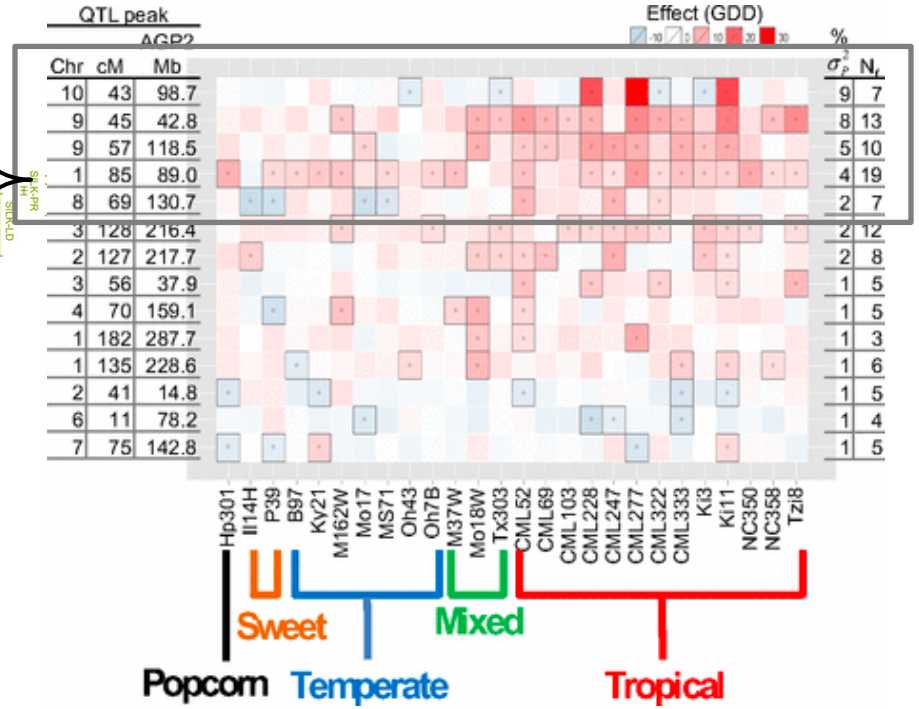
STANDING TALL. "These girls from Washington High School found a fun way to show off the tallest corn in the area in 1946—this stalk measured 26 feet, 1 inch," writes Jane Amos of Clarks Summit, Pennsylvania. "My mom, Fern Mendenhall of Columbus Junction, is second from the top on the right."

Genetic Dissection of Photoperiod Flowering Response

Coles et al. (2010) Genetics 184:799



Hung et al. (2012) PNAS 109:E1913



ZmPR1 (chr 1): *CCT* homolog

ZmPR2 (chr 8): *Vgt1/Rap2.7, ZCN8* (*FT*)

ZmPR3 *(chr 9): Conz1*

ZmPR4* (chr 10): *ZmCCT (GhD7/Ma1 homolog)

How Does Breeding for Adaptation Affect the Potential for Improvement?

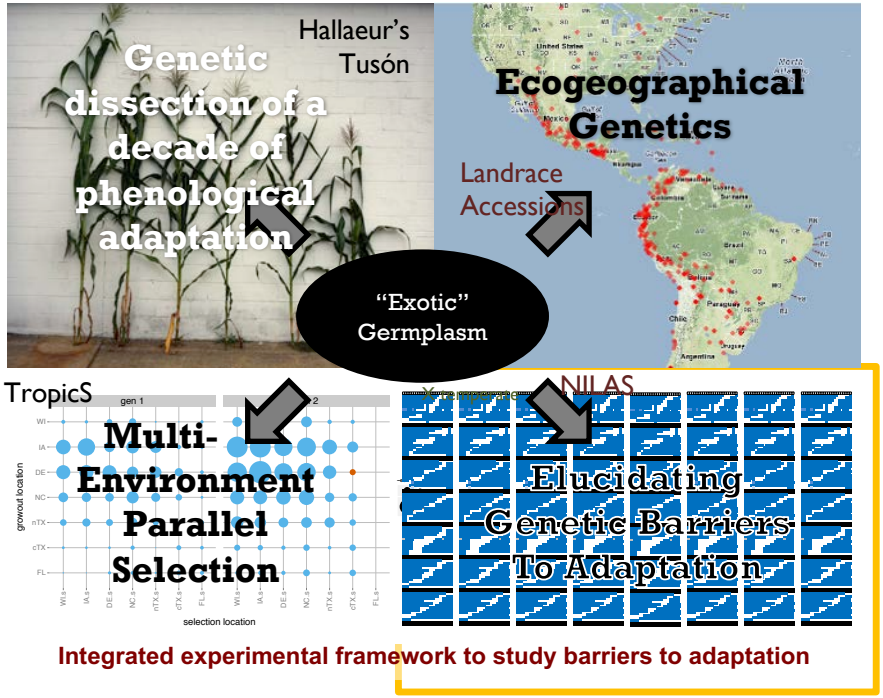
(selection against *ZmPR* alleles)

Hypotheses:

1. Response to photoperiod skews estimates of the genetic merit of haplotypes.
2. Favorable genetic variation is linked to maladaptational variants.

Adaptation Through Latitudinal Artificial Selection

Randy Wisser
Natalia de Leon
Sherry Flint-Garcia
Jim Holland
Nick Lauter
Seth Murray
Wenwei Xu



Integrated experimental framework to study barriers to adaptation

MAIZE ATLAS
Adaptation Through Latitudinal Artificial Selection

USDA United States Department of Agriculture
National Institute of Food and Agriculture

University of Delaware
Wisconsin University of Wisconsin–Madison
Mizzou University of Missouri-Columbia
NC State University
Iowa State University
Texas A&M University
USDA ARS

Climate Variability & Change Challenge Area

Breeding = Mb-scale Genome Context

Injecting diversity into advanced germplasm … from genetics research, expect extensive standing variation across maize chromosomes … segmental haplotypes restructured via crossing over … many assortment combinations possible …

e.g., Under the limiting case of biparental crosses:

$$[2^N \times (2^N + 1)]/2$$

where *N*=haploid chromosome number

Maize: ≈0.5 M unique genotypes for a biparental cross

Genetics and Breeding Consideration: Assortment Component

"Depending primarily on the presence of trait selection pressure, chromosome assortment alone accounted for 40-75% of gain in response to short-term selection."

McClosky and Tanksley (2013) TAG 126:2299

Genetics and Breeding Consideration: Assortment Component

"Depending primarily on the presence of trait selection pressure, chromosome assortment alone accounted for 40-75% of gain in response to short-term selection."

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So what effects are packaged in segmental haplotypes at loci for adaptation (ZmPR1-4) in maize, and how do they change following crossover events?

BREEDING & TRIALING A CONNECTED GENETIC RESOURCE

1

Tropical donors with proven potential for yield improvement

CML10
CML258
CML277
CML341
CML373
Tzi8
Tzi9

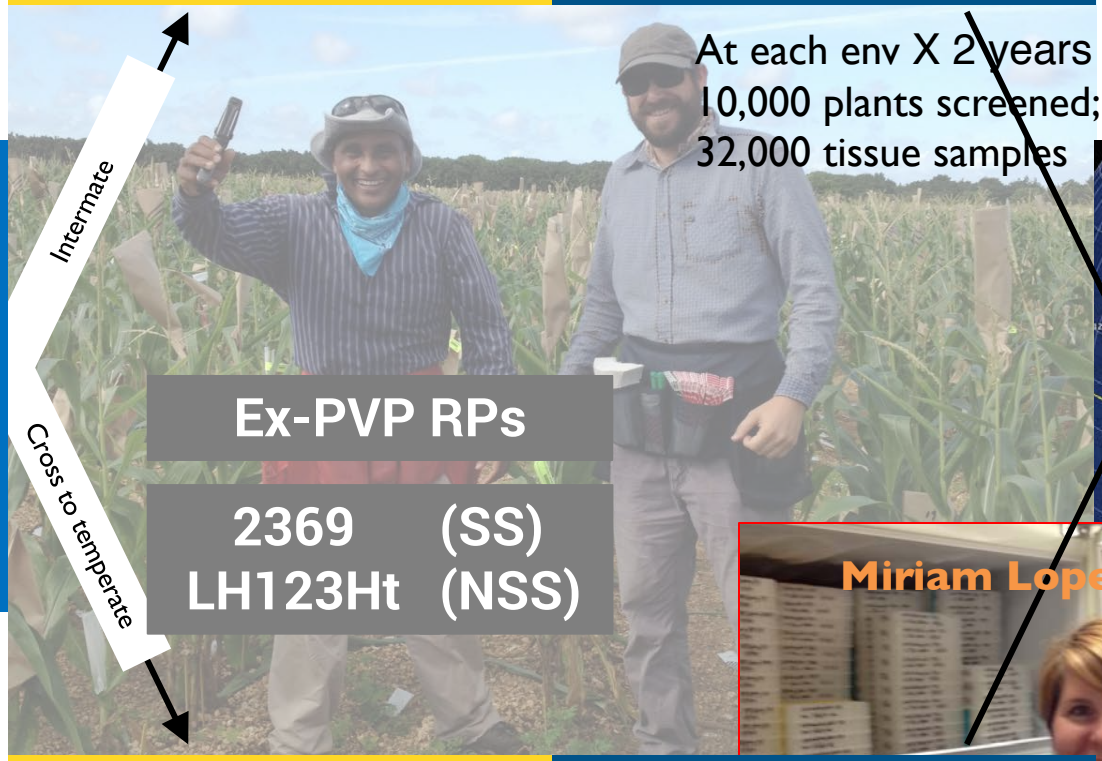
Nelson, P., and M. Goodman (2008) Crop Sci. 48:85-92
Nelson, P., *et al.* 2006 Maydica 51:255-262

Parallel Selection

Env-specific, 2 gens, 8 envs

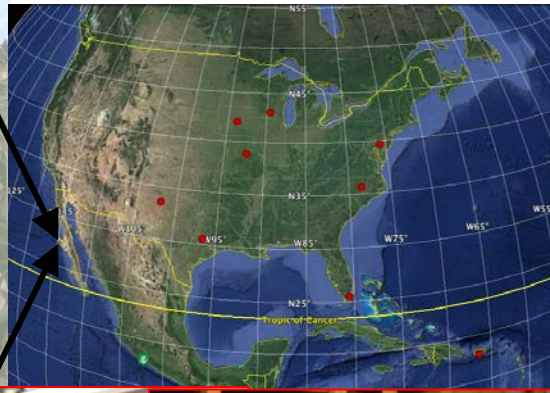
Selection and analysis across latitudinal transect

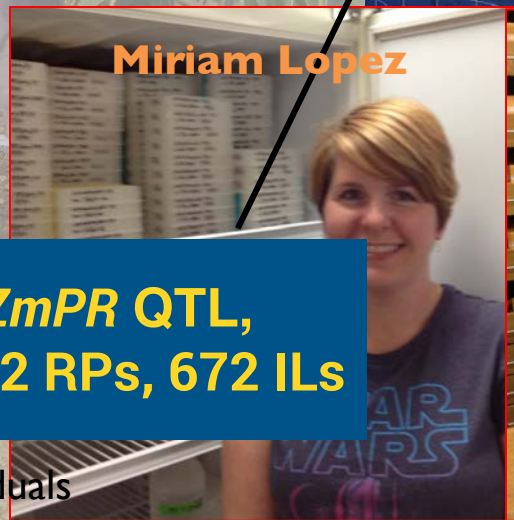
At each env X 2 years
10,000 plants screened; 500 selected
32,000 tissue samples

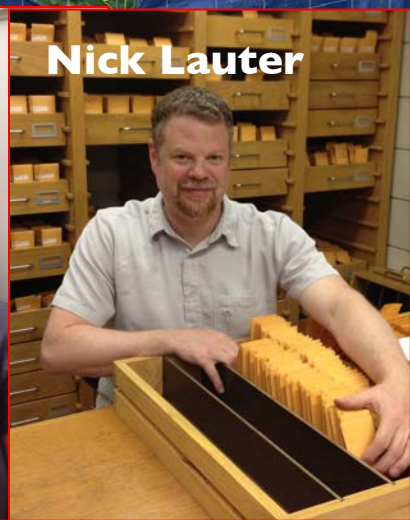


Ex-PVP RPs

2369	(SS)
LH123Ht	(NSS)







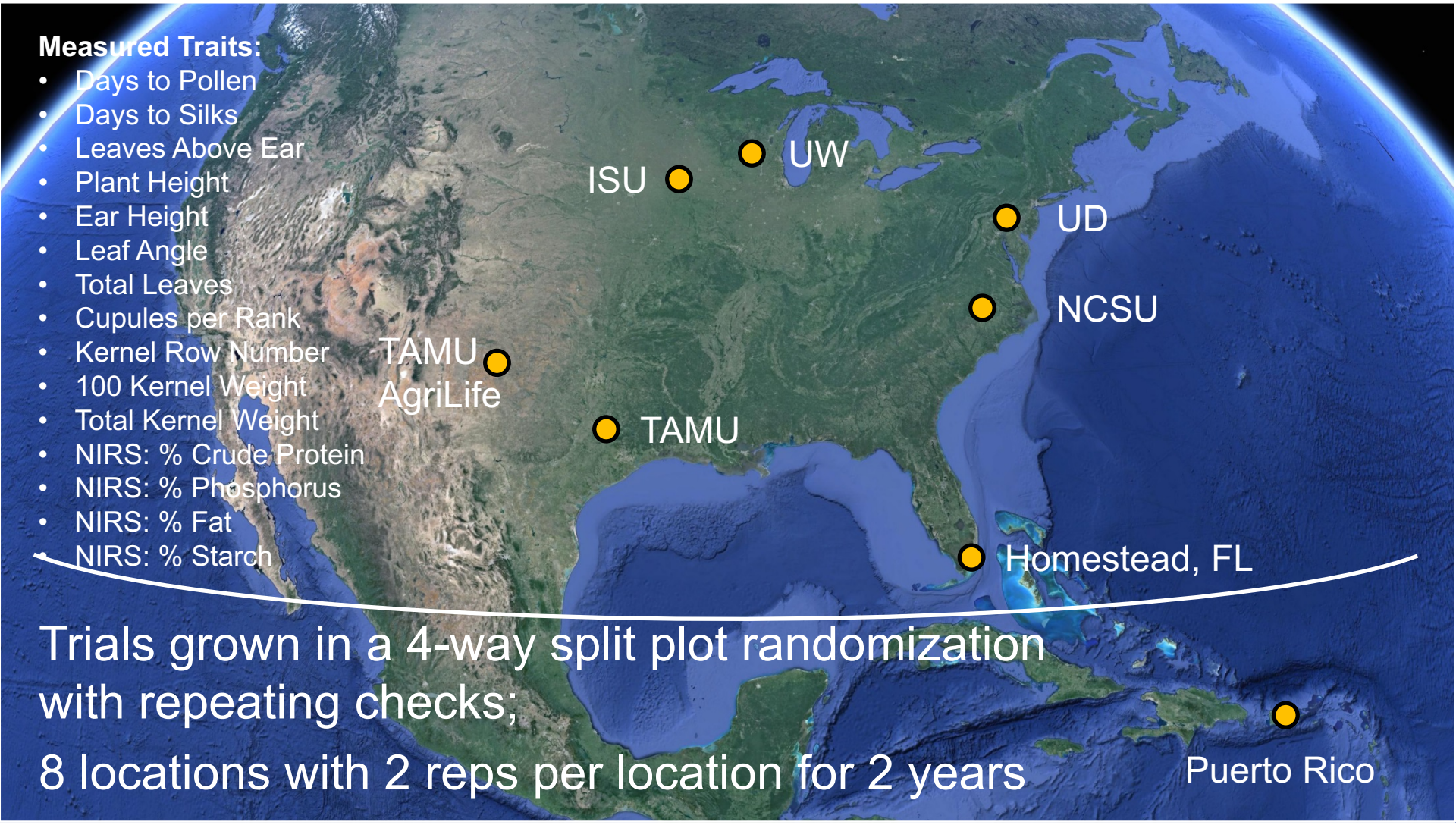
2

Marker-assisted backcrossing

4 *ZmPR* QTL, 7 DPs 2 RPs, 672 ILs

32 markers screened on >50,000 individuals

NILAS Inbred Line Trials



Measured Traits:

- Days to Pollen
- Days to Silks
- Leaves Above Ear
- Plant Height
- Ear Height
- Leaf Angle
- Total Leaves
- Cupules per Rank
- Kernel Row Number
- 100 Kernel Weight
- Total Kernel Weight
- NIRS: % Crude Protein
- NIRS: % Phosphorus
- NIRS: % Fat
- NIRS: % Starch

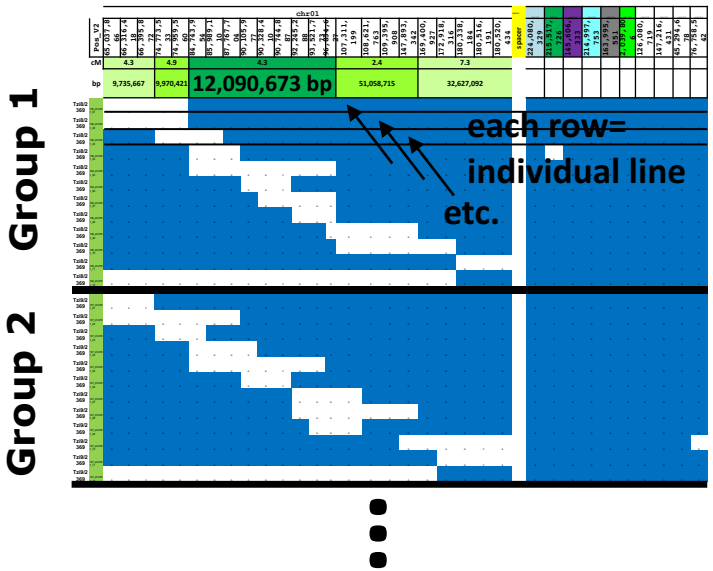
Trials grown in a 4-way split plot randomization with repeating checks;

8 locations with 2 reps per location for 2 years

NILAS Realization

Introgression target interval

Genetic background

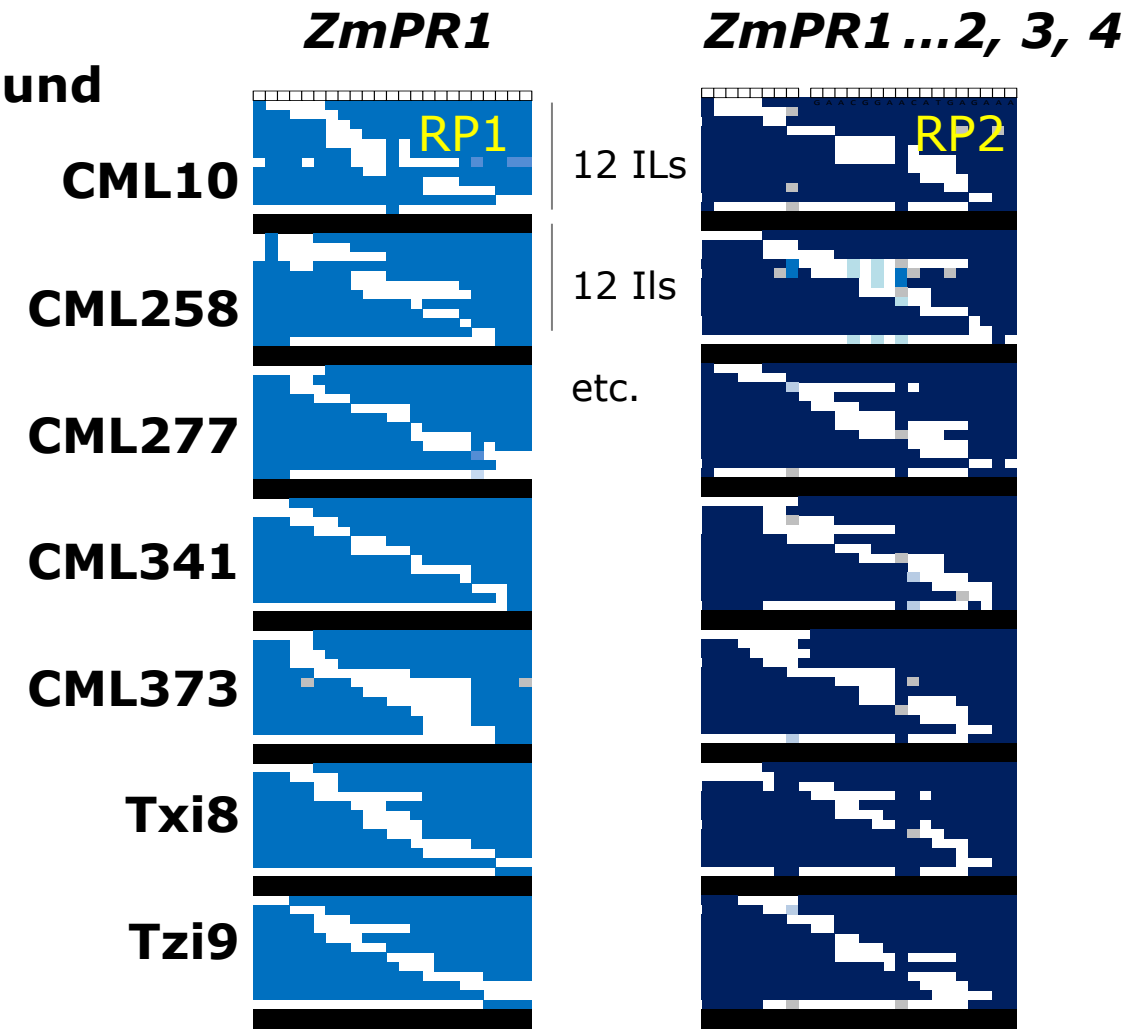


56 groups

7 DP, 2 RP, 4 Loci;

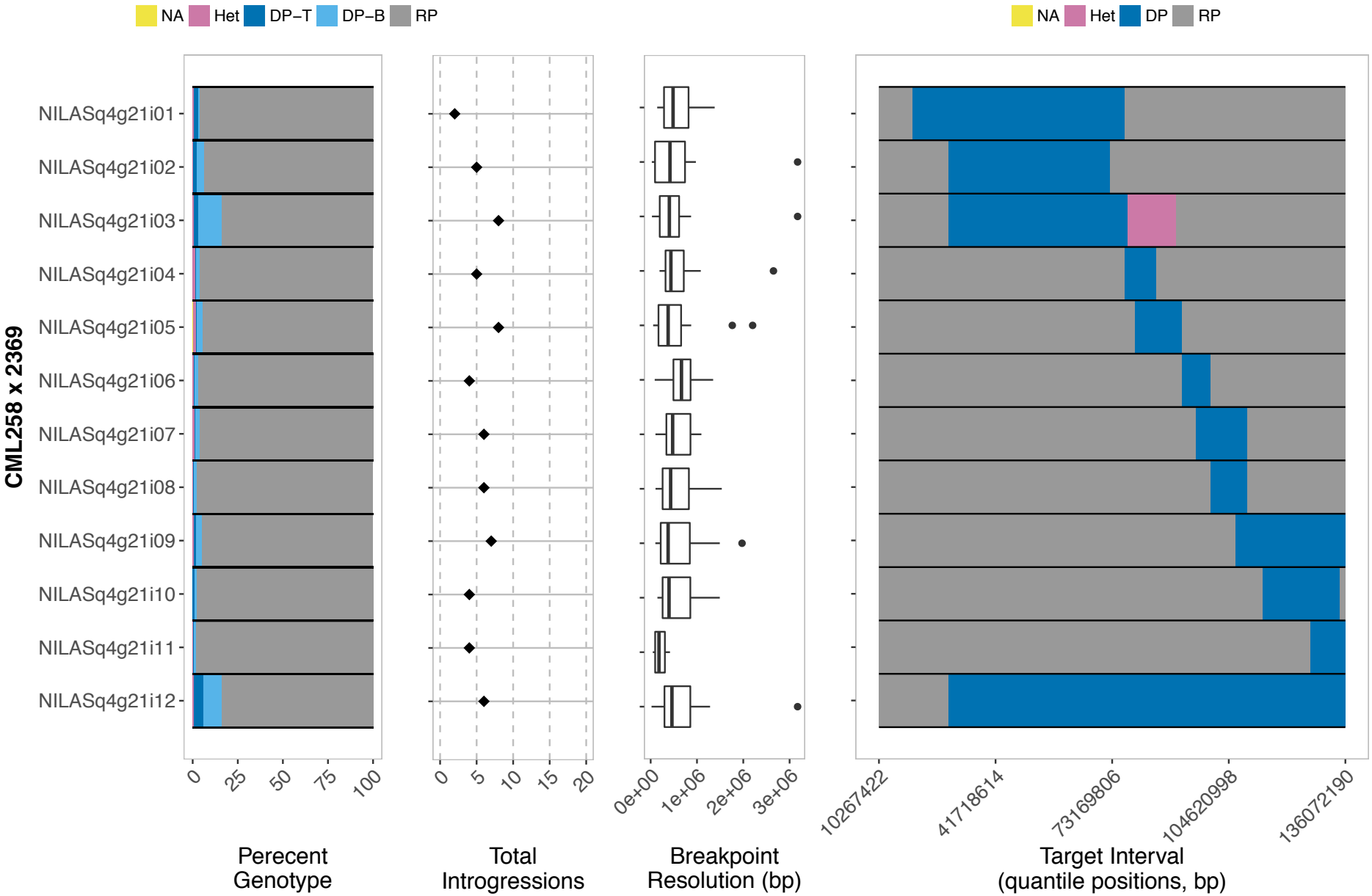
12 ILs each →

672 BC3/4F3:4 lines



Median introgression size: 7.3 Mb

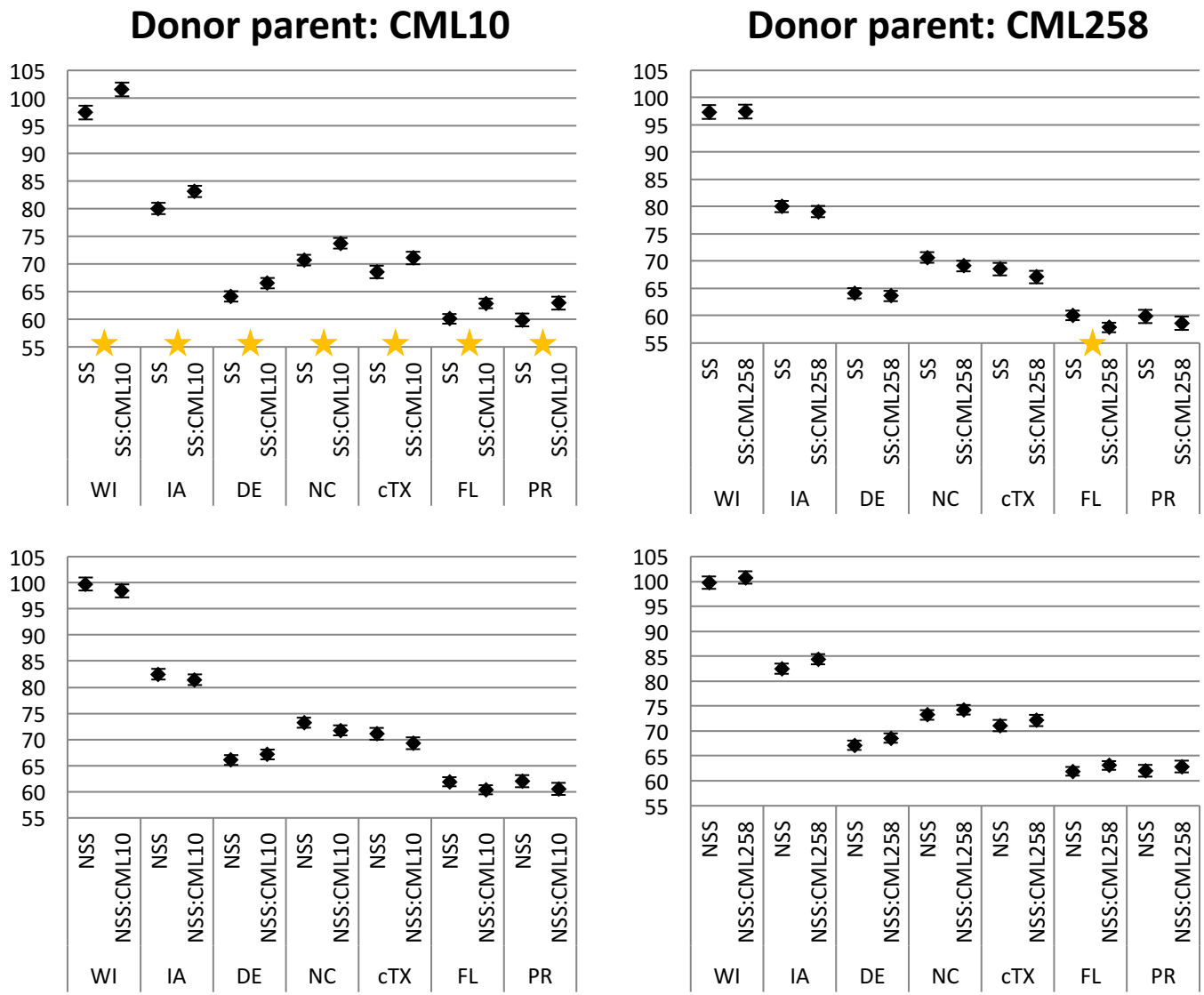
CML258 (DP) x LH123Ht (RP) *ZmPR4*: 1 of 56 groups (12 of 672 Introgression Lines)



Context-Specific Haplotype Effects (genome and environment)

Variety of Phenotypic Effects:

- CML10 QTL full introgression has a significant effect in all locations delaying flowering time in a stiff stalk background. Yet no effect in the non-stiff stalk background
- CML258 full introgression has only one significant effect in one background



David Wills *et al*.

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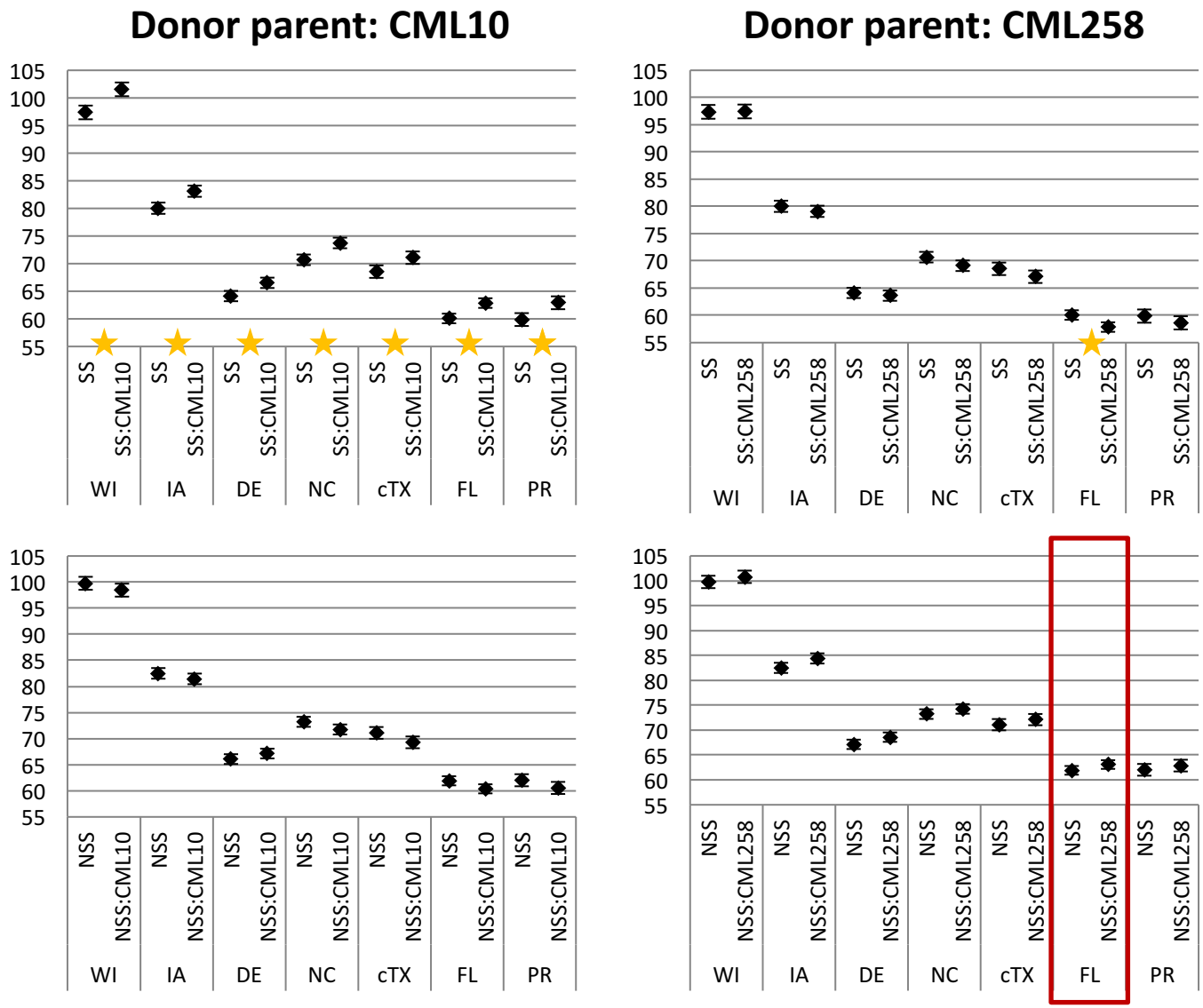
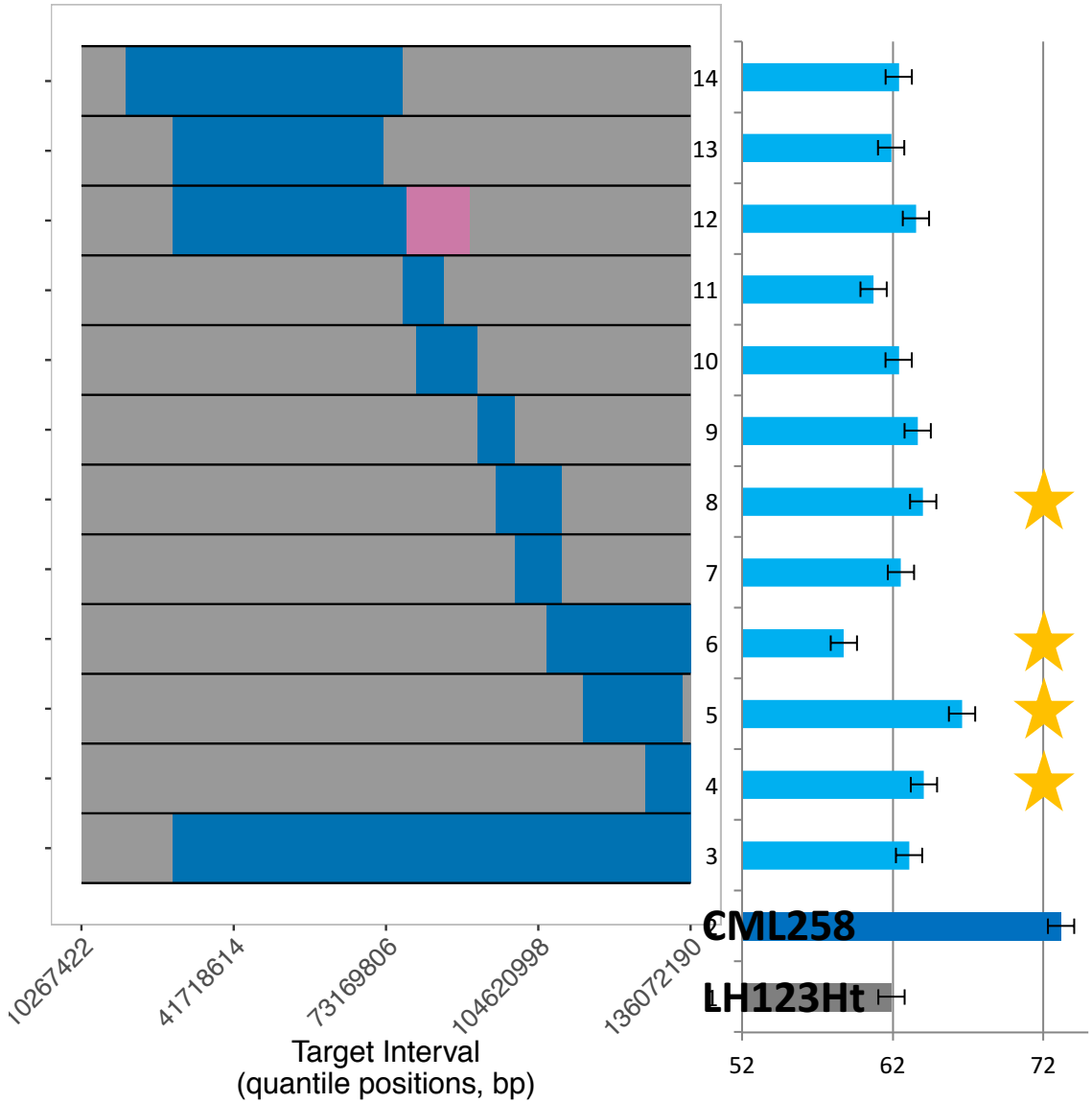


David Wills *et al*.

Fractionation of Haplotype Unlocks Variation

Recombinant Segments:

- Although the introgressed QTL segment does not have a flowering time effect, a number of the recombinant segments do.
- Opposing allele effects underlying "cryptic variation."



David Wills *et al*.

versus

Haplotypes at *ZmPR4 [ZmCCT]*

Extensive local allelic variation associated with a single ZmPR locus…

		Flowering		Plant Architecture						Ear Traits						
	Donor Parent	Days to Pollen	Days to Silks	Plant Height	Ear Height	Number of Leaves	Leaves Above Ear	Leaves Below Ear	Leaf Angle	Ear Diam	# of Kernel Rows	Kernels per Row	YLD potential	# of Kernel	Total Kernel Weight	Cob Length
D E	CML10	--	--	--	--	--	--	--	7.7	--	--	--	--	--	--	--
	CML277	2.8	3.0	--	--	0.8	--	0.9	--	1.6	1.3	--	--	--	--	--
	CML341	3.5	4.3	18.1	17.2	0.8	--	0.7	6.1	2.7	--	--	--	--	--	--
	CML373	--	--	--	--	--	--	--	--	--	--	--	--	-96	--	--
	Tzi8	--	3.0	--	--	--	--	-0.5	--	--	1.6	--	--	--	--	--
	Tzi9	--	--	--	--	--	--	-0.5	--	--	--	--	--	--	--	--
P R	CML10	1.0	1.1	-13.1	--	--	--	--	--	--	--	--	--	--	--	--
	CML277	1.5	--	--	--	--	-0.4	0.7	-4.3	--	--	--	--	-67	-16.9	-1.3
	CML341	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
	CML373	--	--	--	--	--	--	--	--	--	--	--	--	-65	-17.9	--
	Tzi8	--	--	-11.3	-10.6	--	0.4	--	--	--	--	--	89.7	--	--	--
	Tzi9	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

NILAS: Inbred Lines (Multiple Traits)

versus

Haplotypes at *ZmPR4 [ZmCCT]*

Supports hypothesis that photoperiod loci affect response of other traits

		Flowering		Plant Architecture						Ear Traits						
	Donor Parent	Days to Pollen	Days to Silks	Plant Height	Ear Height	Number of Leaves	Leaves Above Ear	Leaves Below Ear	Leaf Angle	Ear Diam	# of Kernel Rows	Kernels per Row	YLD potential	# of Kernel	Total Kernel Weight	Cob Length
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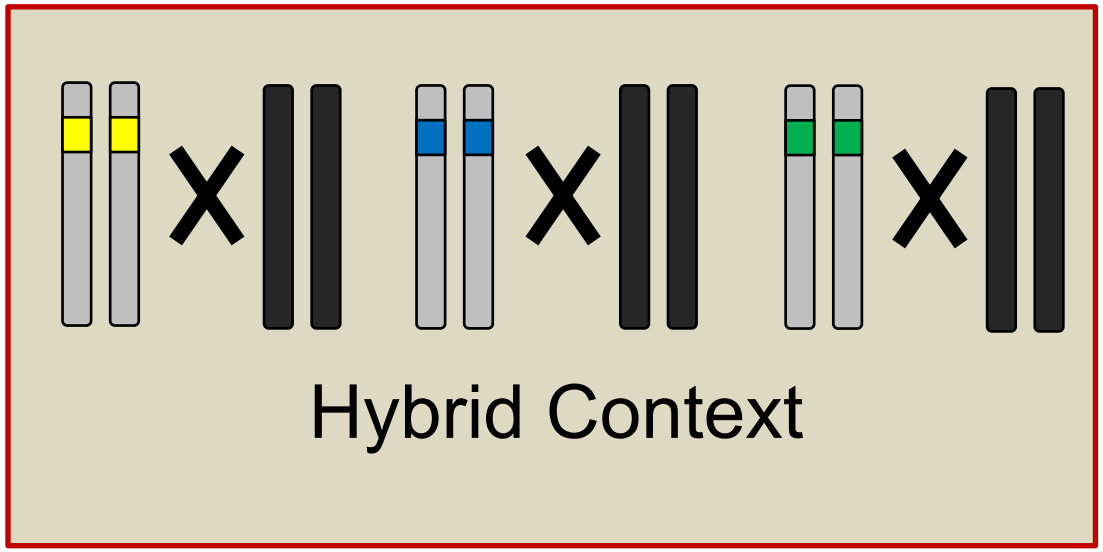
	CML373	--	--	--	--	--	--	--	--	--	--	--	--	-96	--	--
	Tzi8	--	3.0	--	--	--	--	-0.5	--	--	1.6	--	--	--	--	--
	Tzi9	--	--	--	--	--	--	-0.5	--	--	--	--	--	--	--	--
P R	CML10	1.0	1.1	-13.1	--	--	--	--	--	--	--	--	--	--	--	--
	CML277	1.5	--	--	--	--	-0.4	0.7	-4.3	--	--	--	--	-67	-16.9	-1.3
	CML341	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
	CML373	--	--	--	--	--	--	--	--	--	--	--	--	-65	-17.9	--
	Tzi8	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--
	Tzi9	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

CML10 haplotype opposite of the expectation for photoperiod sensitivity

Examine the genetic merit of segmental haplotypes in a hybrid context: (i) the role of photoperiod sensitive alleles as modulators of yield; (ii) pleiotropic and linked variation at *ZmCCT*

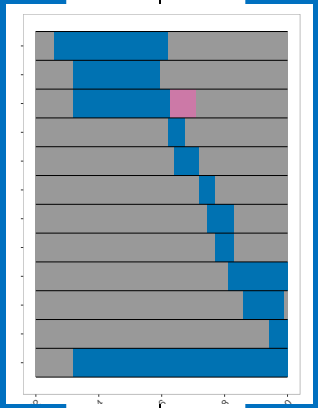


G2F-GxE: NILAS Hybrids (2017)

Segmental haplotypes at flowering time loci act as modulators of yield

***ZmPR1-4* loci**
7 donors
4 introgressions
(centered on *ZmPR loci*)

(112 segmental haplotypes)



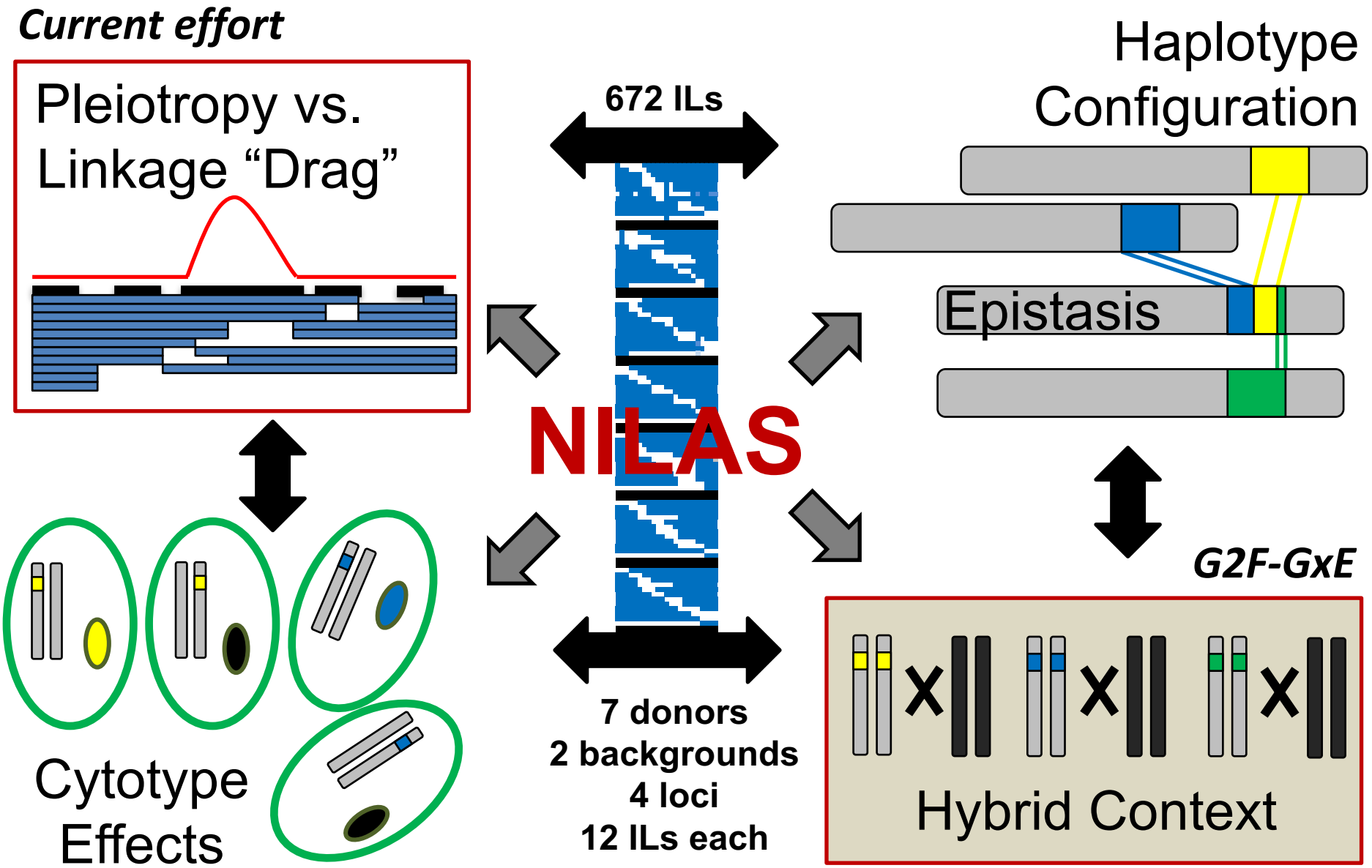
Segmental haplotypes encompassing *ZmCCT* have positive yield effects

***ZmPR4* locus (*ZmCCT*)**
7 donors
12 introgressions

(84 segmental haplotypes)

Design: twice replicated 3-way split plot randomization
(level 1: locus; level 2: donor source; level 3:introgression lines)
with repeating checks of the recurrent parent hybrid

NILAS Platform: Future Potential



THANK YOU

Genomes to Fields

MAIZE ATLAS
Adaptation Through Latitudinal Artificial Selection

USDA
United States Department of Agriculture

National Institute of Food and Agriculture

University of Delaware
Wisconsin University of Wisconsin–Madison
Mizzou University of Missouri-Columbia
NC State University
Iowa State University
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USDA ars