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Identification of SNP Markers Linked to *Wsm2* and QTL for Yield and Yield Components

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Fuentealba¹

1. Texas A&M Agrilife Research
2. Kansas State university
3. University of Idaho
4. Colorado State University
5. USDA-North Dakota

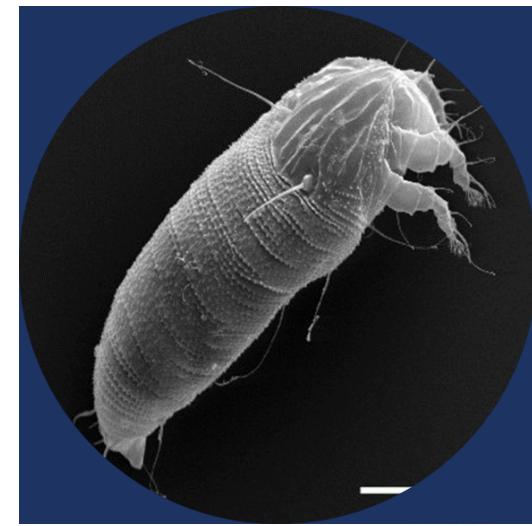


Introduction

- ❖ Genus: *Tritimovirus*; Family: *Potyviridae*
- ❖ Transmission-mainly vectored by WCM (*Aceria tosichella*)
- ❖ 131 accession type documented (<http://www.dpvweb.net>)
- ❖ Minimal diversity in the US among WSMV (Stenger et al. 2002)



www.dpvweb.net



Introduction contd....

❖ Geographic occurrence of WSMV

- US, Australia, Brazil, Argentina, Mexico, Canada, the Czech Republic, Hungary, Iran, Jordan, Mexico, Poland, Rumania, Russia, Turkey, Yugoslavia

❖ Infects-Wheat, Barley, oat, rye, Maize, Sorghum, millets

- MLN = Maize Chlorotic mottle virus+ any virus in Potyviridae

❖ Economic impacts of WSMV (Velandia et al. 2010; Crop Protection 29: 699-703)

- Grain yield- 27.8% - 76.3%
- Biomass-21.4% - 46.4%
- Water use efficiency- 27.6% - 74.4 %



Approach

❖ Genotyping

- 90K SNP markers
- 5995 HQ polymorphic markers used for downstream analysis
- Linkage mapping-JoinMap
- QTL analysis- MapQTL

❖ Phenotypic screening for WSMV resistance

- 217 RILs derived from CO960293-2/TAM 111
- 217 RILs + 3R+ 3S checks
- Screening conducted in GC for 2 seasons

Objectives

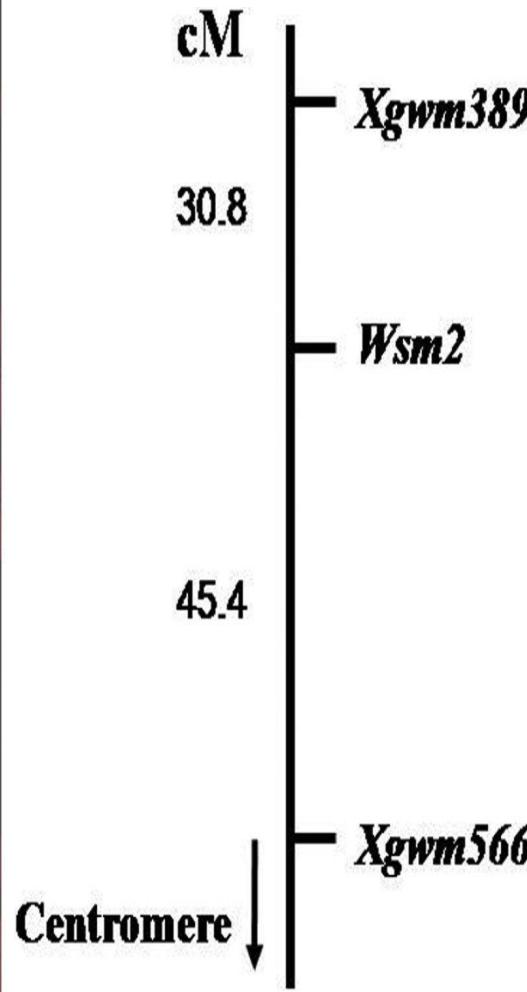
- ❖ *Objective 1: Identify and validate SNP markers that exist in linkage disequilibrium with alleles for WSMV resistant gene*

Two sources of resistance:

- ❖ *Wsm1*
 - ✓ derived through translocation from Intermediate wheatgrass (*Thinopyrum intermedium*)-Friebe et al., 1991)
 - ✓ Mace(PI 651043, Graybosch et al. 2009) and KS96HW10-3 possess *Wsm1*
- ❖ *Wsm2*
 - ✓ identified in CO960293-2 from CAES
 - ✓ Oakley CL (PI 670170, Zhang et al., 2015)
 - ✓ Clara CL (PI 665948; Martin et al., 2015)
 - ✓ Snowmass (PI 65859; Haley et al., 2011)
 - ✓ RonL (PI 648020; Seifers et al., 2007)

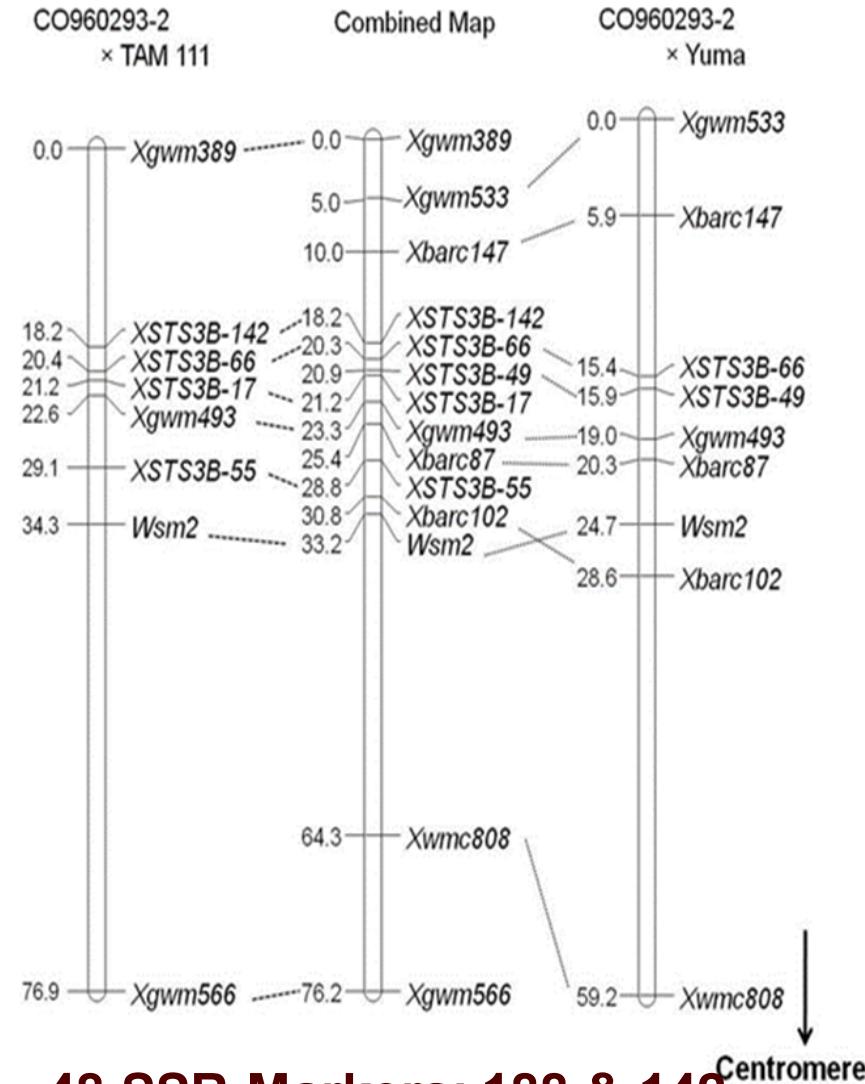


Lu et al 2011; Crop Sci. 51:5-12



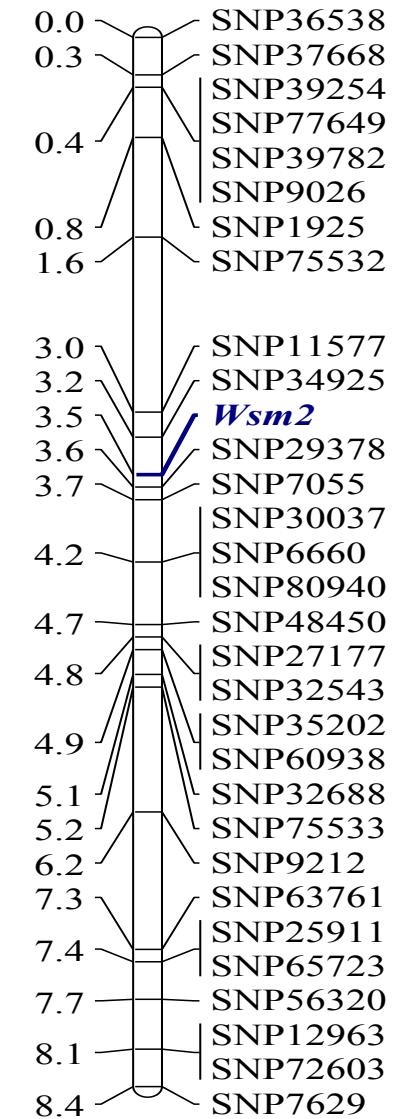
283 SSR Markers;
188 $F_{2:3}$

Lu et al. 2012; Crop Sci. 52:720-728



48 SSR Markers; 188 & 142
 $F_{2:3}$

Current study



5951 SNP
Markers

$R^2 = 91.1\%$



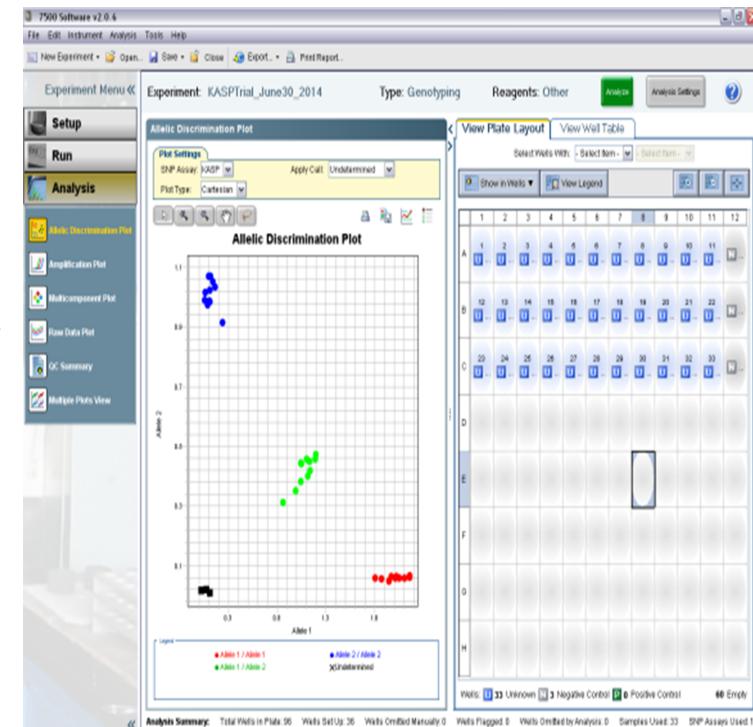
KASP Markers linked to *Wsm2*



**PCR Mixture of DNA,
assay mix containing
primers, reaction mix
with fluorescent label**

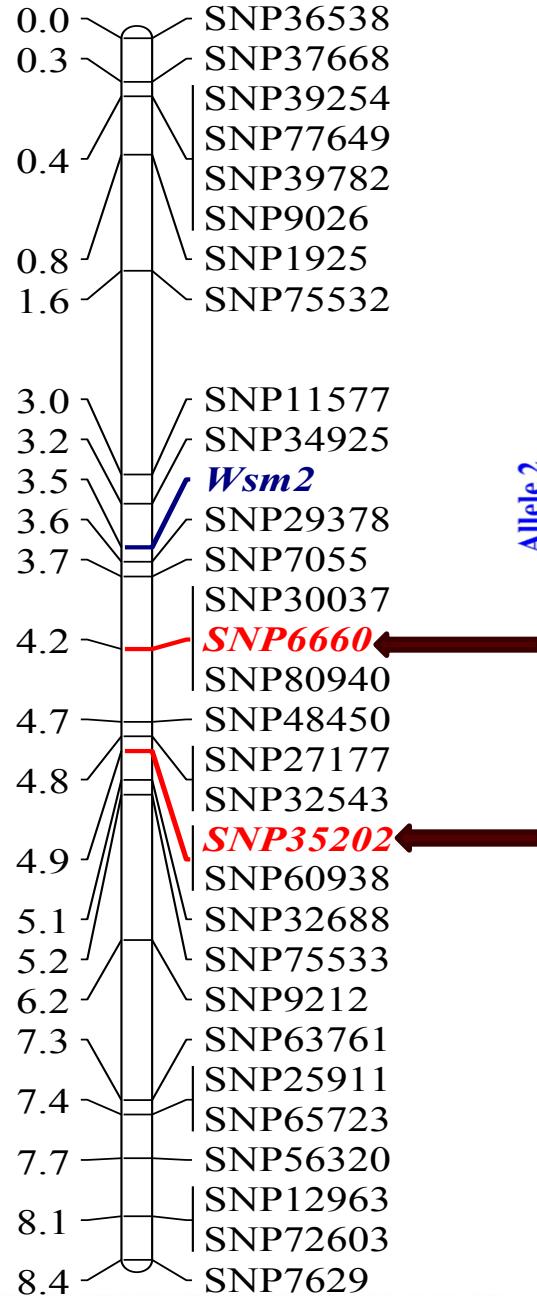


**Real-Time PCR or Plate
reader
Microtitre PCR Plate
96, 384, 1536-well**

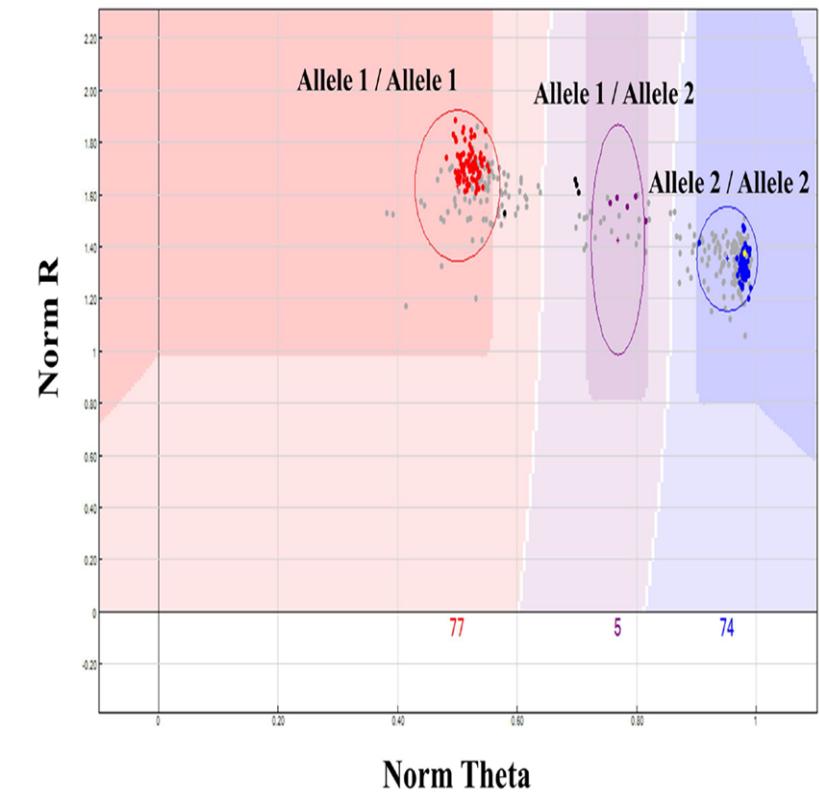
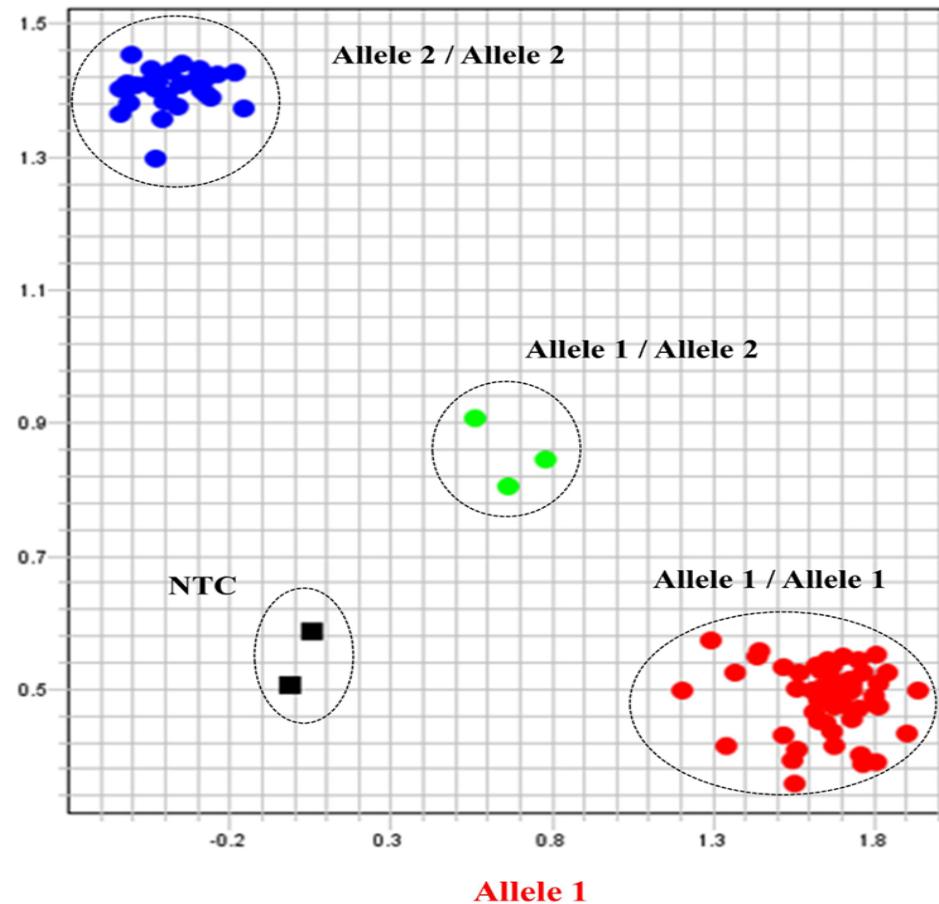


ABI 7500





96 RILs from CT111



Objective 2: Map QTL for yield and yield components under dryland and irrigated conditions

◎ RILs were phenotyped in 8 Env. Using α -lattice or R-C

2013

- Etter (ET13), TX – irrigated
- Aberdeen (ID13), ID – irrigated
- Hays (HY13), KS – dryland

2014

- Bushland (BS14) and Etter(ET14), TX-irrigated
- Walsh, CO-irrigated
- Chillicothe (CH14), TX and Hays (HY14), KS-dryland

◎ Data collection:

- Grain yield (GY)
- Heading date (HD)
- SPM²
- Mean single head weight (MSHW)
- Test weight (TW)
- Kernel weight(TKW)

◎ ANOVA conducted for each env. and across env.

◎ Chromosome map from 90K SNP array used for QTL analysis

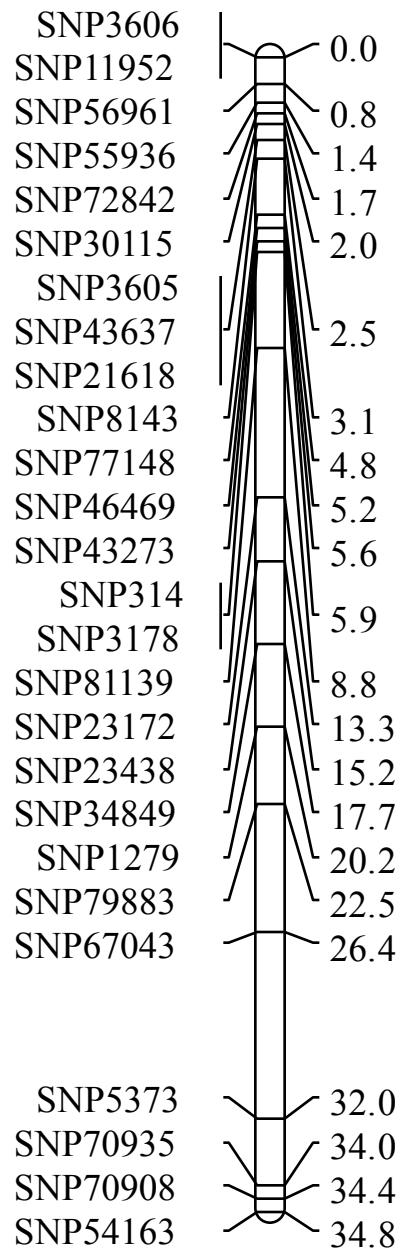
◎ BLUP used for QTL analysis



Summary statistics for grain yield

	2014				2013		
	Bushland	Chillicothe	Etter	Walsh	Etter	Hays	Idaho
Mean	29.1	19.4	52.6	42.4	34.9	57.3	97.9
LSD	9.9	4.6	12.1	13.7	6.7	8.1	33.4
CV	17.1	12.0	11.6	16.3	9.7	7.1	17.3
Sig. ($\alpha=0.05$)	**	**	**	**	**	**	**
$\sigma^2_{\text{genotype}}$	8.9	7.5	11.1	7.3	6.9	19.9	69.3
$\sigma^2_{\text{residual}}$	18.7	4.1	35.1	30.8	10.7	14.9	242.5
H^2	0.5	0.8	0.4	0.3	0.6	0.7	0.4





*QTL for grain yield, yield components
and heading date, 2B*

Q.HD.tamu.2B.BSI4.I



Q.GY.tamu.2B.HYI3.I



Q.GY.tamu.2B.HYI3.I

Q.TKW.tamu.2B.HYI3.I



Q.HD.tamu.2B.CHI4.I



PH.tamu.2B.CHI4.I



Q.TW.tamu.2B.BSI4.I

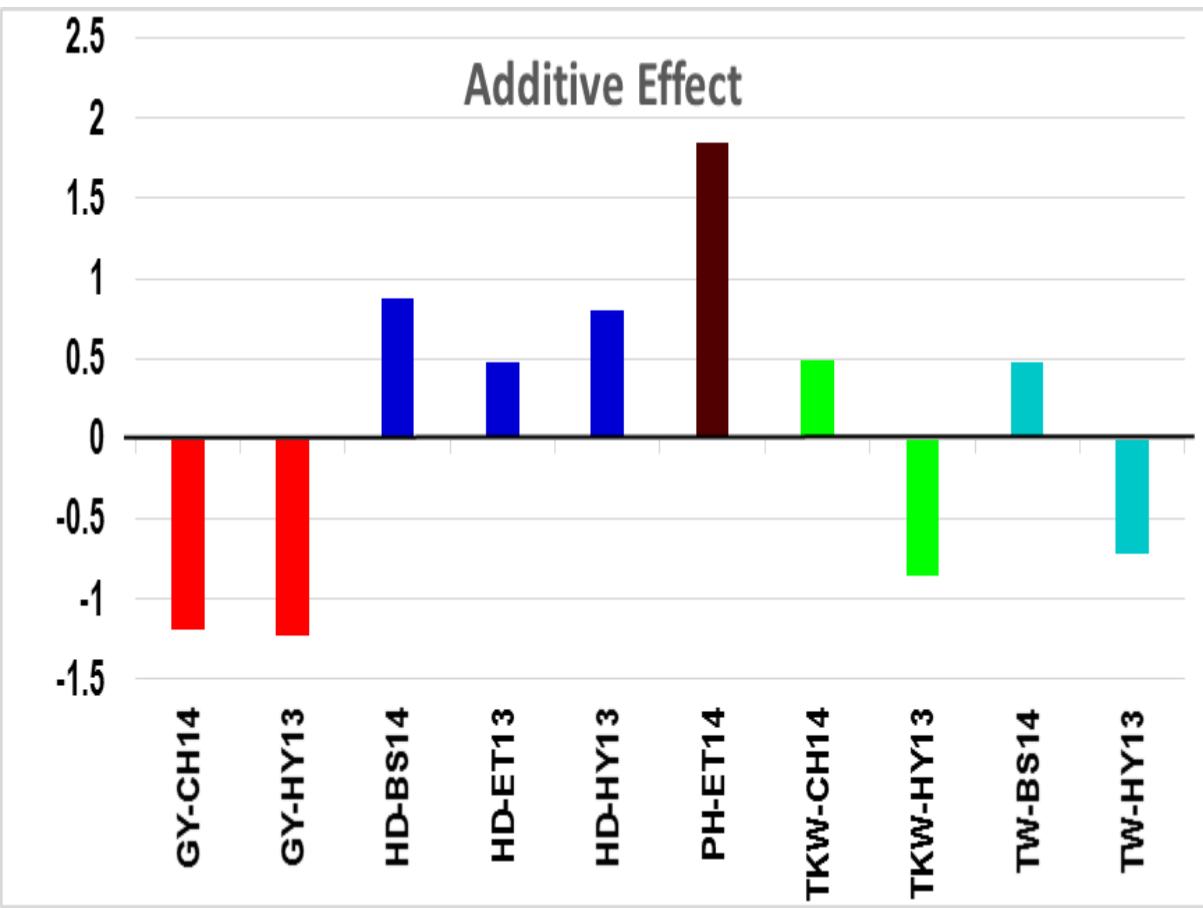
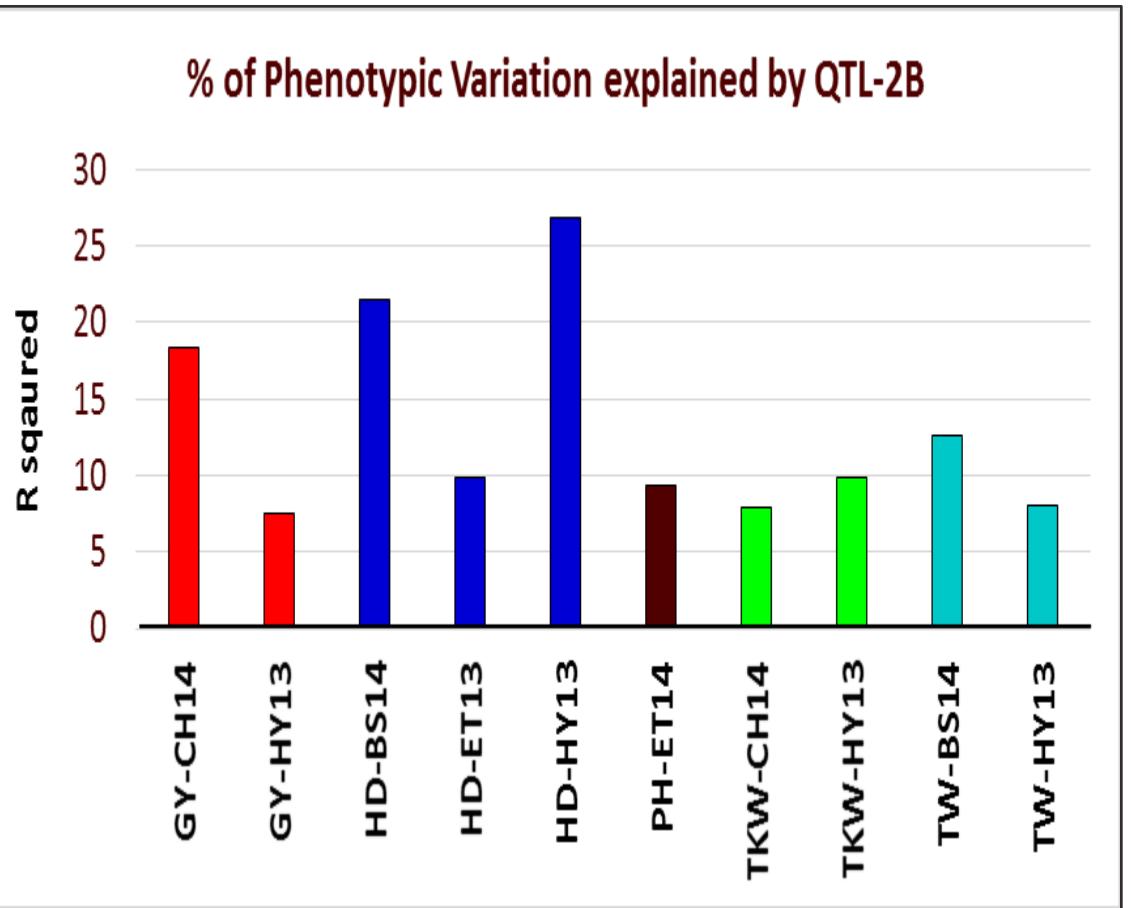


Q.TW.tamu.2B.HYI3.I

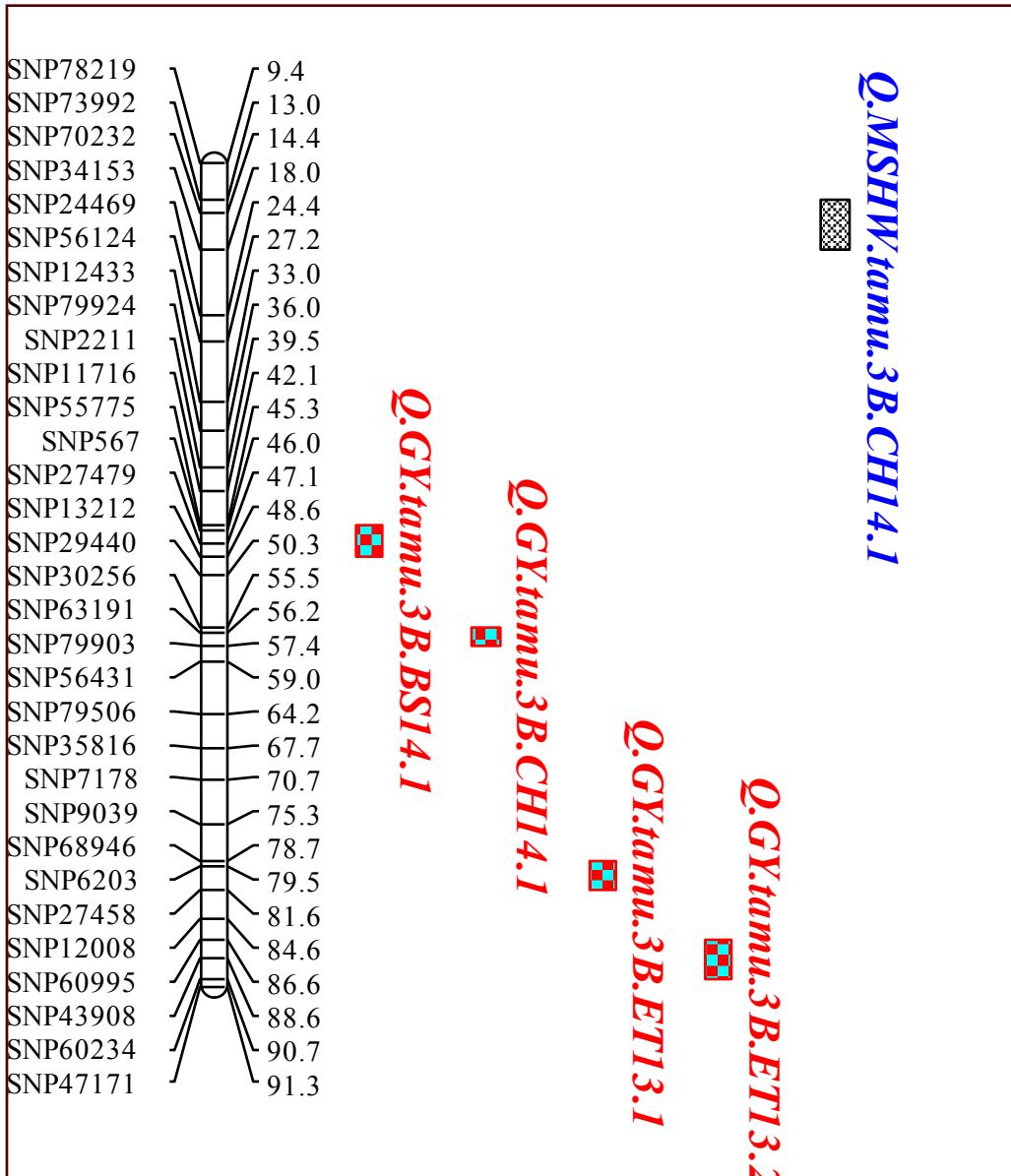


Q.TKW.tamu.2B.CHI4.I





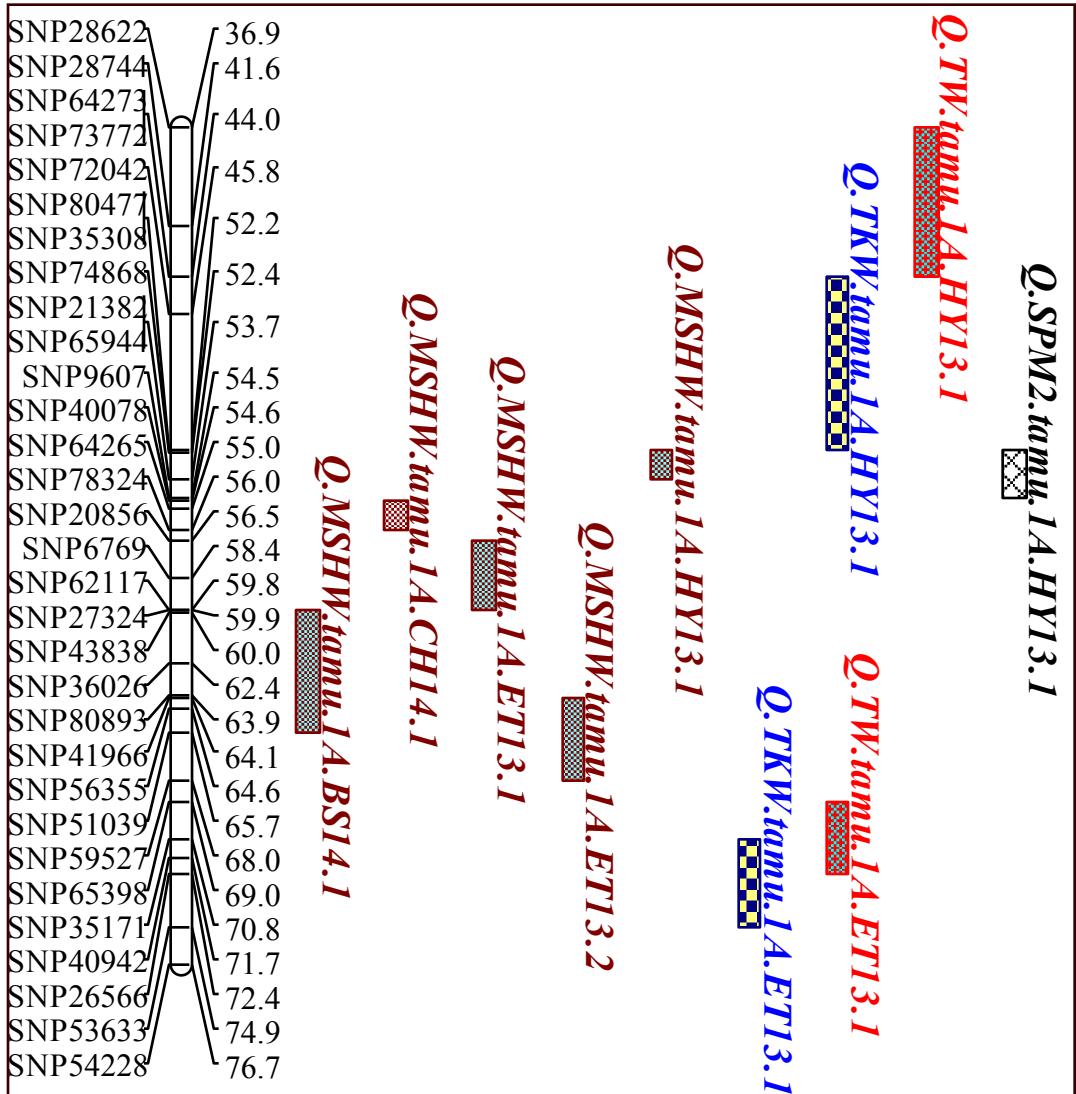
QTL for grain yield and MSHW, 3B



<i>QTL</i>	R^2	Additive
<i>Q.GY.tamu.3B.BS14.1</i>	6.0	1.41
<i>Q.GY.tamu.3B.CH14.1</i>	7.7	0.77
<i>Q.GY.tamu.3B.ET13.1</i>	7.7	0.65
<i>Q.GY.tamu.3B.ET13.2</i>	7.5	0.65
<i>Q.MSHW.tamu.3B.CH14.1</i>	8.4	0.02



QTL for yield components, 1A



QTL	R²	Additive
<i>Q.MSHW.tamu.1A.BS14.1</i>	7.7	-0.03
<i>Q.MSHW.tamu.1A.CH14.1</i>	8.5	-0.02
<i>Q.MSHW.tamu.1A.ET13.1</i>	9.5	-0.03
<i>Q.MSHW.tamu.1A.ET13.2</i>	10.4	-0.03
<i>Q.MSHW.tamu.1A.HY13.1</i>	10.6	-0.03
<i>Q.TKW.tamu.1A.ET13.1</i>	6.8	-0.56
<i>Q.TKW.tamu.1A.HY13.1</i>	6.9	-0.71
<i>Q.TW.tamu.1A.BS14.2</i>	6.7	-0.37
<i>Q.TW.tamu.1A.HY13.1</i>	8.6	-0.74
<i>Q.SPM2.tamu.1A.HY13.1</i>	6.7	23.14

Summary

- A saturated map for *Wsm2* based on 90K SNP markers
- High throughput markers flanking *Wsm2* were developed for MAS
- Putative QTL for yield and yield components are localized on chromosomes 2B, 1A and 3B
- Markers linked to these QTL will be converted to KASP and tested in spring x winter crosses between Kenyan and TAMU cultivars



Acknowledgement



Producers Board and Association
Market Development :: Research :: Education :: Legislative Advocacy



MONSANTO'S
Beachell-Borlaug
International Scholars Program



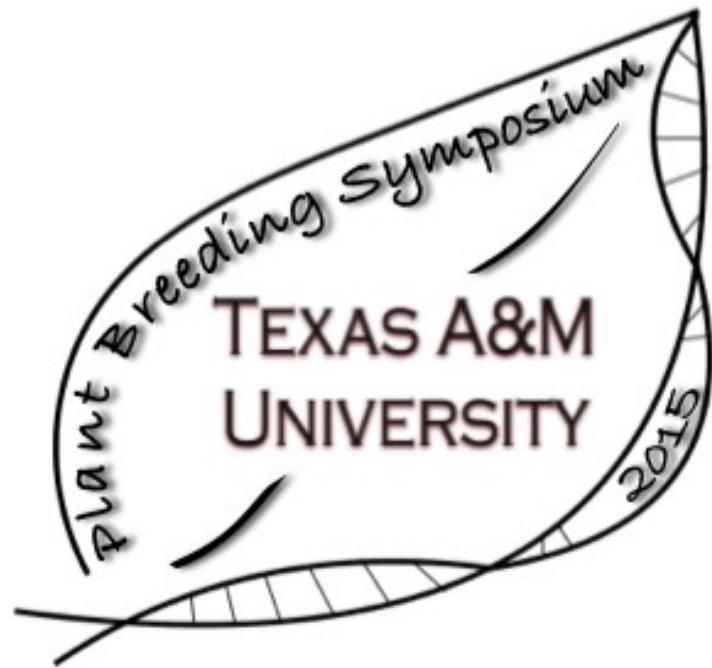
NORMAN E. BORLAUG
LEADERSHIP ENHANCEMENT IN AGRICULTURE PROGRAM



Triticeae CAP
Coordinated Agricultural Project

- **USDA Genotyping lab ND, Fargo**
- **TAMU Wheat Genetics-Amarillo**
- **TAMU Wheat Breeding and Genetics-College Station & Amarillo**
- **Undergraduate(Martin, Nelson, Ashley, Shachter) and graduate students (Reddy, Smit)**
- **Postdoc-Trevis and Suheb**





QUESTION & ANSWER SESSION

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