

Keeping Barley Competitive Through Research

Genomics and Breeding



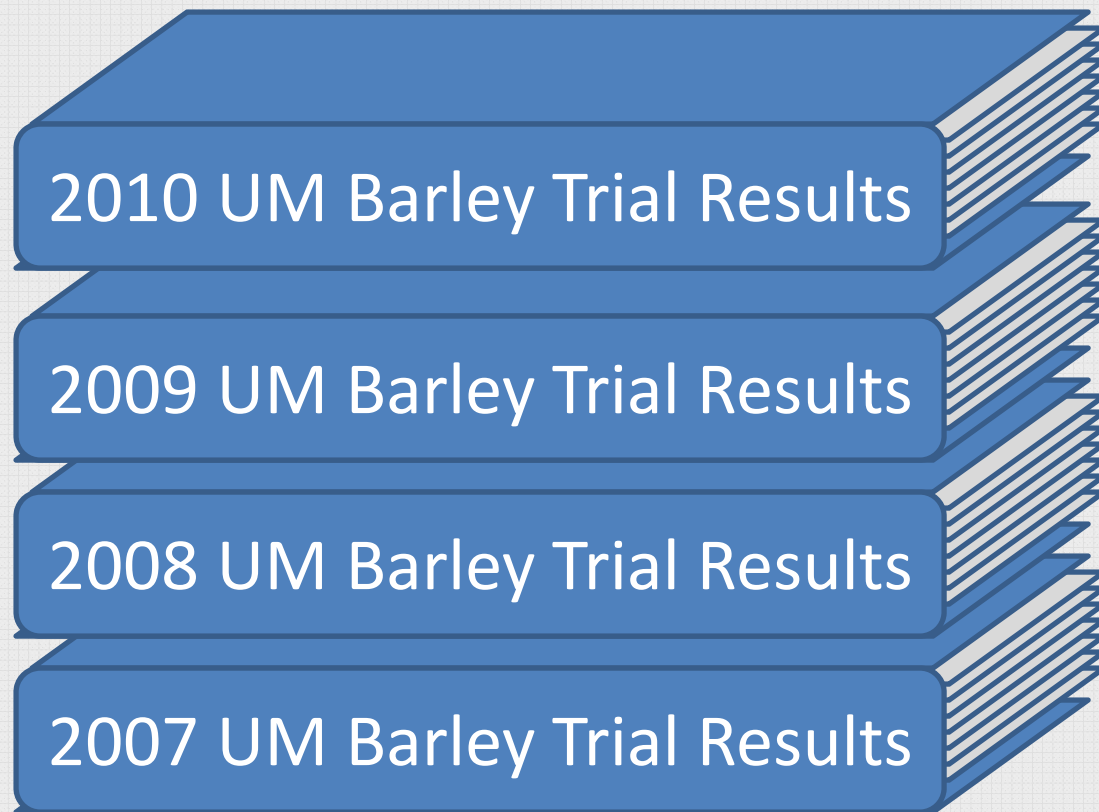
American
Malting
Barley
Association

Kevin Smith University of Minnesota

**2011 Barley Improvement Conference
and Barley CAP Meeting**



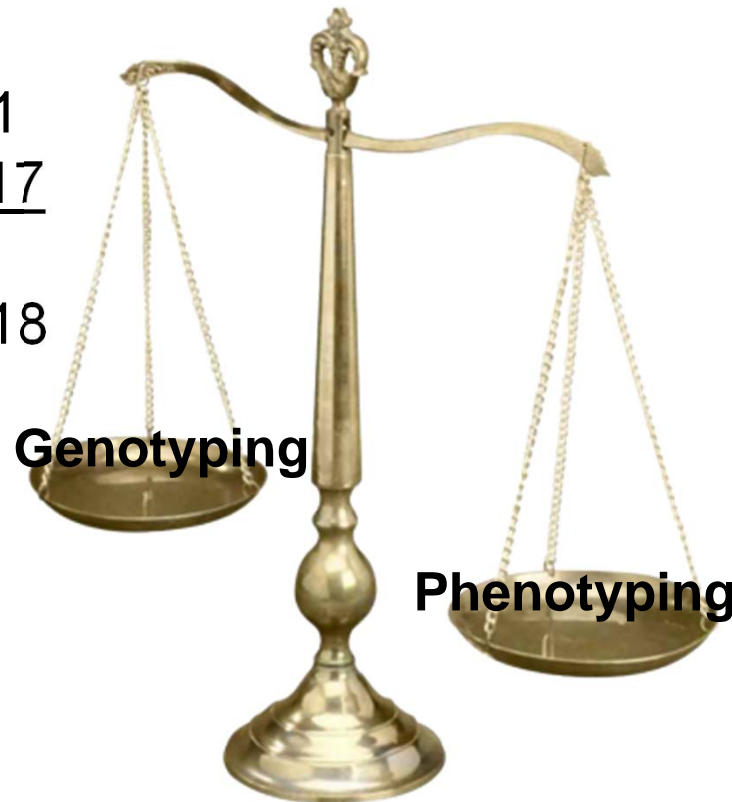
In plant breeding the rate of progress is influenced by trade-offs between speed and accuracy.



Data Costs

Entry 384 SNP

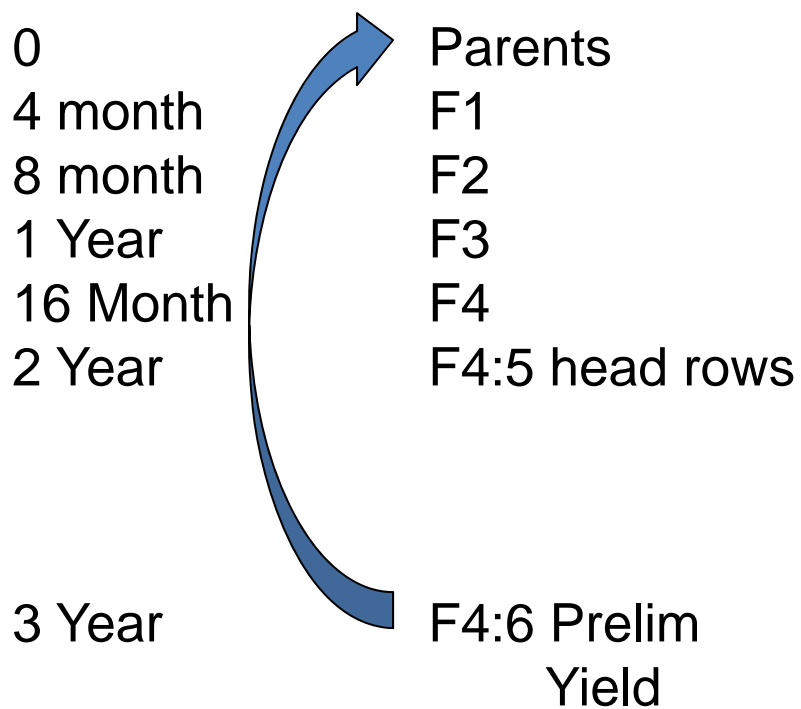
Sample Prep	\$1
<u>Reagents</u>	<u>\$17</u>
Total	\$18



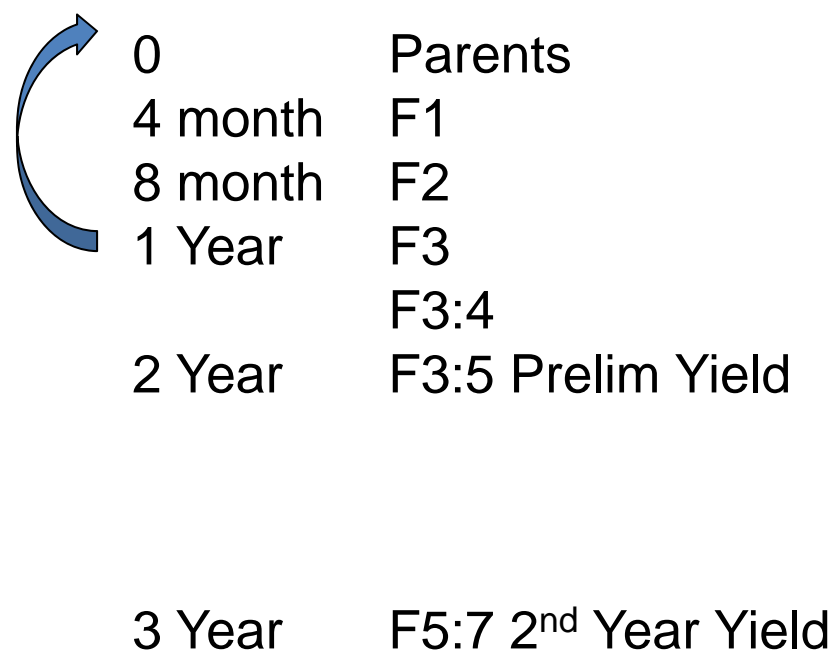
Entry in Single Trial

Yield	\$50
FHB	\$10
Toxin	\$15
<u>Malt Quality</u>	<u>\$100</u>
Total	\$175

Current Breeding Scheme



Genomic Selection Scheme

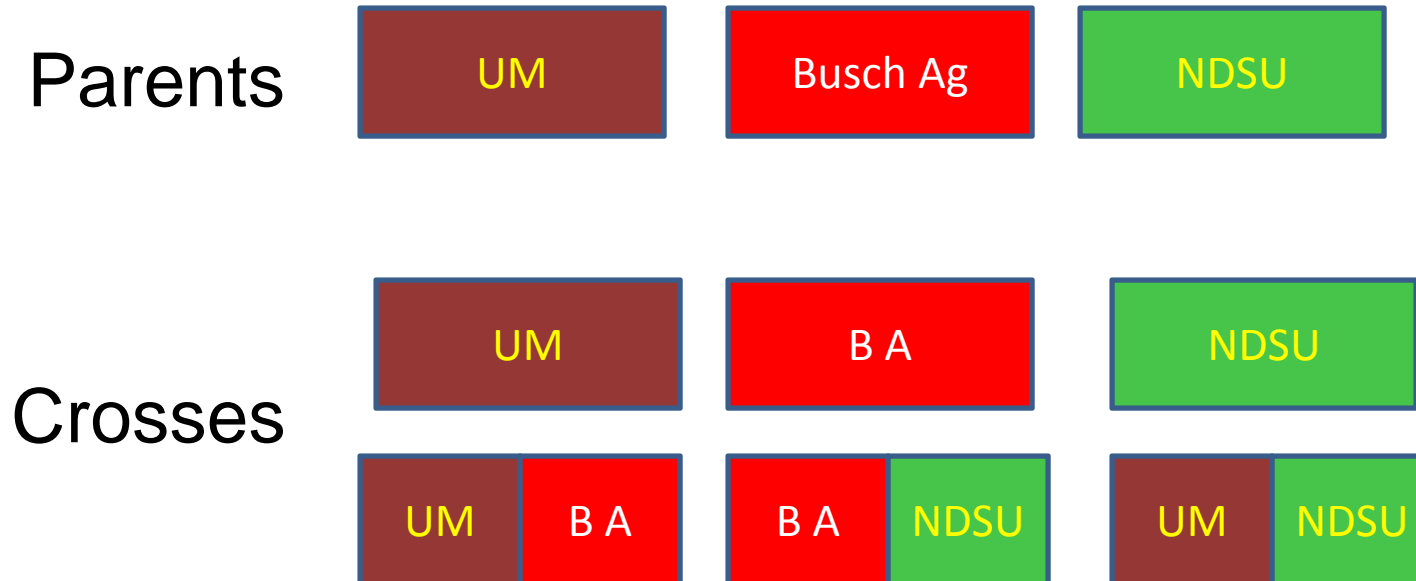


Selection Accuracy for Phenotypic and Genomic Selection

Trait	Heritability	Phenotypic Selection		Genomic Selection
		Check Correlation	PAR Line Correlation	Cross-Validation
Heading Date	0.88	0.95	0.57	0.47
Plant Height	0.87	0.83	0.68	0.72
Yield	0.46	0.44	0.26	0.37



FHB Genomic Selection Project



1440 progeny = 6 cross types x 10 crosses per type x 24 progeny per cross

384 SNPs selected from BOPA1&2 optimized for PIC and genome distribution

Training Data set CAPI, II, II from three programs

Ridge Regression

Shiaoman Chao, Jean-Luc Jannink, Aaron Lorenz,
Rich Horsley, Blake Cooper, Gary Hanning,

GS predicted values for 11 traits on 1920 breeding lines

Lacey	-2.38	4.69	6.42	0.08	-117.00	-5.87	-0.22	0.09	-5.68	0.18	3.56	406.87	727.84
Quest	-17.76	-4.65	-1.04	2.04	36.25	11.35	0.51	0.06	-2.10	8.96	1.13	226.05	643.40
Tradition	-10.32	7.54	5.49	9.01	-141.00	37.33	-0.02	-2.01	-4.59	2.94	4.55	569.52	1330.14
MIN	-26.62	-11.43	-4.82	-10.49	-203.16	-29.51	-1.82	-1.87	-8.90	-4.88	-0.36	-292.99	-96.17
MAX	7.11	15.47	9.54	24.54	62.29	55.02	1.30	2.53	6.44	21.87	14.29	930.77	1391.64
AVE	-9.05	0.51	1.49	8.61	-63.01	10.09	0.09	0.15	-1.48	9.38	5.01	362.50	699.00
	Freq Wt												
x	DON_f	DON	FHB	Aa	Bg	Dp	protein	hd	ht	plump	st	yield	yield_f
G10W037.06	-26.036785	-11.43	-0.08	12.36	-87.88	4.28	-0.57	-1.04	1.08	7.67	8.15	-80.55	231.04
G10W037.05	-12.634535	-2.05	4.48	15.75	-34.40	-12.60	-1.09	-0.74	-1.21	11.55	13.24	5.52	310.02
G10W037.04	-20.93098	-6.54	2.63	12.06	-61.65	6.66	-0.43	-1.04	0.50	1.84	9.81	-267.73	36.12
G10W037.03	-13.563582	-4.89	0.34	17.90	-144.02	26.45	0.59	-0.71	1.65	9.15	8.53	160.00	489.49
G10W037.02	-12.336345	-2.07	2.80	14.67	-8.61	-6.75	-0.34	-0.84	-0.26	7.73	9.87	53.24	366.61
G10W037.01	-12.814291	-5.68	0.05	10.35	-50.78	-11.23	-0.13	-1.25	-0.78	4.36	9.31	78.35	302.92
G10W036.24	-3.2181708	6.09	5.28	8.30	-127.83	12.26	-0.15	-0.80	-5.54	9.28	5.60	823.17	1360.76
G10W036.23	-7.0848412	2.42	2.56	1.89	-59.88	12.59	0.23	-0.89	-3.85	12.20	3.46	598.09	1073.40
G10W036.22	-1.5979616	6.53	5.61	13.03	-136.51	18.48	-0.35	-0.65	-6.43	6.31	6.86	814.85	1291.78
G10W036.21	-9.1445027	-1.30	3.58	9.66	-85.16	23.14	0.04	-0.46	-6.59	5.41	3.64	408.84	654.13
G10W036.20	-5.1177605	2.77	4.06	9.25	-44.29	13.89	0.22	-0.45	-4.70	5.71	3.58	509.14	879.92
G10W036.19	-15.336236	-4.11	-0.48	6.11	-28.36	27.26	0.92	-0.34	-1.25	8.98	1.29	331.65	632.44
G10W036.18	-5.4771292	2.48	3.91	6.87	-52.88	23.73	0.26	-0.77	-4.12	11.92	3.21	477.44	811.91
G10W036.17	-2.5725907	6.00	6.66	8.70	-150.35	23.64	-0.35	-0.88	-6.77	6.63	4.33	723.18	1194.45
G10W036.16	-9.4996327	0.69	1.96	4.86	-45.28	14.34	0.67	-0.41	-4.11	7.18	2.43	382.44	736.38

What resources do we have to support implementation of GS?

- **Marker platform** - 3K BOPA1&2, new 9K SNP assay
- **USDA Regional Genotyping Centers** – Fargo, Raleigh, Pullman, Manhattan
- **Trait and Marker Database** – THT, *developing T3*
- **User friendly modeling tools** – TASSEL (Ridge Regression)
- **Phenotyping Capacity** – breeding trials, regional nurseries, disease trials, USDA quality lab, DON testing labs

What do we need to support implementation of GS?

- Continue to expand, improve phenotyping
- Coordinated phenotyping efforts to feed the database
- Long term support for database maintenance and development.
- Breeders analysis toolbox (T3)
- Empirical and simulation-based evaluation of GS strategies and approaches for a wide range of traits, regions, germplasm.