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Oat genomics: the state of the art, illustrated by a model trait

Charlene P. Wight, Biniam T. Hizbai, Kyle M.
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Canada



13.7

Cosmos And Culture



The Liberating Embrace Of Uncertainty

May 15, 2012

by Adam Frank, National Public Radio blog

“The only constant is change... and yet, in spite of all evidence to the contrary, we exhaust ourselves in an endless search for solidity. We hunger for something that lasts...we hunger for certainty.

That is a big problem.”

An RFLP-based linkage map of oats based on a cross between two diploid taxa (*Avena atlantica* × *A. hirtula*)¹

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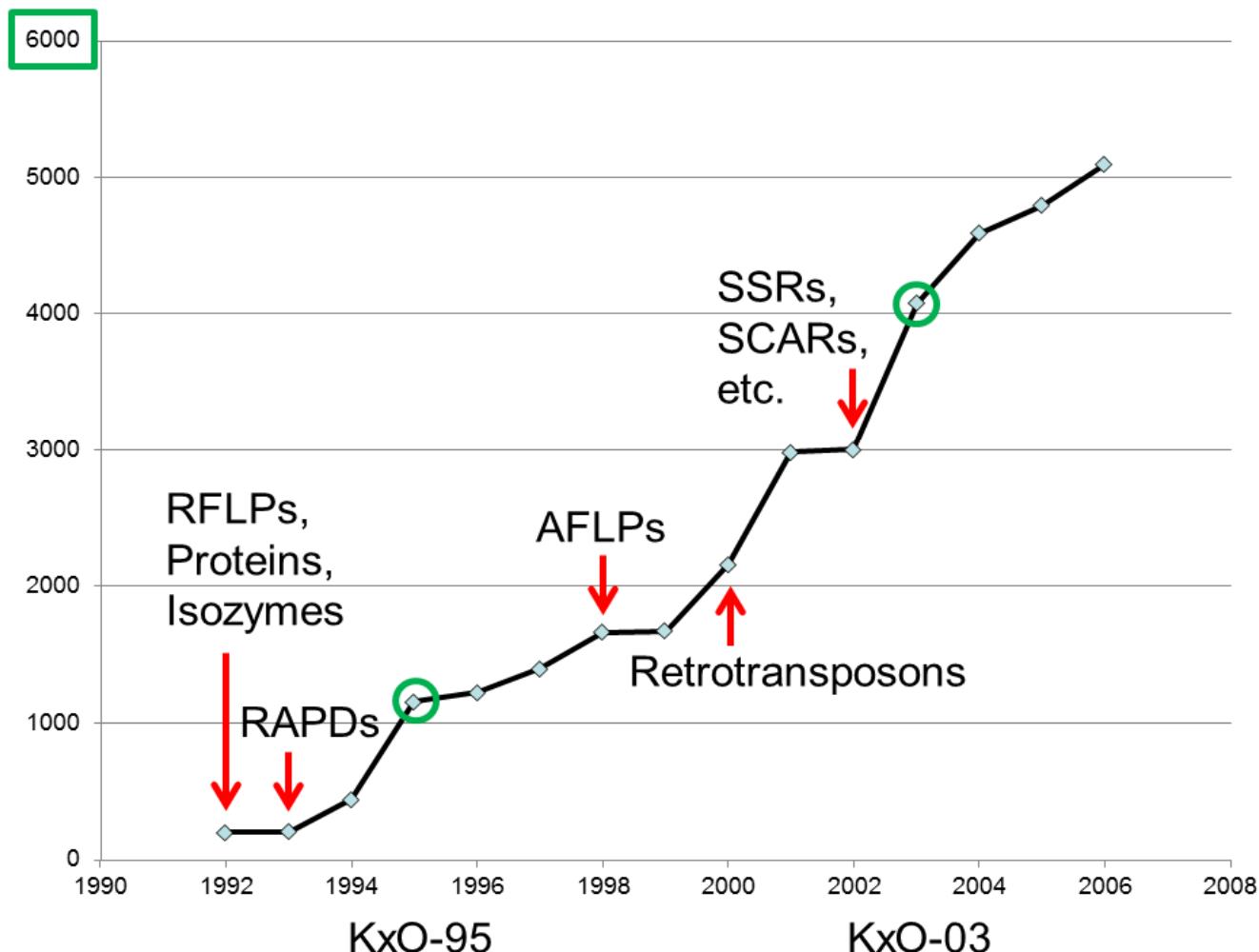
Accepted May 7, 1992

O'DONOUGHUE, L. S., WANG, Z., RÖDER, M., KNEEN, B., LEGGETT, M., SORRELLS, M. E., and TANKSLEY, S. D. 1992. An RFLP-based linkage map of oats based on a cross between two diploid taxa (*Avena atlantica* × *A. hirtula*). *Genome*, **35**: 765–771.

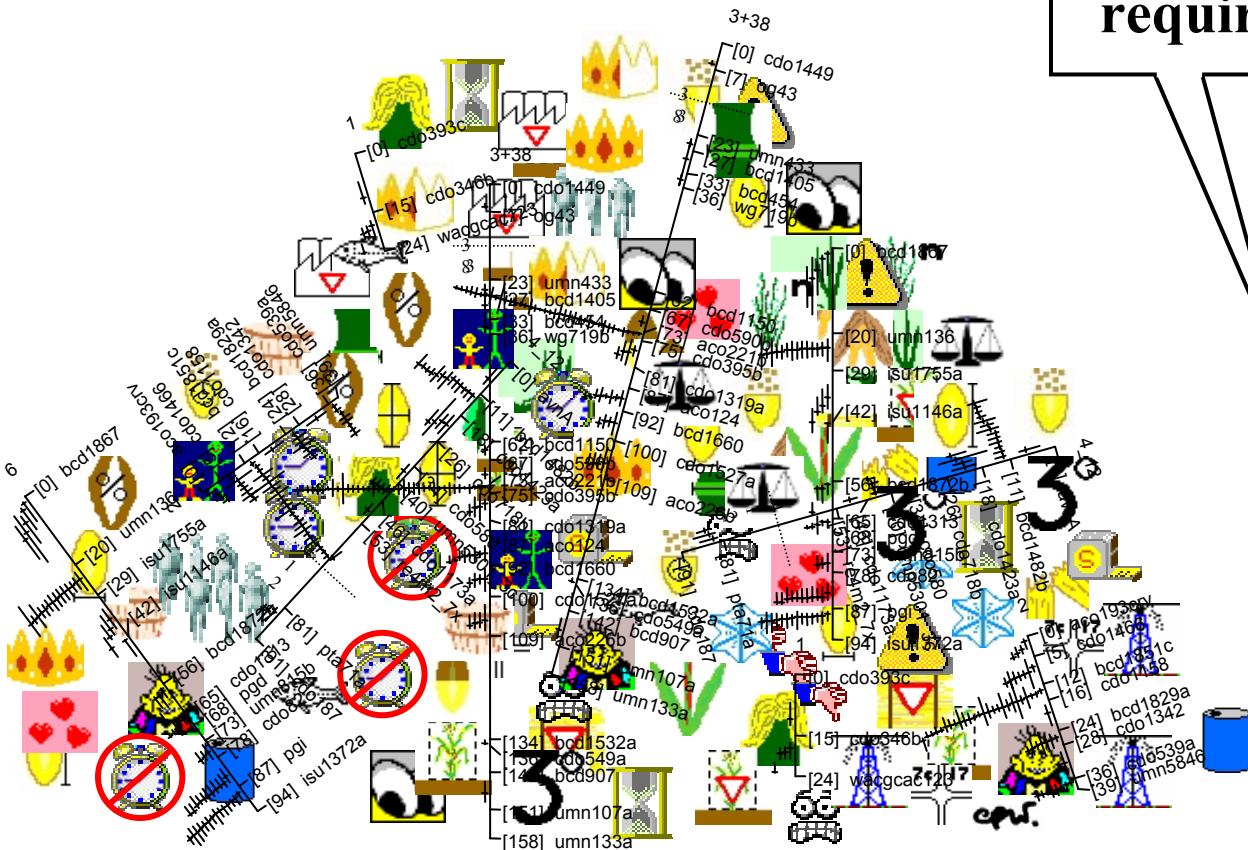
A restriction fragment length polymorphism (RFLP) map for the A genome of *Avena* has been developed using F₃ families from the cross *A. atlantica* × *A. hirtula*. The main source of markers were an oat cDNA and a barley cDNA library. A total of 194 RFLP markers was used, 192 of which were mapped or assigned to linkage groups. Seven main linkage groups, presumably corresponding to the seven chromosomes of the haploid genome, were identified. The linkage groups varied in size from 30 to 118 cM for a total map length of 614 cM. This map provides a tool for the interpretation of genome organization in *Avena* and for marker selection in the development of a map of hexaploid oats.

Key words: restriction fragment length polymorphism, *Avena*, mapping.

Number of published oat markers available as of 2006:



**“Some assembly
required....”**





Consultative Group on International Agricultural Research



Triple A Framework

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Availability, Accessibility and Applicability of the CGIAR Research Outputs

Research organizations like the CGIAR cannot be satisfied just knowing they have produced high quality science. It is essential that the outputs of their research are communicated and put to use, in the village, on the ground, in the lab, or across the negotiating table.

The Triple-A Framework developed by the ICT-KM Program seeks to help CGIAR Centers and Programs and their scientists decide on the level of Availability, Accessibility and Applicability (AAA) they want for their research outputs, and also the pathways with which to turn these outputs into International Public Goods.



Oat Database Search

Search by:

Composite map

all diploid tetraploid hexaploid

Composite map traits

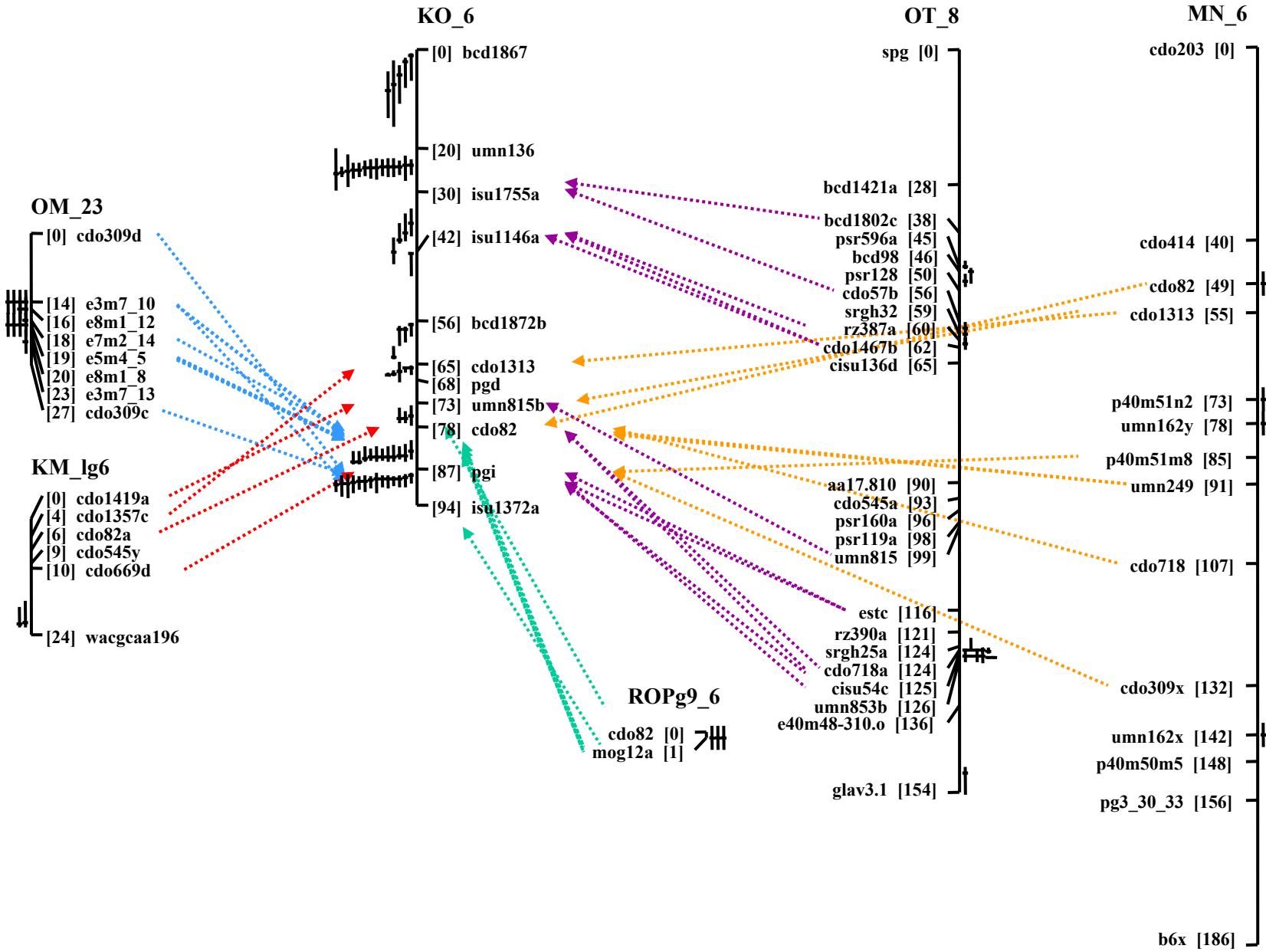
[\(icon legend\)](#)

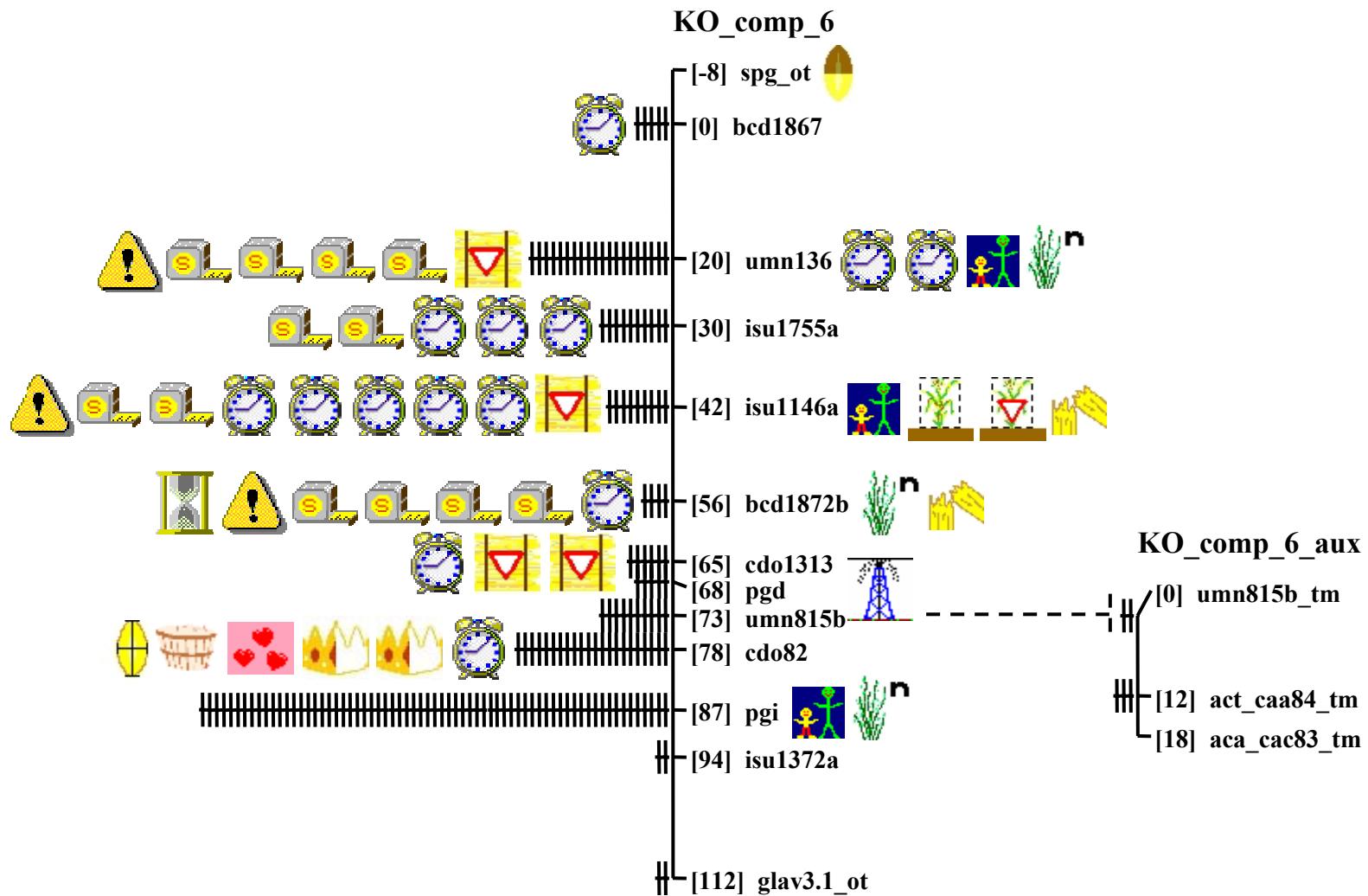
Composite map markers

Composite map population

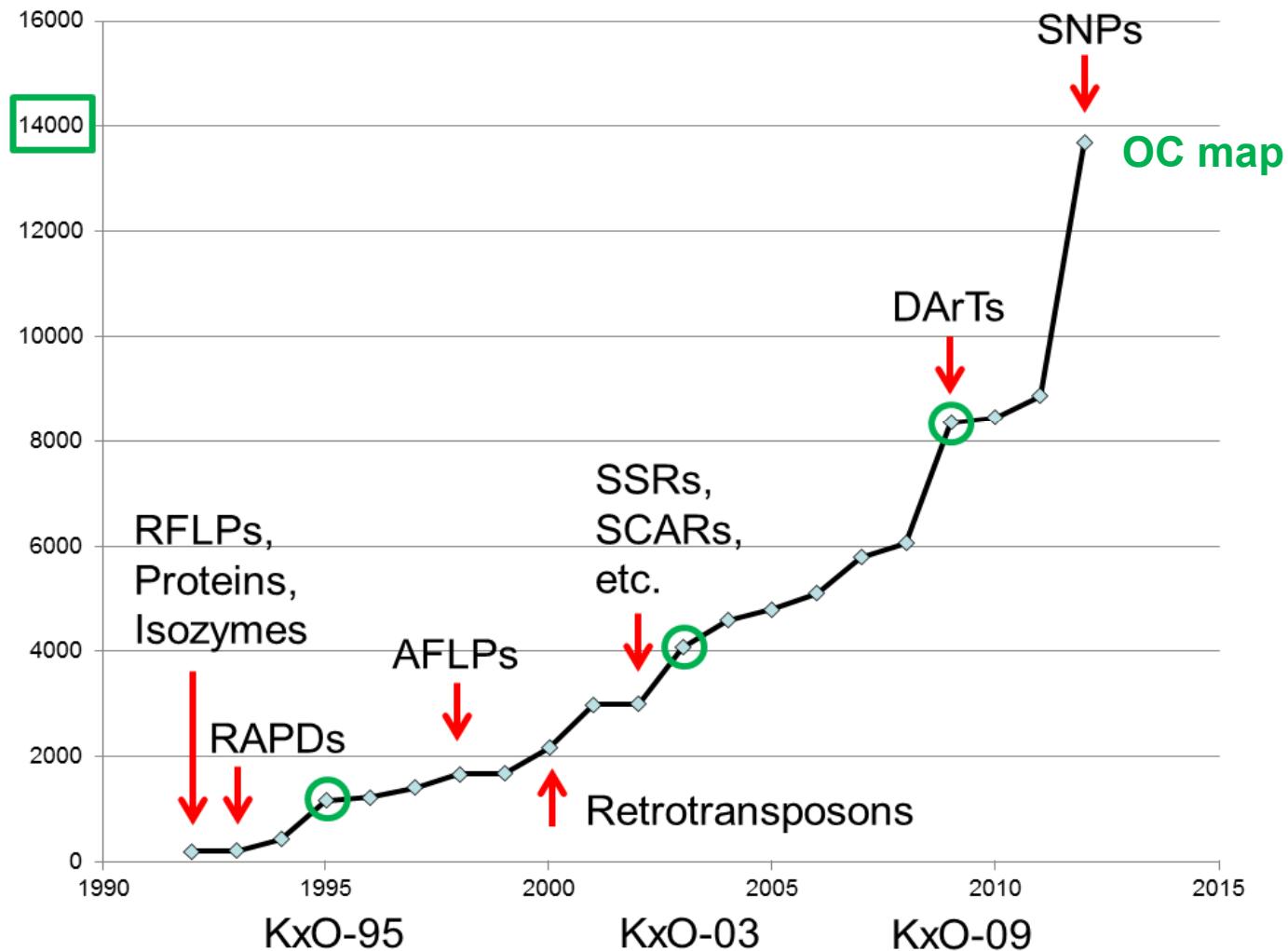
Produced by Charlene Wight & Diane Bergeron, Agriculture and Agri-Food Canada

<http://avena.agr.gc.ca/oatgenes/>

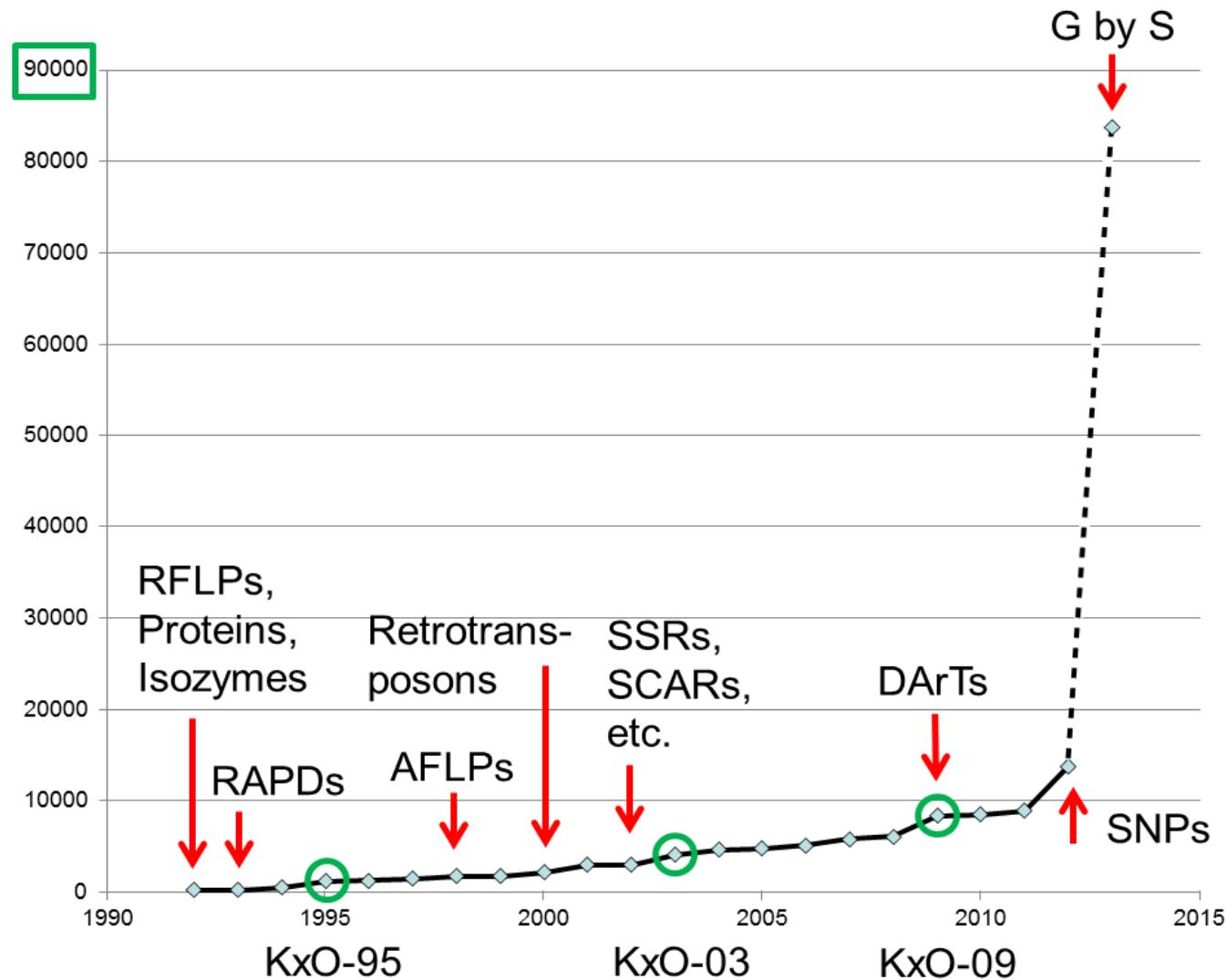




Number of published oat markers available as of 2012:



Number of mapped oat markers available including G by S:



Partial genotype data from an association mapping population:

Marker		9741A41-4-6-86	AC_Marie	Ajay	AC_Assiniboina/S42	Eurabbie	Fulghum	Kangaroo	MN841801-1	Mortlock	Noble-2	Nortline	Potoroo	Sunill-1	Wintok	Aveny	Belinda	Bia	Blaze	Brochan	Buffalo	Bullion	Bulwark	CDC_Boyer	CDC_Weaver	Cl_1712	Cl_4706	Cl_9416-1	Cascade	Cilla	Coker227	Coker833	D921-643	Dal
oPt-0003		1	0	1	1	0	0	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1			
oPt-0011		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1	1	1	1	1	0	0	1	0	1	0				
oPt-0026		1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0				
oPt-0028		1	0	1	0	1	1	0	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1				
oPt-0032		1	0	1	1	0	0	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	0	0	1	1	0	1				
oPt-0075		0	1	1	1	1	1	0	0	1	0	1	1	1	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	0				
oPt-0075_c		0	1	1	1	1	1	0	0	1	0	1	1	1	0	1	0	0	0	1	1	1	0	1	0	1	0	0	0	0				
oPt-0096		1	1	0	1	1	0	1	1	0	1	0	0	0	1	0	1	1	1	0	0	1	0	1	1	1	0	0	1	1				
oPt-0101		0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1	1	1	0	0	0	1	0	0				
oPt-0101_c		0	1	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0				
oPt-0114		0	1	0	0	0	1	1	0	1	0	0	1	1	0	1	1	1	0	1	0	0	0	0	1	0	1	0	0	0				
oPt-0120		0	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	1	1	1	1				
oPt-0121		1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	0	0	1	1	1	1			
oPt-0121_c		1	1	1	1	1	0	1	1	1	1	0	1	1	1	0	1	1	1	1	0	1	1	1	1	0	0	1	1	1	1			
oPt-0123		0	1	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	1	0	0	1	0	0	0				
oPt-0136		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	0				
oPt-0136_c		1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	0	1				
oPt-0138		1	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1				
oPt-0148		0	0	0	0	0	0	0	1	0	0	1	0	1	0	1	1	1	0	0	0	1	1	0	0	0	1	0	0	0				
oPt-0173		1	1	0	1	1	1	0	1	0	1	1	1	1	1	0	1	1	1	1	1	1	1	1	0	1	1	1	1	1				
oPt-0173_c		1	1	0	1	1	1	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1				
oPt-0177		0	1	0	1	1	1	1	0	1	1	1	1	0	1	0	1	0	1	1	1	1	1	0	0	1	1	0	1					
oPt-0186		1	0	1	0	0	0	1	0	0	1	0	0	0	1	0	0	0	1	1	1	0	1	0	0	0	1	1	1	1				
oPt-0220		1	0	1	1	0	0	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	0	0	1	0	1	1	1				
oPt-0233		1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1				
oPt-0322		1	0	0	0	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1				
oPt-0334		0	0	1	0	0	1	1	0	0	0	1	0	1	0	0	0	0	0	1	1	1	0	0	0	1	0	1	0	1				
oPt-0338		0	0	0	1	1	0	0	1	0	0	1	0	1	1	1	1	0	0	1	0	0	1	1	0	0	1	0	0	1				
oPt-0344		1	0	1	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1				
oPt-0350		1	1	1	1	1	0	1	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	1	1	0	0	1				
oPt-0354		1	0	1	1	1	1	0	1	0	0	0	1	0	1	1	1	1	1	1	1	1	1	0	0	0	1	1	0	1				
oPt-0373		0	1	1	1	0	1	0	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	1	1	1	1	1				
oPt-0401		0	0	0	0	0	1	0	1	0	0	0	1	0	0	1	0	1	0	0	0	0	1	0	1	1	0	0	0	0				
oPt-0419		0	1	0	0	0	0	1	0	0	0	1	0	0	1	0	0	1	0	1	0	1	1	0	0	0	0	0	0	0				
oPt-0427		1	0	1	1	1	0	0	0	0	1	1	1	1	1	1	1	1	1	1	1	1	1	0	1	0	1	1	1	1				

Flae
lus
CAT Flaemi
KGA ro
CAA Flae
YYG
TTAGF
C
ATTACAC
ATATGGG
AGAOTCA
GGG-ASC

!Some assembly required... ,

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Welcome to InterStore_{DB}

A generic integration resource for genetic and genomic data

InterStoreDB is a suite of closely linked web-based tools designed to assist researchers in navigating from phenotype to genotype.

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Disease Resistance		
Milling		
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Web InterStores

ward genetics approach.



er purpose and non-infringement of the proprietary material on these web pages. However, it accepts no

Our new database concept is

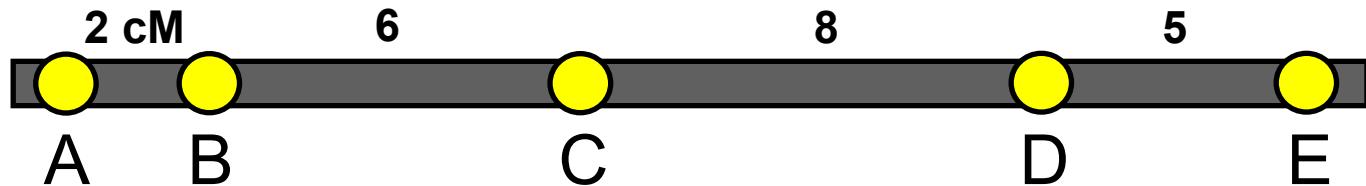
“IMPairED”

Integrated Marker Pair-Enhanced
Database

What if we looked less at the maps and more at the markers themselves?

- Marker associations and map orders are calculated based on the number of recombinations between any two pairs of markers in a data set.
- We can take advantage of this by extending the concept from looking within one population to looking across populations.

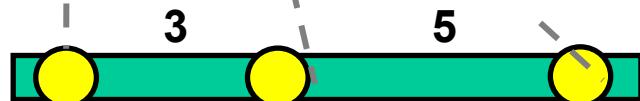
Actual
linkages



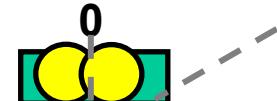
Map 1



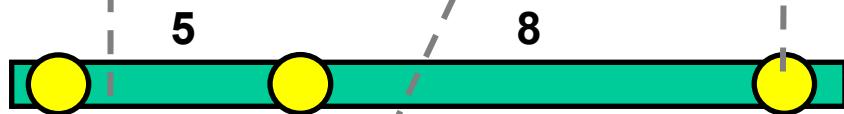
Map 2



Map 3



Map 4



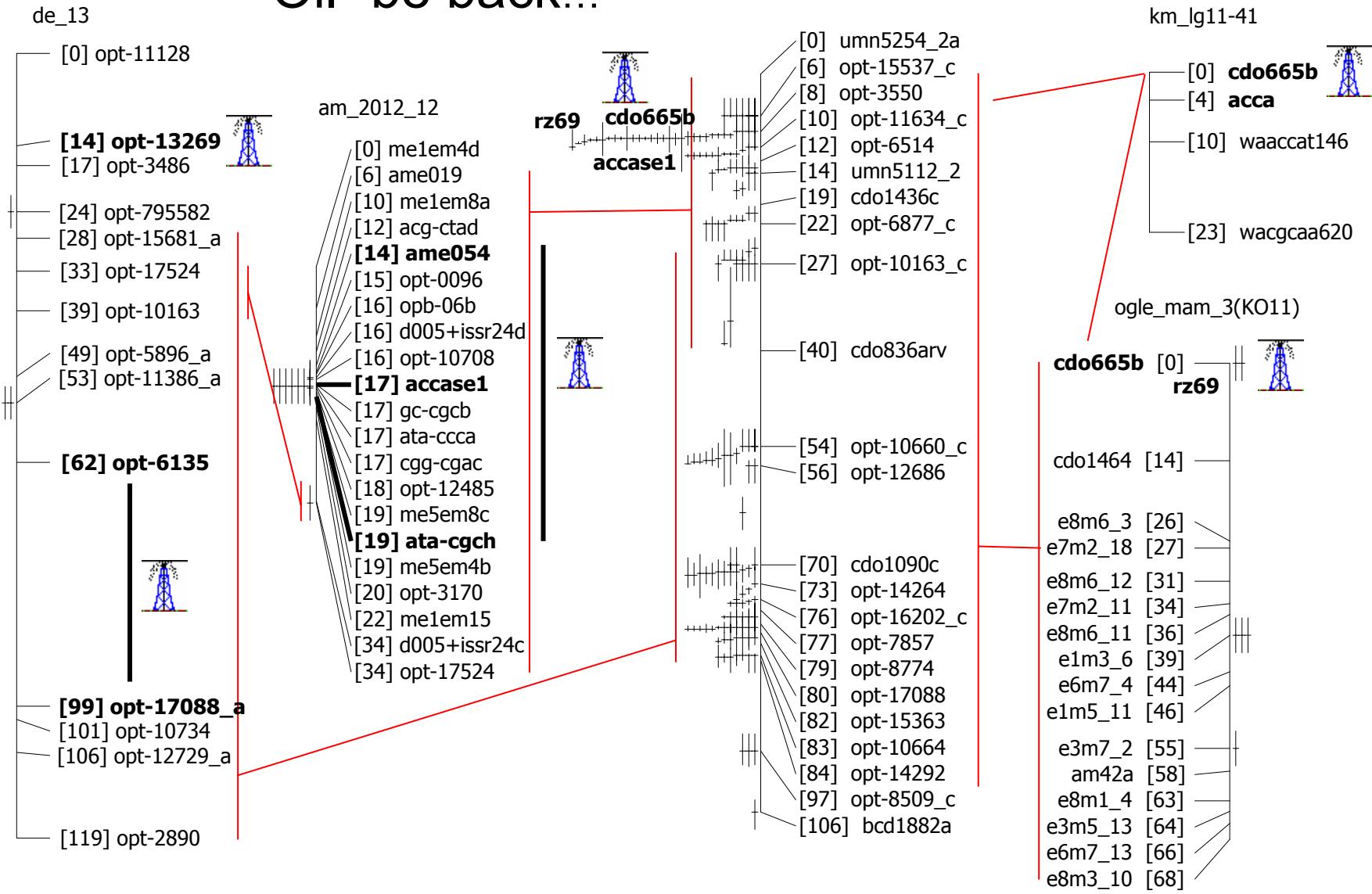
Map 5



Advantages of having direct access to pairwise distances:

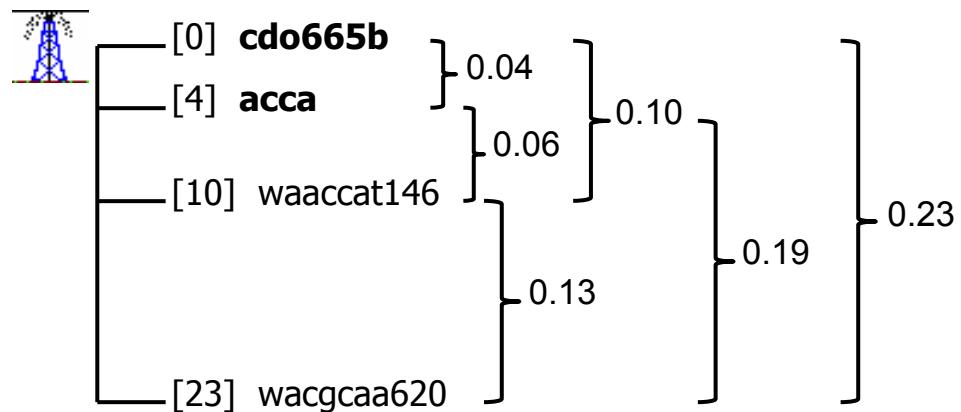
- Provides a direct way to list markers linked to a target.
- Can represent LD distances that cannot be resolved in a map (LD may give stronger evidence of tight linkage).
- Can show critical ambiguity that is lost in a consensus map (could be important to know if a marker has two potential locations).

“Oil” be back...



Pair-wise
recombination
distances can be
derived from the
graphical
representation of
a map...

km_lg11-41



although it's more accurate to calculate them using raw genotype scores:

cdo665b	4	1	4	1	4	4	0	4	1	4	4	4	4	1	1	4	1	4	1	4	1	1	4	1	1	1	4	4	1	4	4	1	4
ACCa	3	5	3	5	3	3	5	3	5	3	3	3	3	3	5	5	5	3	5	5	3	5	5	5	3	5	3	3	3	5	3	3	3
waaccat146	0	5	3	5	3	3	5	3	5	3	3	3	3	3	5	3	5	5	3	5	3	5	5	3	5	3	0	5	5	3	3	5	3
waccaa620	0	5	3	5	3	3	5	3	5	3	3	3	3	5	3	3	5	3	3	5	5	5	3	5	3	3	5	5	5	5	3	3	3

Markers found linked to oil marker cdo665b using “IMPairED”:

Map	Trait	Published_marker	M1	minr	maxr	dif	aver	NI	NP
KO	Oil	cdo665b	GMI_ES01_c17183_31	0	0	0	0	50	1
KM	Oil	cdo665b	GMI_ES01_c17183_31	0	0	0	0	50	1
KO	Oil	cdo665b	GMI_ES01_c825_535	0	0	0	0	48	1
KM	Oil	cdo665b	GMI_ES01_c825_535	0	0	0	0	48	1
KO	Oil	cdo665b	CDO783RV	0.008	0.008	0	0.008	59	1
KM	Oil	cdo665b	CDO783RV	0.008	0.008	0	0.008	59	1
KO	Oil	cdo665b	CSU36c	0.008	0.008	0	0.008	59	1
KM	Oil	cdo665b	CSU36c	0.008	0.008	0	0.008	59	1
KO	Oil	cdo665b	RZ69	0.008	0.008	0	0.008	60	1
KM	Oil	cdo665b	RZ69	0.008	0.008	0	0.008	60	1
KO	Oil	cdo665b	oPt_0473_c	0.013	0.013	0	0.013	76	1
KM	Oil	cdo665b	oPt_0473_c	0.013	0.013	0	0.013	76	1
KO	Oil	cdo665b	oPt_0473	0.014	0.014	0	0.014	72	1
KM	Oil	cdo665b	oPt_0473	0.014	0.014	0	0.014	72	1
KO	Oil	cdo665b	GMI_ES17_c1315_660	0.021	0.021	0	0.021	47	1
KM	Oil	cdo665b	GMI_ES17_c1315_660	0.021	0.021	0	0.021	47	1
KO	Oil	cdo665b	Wacgcac612	0.027	0.027	0	0.027	55	1
KM	Oil	cdo665b	Wacgcac612	0.027	0.027	0	0.027	55	1
KO	Oil	cdo665b	GMI_ES15_c14140_12	0.033	0.033	0	0.033	46	1
KM	Oil	cdo665b	GMI_ES15_c14140_12	0.033	0.033	0	0.033	46	1
KO	Oil	cdo665b	oPt_0096	0.035	0.035	0	0.035	72	1
KM	Oil	cdo665b	oPt_0096	0.035	0.035	0	0.035	72	1
KO	Oil	cdo665b	avjp2349	0.037	0.037	0	0.037	27	1
KM	Oil	cdo665b	avjp2349	0.037	0.037	0	0.037	27	1
KO	Oil	cdo665b	avjp3983	0.037	0.037	0	0.037	41	1
KM	Oil	cdo665b	avjp3983	0.037	0.037	0	0.037	41	1
KO	Oil	cdo665b	avjp497	0.037	0.037	0	0.037	41	1
KM	Oil	cdo665b	avjp497	0.037	0.037	0	0.037	41	1

(cont.)

The “IMPairED” concept database:

- Stores pair-wise linkage distances from raw genotype scores and published maps to make marker choice easier and more precise,
- can help us make the available genetic linkage and phenotypic association data more accessible, and, therefore, more applicable.

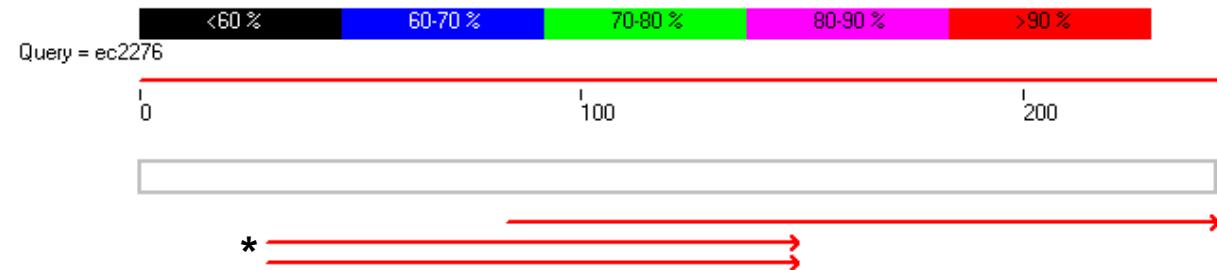
We believe that this will add value to existing and future oat community databases such as TAT.



谢谢

Thank you!

Charlene P. Wight, Biniam T. Hizbai, Kyle M. Gardner, Philippe Couroux,
and Nicholas A. Tinker (ECORC, Agriculture and Agri-Food Canada,
Ottawa)



cd01423 (ec2276)

Contig has one cdo1423 sequence.

File Edit Format View Help

Query= ec2276
(244 letters)

Sequences producing significant alignments:

	(bits)	Value
GMI_ES01_lrcl2306_239	262	4e-071
GMI_ES15_c8238_156	218	5e-058
GMI_ES02_c16818_188	218	5e-058

>GMI_ES01_lrcl2306_239
Length = 202

Score = 262 bits (132), Expect = 4e-071
Identities = 155/162 (95%), Gaps = 1/162 (0%)
Strand = Plus / Plus

Query: 83 aactctcaagagctggatagaatgtgatggtgagctatgccactattcttaatgcagt 142
sbjct: 1 aactctcaagagctggatcngtataatgtgatggtgagctatgccactattcttaatgcagt 60

Query: 143 cgagtgtactttggagattgggtgtctaaaggacattctgtggagagatcaaagctgg 202
sbjct: 61 cgagtgtactttggagattgggtgtcgaaaggacattcntrggagagatcaaagctgg 120

Query: 203 cattgggggtgtcgaaatggggagattgtggattcatgtcgaca 244
sbjct: 121 cattgggggtgtcgaaaggggagtttgt-gattcatgtcgaca 161

>GMI_ES15_c8238_156
Length = 121

Score = 218 bits (110), Expect = 5e-058
Identities = 118/121 (97%)
Strand = Plus / Plus

Query: 29 tggcattgtatggaaaggatcagcttagggatgagaaggtaagggtggaaagtcaaactct 88
sbjct: 1 tggcattgtatggaaaggatcagcttagggatgagaaggtaatgtggaaagtcaaactct 60

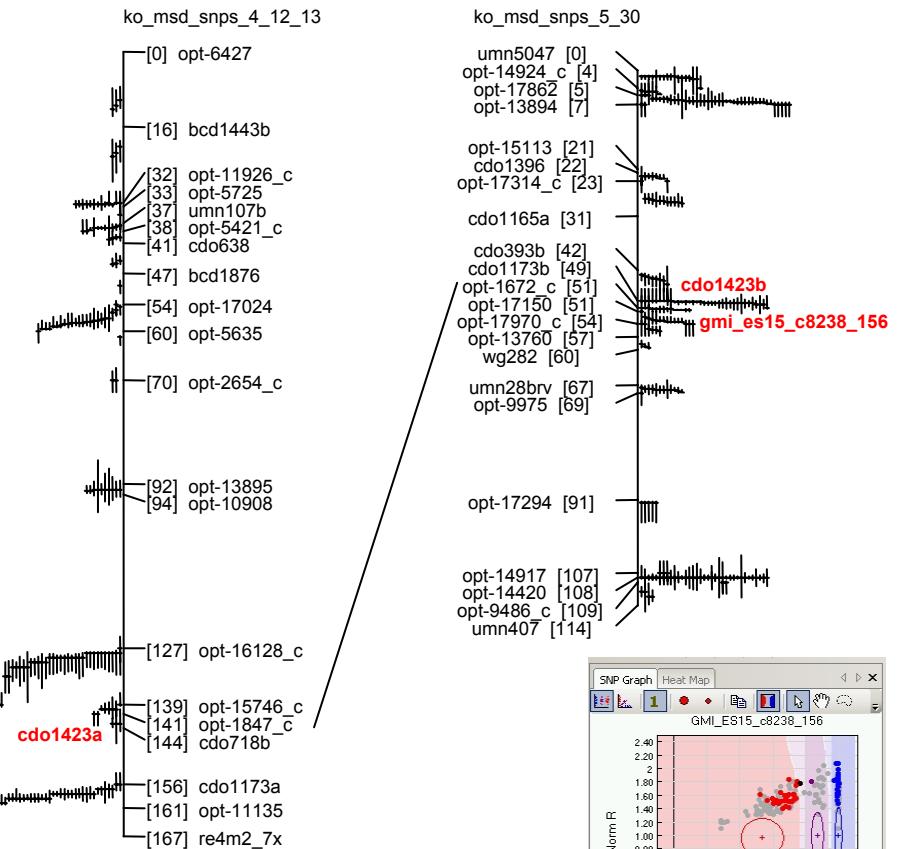
Query: 89 caagagctggatagaatgtgatggtgagctatgccactattcttaatgcagtcgagt 148
sbjct: 61 naagagctggatcagtaatgtgatggtgagctatgccactattcttaatgcagtcgagt 120

Query: 149 t 149
sbjct: 121 t 121

>GMI_ES02_c16818_188
Length = 121

Score = 218 bits (110), Expect = 5e-058
Identities = 118/121 (97%)
Strand = Plus / Plus

Query: 29 tggcattgtatggaaaggatcagcttagggatgagaaggtaagggtggaaagtcaaactct 88
sbjct: 1 tggcattgtatggaaaggatcagcttagggatgagaaggtaatgtggaaagtcaaactct 60



QTL: yld (close to rust/avns), HD

