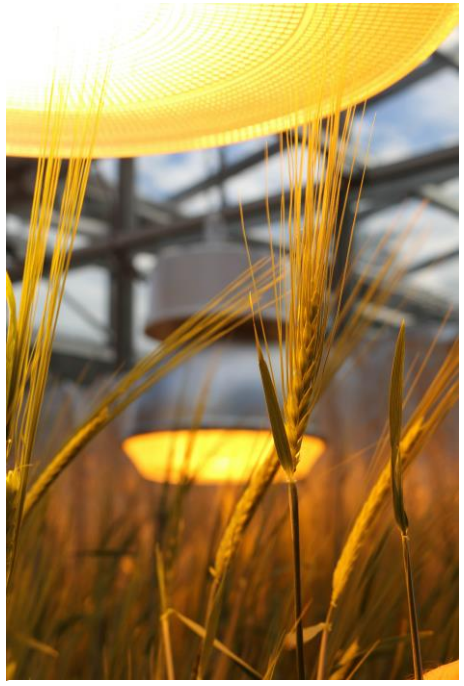
Accelerating wheat breeding for end use quality with multi-trait genomic predictions incorporating near infra red and nuclear magnetic resonance derived phenotypes

Ben Hayes, Joe Panozzo, Cassandra Walker Ai-Ling Choy, Surya Kant, Debbie Wong, Josquin Tibbits, Hans Daetwyler, German Spangenberg, Matthew Hayden



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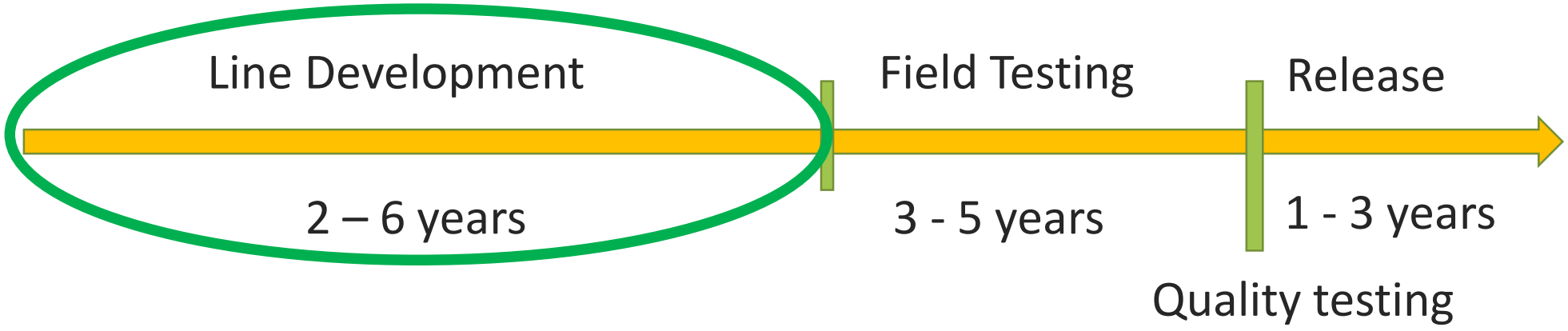
Traditional breeding pipeline for new wheat cultivars



Need to accelerate development of improved cultivars

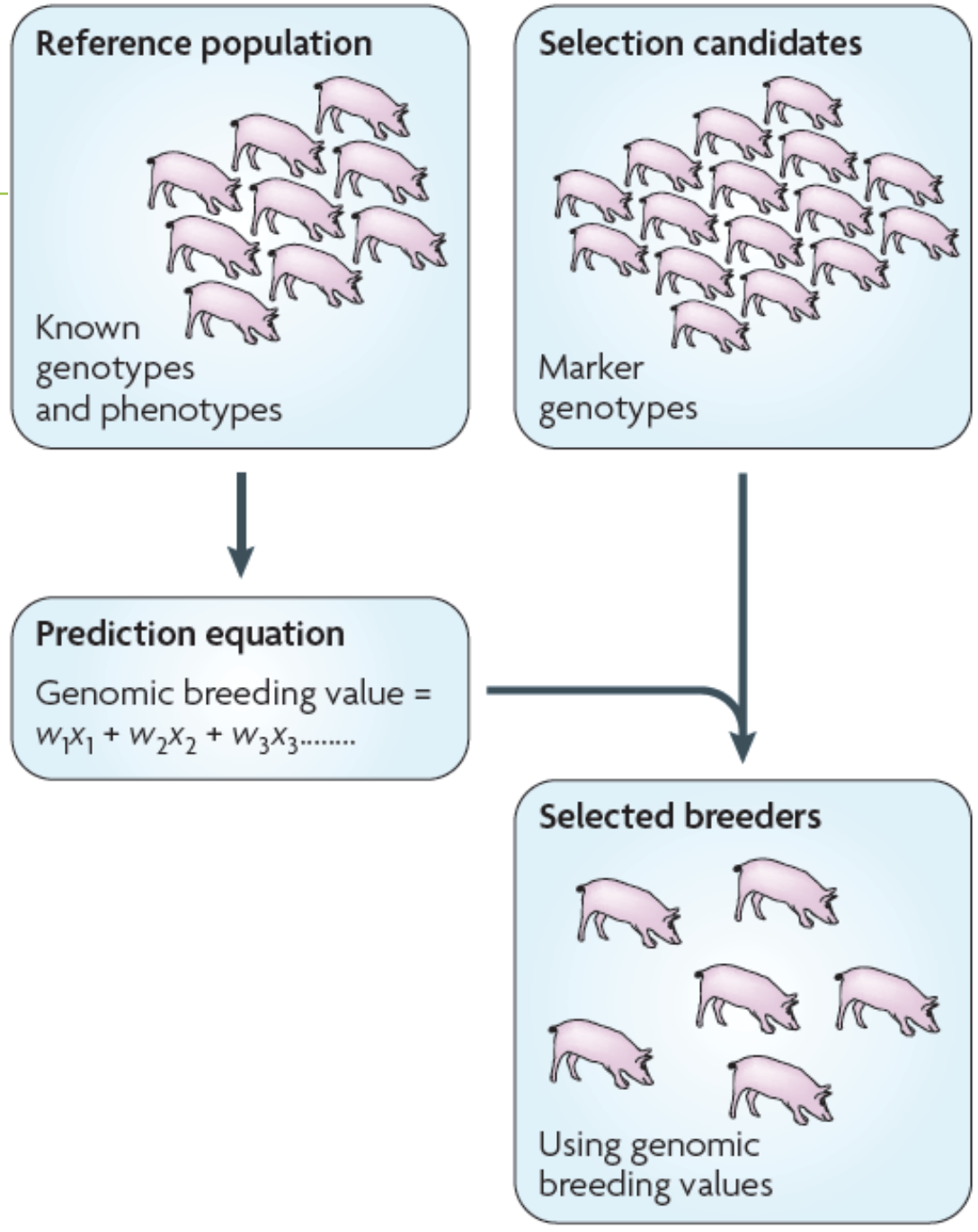
End use quality traits among most important in wheat breeding

Difficult to breed for, as assays require flour quantities that can only be obtained late in the breeding cycle, and are expensive

Ideal target for **Genomic Selection**

Genomic selection

Large reference populations ('000s of lines) required for accurate genomic selection



Genomic selection for end use quality

- Challenging to assemble reference populations for end use quality, given cost of assays, and need for large amounts of flour

- Can we use proxies?
  - Near Infra Red (NIR) derived phenotypes
  - Nuclear Magnetic Resonance (NMR) derived phenotypes

- And measured on small amounts of flour, in a large number of lines

Genomic selection for end use quality

- Reference population with phenotypes on both real end use quality assays and NIR/NMR predictions

- How to analyse, genetic correlations between real trait and NIR/NMR trait might be <1 ?
- Multi-trait approach

Treat industry end use assay and NIR/NMR derived phenotype for this trait as different, but potentially correlated traits

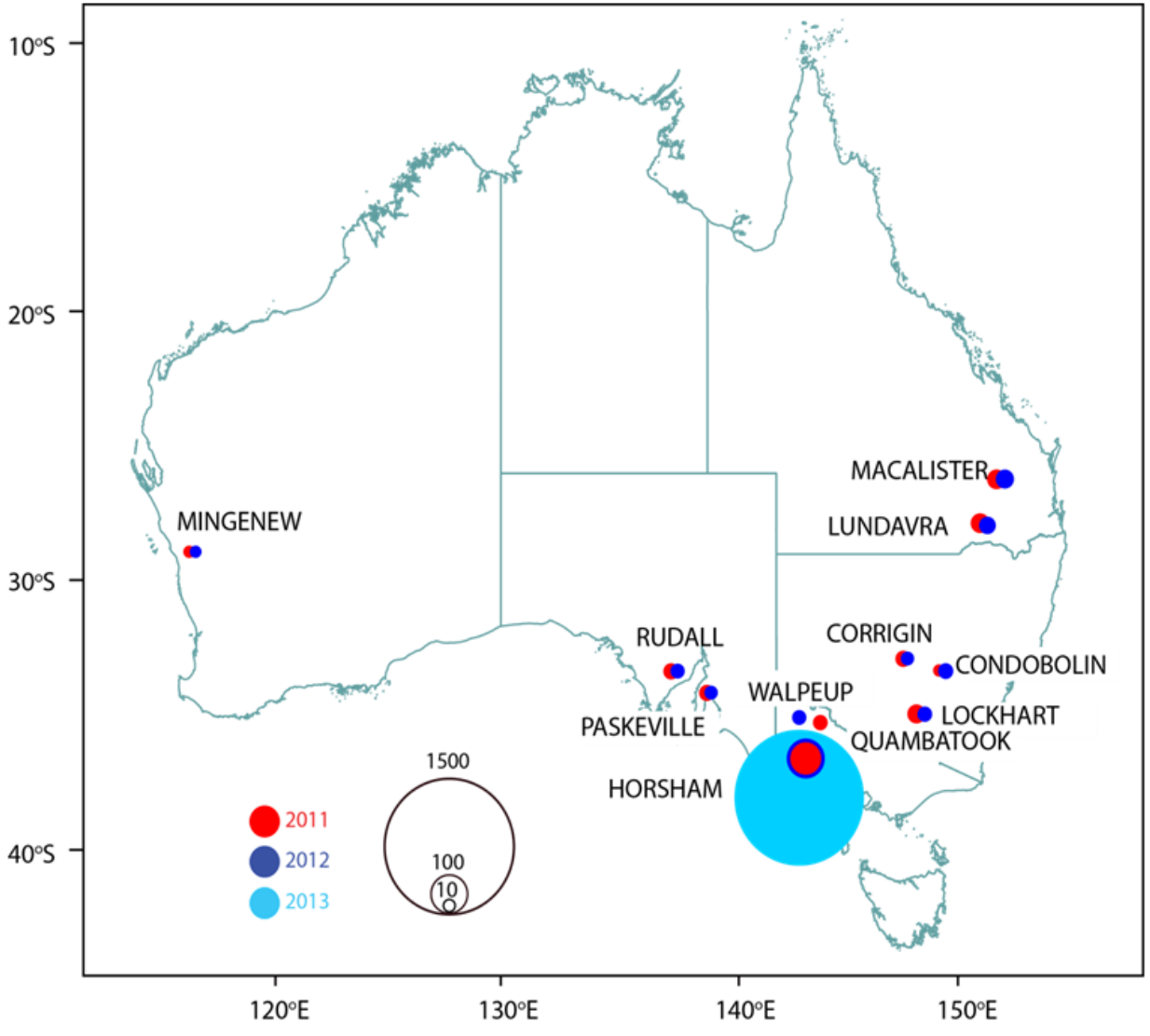
Genomic selection for end use quality

- Reference population with phenotypes on both real end use quality assays and NIR/NMR predictions
- How to analyse, genetic correlations between real trait and NIR/NMR trait might be <1 ?
- Multi-trait approach
- **Aim:** Assess accuracy of genomic prediction for end use quality (19 traits) using multi-trait approach

Reference populations

- 2420 bread wheat accessions (hard and soft wheats) from
  - Australian released varieties from the Australian Winter cereal collection with known grain quality and end use characters,
  - Breeding germplasm,
  - A number of synthetic derivatives
- In 2011-12, 920 accessions grown in under rain-fed field conditions at Horsham, Victoria, Australia.
- In 2013, 1,500 accessions grown under irrigated and rain-fed conditions
- Released varieties grown in National variety trials
  - The NVT trails included multiple evaluation sites across Australia.

Reference populations



Reference populations

- 398 accessions with industry end use quality assays
- All 2420 with NIR/NMR derived phenotypes
- All genotyped Illumina 90K SNP array, used 51,208 SNP

Reference populations

		NIR R^2	NMR R^2
Grain traits			
	Test Weight (Kg/hL)	0.67	0.75
	Grain Protein (%)	0.96	0.90
	Grain Hardness (PSI)	0.86	0.80
Milling traits			
	Milling Yield (%)	0.49	0.77
	Ash (%)	0.53	0.73
	Starch Damage (%)	0.85	0.84
	Flour brightness (L*)	0.83	
	Flour colour (a*)	0.85	
	Flour colour (b*)	0.90	

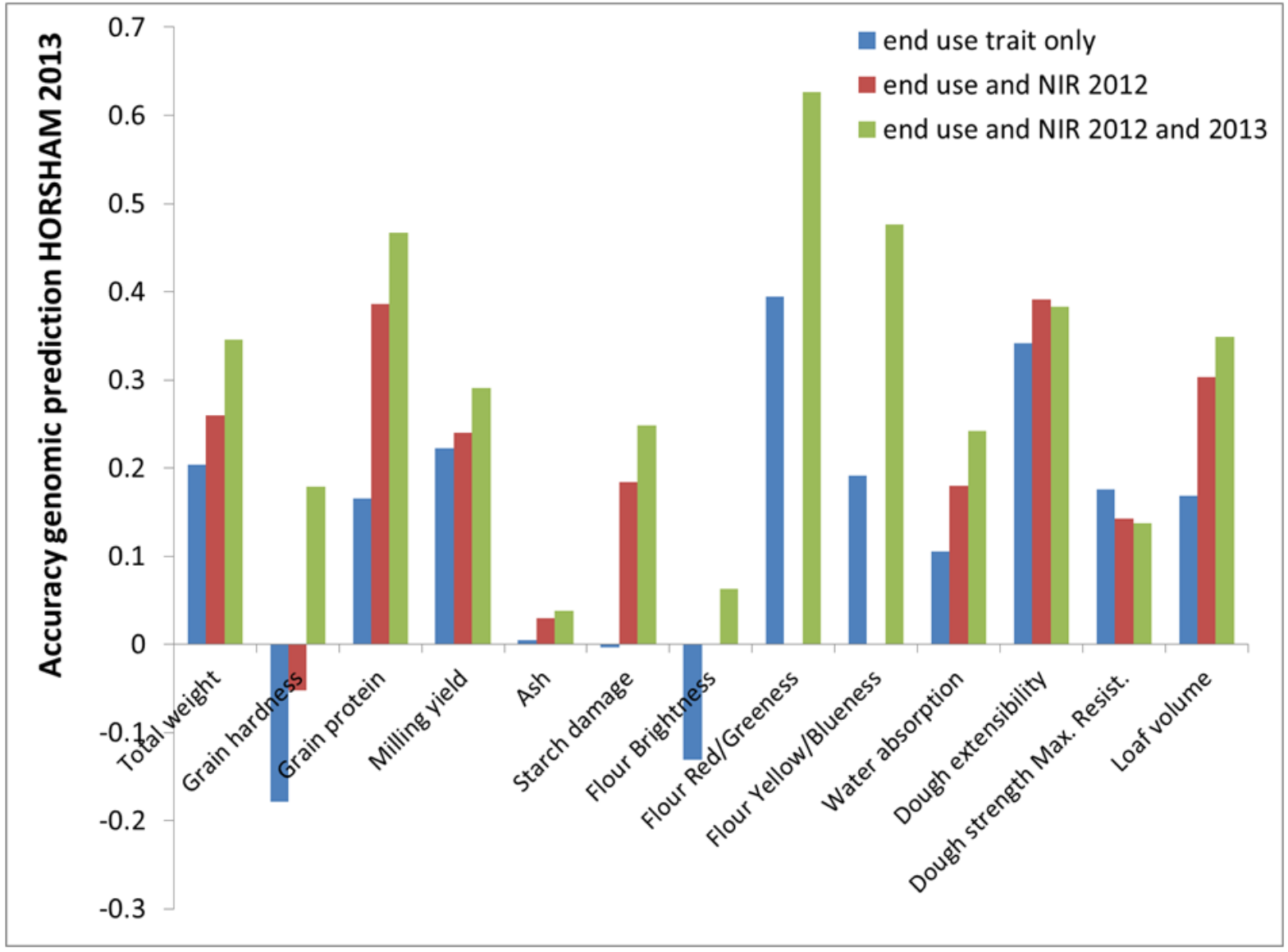
Reference and validation populations

	NIR R^2	NMR R^2
Dough rheology		
Water Absorption (%)	0.68	0.80
Extensibility (cm)	0.71	0.74
Maximum Resistance (BU)	0.62	0.69
Baking traits		
Loaf Volume (mL)	0.62	0.73

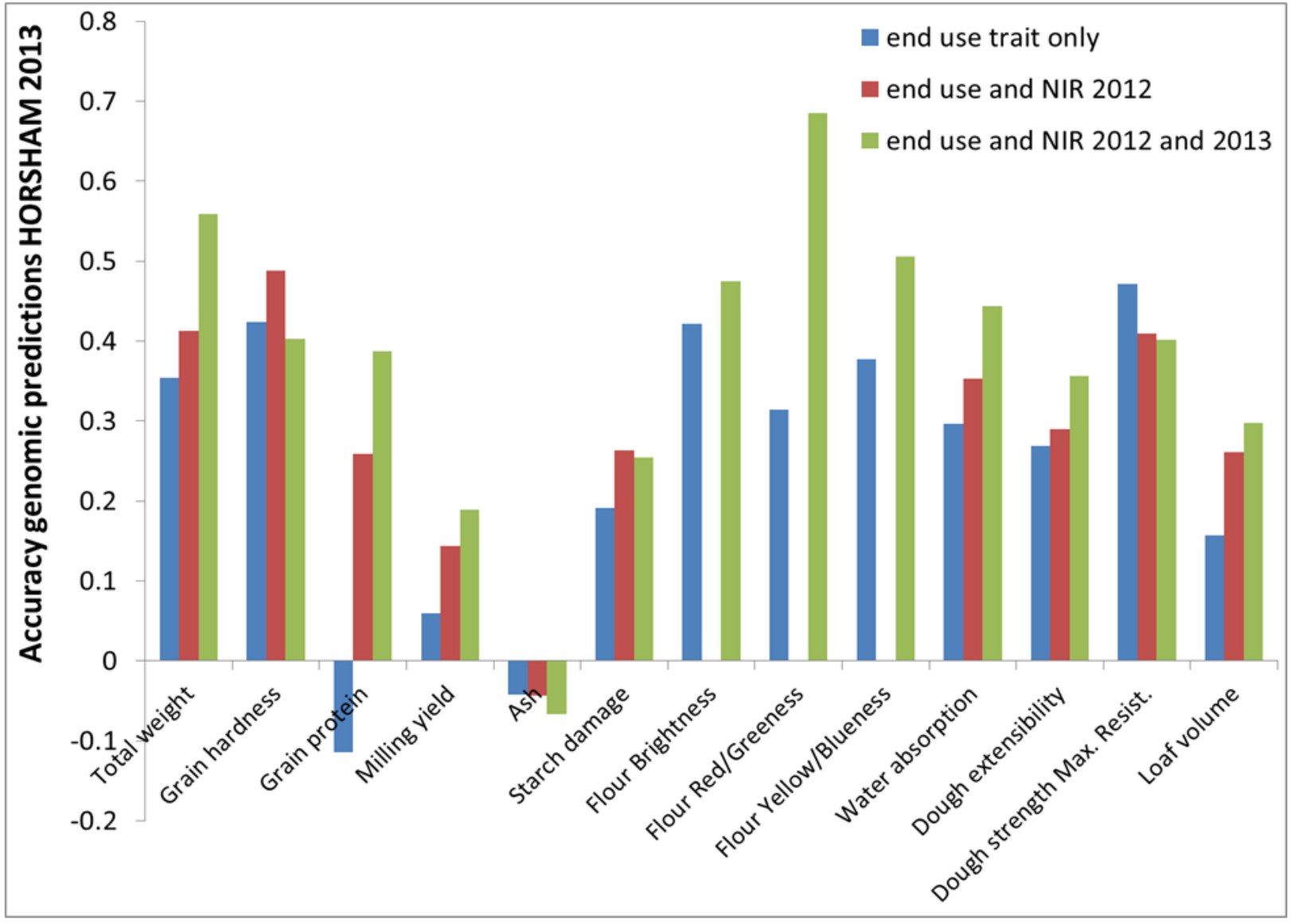
Genomic predictions

- Genomic BLUP
- Multi-trait: treat industry end use assay and NIR/NMR derived phenotype for this trait as different, but potentially correlated traits
- **Validate against industry end use assay trait**
- Validation population -> Horsham 2013, 116 Accessions
- Separately for hard wheats (n=74) and soft wheats (n=42)

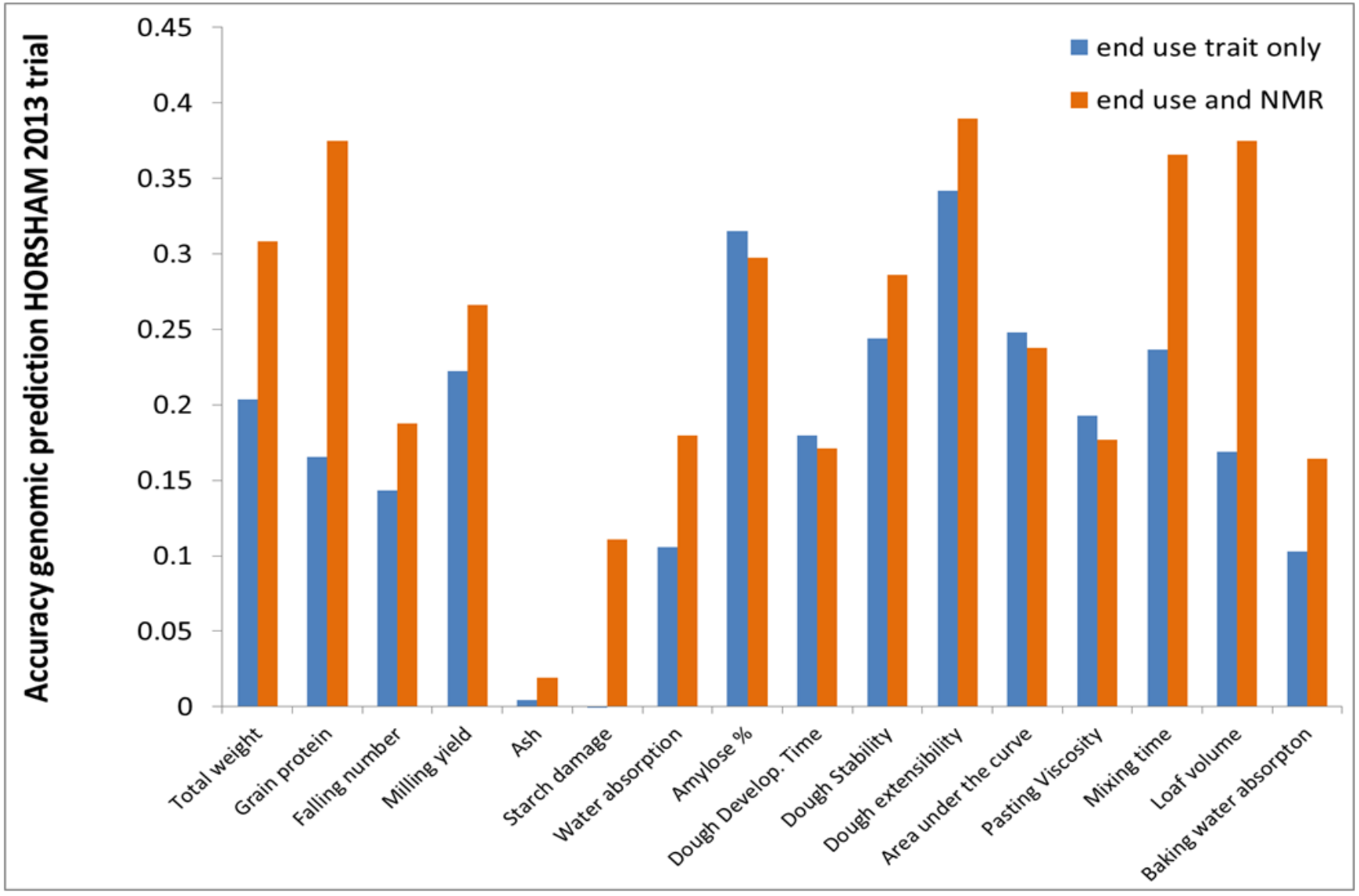
Results – hard wheats NIR



Results – soft wheats NIR



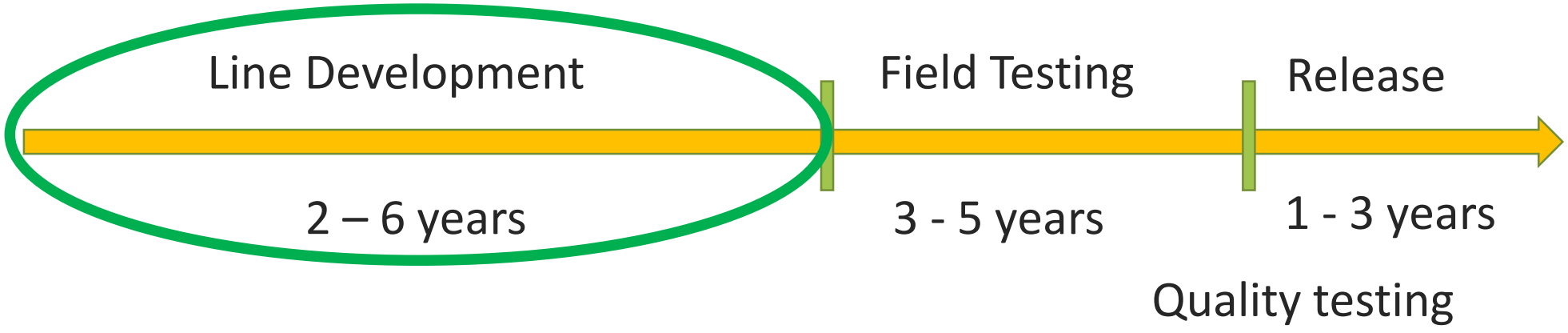
Results – hard wheats NMR



Results – accuracy of predictions

	Traits used in prediction			
Traits	**End use assays only**	**End use assay and NIR**		**End use assay and NMR**
		2011-2012	2011-2012-2013	
Grain traits	0.14	0.21	0.39	0.34
Milling traits	0.10	0.14	0.16	0.12
Dough rheology traits	0.28	0.29	0.33	0.29
Baking traits	0.20	0.28	0.32	0.35

Traditional breeding pipeline for new wheat cultivars



Increase rates of gain for end use quality traits

Remove lines early that will fail quality tests

$$R_t = \frac{ir_{\sigma_A}}{y}$$

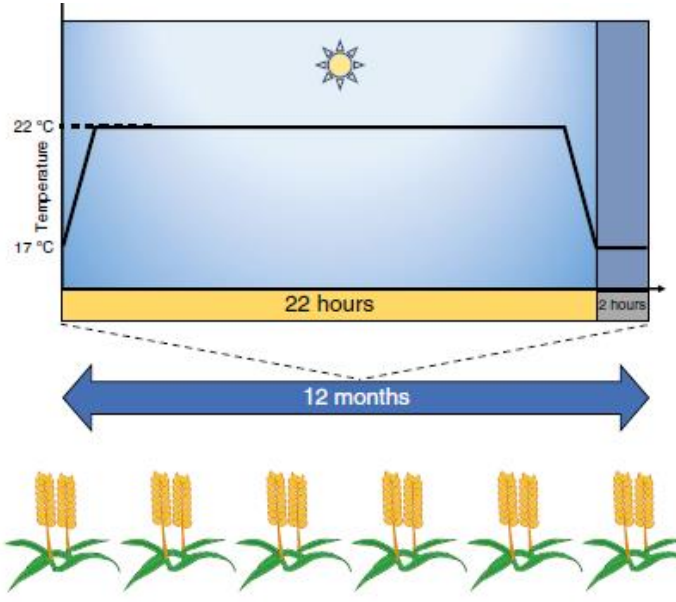
selection intensity
selection accuracy
genetic variance
genetic gain over time
years per cycle

Speed Breeding (University of Queensland)

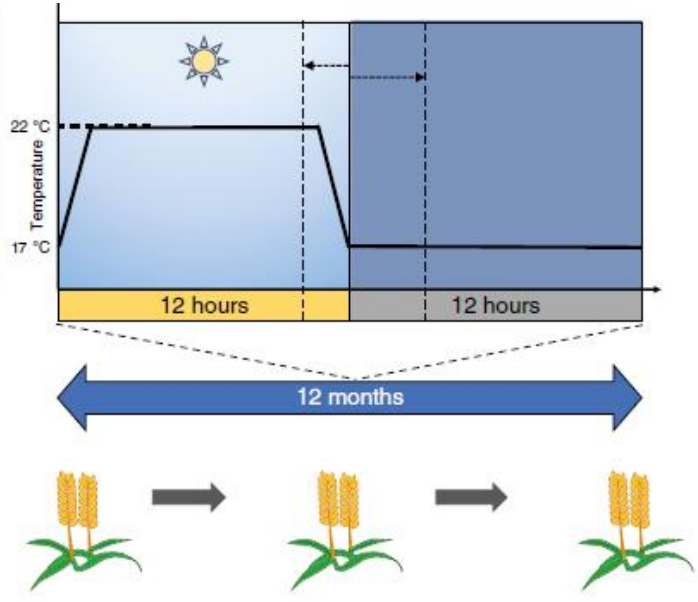
Watson and Ghosh et al. (2018)
Nature Plants **4**, 23–29

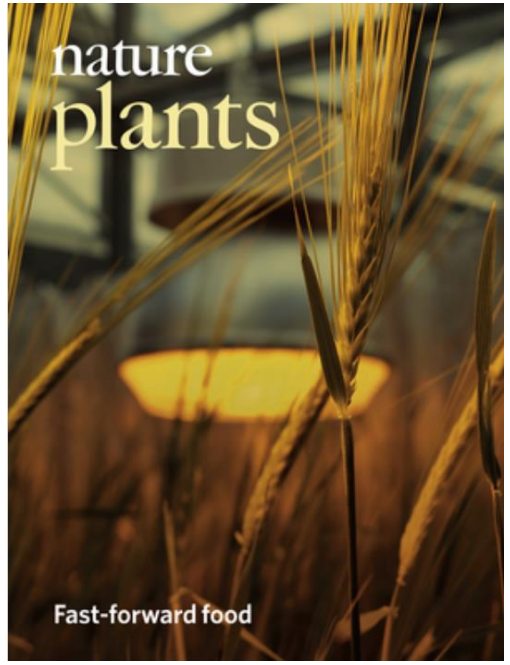
Wheat

Speed Breeding



Glasshouse control





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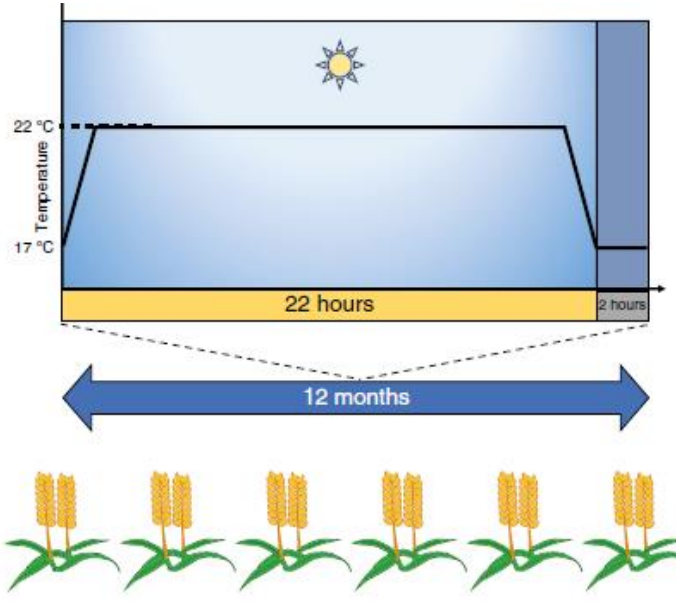
Speed Breeding



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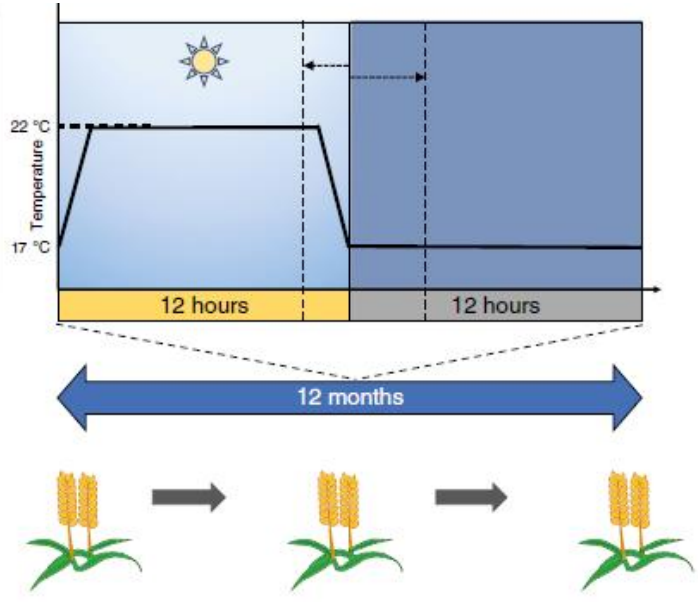

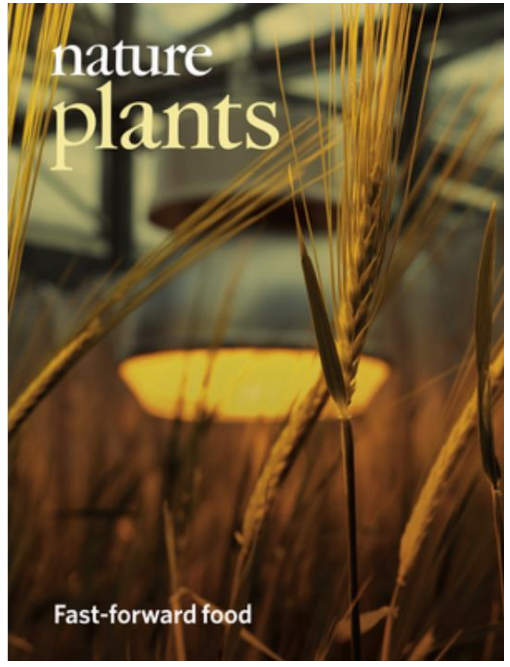

Genomic selection + speed breeding
= double rates of gain for end use quality traits

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Conclusion

- Large reference populations for end use quality traits can be assembled with NIR/NMR derived phenotypes
  - overcomes costs, amount of flour required restraints
- Multi-trait approach takes into account correlation between end use assay and NIR/NMR phenotype < 1
  - Produces genomic breeding values for end use assay, but uses information from NIR/NMR predictions
- Use genomic breeding values to screen out lines that will fail quality testing early
- GS + speed breeding to double rate of gain for end use quality traits

Acknowledgements

Co-authors
Joe Panozzo, Cassandra Walker Ai-Ling Choy, Surya Kant, Debbie Wong, Josquin Tibbits, German Spangenberg, Hans Daetwyler, Matthew Hayden

Results – correlation end use assay, NIR/NMR trait

Trait	NIR	NMR
Test Weight	0.79	0.69
Grain Hardness	0.79	
Grain Protein Content	0.81	0.64
Milling yield	0.35	0.77
Falling Number		0.58
Starch Damage	0.69	0.44
Flour Brightness	0.74	
Flour Red/Greeness	0.88	
Flour Yellow/Blueness	0.89	
Amylose percentage extracted starch		0.43
Water absorption	0.59	0.44
Extensibility	0.39	0.85
Area under the curve		0.98
Pasting Viscosity		0.45
Maximum Resistance	0.20	
Mixing time		0.62
Loaf Volume	0.57	0.77