Genetics and Progress in Soft Wheat Quality

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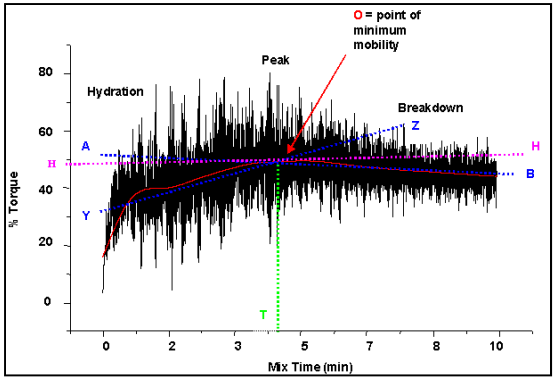


Genetics: Mapping Efforts

- Used CAP $ to phenotype six 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

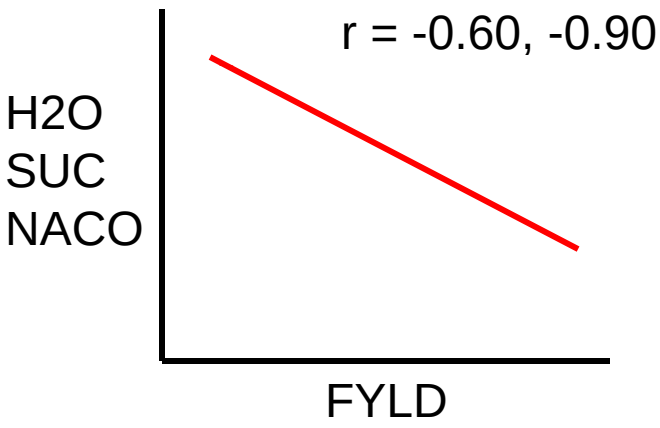
Rationale

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

Measures of Quality Used in All Analyses

- **Water absorption (WA SRC)**
- **Starch damage (SO SRC)**
- **Pentosans (SU SRC)**
- **Flour Yield (FY)**

ACT LIKE ONE TRAIT



- **Gluten strength (LA SRC)**

- Softness Equivalent (SE)

- Flour Protein (FP)

- Test Weight (TW)

Populations & Current Phenotyping & Genotyping

	PI	Pedigree	# Lines	Markers	Number of Envs
	Sorrells	**Foster/Kanqueen**	**90**	254 SSR and AFLP (DArTs being added)	**3 (NY, OH)**
	Johnson	**SS 550/PIO 26R46**	**150**	153+ SSRs	**4 OH, 2 GA**
*	**Griffey**	**Jaypee/USG 3209**	**125**	230 SSR + DArT	**4 (VA,NC)**
*	**Sneller**	**Foster/PIO 25R26**	**175**	162 SSR	**4 (OH, NY)**
*	**Ohm**	**92201/91193**	**190**	245 DArT and SSR	**4 (IN, NY, OH)**
	Sorrells	**Cayuga/Caledonia**	**155**	256 SSR and AFLP (DArTs being added)	**4 for Starch Dam, 2 for others**
*	**Ohio State, USDA SWQL**	**Association Analysis**	**187**	~600 DArTs, SSRs, others	**9 (NY, OH, IN, KY, VA)**

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
	112				75	

Association Analysis
606 DArT markers, 7 Traits, 4,242 Tests

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

Mean

9 PCs – 69%
Axes of Ancestry
Covariates

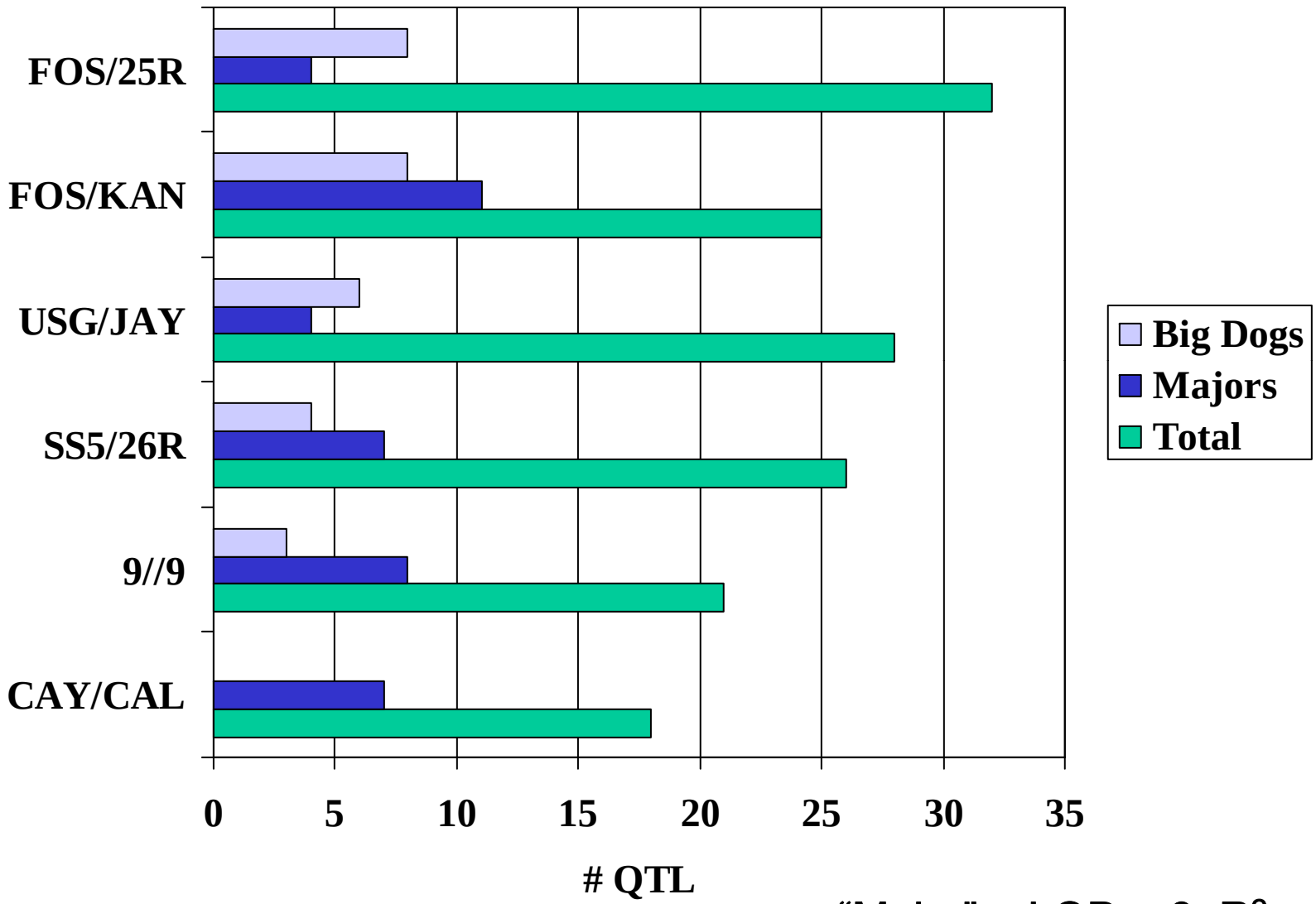
Marker Effect
Fixed

Polygene
Effect:
Covariance
of relatives
Random

Results: Phenotypes

- **Traits are very heritable, h^2 generally > 0.75**
- **Significant genetic variation found in all populations for all traits**
- **Correlations were similar to the expectations**
  - **In AA population Gluten Strength and penotosans were correlated (r = 0.20)**
  - **Softness and flour protein were correlated (r = -0.55)**

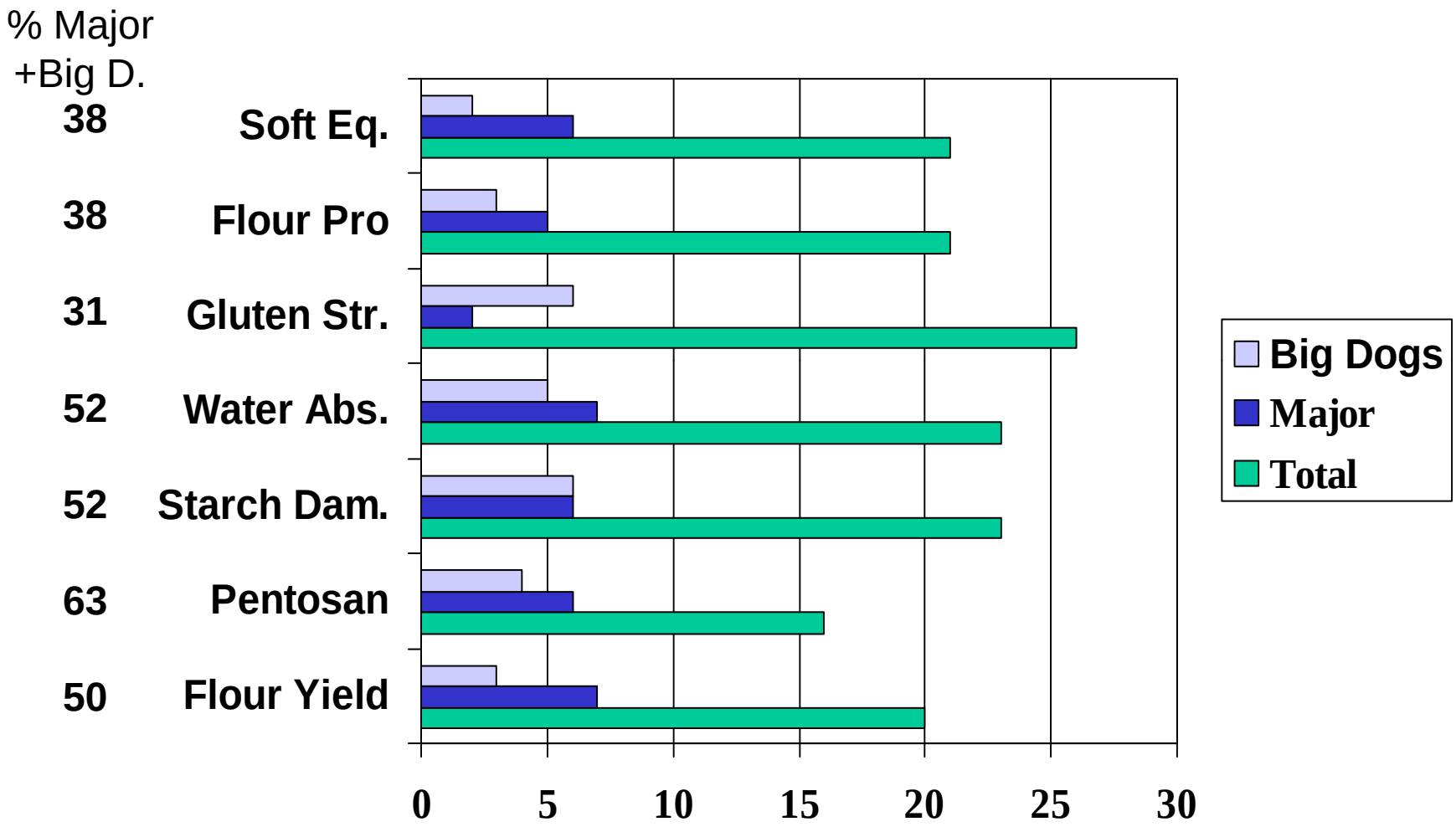
Biparental: Number of QTL by population



"Major" = LOD > 3, R^2 > 0.12

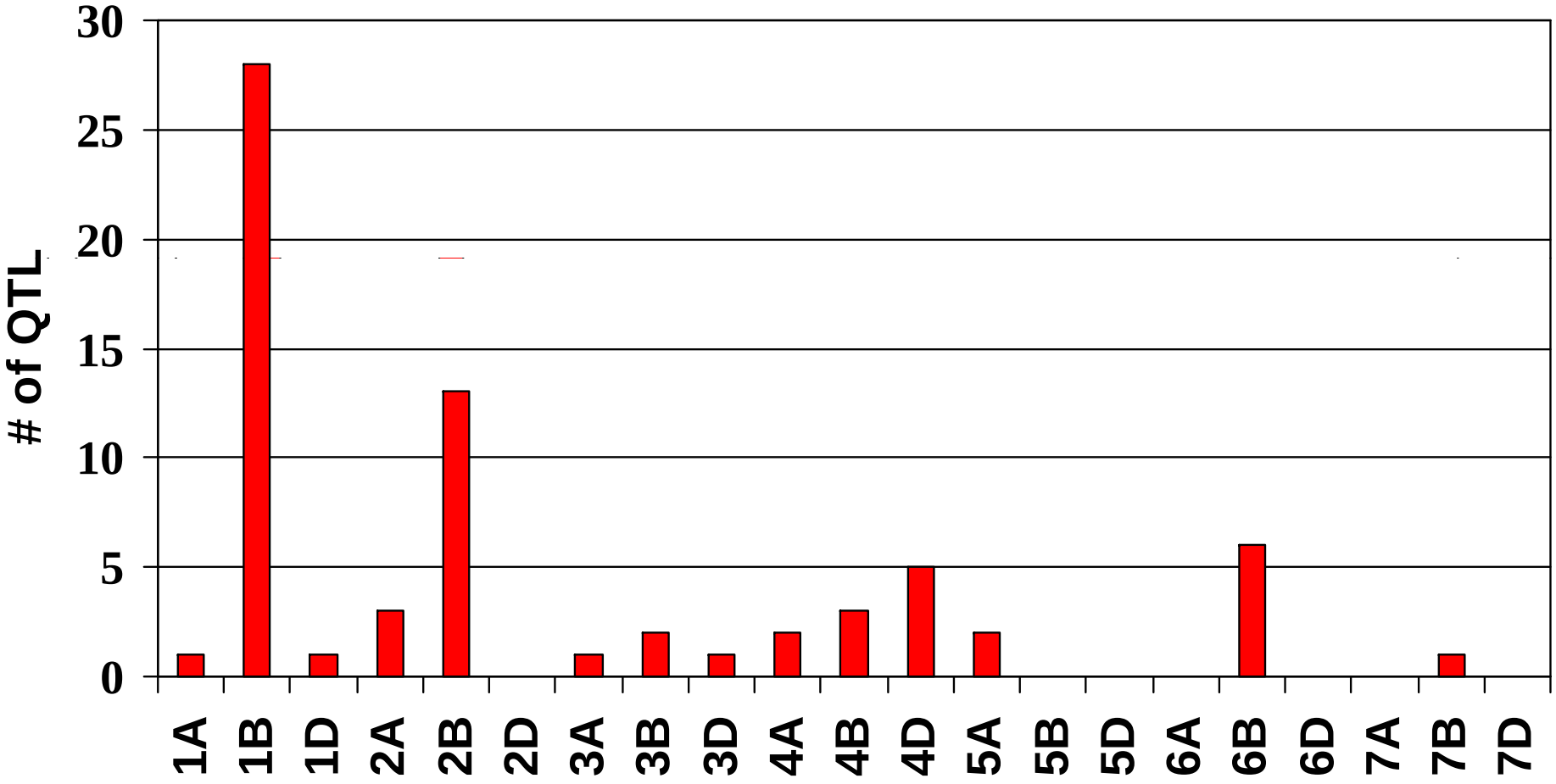
"Big Dog" = LOD > 6, R^2 > 0.20

Biparental: Number of QTL by trait

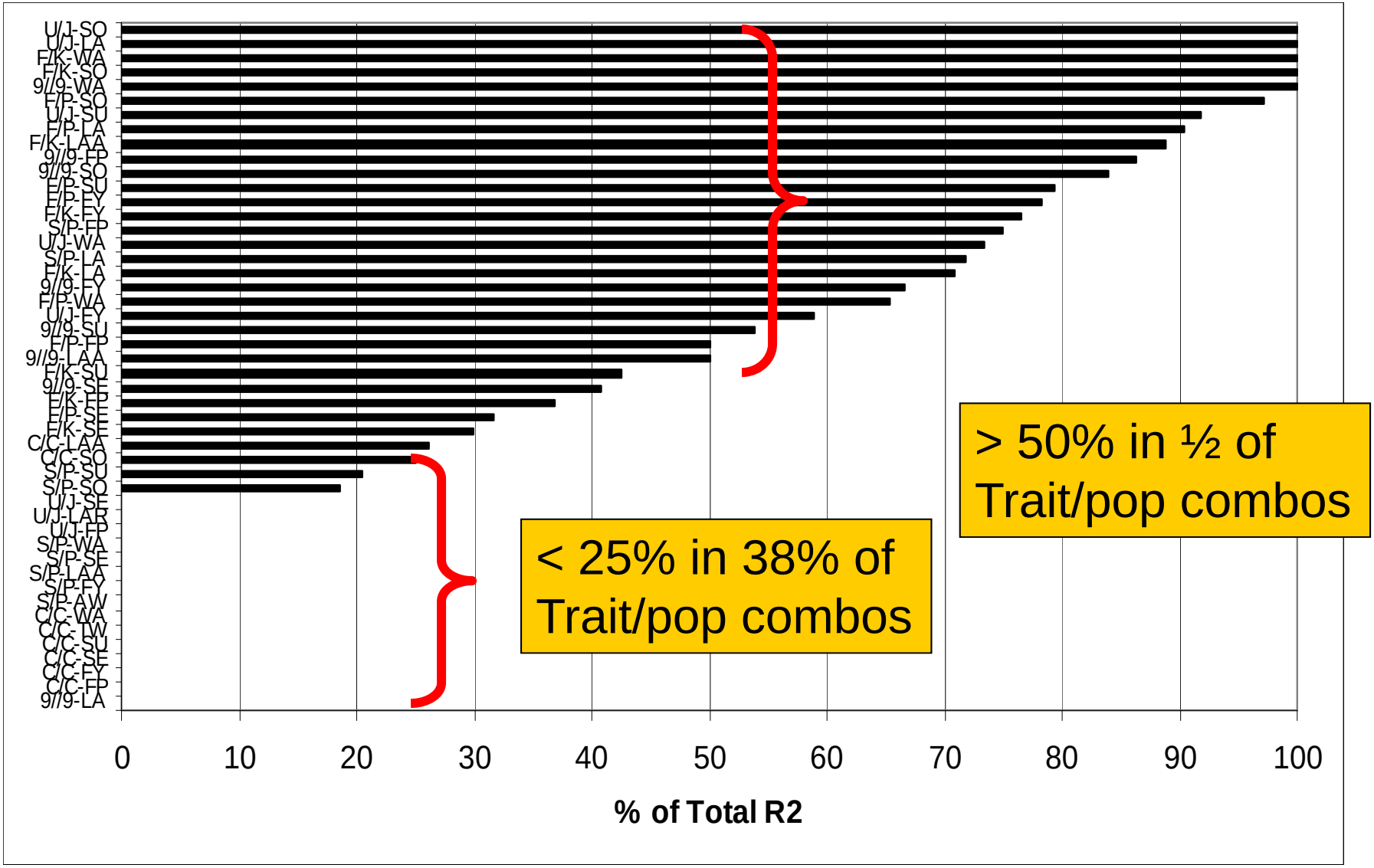


"Major" = LOD > 3, R^2 > 0.12
"Big Dog" = LOD > 6, R^2 > 0.2

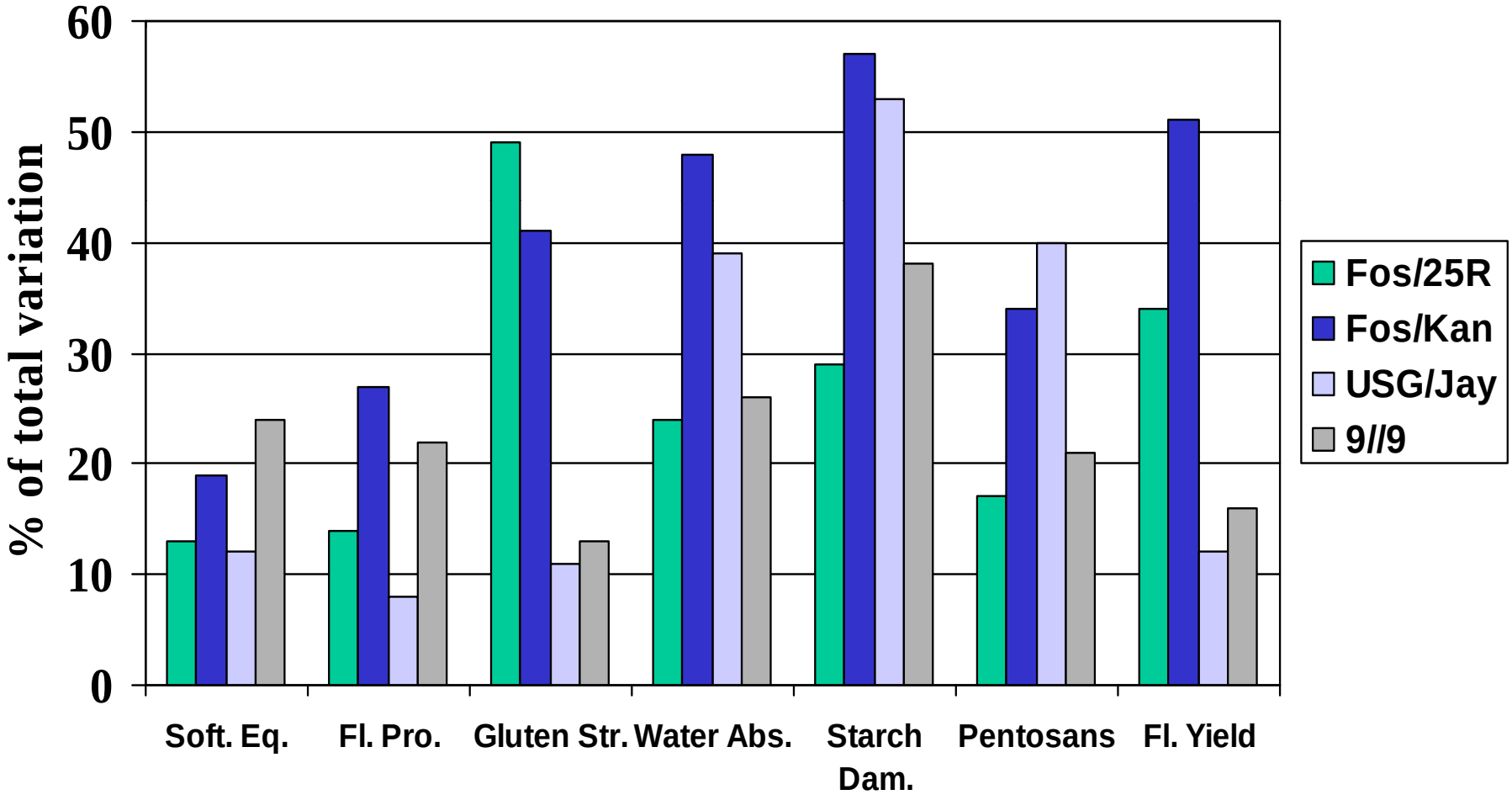
Biparental Mapping: Location of QTLs



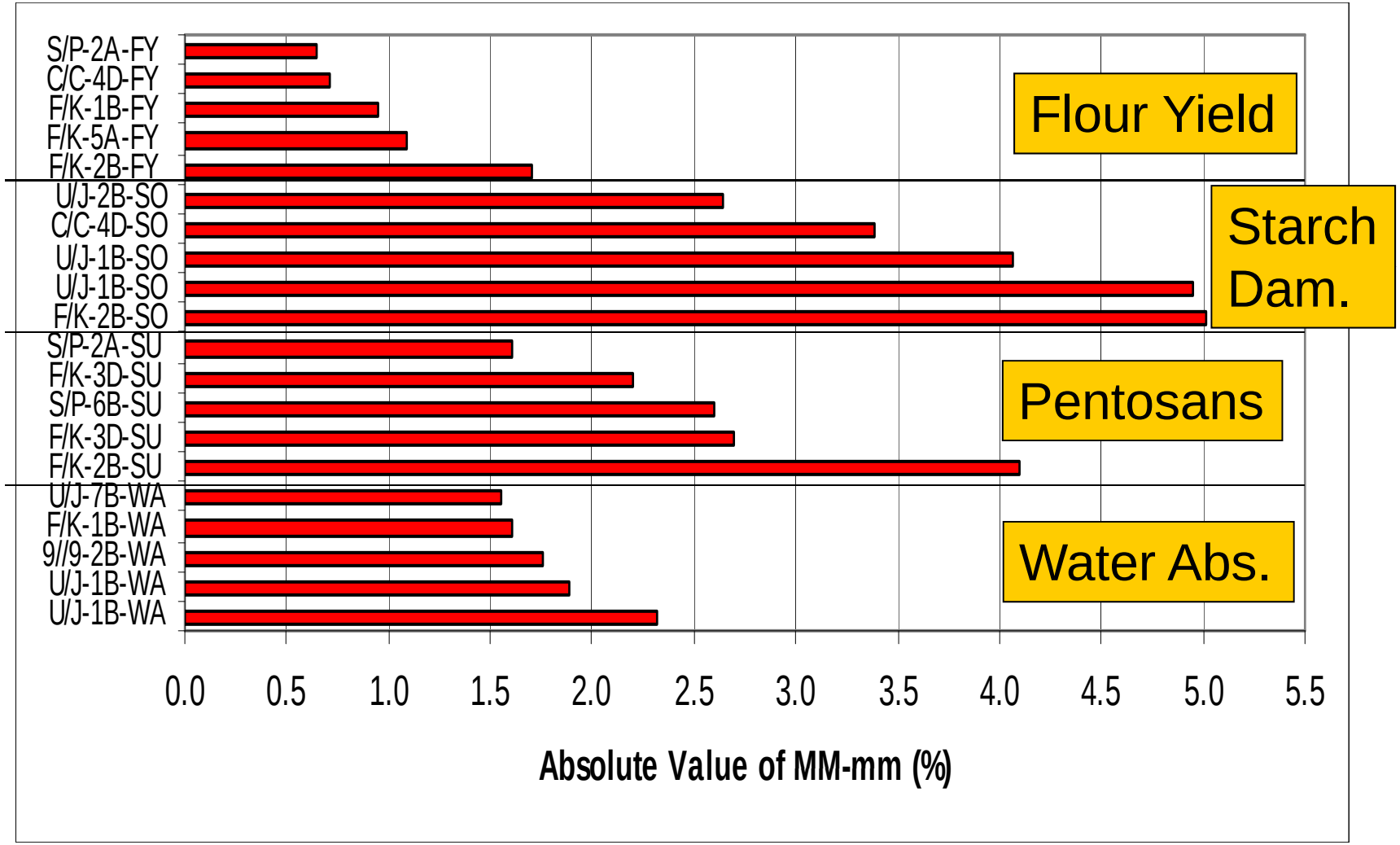
% of total R2 of significant QTL accounted for by QTL from 1B & 2B
42 Trait, Population Combinations



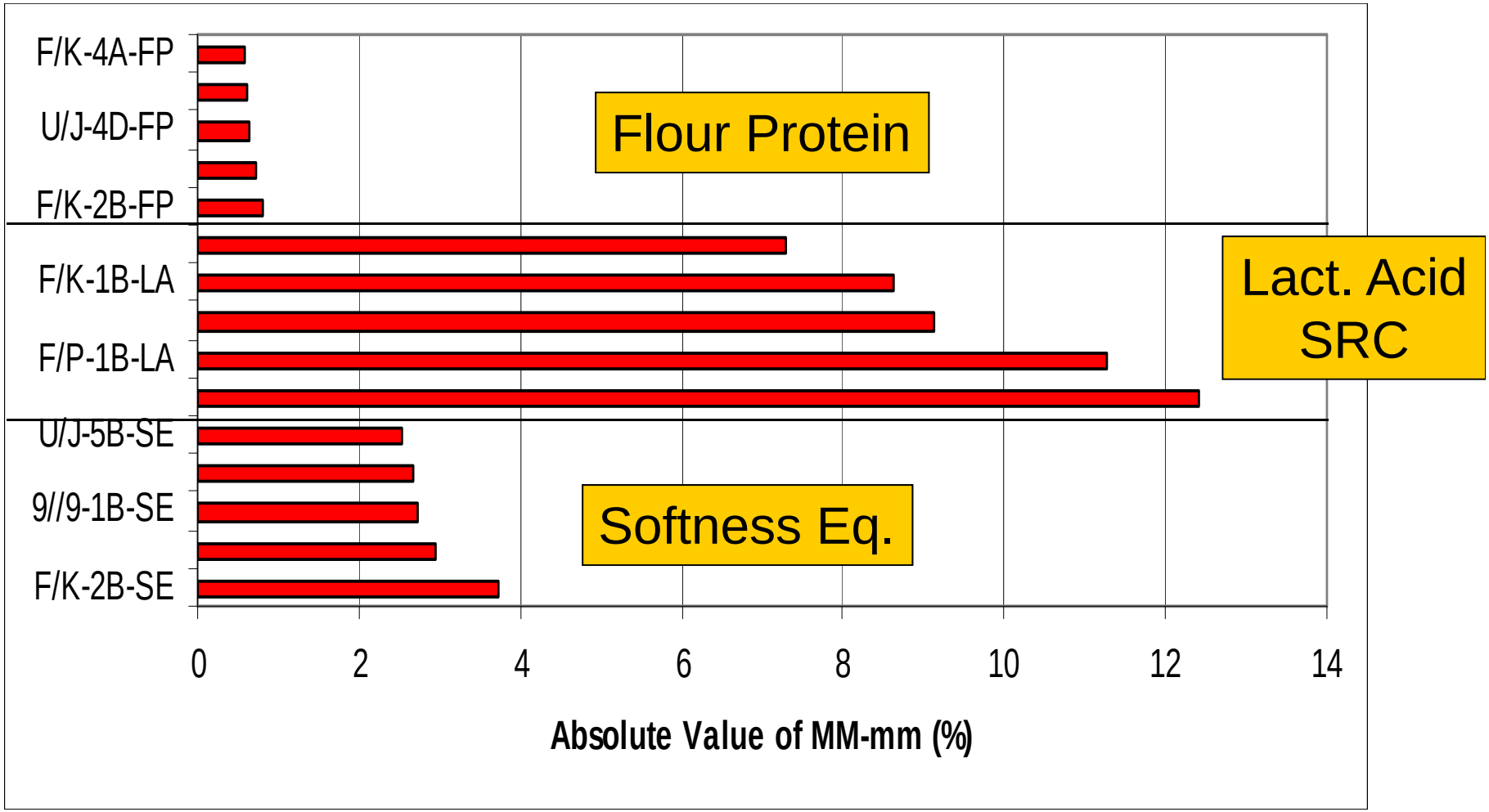
% of Total Variation Modeled by 1B and 2B Markers: Multiple Regression



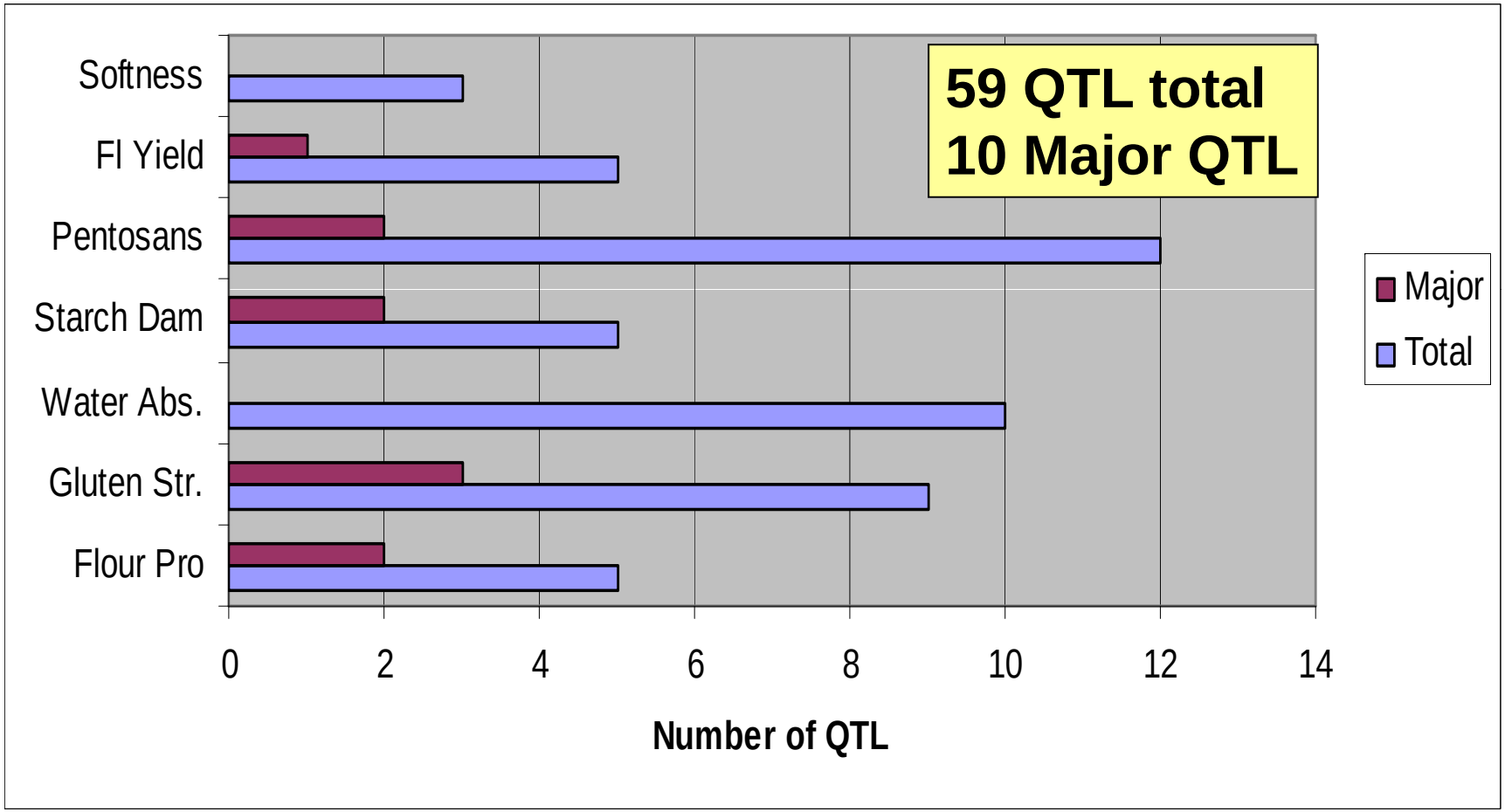
Effect on Traits



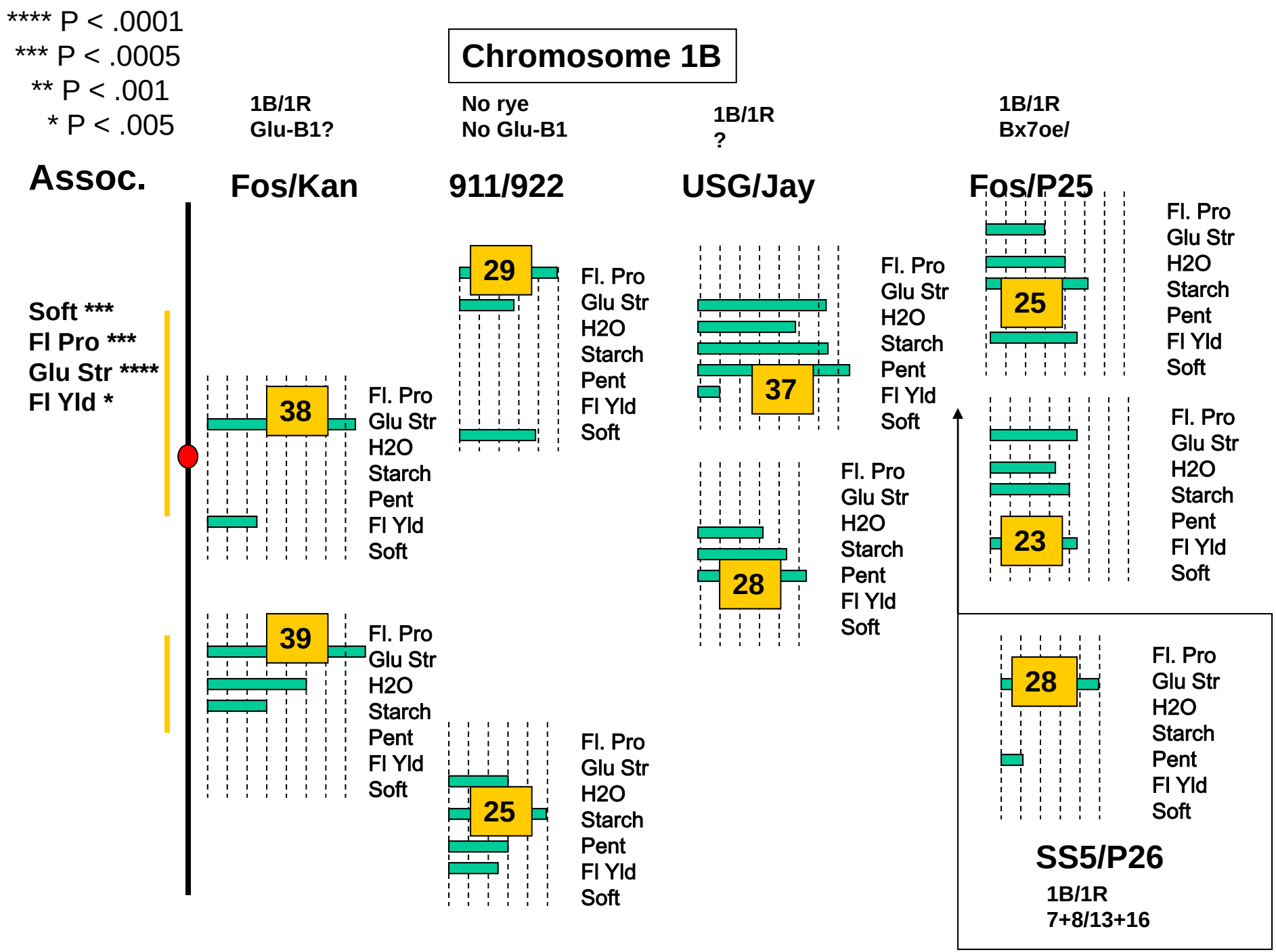
Effect on Traits



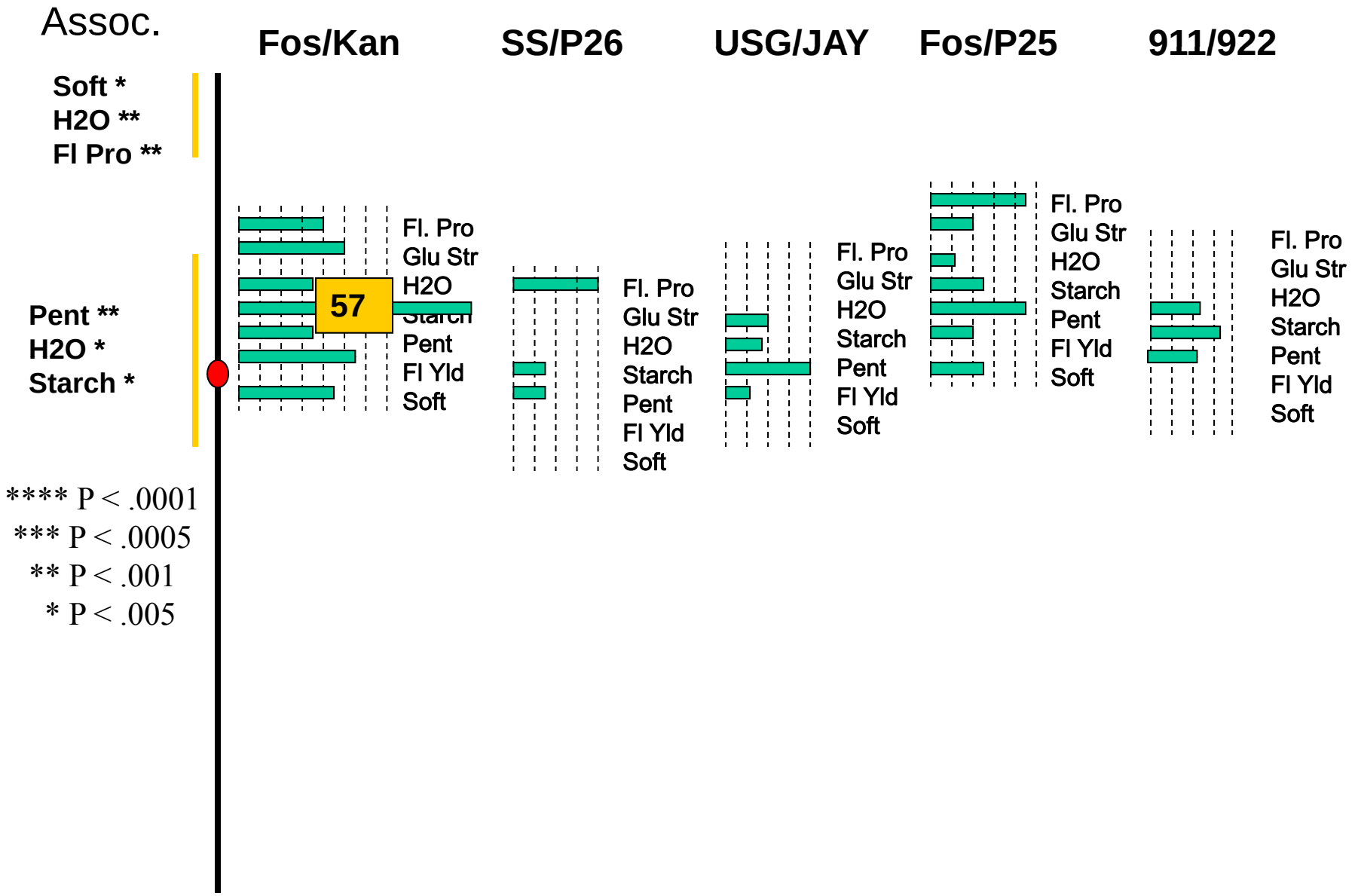
Assoc. Analysis: Number of QTL by Trait

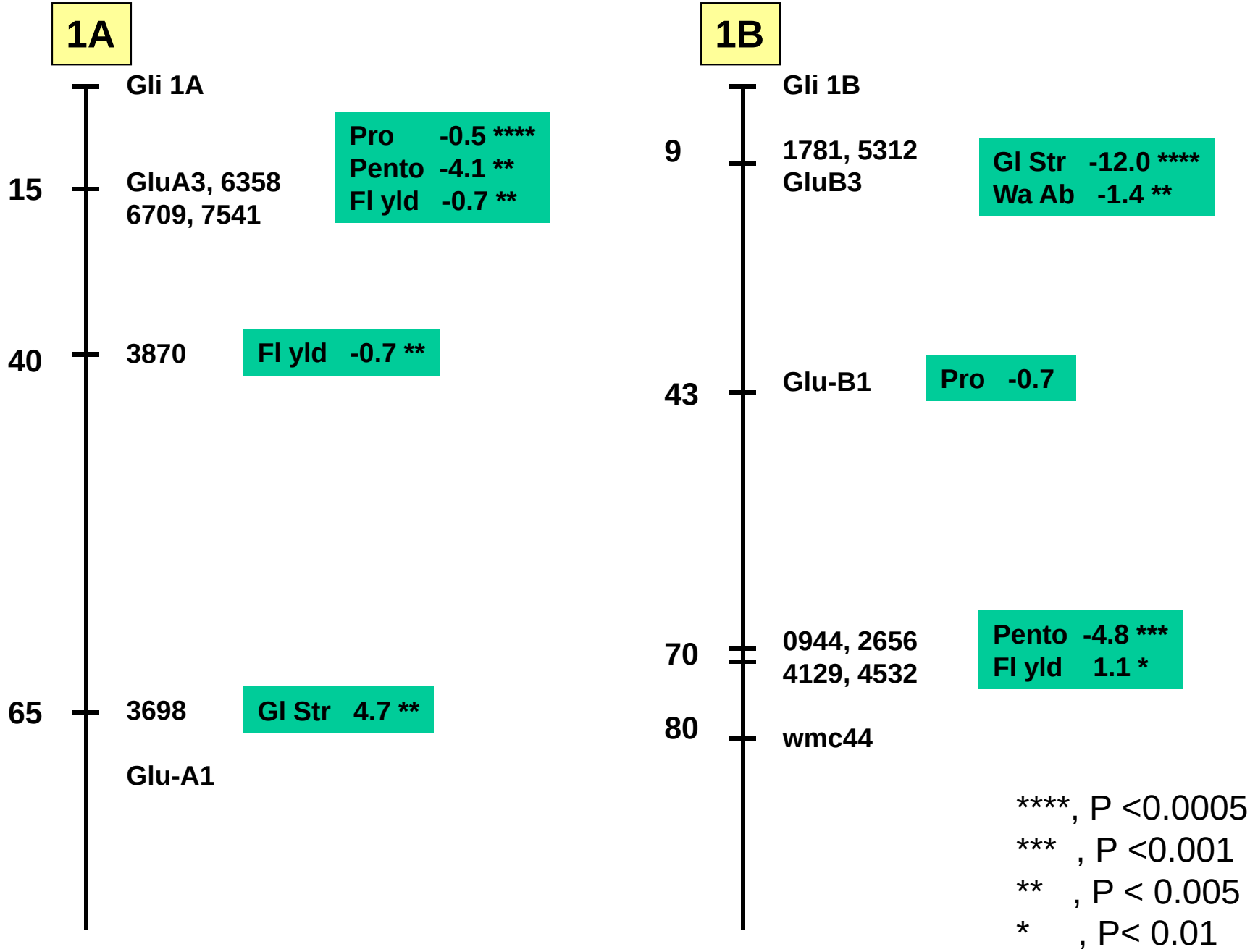


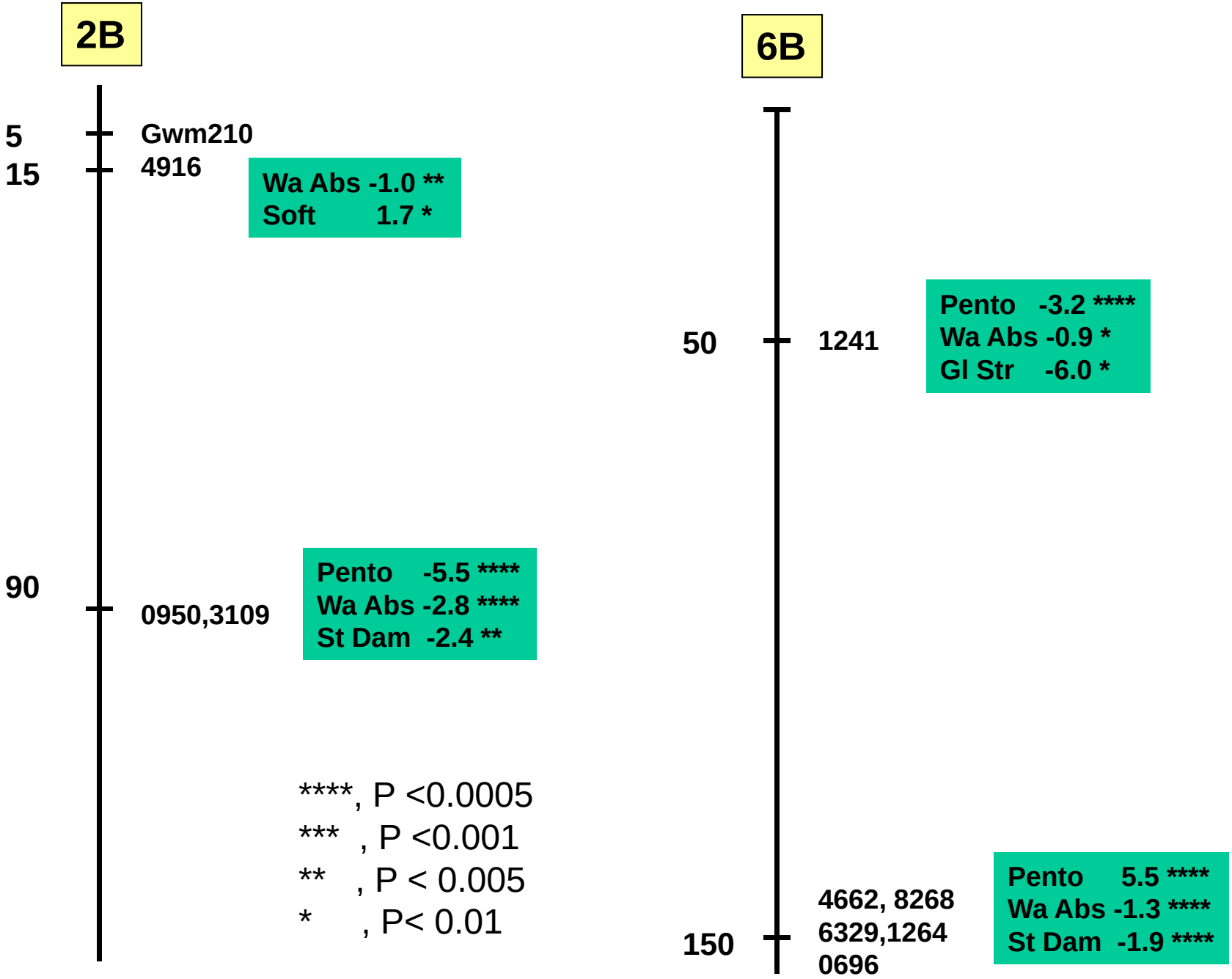
"Major" had a probability <0.0005


**** P < .0001
*** P < .0005
** P < .001
* P < .005
Chromosome 1B
Assoc.
Soft ***
Fl Pro ***
Glu Str ****
Fl Yld *
1B/1R
Glu-B1?
Fos/Kan
38
39
Fl. Pro
Glu Str
H2O
Starch
Pent
Fl Yld
Soft
No rye
No Glu-B1
911/922
29
25
1B/1R
?
USG/Jay
37
28
1B/1R
Bx7oe/
Fos/P25
25
23
28
SS5/P26
1B/1R
7+8/13+16

Chromosome 2B



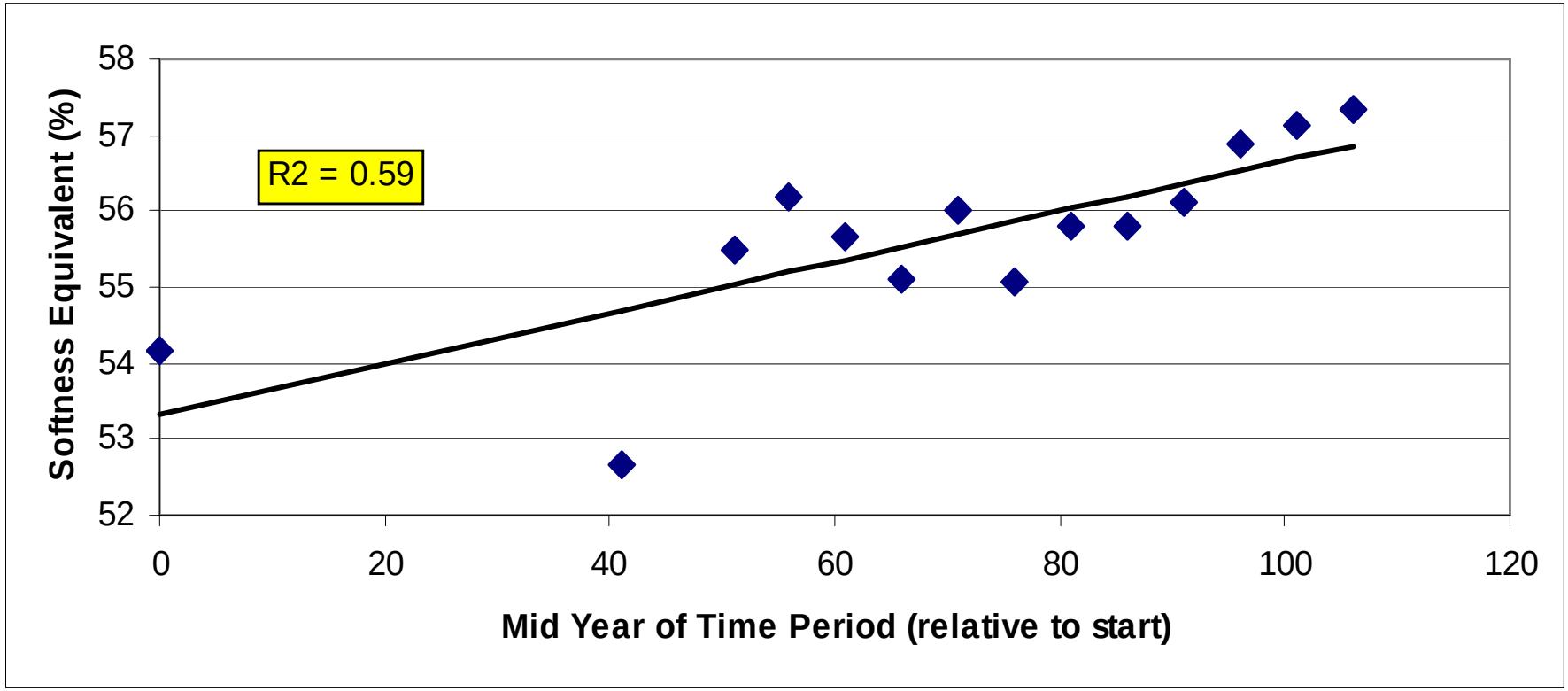

1A
Gli 1A
15
GluA3, 6358
6709, 7541
Pro -0.5 ****
Pento -4.1 **
Fl yld -0.7 **
40
3870
Fl yld -0.7 **
65
3698
Gl Str 4.7 **
Glu-A1
1B
Gli 1B
9
1781, 5312
GluB3
Gl Str -12.0 ****
Wa Ab -1.4 **
43
Glu-B1
Pro -0.7
70
0944, 2656
4129, 4532
Pento -4.8 ***
Fl yld 1.1 *
80
wmc44
****, P <0.0005
*** , P <0.001
** , P < 0.005
* , P< 0.01

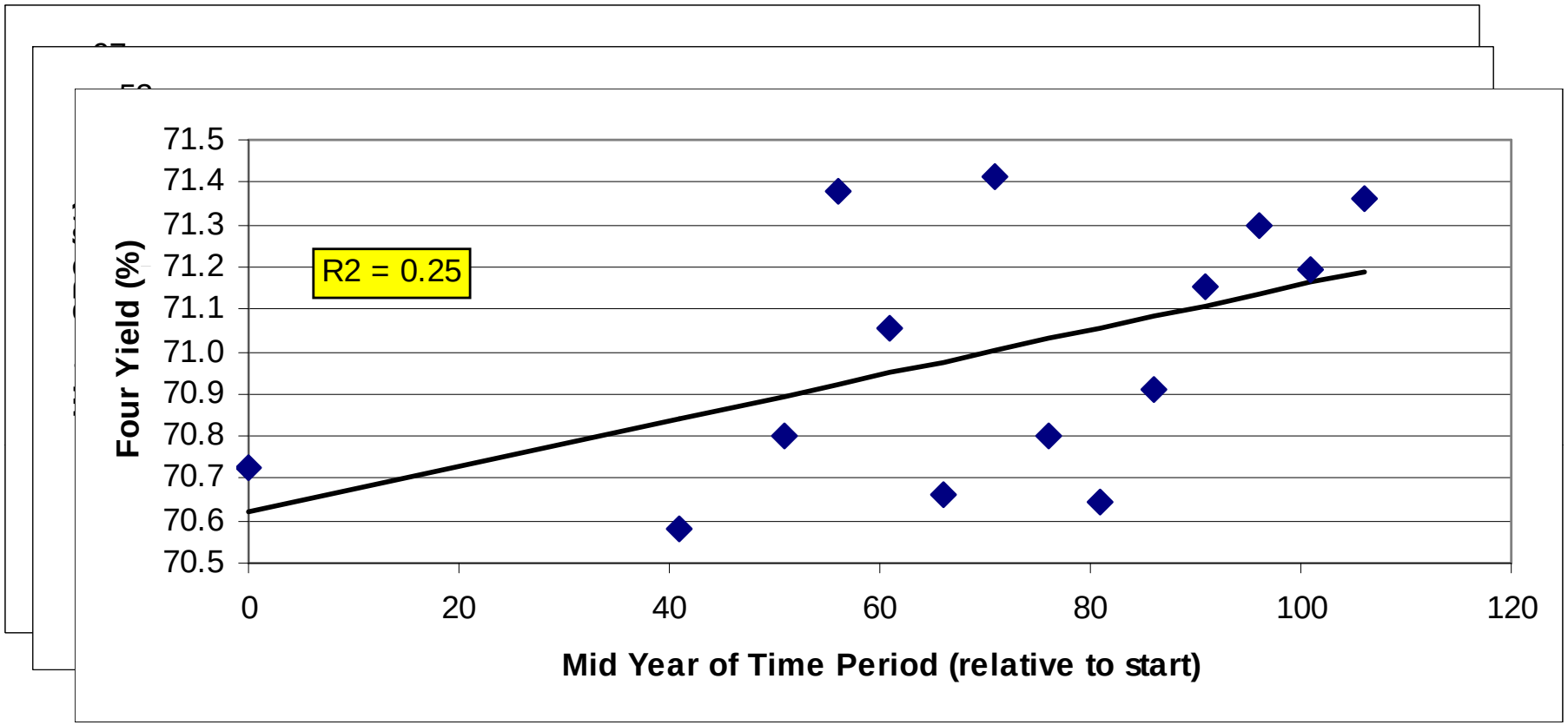

2B
5
15
90
Gwm210
4916
Wa Abs -1.0 **
Soft 1.7 *
Pento -5.5 ****
Wa Abs -2.8 ****
St Dam -2.4 **
0950,3109
****, P <0.0005
*** , P <0.001
** , P < 0.005
* , P< 0.01
6B
50
150
1241
Pento -3.2 ****
Wa Abs -0.9 *
Gl Str -6.0 *
4662, 8268
6329,1264
0696
Pento 5.5 ****
Wa Abs -1.3 ****
St Dam -1.9 ****

What We Know

- Traits are VERY Heritable
- Genetic variation is abundant
- Genes with large effects are identified
- “Fair” markers in place
- Great service labs (SWQL, SG Genotyping)

So Is Quality Getting Better?



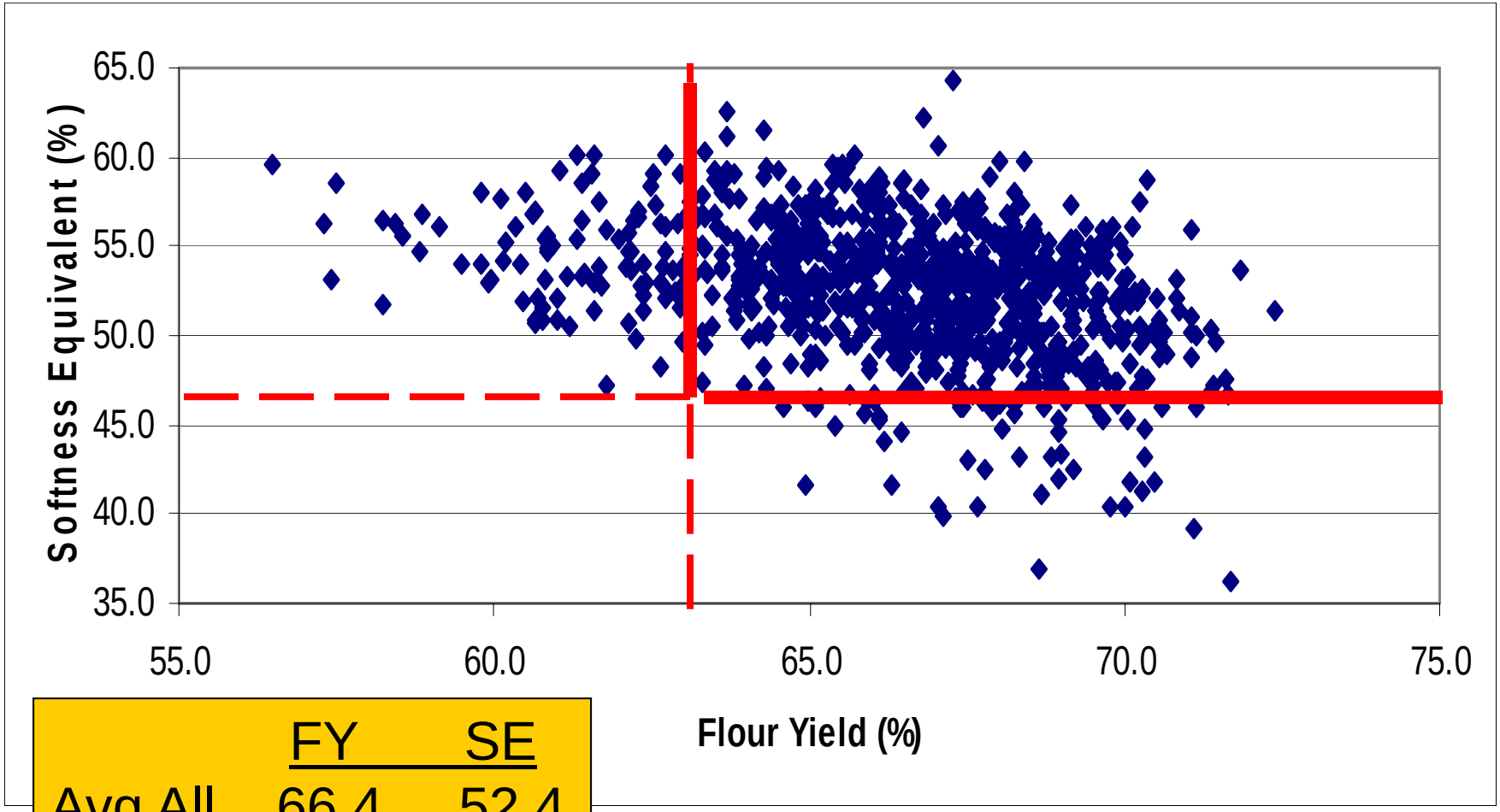


Much Greater Progress can Occur

Methodology, Markers, Motivation

- Parent Selection
  - Phenotypes Matter
  - Data Base
  - Marker profile of key genes
- Selection Pressure
  - Larger population sizes
  - Higher standards

SE and Flour Yield of 959 Lines



	FY	SE
Avg All	66.4	52.4
Avg Sel	67.3	53.8

Methodology, Markers, Motivation

- Marker-Assisted Selection
  - Better markers are needed
  - Routine, like FHB
  - In conjunction with MAS for other traits
  - Can increase selection pressure
  - Build marker-based selection index based on 1B and 2B (maybe 6B too)

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 many of the large effect QTL reported in the 6 biparental mapping pops
- MAS should be worthwhile for some QTL

QTL from Association Analysis Compared to QTLs from Biparental Crosses

Highly Significant DArT Associations

Type of Result	# QTL
AM and Biparental results were similar	**18**
AM and Biparental results were *NOT* similar	**6**
DArT location known, but poorly mapped in biparentals	**3**
DArT marker not assigned a location	**8**

Major (R2 > 20%) and Mid-Major (R2 > 10%) QTL from six biparental mapping populations from CAP program

Xsome	Trait	Bi-Part	AA		Xsome	Trait	Bi-Par	AA
IAS	Pro	0/5	***		2BL	Wa Abs	2/5	***
1AS	Soft	2/5	Not sig		**2BL**	**Soft**	**1/5**	*****
1AS	Wa Abs	2/5	*		3AL	Pro	0/4	**
1BC	**Gl Str**	**5/6**	********		3BC	Soft	0/4	*
1BC	**Wa Abs**	**3/6**	******		3BC	Wa Abs	0/4	**
1BL	**Wa Abs**	**2/2**	******		4AS	Soft	1/2	**
1BL	Gl Str	1/2	Not Sig		4AS	Pro	1/2	Not Sig
1DL	Gl Str	3/3	*		4BL	Gl Str	4/4	Not Sig
2AC	Pro	3/5	Not Sig		4BL	Pro	1/4	Not Sig
2AC	**Wa Abs**	**4/6**	******		**4DS**	**Wa Abs**	**2/3**	******
2BS	**Wa Abs**	**5/6**	********		**6BS**	**Wa Abs**	**1/4**	******
2BS	**Soft**	**3/6**	*******		6BS	Pro	0/4	*

R^2 (x100) of QTL on 1B near centromere

	Fo/K	Fo/25	S/26	Ja/U	9/9	Ca/C	AM
Protein							
Glu Strgth	38	32	37	31	12	10	****
Water Abs	5	12		19			*
Starch Dam				28			
Pentosans		22		25			***
Fl. Yield	12	30		9			*
Soft Eq.							

☐ = not significant

nm = no marker

****, P <0.0005

*** , P <0.001

** , P < 0.005

* , P< 0.01

R^2 (x100) of QTL on 2B Short Arm

	Fo/K	Fo/25	S/26	Ja/U	9/9	Ca/C	AM
Protein	25	24	19				
Glu Strgth		9		5			
Water Abs	18	2		11	9		****
Starch Dam	57†		7	11	10	12	**
Pentosans	17	24	8	7		8	****
Fl. Yield	27	16		8			
Soft Eq.	23	13			5		small

☐ = not significant

nm = no marker

† 90 lines

****, P <0.0005
***, P <0.001
**, P < 0.005
*, P< 0.01

Conclusions 2

- Significant associations were detected
- Structure likely not much of a problem, rare alleles are
- Known genes were validated
- Results of association mapping and biparental were *similar*:
  - All major QTL from bi-parentals were detected
  - Alignment is difficult, consensus ≠ agreement

Alignment of Other Large Effect QTL

	Fos/Kan	SS5/P26	USG/Jay	Fos/P25	911/922	Cay/Cal	Assoc. An.
4D	No Markers	No Markers	**Fl Pro 20%** 4DL	Non-Sig	Non-Sig	**Fl Pro19%** 4DS	Non-Sig
5AS	**Soft 19%**	No Markers	Fl Pro 6%	No Markers	**Soft 12%**	No Markers	Non-Sig
5B	No Markers	No Markers	**Fl Yld 19%**	Non-Sig	No Markers	Non-Sig	**Pentos **** **H2O *** **Fl Yld ***
6AS	Non-Sig	No Markers	Non-Sig	No Markers	No Markers	Non-Sig	**Starch *****
6BC	Non-Sig	**Pentos 22%** **H2O 27%** Starch 13% Fl Yld 8%	No Markers	Non-Sig	Non-Sig	No Markers	**Pentos ****** H2O ** **Glu Str ******
7B	Non-Sig	No Markers	**Pentos 12%** **H2O 12%** **Soft 17%**	No Markers	**Fl Pro 17%** **Glu Str 11%** **Pento 12%**	No Markers	**Pentos ***** **Glu Str *** **Fl Pro ***

Ed’s Table of effects

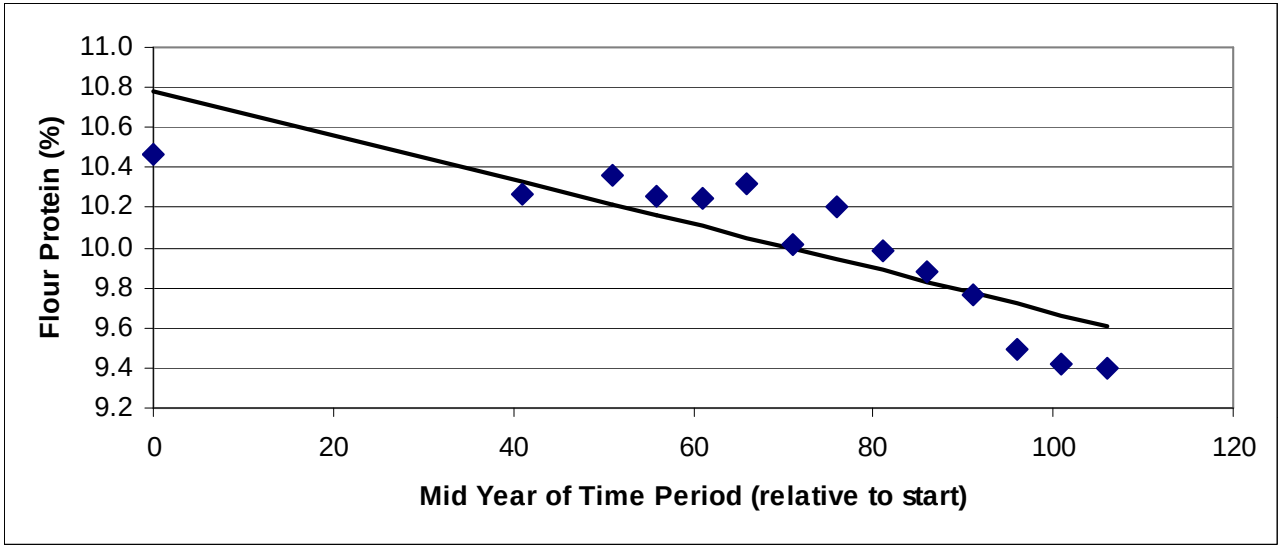
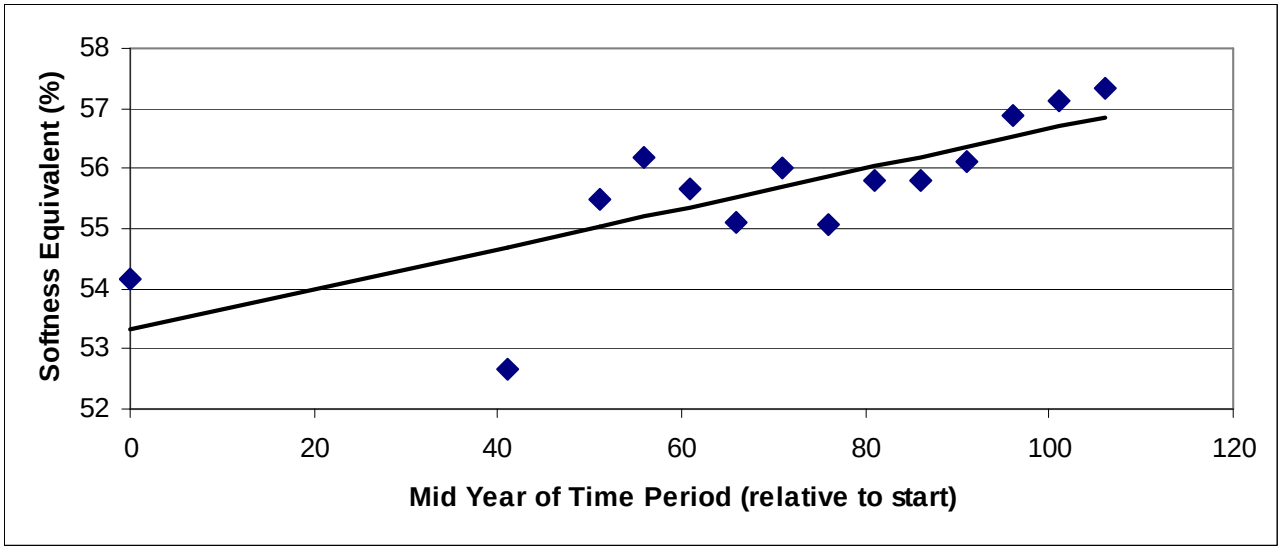
Marker	Origin	Type of gene	FPRO	WATER	NACO	SUC	LA	LAADJ	SE	FYLD	CDIA	TG
Barc07	Sr36	Disease										
FHB1	umn10Fd	Disease										
Glu1D		Functional	5.4*				12.2***	9.7**	6.1*			
gwm261Nd	Rht 8	Functional		3.8*	5.7***	2.9*						
Rht*	Rht1&2	Functional	71.2***			4.6*	6.3*		19.2***		24.4***	23.4***
Ppd1-2D	Ppd	Functional	15.2***									
1B/1R		Functional		4.5*			11.0***	11.0***				
gwm312	SSxP	QTL										
Barc17	FxKQ	QTL								2.8*		

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 2B effects

Phenotypic Changes over Time

Protein



Softness Equivalent