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Breeding for an "ideal" Milling Oat: Challenges and Strategies

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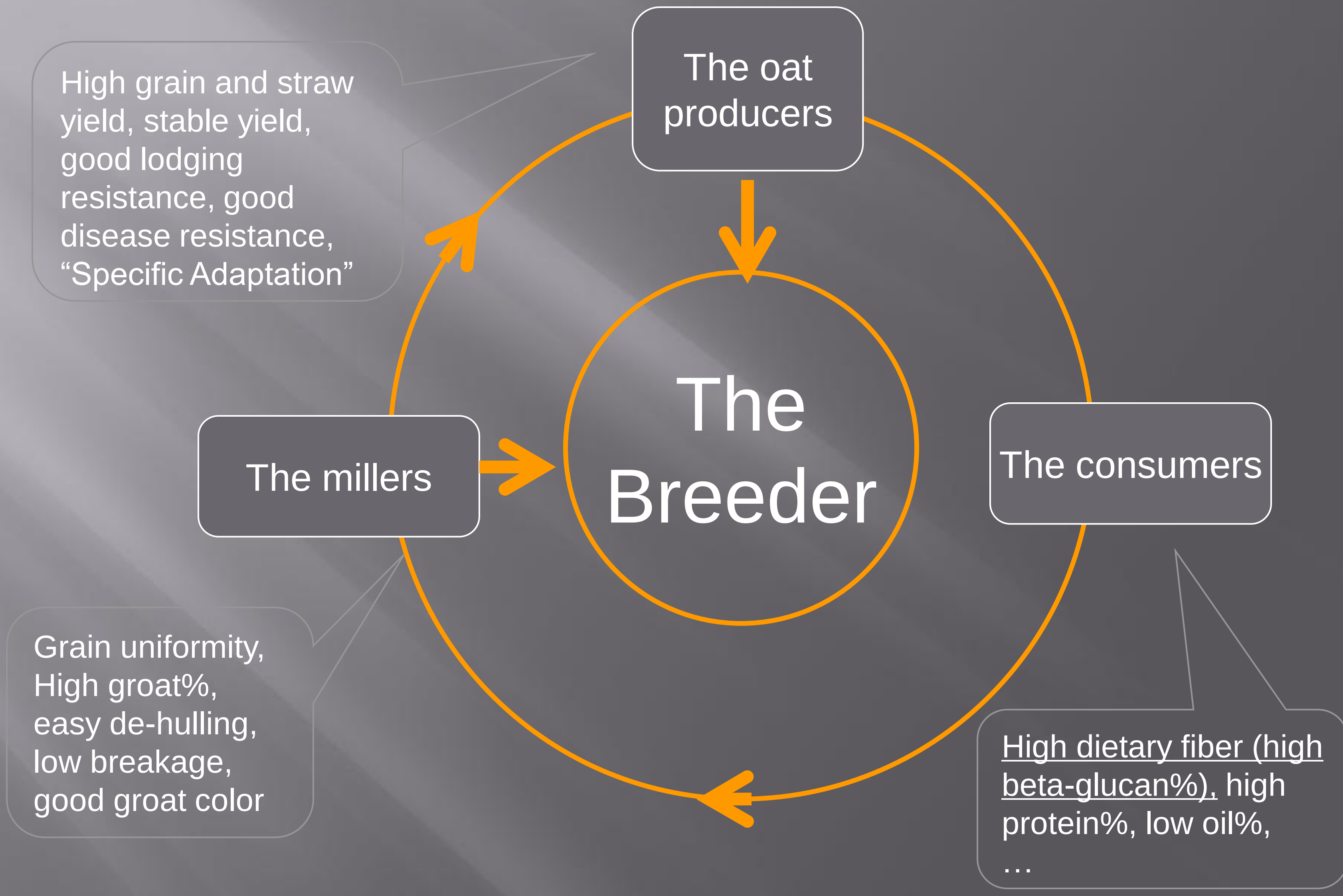
What makes an ideal milling oat?



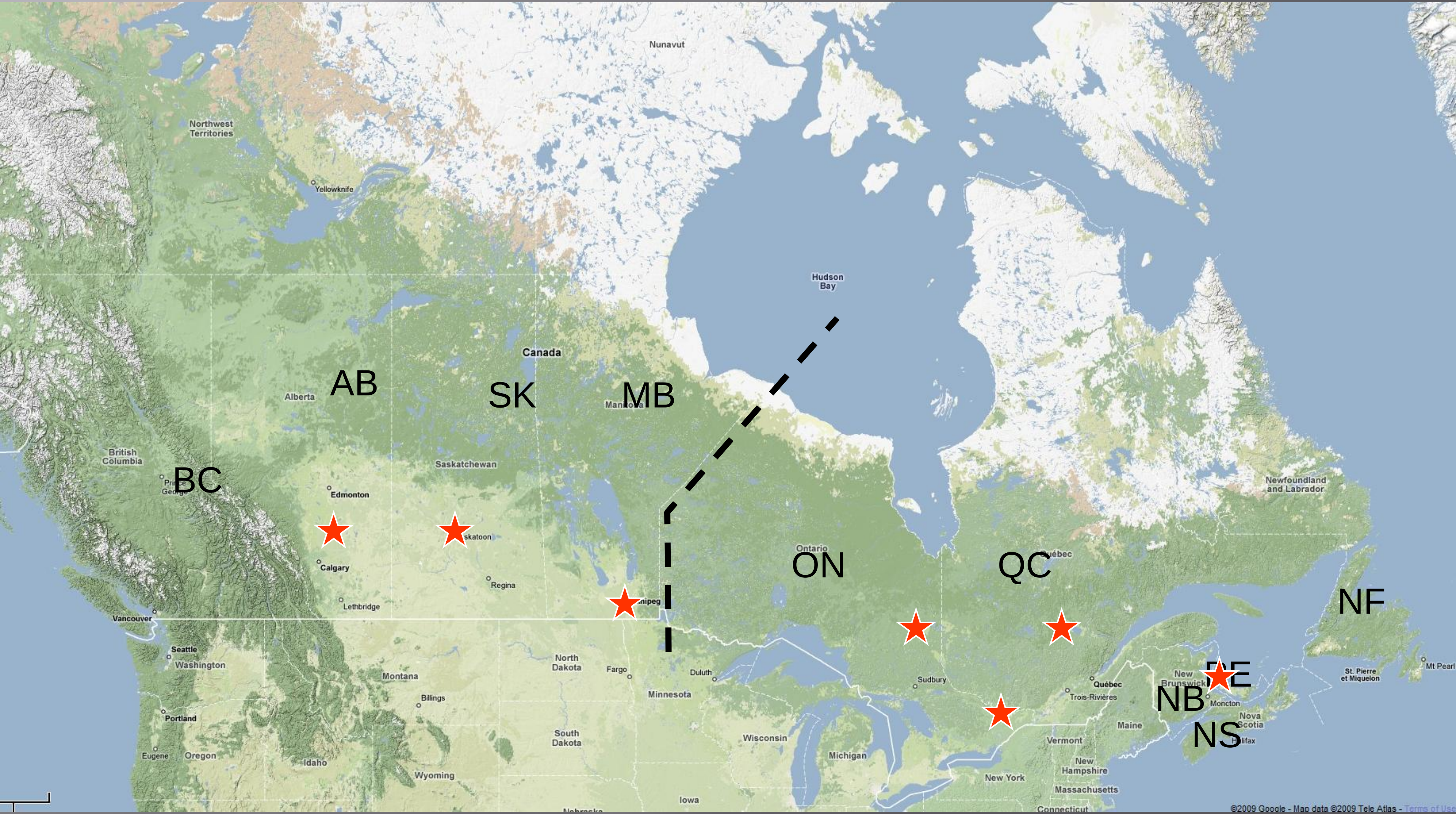
It is not easy!

- Challenges
- Strategies

The 2011 Nationwide Oat Test in Canada

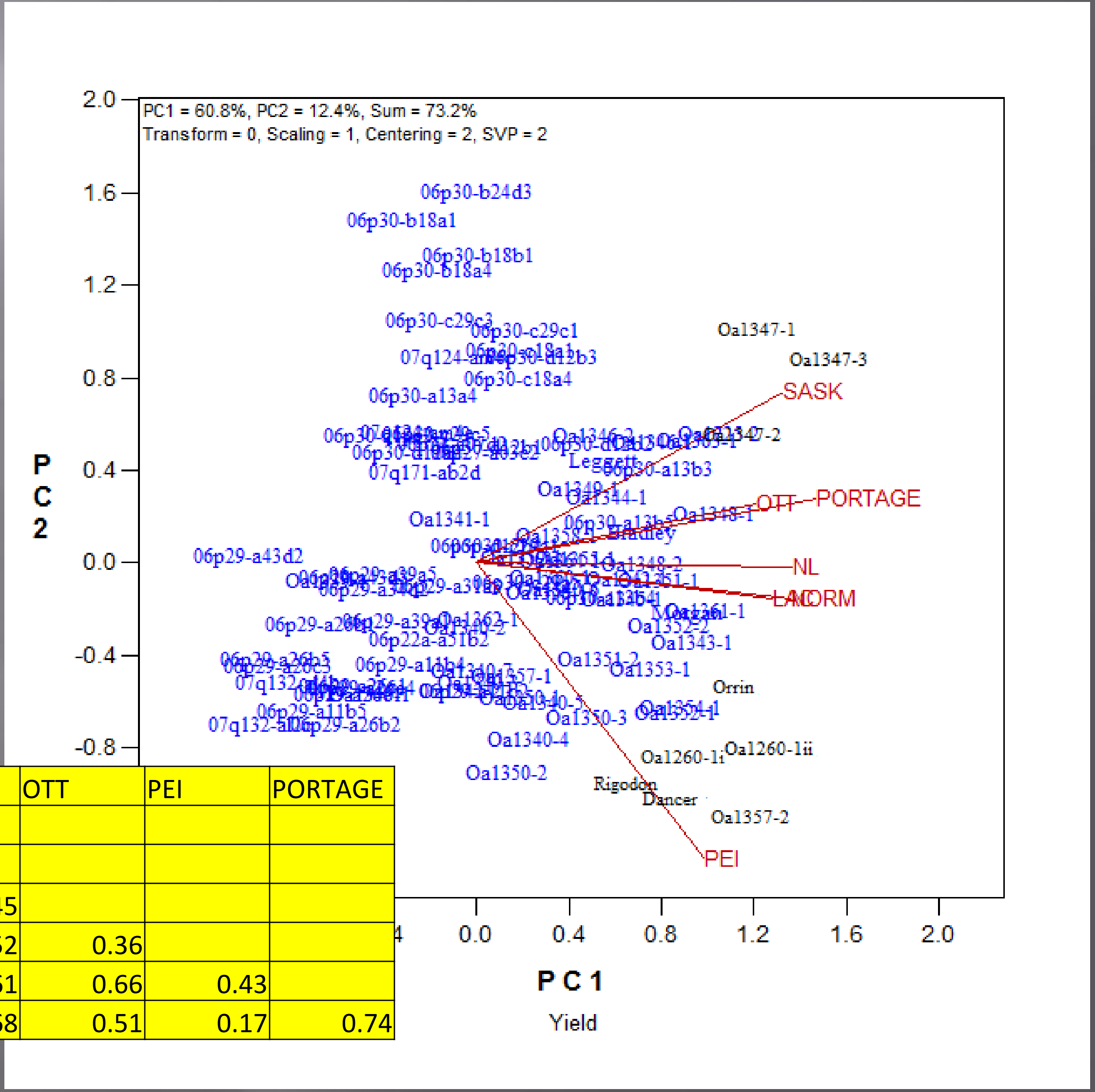
- Entries
  - 45 new lines from CRC-AAFC, Winnipeg
  - 45 new lines from ECORC-AAFC, Ottawa
  - 6 checks representing the oat production regions of Canada
- Locations
  - 3 west and 4 east locations
- Traits measured

Test Location Across Canada



Yield

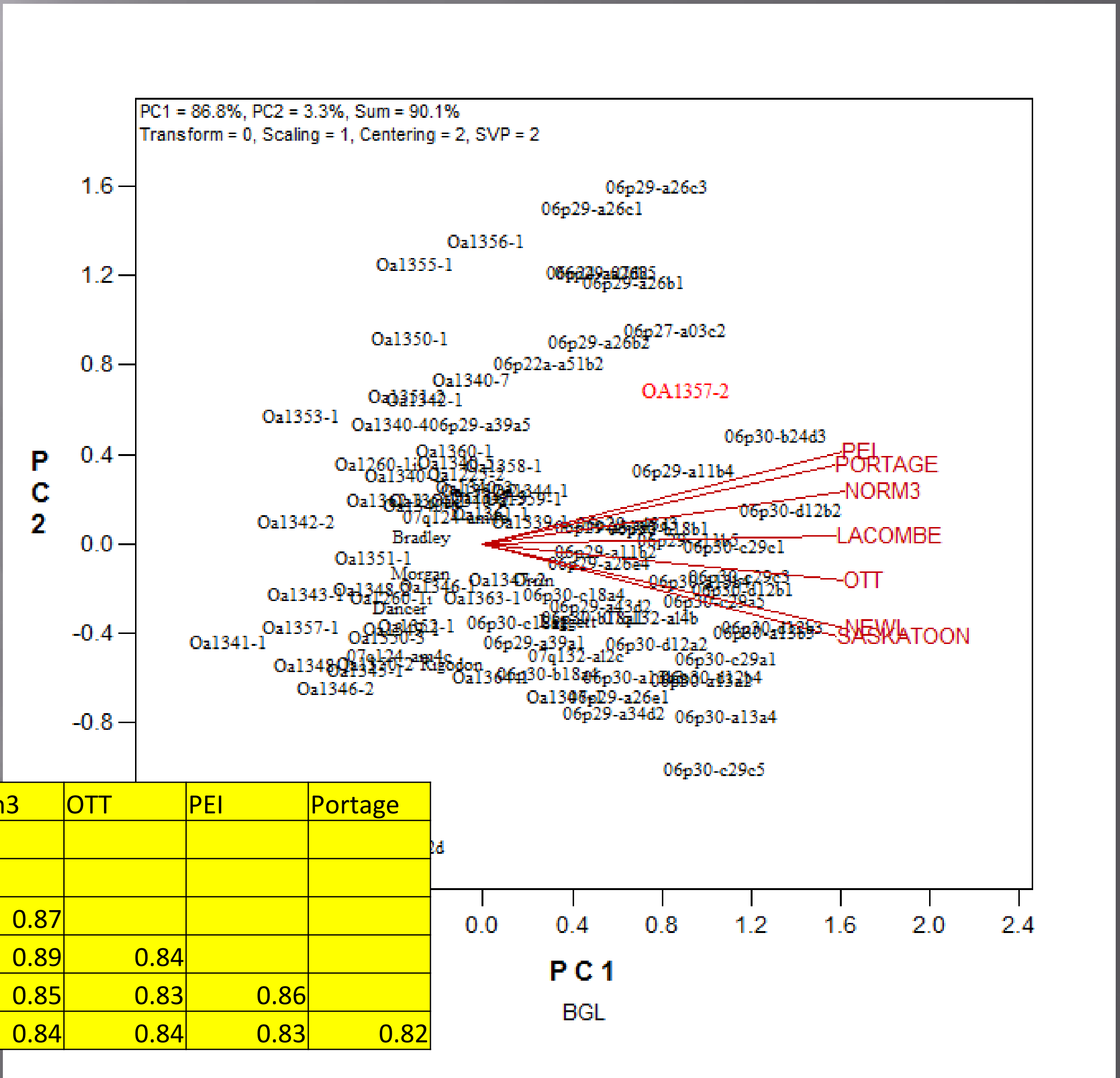
The genotype by location interaction relative to the genotype main effect was not very large, except that PEI was more different from other locations. So selection based on mean yield is a reasonable option, which will simplify the discussion.



	LAC	NL	NORM	OTT	PEI	PORTAGE
NL	0.56					
NORM	0.62	0.58				
OTT	0.39	0.62	0.45			
PEI	0.44	0.47	0.52	0.36		
PORTAGE	0.62	0.69	0.61	0.66	0.43	
SASK	0.57	0.56	0.68	0.51	0.17	0.74

Beta-glucan

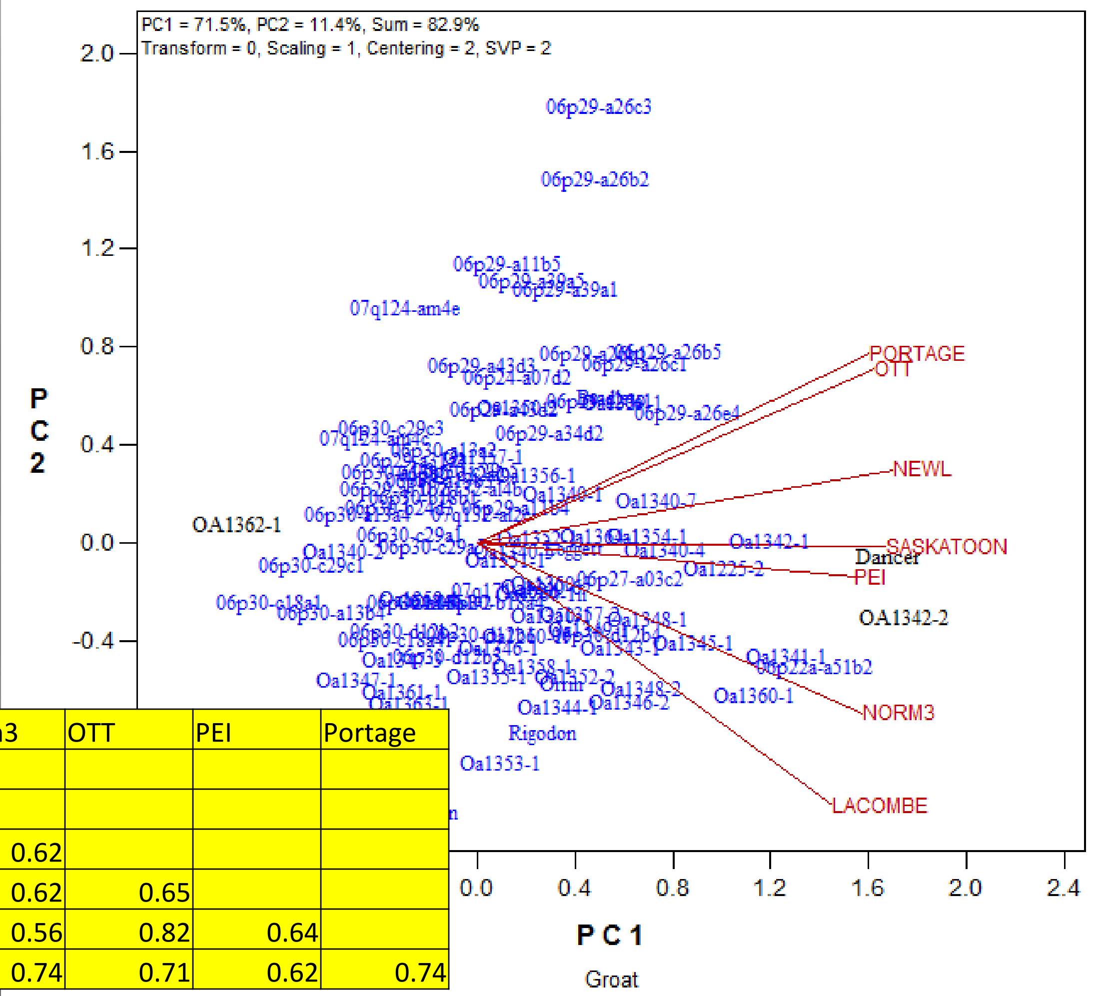
Data from two locations so far. The two locations were highly correlated. So selection based on mean is a reasonable option, which will simplify the discussion. CRC lines tended to have high BGL while ECORC lines have low BGL.



	Lacombe	NEWL	norm3	OTT	PEI	Portage
NEWL	0.85					
norm3	0.84	0.85				
OTT	0.84	0.92	0.87			
PEI	0.86	0.83	0.89	0.84		
Portage	0.81	0.83	0.85	0.83	0.86	
Saskatoon	0.82	0.88	0.84	0.84	0.83	0.82

Groat

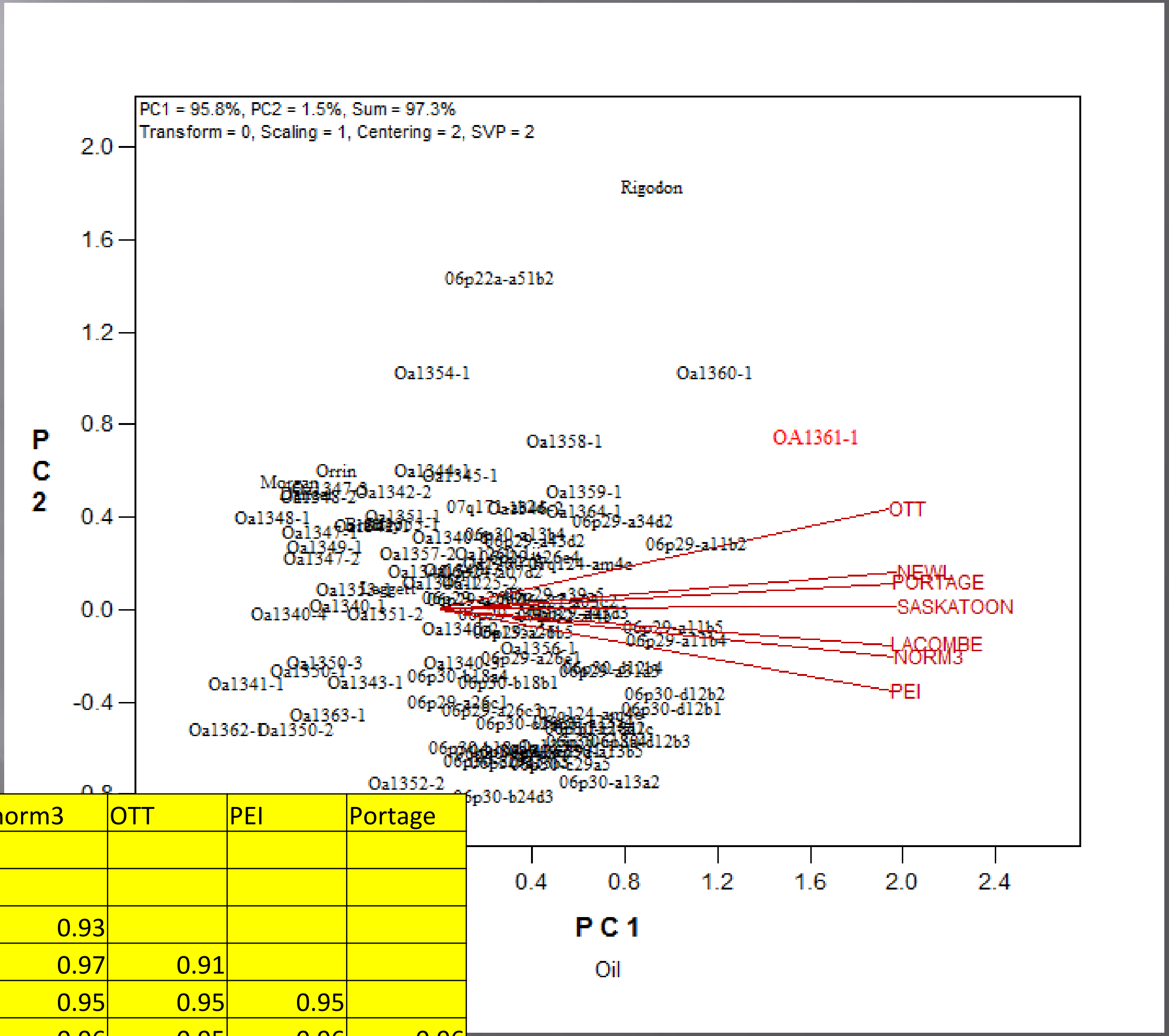
The genotype by location interaction relative to the genotype main effect was not very large. So selection based on mean values is a reasonable option, which will simplify the discussion.



	Lacombe	NEWL	norm3	OTT	PEI	Portage
NEWL	0.64					
Norm3	0.77	0.64				
OTT	0.45	0.80	0.62			
PEI	0.64	0.69	0.62	0.65		
Portage	0.45	0.79	0.56	0.82	0.64	
Saskatoon	0.65	0.76	0.74	0.71	0.62	0.74

Oil

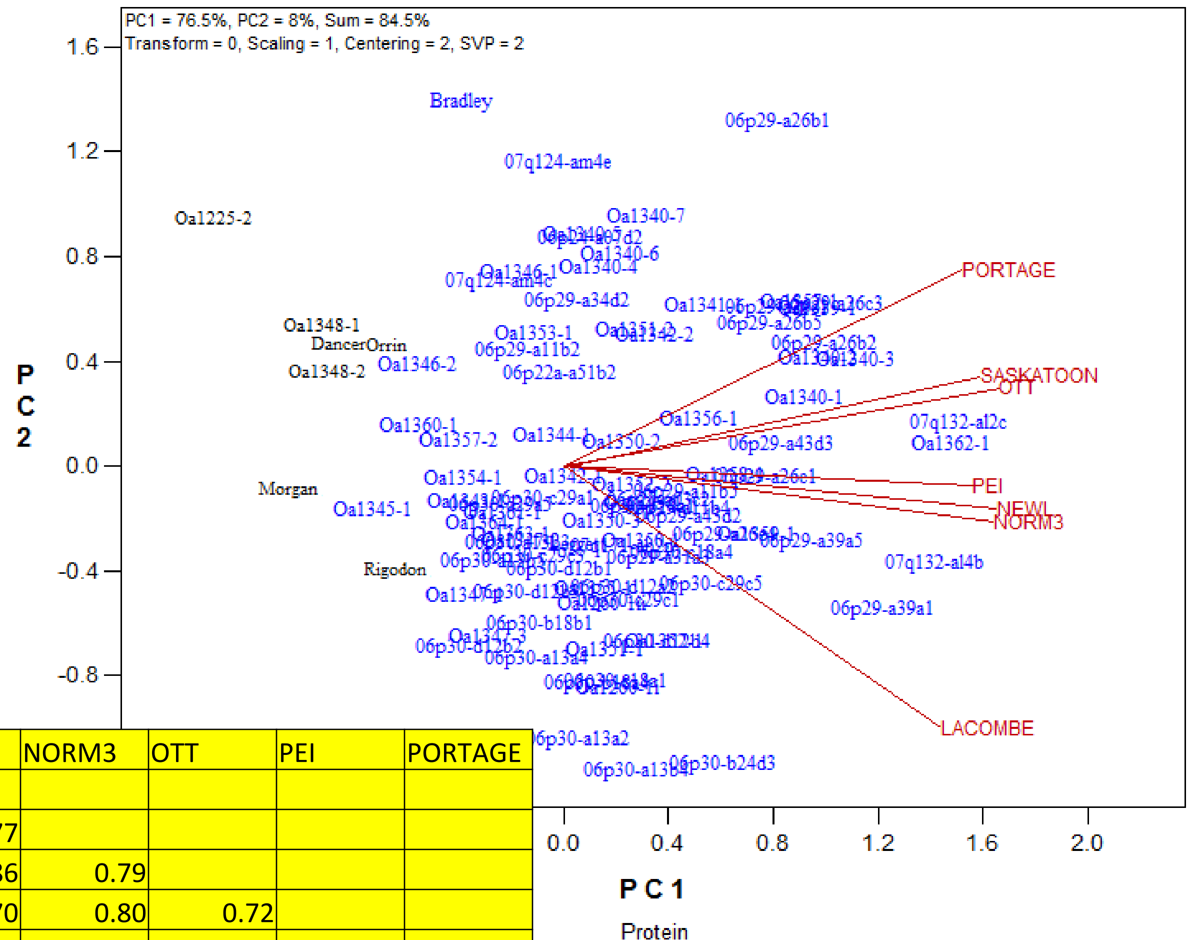
The genotype by location interaction relative to the genotype main effect was very small. So selection based on mean values is a reasonable option, which will simplify the discussion.



Row/Col	Lacombe	NEWL	norm3	OTT	PEI	Portage
NEWL	0.95					
norm3	0.95	0.96				
OTT	0.93	0.97	0.93			
PEI	0.95	0.95	0.97	0.91		
Portage	0.93	0.97	0.95	0.95	0.95	
Saskatoon	0.97	0.97	0.96	0.95	0.96	0.96

Protein

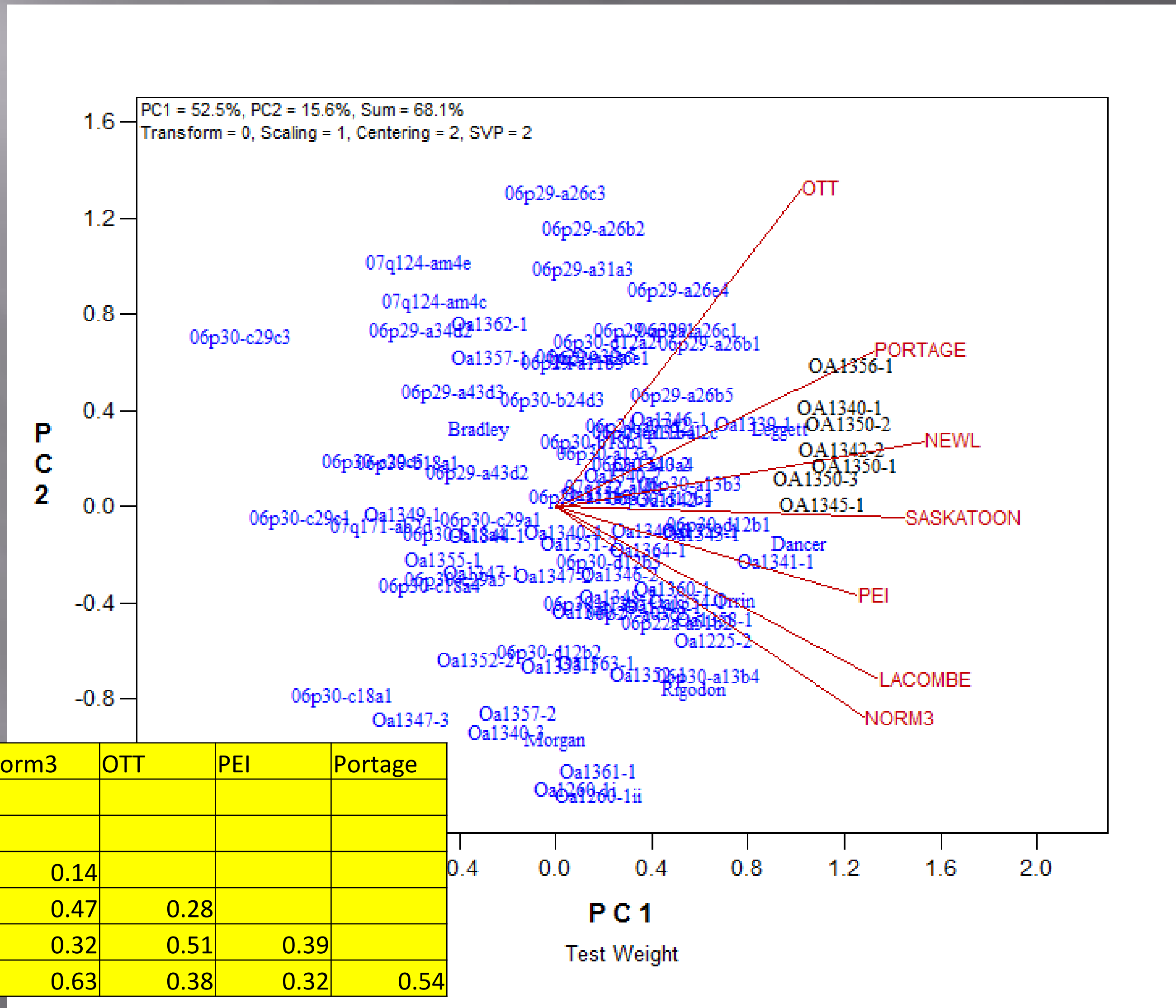
The genotype by location interaction relative to the genotype main effect was not very large. So selection based on mean yield is a reasonable option, which will simplify the discussion.



	LACOMBE	NEWL	NORM3	OTT	PEI	PORTAGE
NEWL	0.77					
NORM3	0.73	0.77				
OTT	0.64	0.86	0.79			
PEI	0.66	0.70	0.80	0.72		
PORTAGE	0.50	0.72	0.68	0.80	0.70	
SASKATOON	0.60	0.75	0.77	0.80	0.71	0.74

Test-Weight

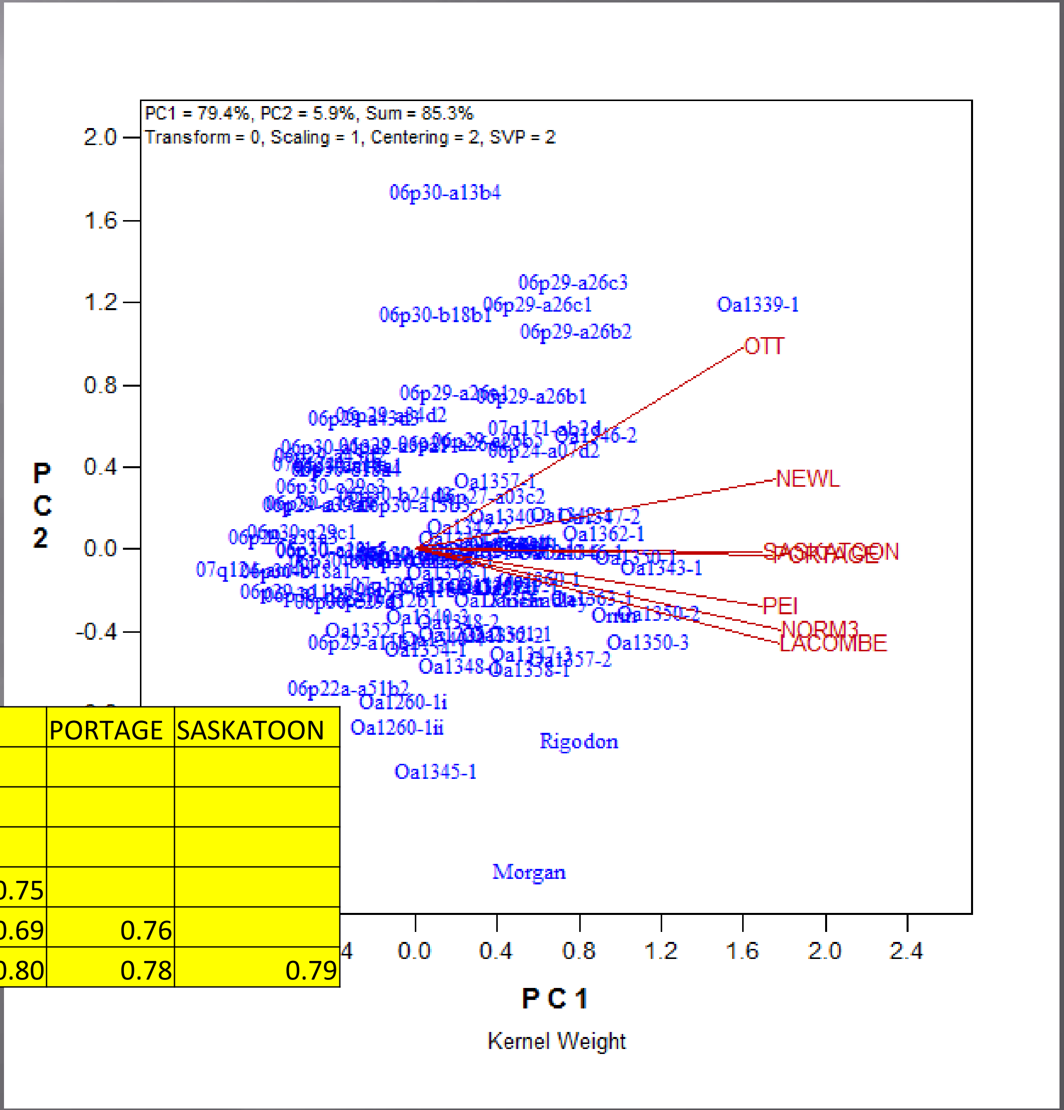
The genotype by location interaction relative to the genotype main effect was not very large. So selection based on mean values is a reasonable option, which will simplify the discussion.



	Lacombe	NEWL	norm3	OTT	PEI	Portage
NEWL	0.58					
norm3	0.53	0.43				
OTT	0.14	0.51	0.14			
PEI	0.50	0.51	0.47	0.28		
Portage	0.41	0.56	0.32	0.51	0.39	
Saskatoon	0.48	0.59	0.63	0.38	0.32	0.54

Kernel-Weight

The genotype by location interaction relative to the genotype main effect was not very large. So selection based on mean values is a reasonable option, which will simplify the discussion.



	LACOMBE	NEWL	OTT	PEI	PORTAGE	SASKATOON
NEWL	0.78					
OTT	0.67	0.77				
PEI	0.79	0.75	0.68			
PORTAGE	0.82	0.81	0.71	0.75		
SASKATOON	0.77	0.78	0.68	0.69	0.76	
NORM3	0.89	0.78	0.69	0.80	0.78	0.79

Undesirable correlations

Traits	TWT	TKW	GROAT	YIELD	OIL	PROTEIN
TKW	0.46**					
GROAT	0.52**	0.37**				
YIELD	0.07	0.38**	0.13			
OIL	-0.12	-0.49**	-0.26*	-0.38**		
PROTEIN	0.05	-0.04	-0.19	-0.67**	0.06	
BGL	-0.26*	-0.47**	-0.43**	-0.38**	0.57**	0.09

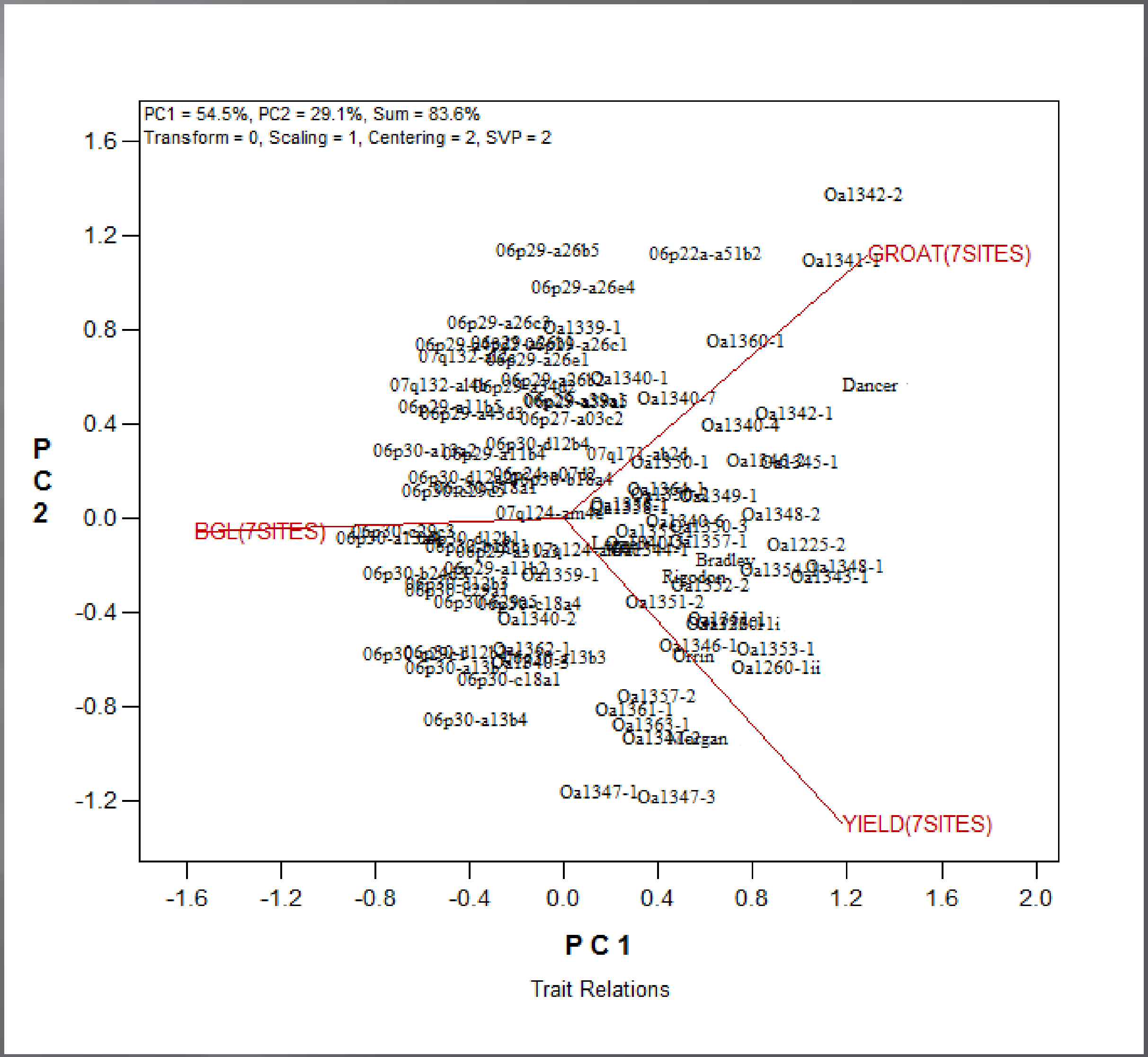
Relationship among traits

Challenges

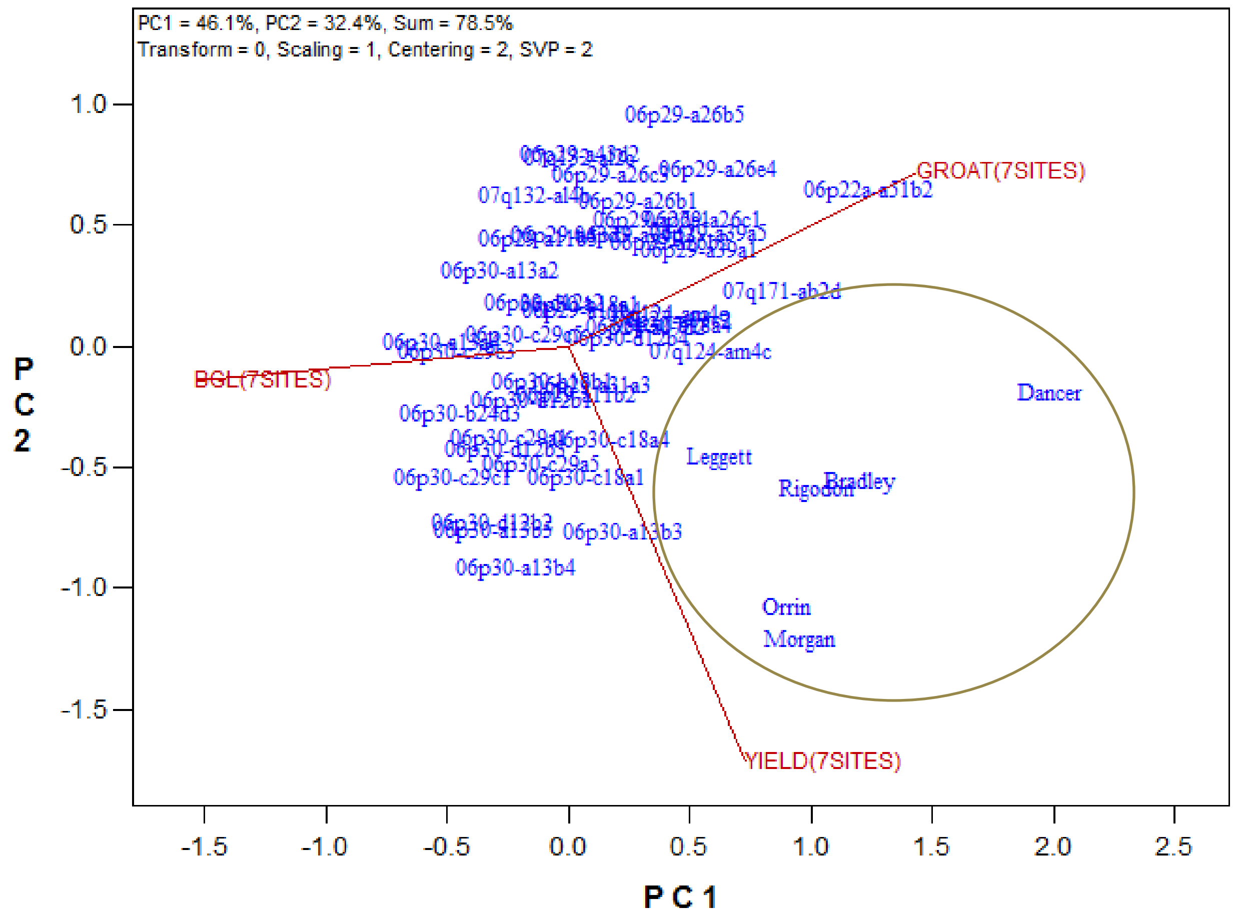
- High level for a desirable trait—not even a challenge!
- Association between any two traits does not seems to be too strong to be combined in a single genotype—not a difficult challenge
- However, when more traits are considered, it becomes a real challenge!

Yield, groat, and BGL

- CRC lines tended to have higher BGL but lower groat and yield

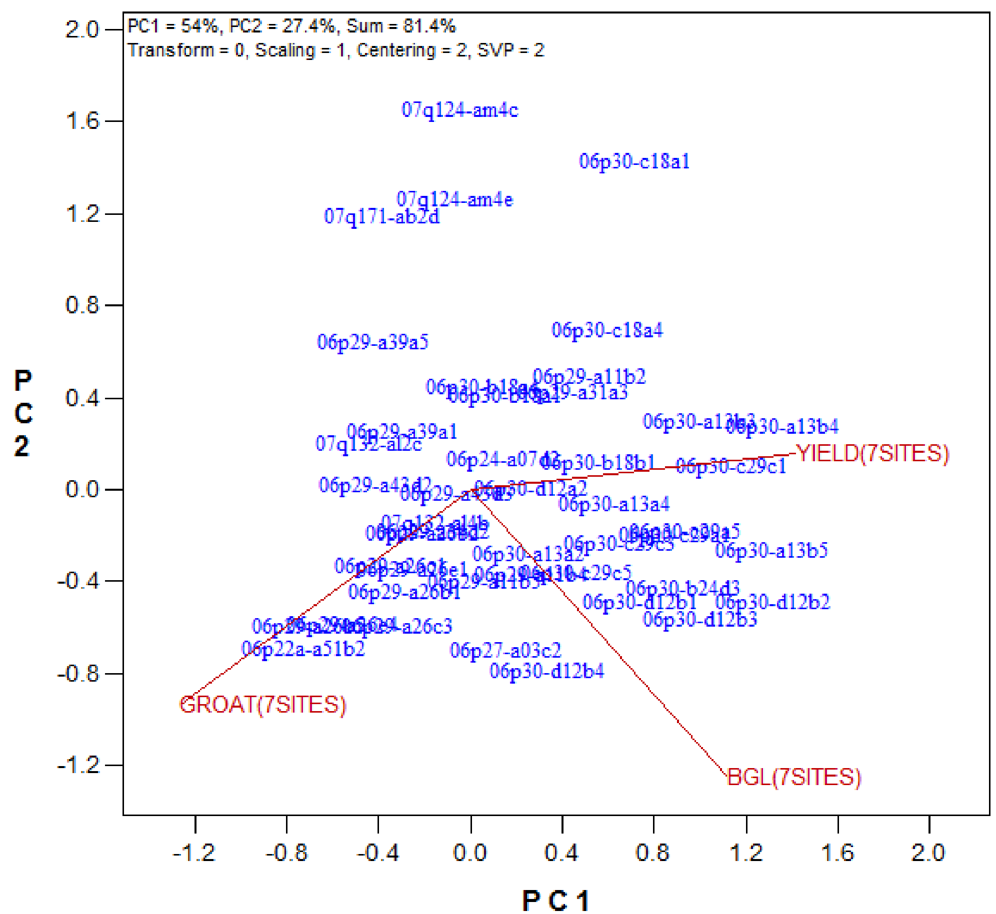


CRC lines plus checks



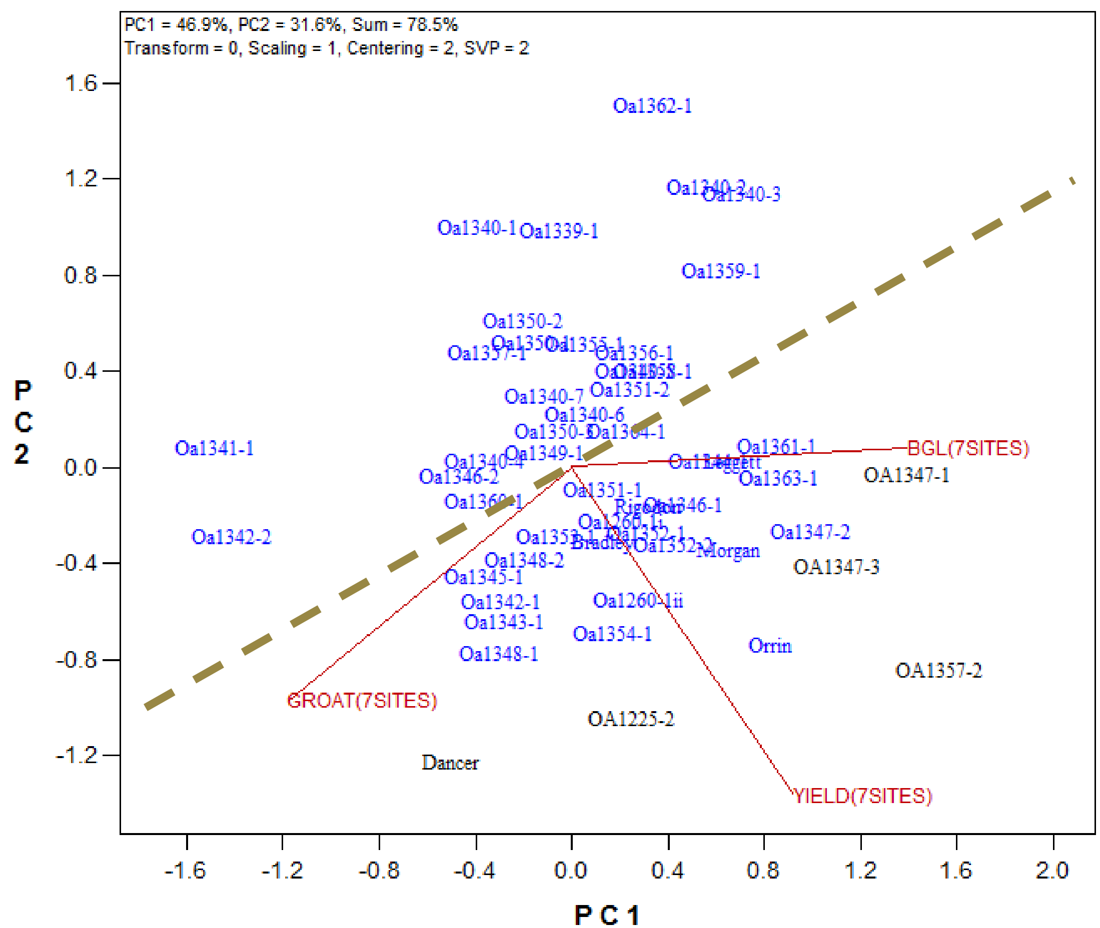
CRC lines only

CRC lines only



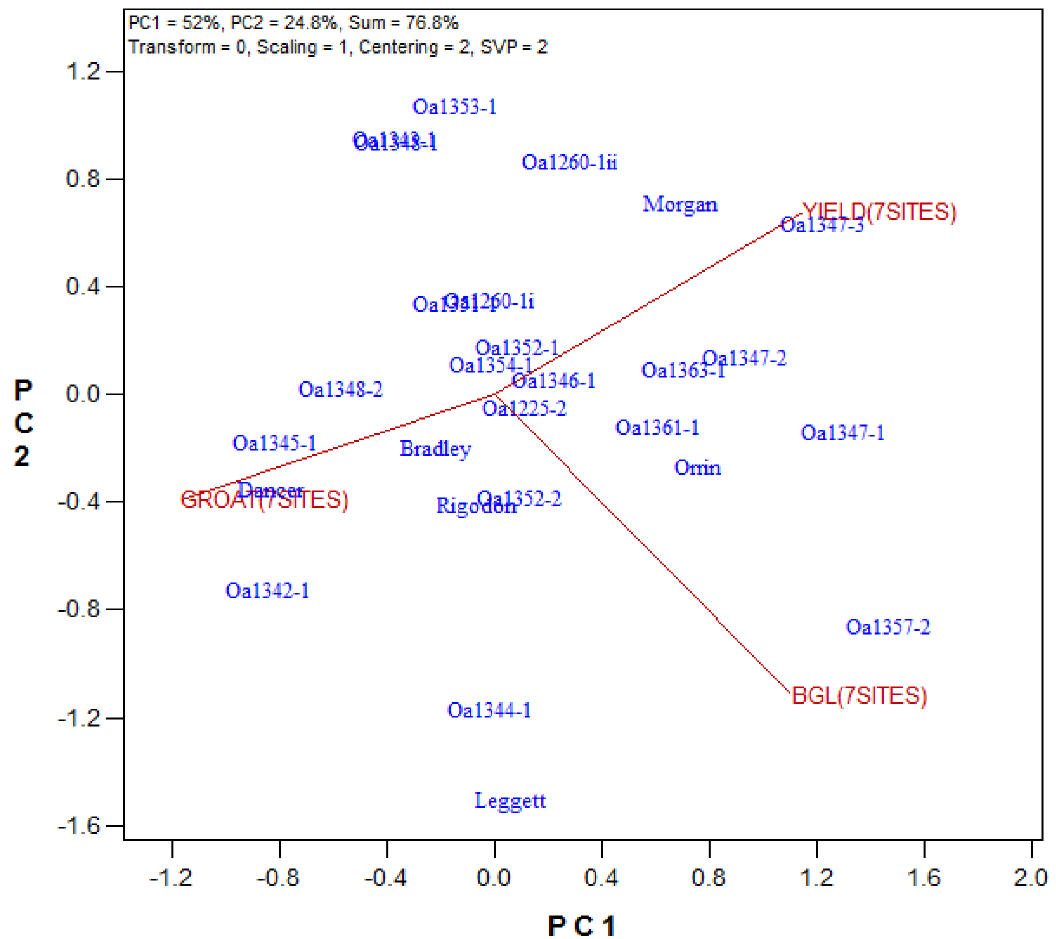
CRC lines only, checks exlcuded

ECORC lines



ECORC lines only

ECORC lines with higher yields

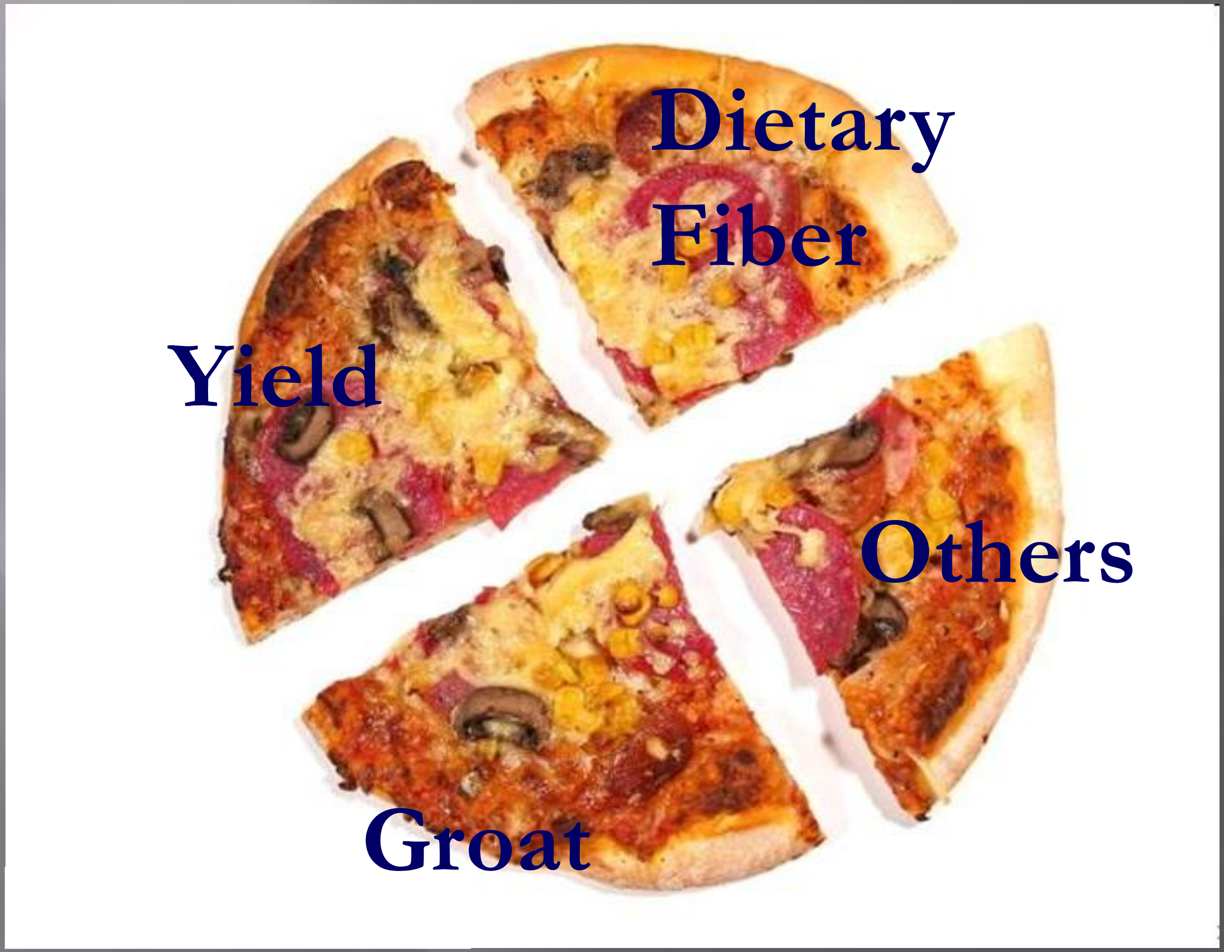


Relationship among traits

The three-way association persists…

- Depending on the population of genotypes, there was always a negative, undesirable correlation
  - Yield vs. groat, or
  - Groat vs. beta-glucan, or
  - Yield vs. beta-glucan
- No genotype was best for all three traits, ever

Breeding for an ideal milling oat is more than "a piece of cake"!

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Why so?

- The undesirable associations among the breeding objectives are logically inevitable

$$\text{Groat\%} = \frac{\text{Groat Yield}}{\text{Grain Yield}}$$

$$\text{BGL}(\%) = \frac{\text{BGL Yield}}{\text{Groat Yield}}$$

$$BGL\% = \frac{BGL\,\text{Yield}}{\text{Groat\%} \times \text{Grain Yield}}$$

A two-step strategy

Given an “ideal” cross and therefore a promising selection population:

- Set a minimum requirement for each trait and do an initial screening (independent culling)
- Set weights to the breeding objectives (desirable traits) to calculate an Selection Index and rank preselected genotypes based on the selection index

Step 1: Set a minimum requirement for each trait using the check cultivars for initial screening

Genotype	GROAT	YIELD	BGL	All Pass
Bradley	Pass	Pass	Pass	YES
Dancer	Pass	Pass	Pass	YES
Leggett	Pass	Pass	Pass	YES
Morgan	Pass	Pass	Pass	YES
Orrin	Pass	Pass	Pass	YES
Rigodon	Pass	Pass	Pass	YES
OA1225-2	Pass	Pass	Pass	YES
OA1342-1	Pass	Pass	Pass	YES
OA1344-1	Pass	Pass	Pass	YES
OA1346-1	Pass	Pass	Pass	YES
OA1352-1	Pass	Pass	Pass	YES
OA1352-2	Pass	Pass	Pass	YES
OA1354-1	Pass	Pass	Pass	YES
OA1357-2	Pass	Pass	Pass	YES

For each trait, use the level of the poorest Check cultivar as the minimum requirement

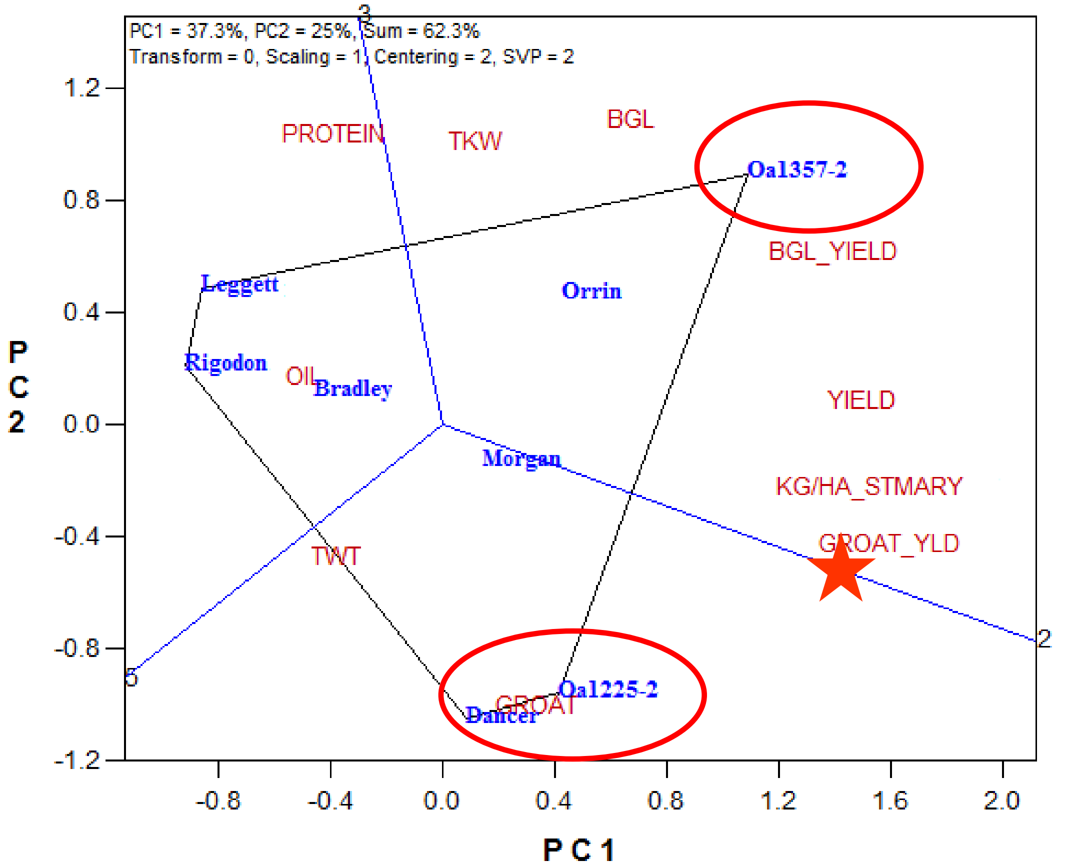
Step 2: Set weights to the breeding objectives to calculate a Selection Index: an example

Trait	Weight
YIELD	1.0
GROAT	1.0
BGL	1.0
TWT	0.6
KW	0.5
PROTEIN	0.5
OIL	-0.6

Rank the selected genotypes on the Selection Index

Trait	GROAT	YIELD	BGL	TWT	Yield (Rust)	TKW	PROTEIN	OIL	Selection Index
OA1357-2	**0.94**	**1.00**	**1.00**	**0.94**	**0.93**	**0.96**	**0.92**	**0.80**	**0.99**
Orrin	0.94	0.98	0.91	0.99	0.90	**1.00**	0.89	0.75	0.97
Leggett	0.94	0.87	0.93	**1.00**	0.92	0.92	0.97	0.79	0.95
Dancer	1.00	0.93	0.81	**1.00**	0.92	0.92	0.87	0.72	0.95
OA1342-1	0.98	0.88	0.82	0.97	0.98	0.96	0.96	0.76	0.94
OA1352-2	0.94	0.91	0.86	0.93	0.93	0.90	0.99	0.79	0.93
Morgan	0.92	0.97	0.83	0.95	0.92	0.93	0.85	0.70	0.93
OA1346-1	0.93	0.92	0.83	0.97	0.94	0.96	0.94	0.82	0.93
OA1344-1	0.94	0.87	0.90	0.93	**1.00**	0.86	0.96	0.81	0.93
OA1225-2	0.97	0.96	0.85	0.98	0.92	0.87	0.82	0.85	0.92
Bradley	0.95	0.90	0.83	0.94	0.89	0.95	0.93	0.77	0.92
OA1354-1	0.96	0.94	0.82	0.97	0.87	0.85	0.92	0.81	0.92
OA1352-1	0.93	0.92	0.82	0.97	0.90	0.80	**1.00**	0.88	0.90
Rigodon	0.94	0.90	0.85	0.98	0.85	0.96	0.89	**1.00**	0.89

Trait profile of OA1357-2



Which is best for what

Conclusion: challenges

- Two-trait associations—does not seem to be so difficult
- Three-trait or multi-way association— is persistent, and logically inevitable

Conclusion: strategies

Given a promising breeding population, selection should be conducted in two steps:

1. Set a minimum requirement for each trait and conduct an initial screening
2. Set Weights to the breeding objectives (desirable traits) and calculate an Selection Index

   —is it possible to have some “official” or consensus weights?

   --Is it more (or less) practical for the molecular scientists to treat the “Selection Index” as a “trait” in MAS?

Conclusion: result

- The new oat line OA1357-2 appeared to have an improved package of yield, BGL, groat, and other desirable traits
- Using OA1357-2 as a parent may lead to further improvement (e.g., crossing with Dancer)

Acknowledgement

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THANK YOU!