

# QTL for Soft Wheat Quality

## OSU

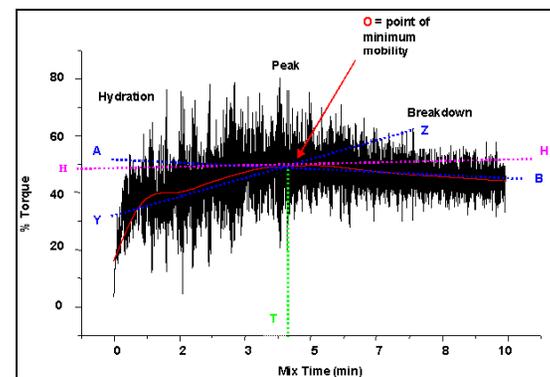
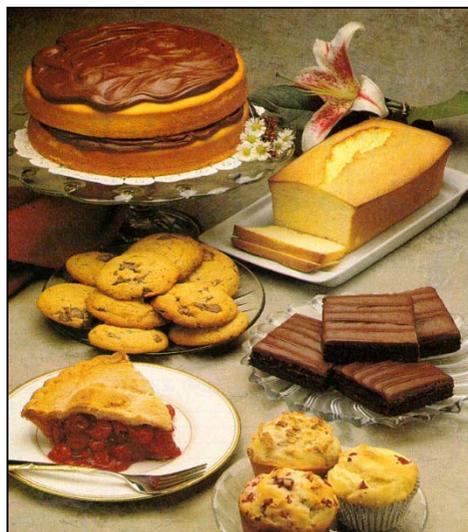
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## USDA SWQL

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Funding  
CSREES NRI CAP  
ARS – Wooster, Raleigh  
State Universities

# Approach & CAP Funding

- CAP funded phenotyping of 6 biparental populations for soft wheat quality
- Populations were primarily developed for other traits
- Genotyping of populations was funded by either CAP or other sources
- Non-CAP mapping work was added

# Rationale

- Mapping in multiple populations provided a broad perspective of genetics
- Value of QTL discovered in multiple populations

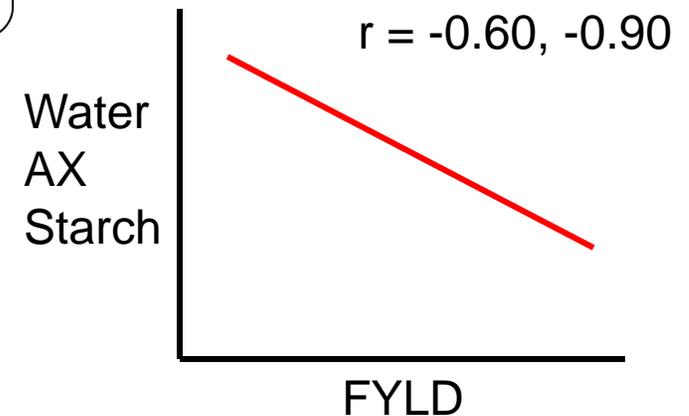
# Conclusions

- Major QTLs were identified that affect all components of soft wheat quality
- Chromosomes 1B and 2B were important in most populations and for most traits
- Large effect QTL from other regions were detected in > 1 population. Repeated yet more population specific than the 1B and 2B QTL.
- Association Analysis detected in the general chromosome regions many of the large effect QTL reported in the 6 biparental mapping pops, but specific markers may not be significant.
- Mapping major translocations and functional genes necessary for understanding variation

## Key Components of Soft Wheat Quality Used in All Analyses

- **Water absorption (Water SRC)**
- **Starch damage (Na Carb. SRC)**
- **Arabinoxylan (Sucrose SRC)**
- **Flour Yield**
  
- **Gluten strength (Lactic acid SRC)**
  
- Softness Equivalent  
(Flour particle size = Break flour yield)
  
- Flour Protein
  
- Test Weight

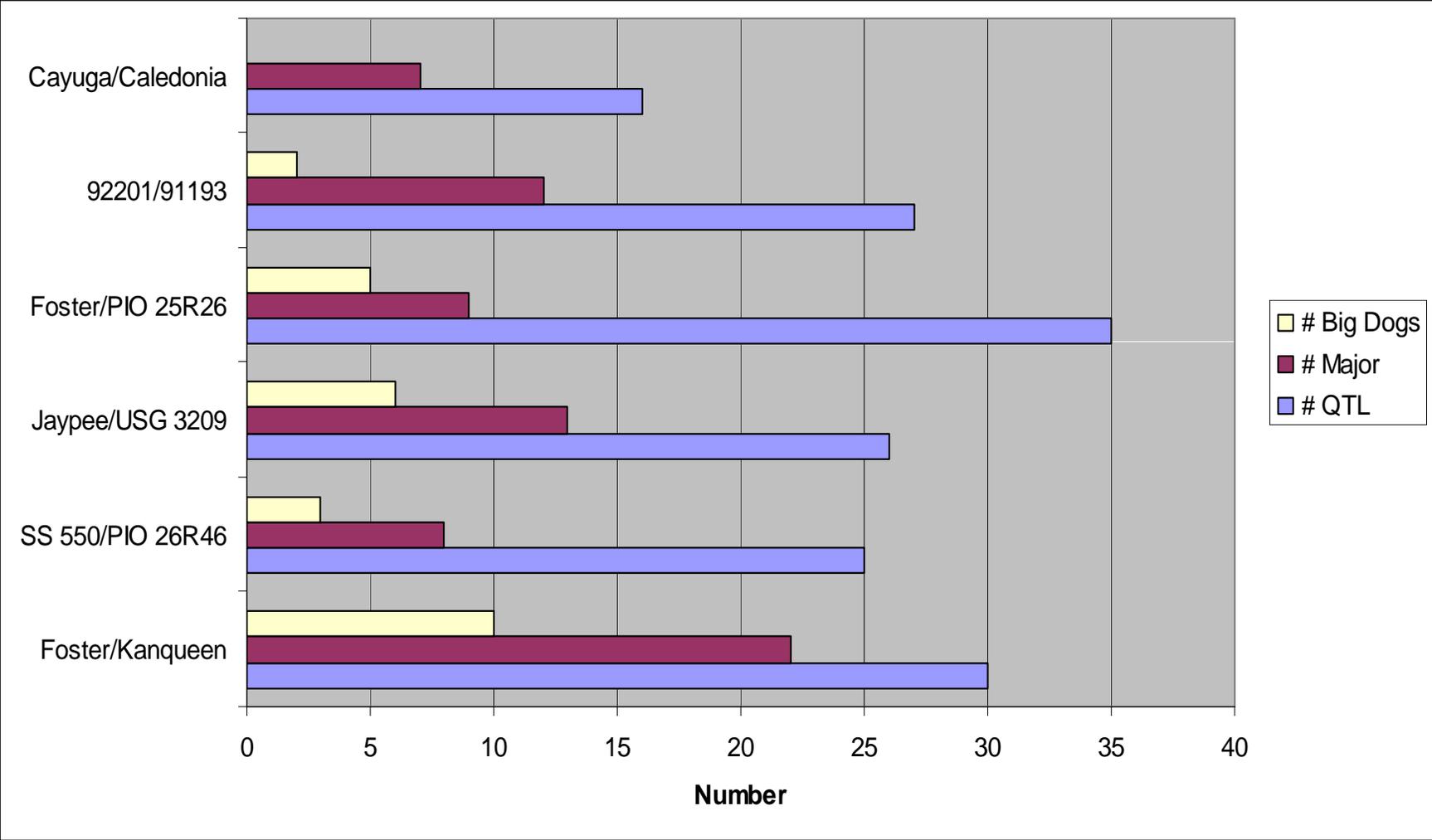
ACT LIKE ONE TRAIT



## Populations & Current Phenotyping & Genotyping

PI	Pedigree	# Lines	Markers	Number of Envs
<b>Sorrells</b>	<b>Foster/Kanqueen</b>	<b>90</b>	254 SSR and AFLP (DArTs being added)	<b>3 (NY, OH)</b>
<b>Johnson</b>	<b>SS 550/PIO 26R46</b>	<b>150</b>	153+ SSRs	<b>4 OH, 2 GA</b>
<b>Griffey</b>	<b>Jaypee/USG 3209</b>	<b>125</b>	220 SSR, 363 DArT	<b>3 (VA,NC)</b>
<b>Sneller</b>	<b>Foster/PIO 25R26</b>	<b>175</b>	163 SSR	<b>4 (OH, NY)</b>
<b>Ohm</b>	<b>92201/91193</b>	<b>190</b>	383 DArT and SSR	<b>3 (IN, NY, OH)</b>
<b>Sorrells</b>	<b>Cayuga/Caledonia</b>	<b>155</b>	256 SSR and AFLP (DArTs being added)	<b>4 for Starch Dam, 2 for others</b>
<b>Ohio State, USDA SWQL</b>	<b>Association Analysis</b>	<b>187</b>	~600 DArTs, SSRs, others	<b>9 (NY, OH, IN, KY, VA)</b>

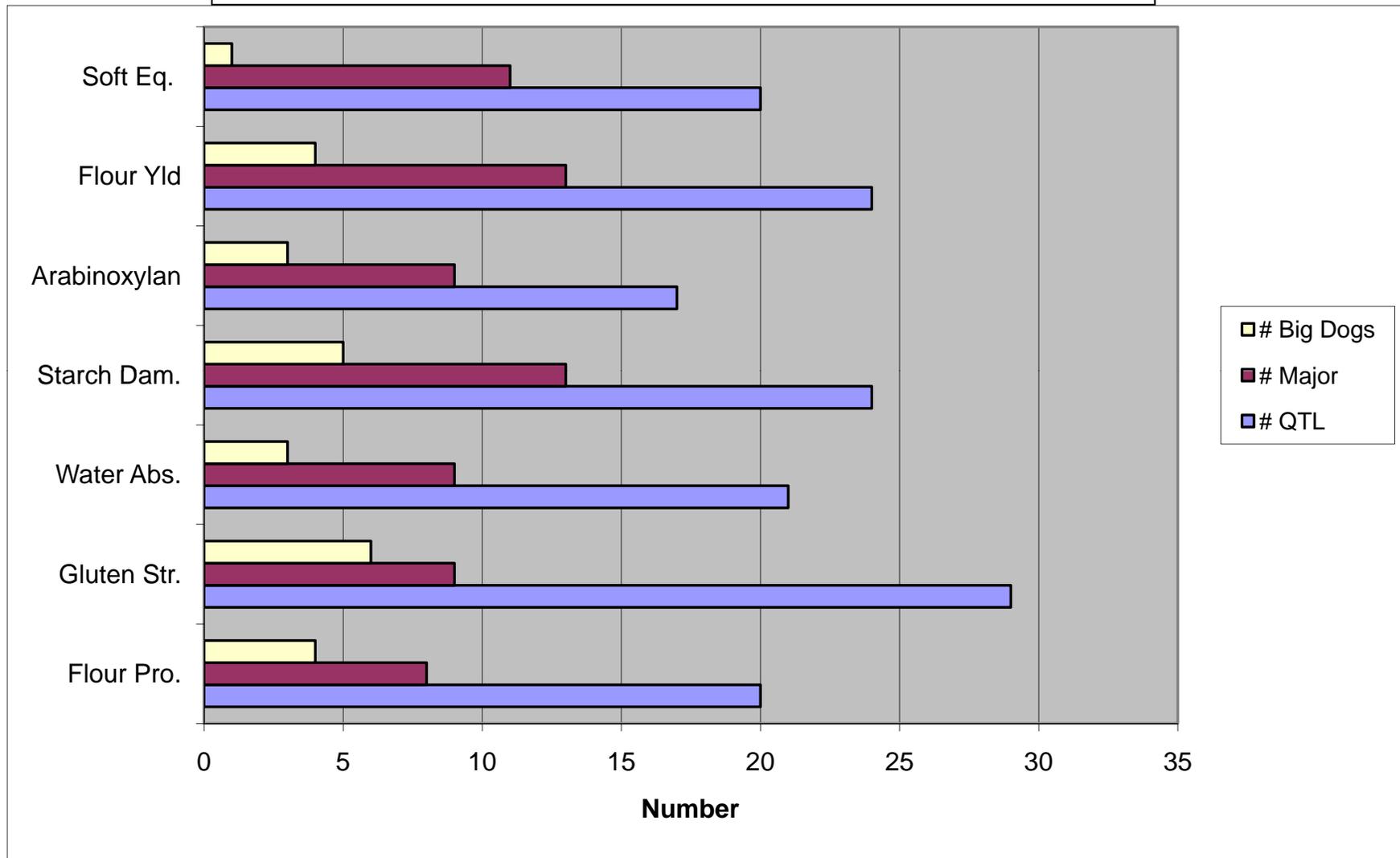
# Biparental: Number of QTL by population



“Major” =  $LOD > 3$ ,  $R^2 > 0.12$

“Big Dog” =  $LOD > 6$ ,  $R^2 > 0.2$

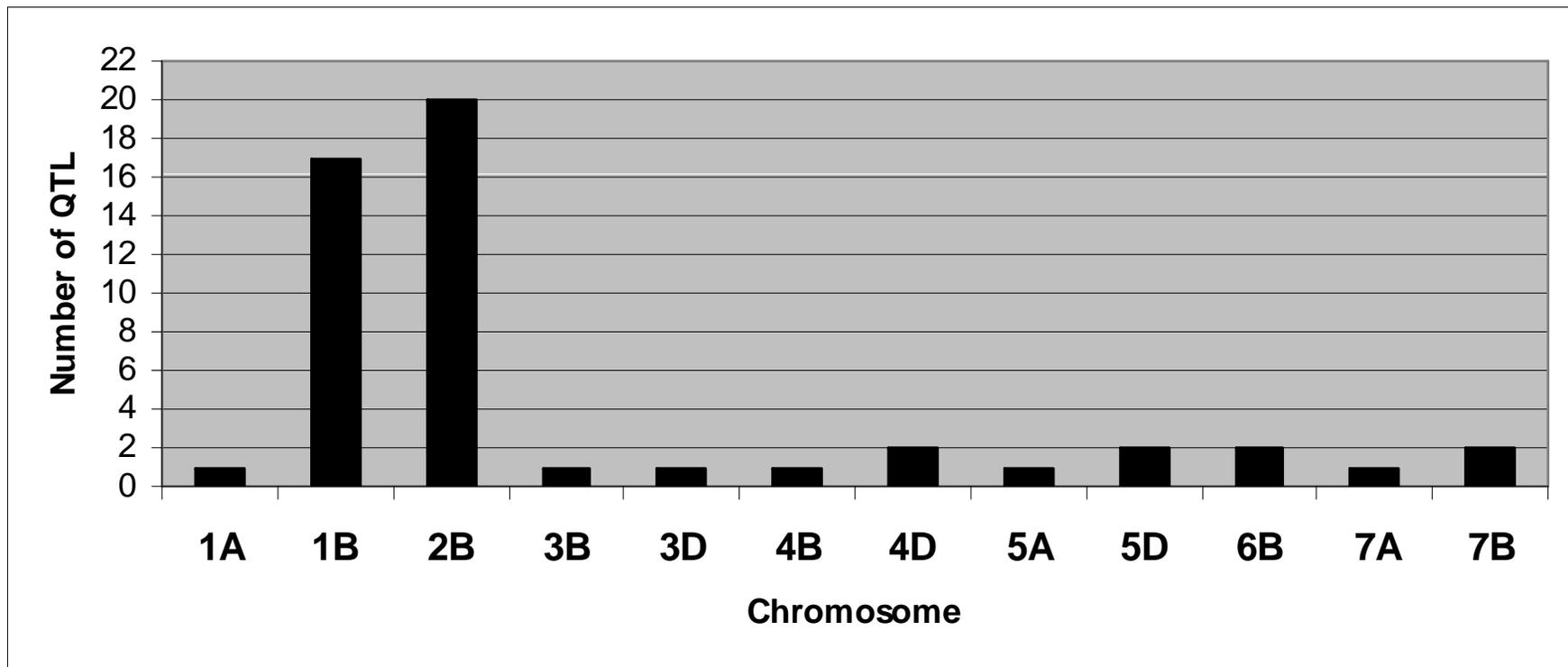
## Biparental: Number of QTL by trait



“Major” = LOD > 3,  $R^2 > 0.12$

“Big Dog” = LOD > 6,  $R^2 > 0.2$

# Biparental Mapping: Location of QTLs with $R^2 > 0.15$



\*\*\*\* P < .0001

\*\*\* P < .0005

\*\* P < .001

\* P < .005

# Chromosome 1B

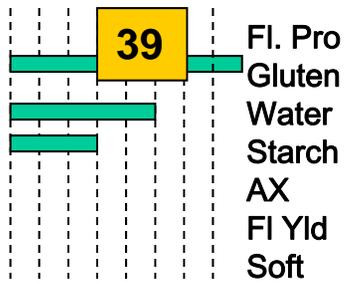
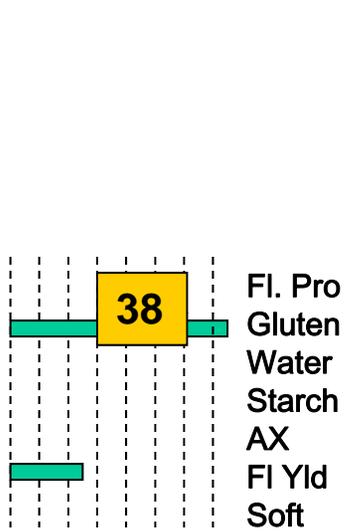
## ASSOC.

Soft \*\*\*  
FI Pro \*\*\*  
Gluten \*\*\*\*  
FI Yld \*

AX\*  
FI Yld \*\*\*

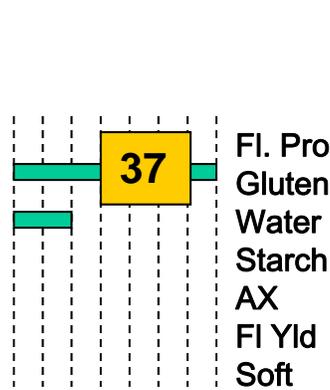
1B/1R  
Glu-B1?

### Fos/Kan



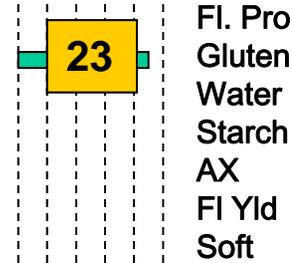
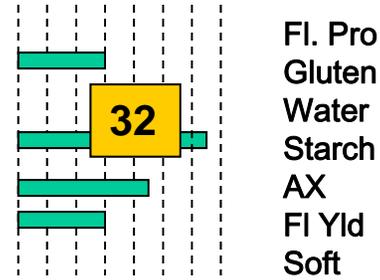
1B/1R  
7+8/13+16

### SS5/P26



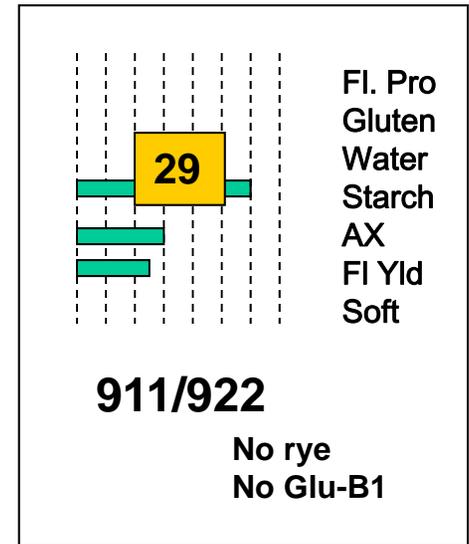
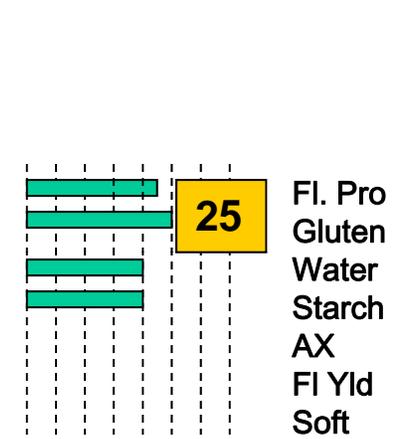
1B/1R  
?

### USG/Jay



1B/1R  
Bx7oe/

### Fos/P25



### 911/922

No rye  
No Glu-B1

# Chromosome 2B

ASSOC.

Fos/Kan

SS/P26

USG/JAY

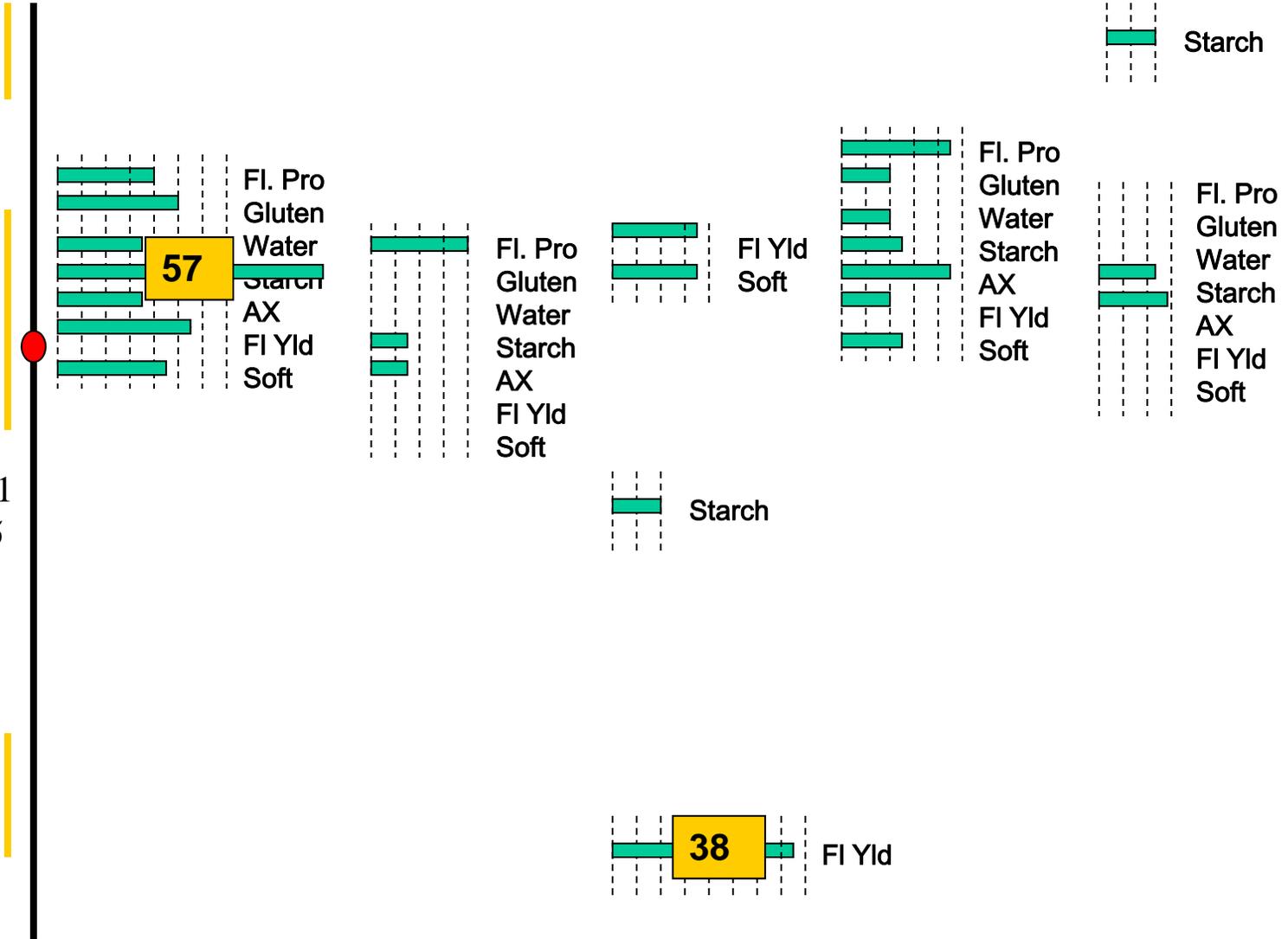
Fos/P25

911/922

AX \*  
Water \*\*  
FI Pro \*\*

AX \*\*  
Water \*  
Starch \*

\*\*\*\* P < .0001  
\*\*\* P < .0005  
\*\* P < .001  
\* P < .005



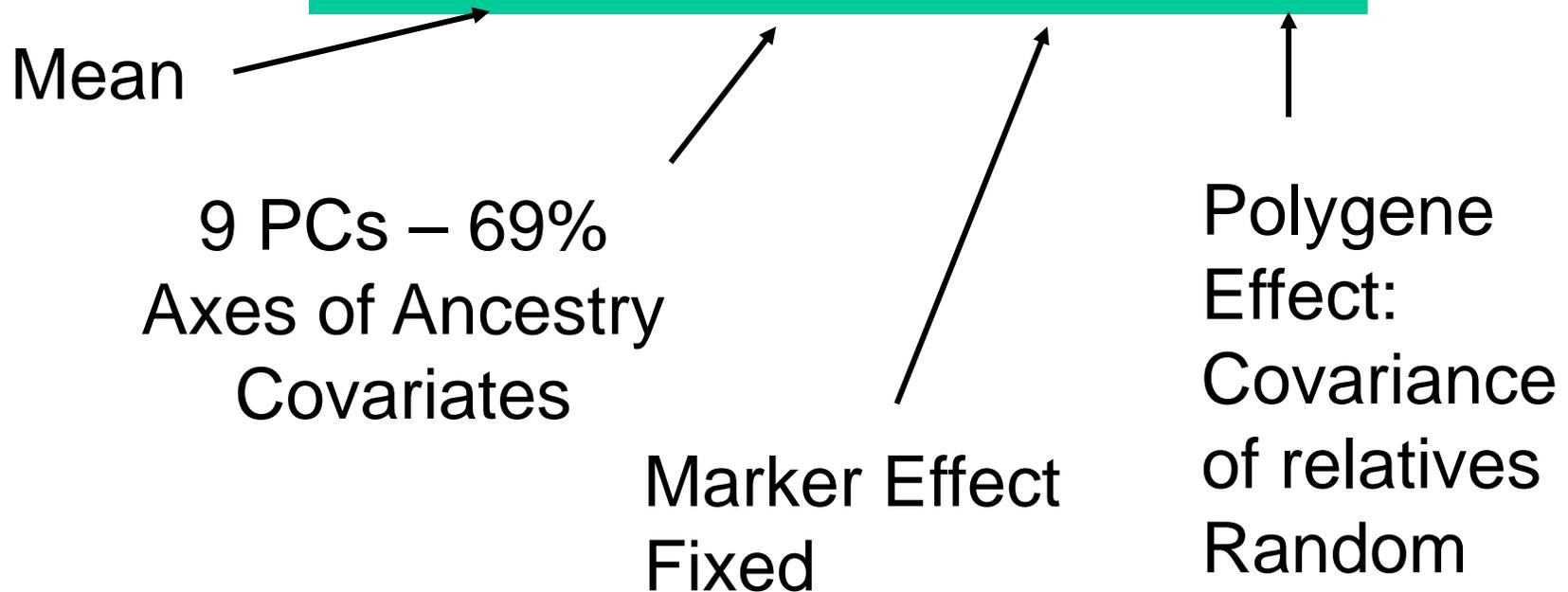
## Association Analysis Population: 187 Genotypes

Source	# Entries	Years		Source	# Entries	Years
Canada	7	1985-2001		AR	14	1975-2003
IL	5	1915-1999		FL	2	1994
IN	44	1915-2001		GA	5	1947-2000
KY	1	1997		KS	2	1897-1946
MI	11	1881-1993		MD	4	1837-1975
NY	17	1893-1998		MO	7	1830-1976
OH	20	1808-2003		NC	9	1959-2002
PA	3	1870-1951		SC	16	1921-1996
WI	4	1974-1991		TN	1	1900
				TX	1	1984
				VA	14	1852-2001

# Association Analysis

606 DArT markers, 7 Traits,  
4,242 Tests

$$P = Xb + Pw + Sa + Zv$$



All quality traits were very heritable,  $h^2$  generally  $> 0.75$

# Genes of known function have an effect in the Assoc. Analysis

Micro-satellite	Flour protein	Gluten (Lactic Acid SRC)	AX (Sucrose SRC)	Starch Damage (Na carb. SRC)	Softness equivalent	Flour yield	Cookie diameter
Glu1D	0.3%*	8.1%***			1.6%*		
1BL:1RS		15.1%**					
Rht8 gwm261Nd			3.9%*	2.7%***			
Rht1&2 vs. Tall	0.7%***	5.1%*	1.7%*		2.3%***		0.4cm***
Ppd1	0.5%***						

Number represent the 2a effect of substituting the alleles that are most different for quality

## QTL markers from bi-parental populations have limited prediction power in Assoc. Analysis

Micro-satellite	Flour protein	Gluten (Lactic Acid SRC)	AX (Sucrose SRC)	Starch Damage (Na carb. SRC)	Softness equiv.	Flour yield	Cookie diameter
wmc25a 2BS FxKQ		10.1%*				0.9%*	
gwm429 2BS FxKQ	0.5%**	9.8%**					0.4cm*
barc98A 2BS FxKQ	0.4%*		2.5%**	1.4%***		0.8%*	0.4cm*
Barc126 7D CxC							
gwm312 2A SSxP							
Barc17 1A FxKQ					0.9%*		

Number represent the 2a effect

# DArT QTL on Chromosome 1B

## Assoc. Analysis Excluding 1BL:1RS Lines

DArT	Gluten (Lactic Acid SRC)	AX (Sucrose SRC)	Starch Damage (Na carb. SRC)	Water Absorp. (Water SRC)	Softness equivalent	Flour yield	Cookie diameter
wPt4532 and others	Linked on 1BL but independent of Glu-1B		2.1%**	4.0%**		-1.0%***	
wPt1781			2.1%**	2.2**			
wPt8168		3.8%**				-1.4%**	-0.3cm*
wPt6427				-4.5%**	-5.8%*		
wPt3753	-5.9%*	Independent		-0.8%*	1.4%*		0.3cm**
wPt0328	-5.6%*		Linked to Glu-1B		-1.4%*		
wPt5312	15.1%***						

Numbers represent the 2a effect

# DArT QTL on Chromosome 2B Assoc. Analysis Excluding Sr36 Translocation Lines

DArT	Gluten (Lactic Acid SRC)	AX (Sucrose SRC)	Starch Damage (Na carb. SRC)	Water Absorp. (Water SRC)	Softness equivalent	Flour yield	Cookie diameter
wPt5195 wPt0643	0.4%***			0.9%**	-2.7%***		-0.2cm*
wPt2106	-0.3%*	-3.2%*		-0.9%*	2.2%*		0.4cm**
wPt3109		4.2%*	1.8%*	1.3%**			-0.4cm*
wPt4916	Loosely linked to each other and Barc10 on 2BS			1.2%***	-2.5%*		
wPt0100					-0.9%**		0.7%*
wPt6567		-8.4%*	-4.5%**		Independent		

Numbers represent the 2a effect

# Future

- MAS for key QTL with repeated effects
- Develop selection indices, methods based on effects from 1B and 2B.
- Determine function of genes underlying the 1BL and 2BS effects
- For Assoc. Analysis to work well will require SNP within ESTs. Preferably of known function.