PRIFYSGOL ABERYSTWYTH UNIVERSITY

Oat MAGIC

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Sefydliad y Gwyddorau Biolegol, Amgylcheddol a Gwledig
IBERS ABERYSTWYTH
Institute of Biological, Environmental and Rural Sciences

Oat breeding at IBERS

- Winter and spring oats
- Husked and naked oats

65% of oats used in UK bred in Aberystwyth

www.QUOATS.ORG

HARNESSING NEW TECHNOLOGIES FOR SUSTAINABLE OAT PRODUCTION AND UTILISATION

❖The ***Qu****ality* ***Oats*** (QUOATS) project brings together research organisations, levy boards, and industrial partners representing the oat production chain and the end users of the crop.

From breeder to plate, this project aims to harness new technologies to advance the yield, value and functionality of oats.

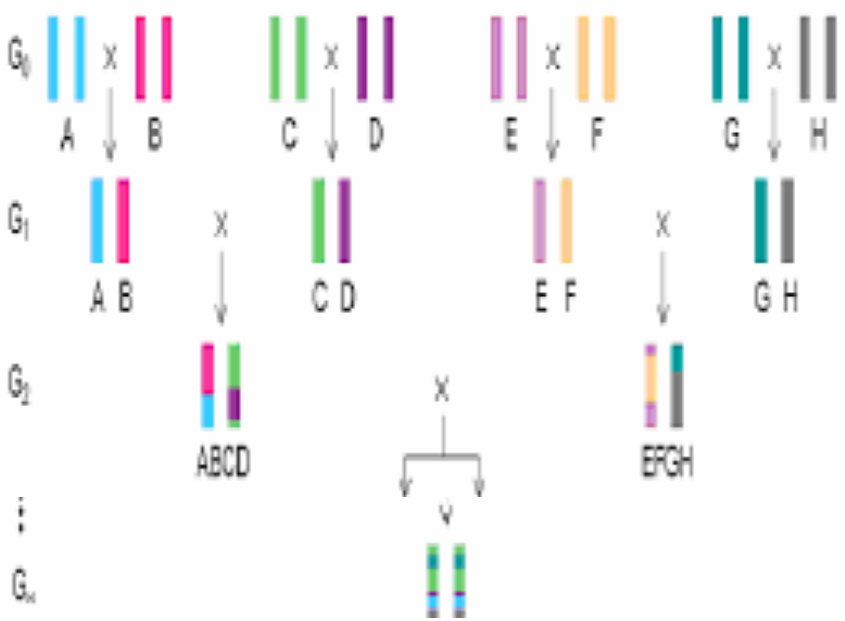
- **In the U.K. oats are grown for human food (70%) and animal feed (30%).**
- **Key traits for improvement:**
  - **YIELD (and its components)**
  - **Lodging resistance (increase yield stability)**
  - **Disease resistance and cold tolerance (increase yield stability)**
  - **Milling quality**
  - **β-glucan (enhanced health benefits)**
  - **Oil content and low lignin husk (increase feed value)**
  - **Nitrogen Use Efficiency (improve sustainability)**

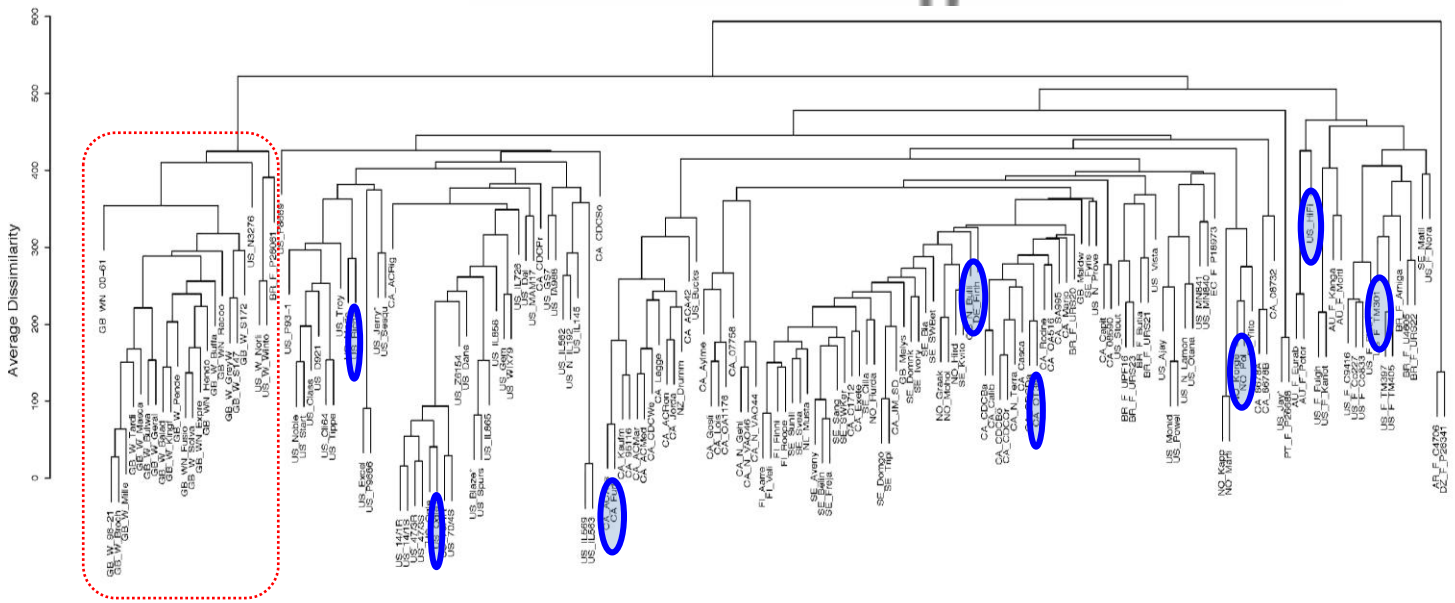
Population development

- **Bi-parental**
- **Association mapping (including spring oat population and European landrace collections)**
- **Wild relatives (diploid, tetraploid and hexaploid)**
- **MAGIC population**
- **Nested Association Mapping (NAM)**
- **TILLING**
- **QTL-NILs**
- **Breeding programme crosses for testing/ validation of MAS and genomic selection**

Spring oat MAGIC population development

8 spring oats chosen to sample world-wide genetic and phenotypic diversity (highlighted in blue in dendrogram from results from DArT analysis)





Winter oats

Stages in MAGIC population development

2009: 1st generation of crosses successfully completed (28 x 2 way crosses)

		1	2	3	4	5	6	7	8
		Ogle	TAM O-301	Ac Assiniboia	HiFi	CDC Dancer	Firth	Pol	CDC SolFi
1	Ogle								
2	TAM O-301	12							
3	Ac Assiniboia	13	23						
4	HiFi	14	24	34					
5	CDC Dancer	15	25	35	45				
6	Firth	16	26	36	46	56			
7	Pol	17	27	37	47	57	67		
8	CDC SolFi	18	28	38	48	58	68	78	

Female panicle selected and emasculated

Set-up cross

Male pollen donor

2010: 2nd generation of crossing successfully completed (28 crosses combining 4 genotypes)

2011: 3rd generation of crossing successfully completed (42 crosses combining 8 genotypes)

1st generation of single seed descent (SSD) harvested October 2011 (population size >500 individuals)

2012: 2rd generation of SSD harvested June 2012

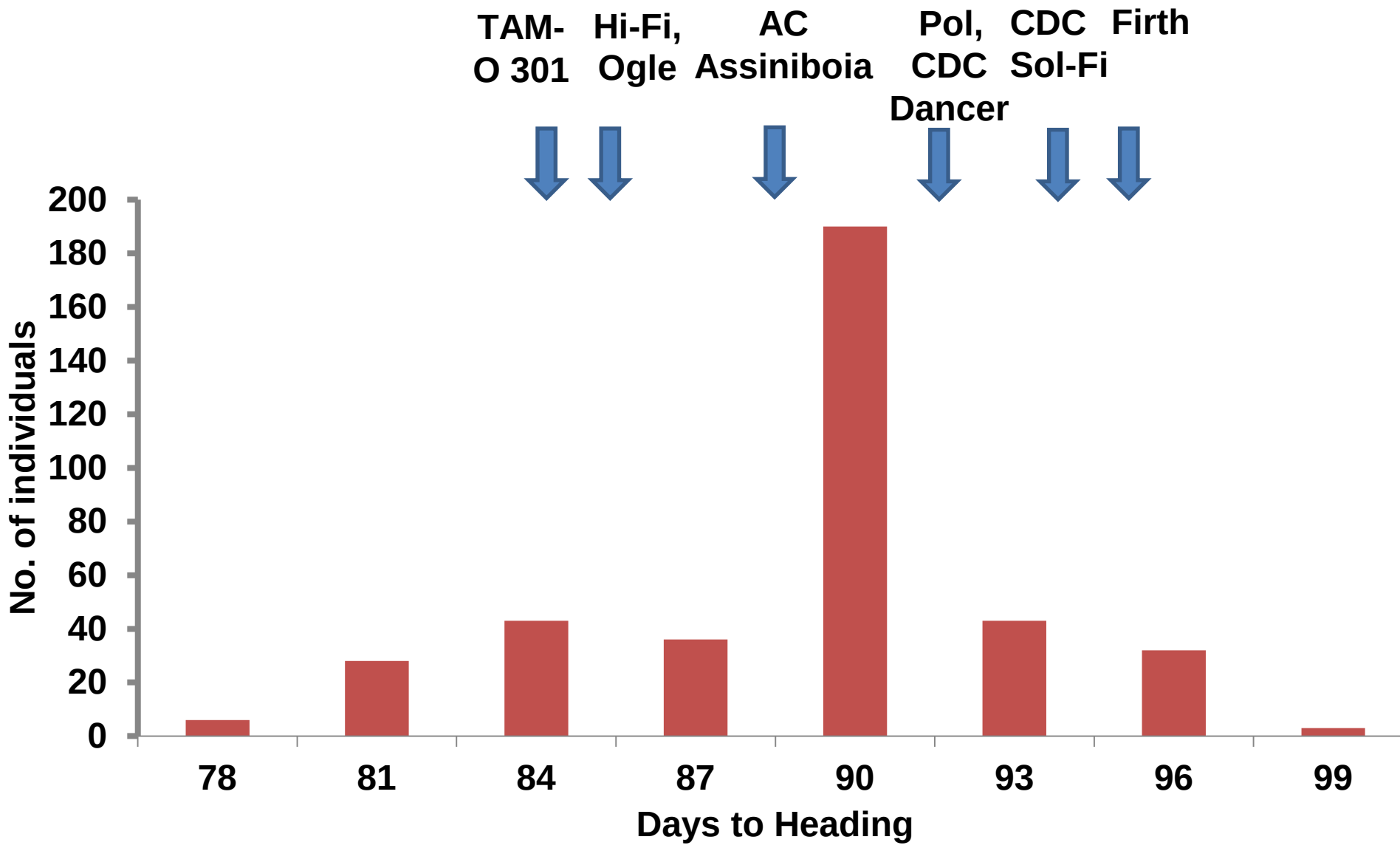
3rd generation of SSD harvested December 2012

2013: 4th generation of SSD sown February 2013 and population size increased

5th generation of SSD due to be sown August 2013

Population on schedule for first field sowing in Spring 2014

Range in flowering time, MAGIC S4s



NAM populations

Common parent is Firth (spring); 17 populations currently at F5 (mostly 60 individuals or less).

Parents - 7 high β-glucan, 2 low β-glucan; 4 landraces; 4 wild species introgressions; 1 naked; all spring

Additional populations in progress (at F3) - three winter crosses; one European elite; one Australian hay cultivar, one putative Turkish ancestral domesticate, one early Scandinavian

Additional F2 progeny being grown of selected populations for finer mapping of selected regions (NUE, equivalents of rice domestication QTL regions) (additional 60-200 as seed available)

Fine mapping using segregating F4s (HIF approach)

Molecular breeding in oats has until recently been limited due to lack of available markers

- SSRs
- DArT (Oat DArT consortium)

Use of NGS for genotyping and comparative genomics has revolutionised this

- Sequence-based SNP markers
  - Illumina oOPA
    - GoldenGate® (3,072)
    - *Infinium*® (5,743)
  - KASPar (874)
- Physically anchored consensus map
- Genotype-by-sequencing (GbyS)

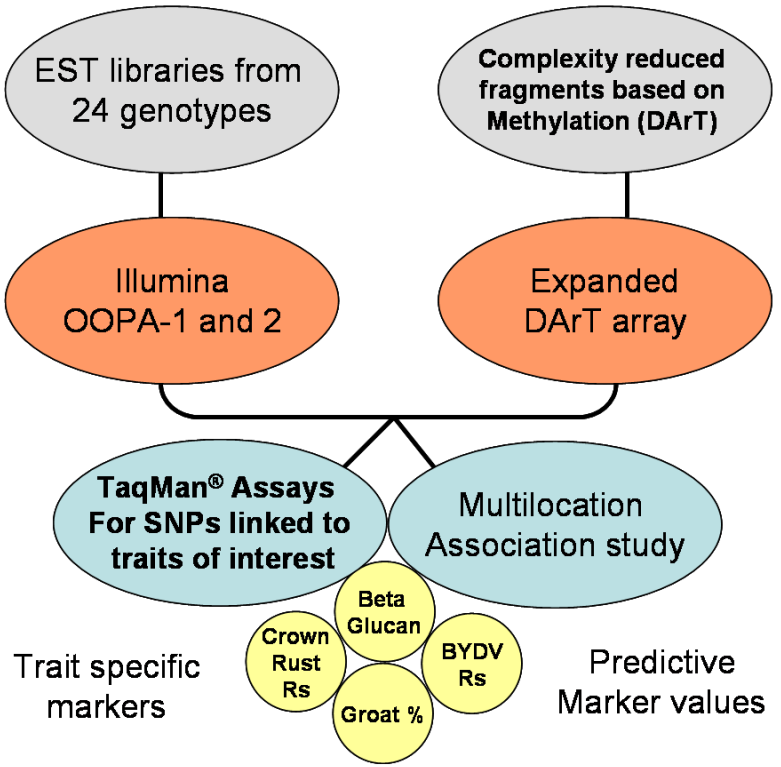
Collaborative Oat Research Enterprise (CORE)

Big Avena SNP Strategy

Eric Jackson
Don Obert
Shiaoman Chao
Nick Tinker
Gina Brown-Guedira
Joe Anderson
Jean-Luc Jannink
Gerry Lazo
Asmund Bjornstad
Mike Bonman
Steve Harrison
Mike McMullen
Jennifer Mitchell-Fetch
Heidi Kaepplar

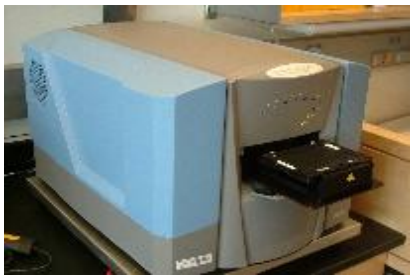
Catherine Howarth
Mark Sorrells
Herb Ohm
Weikai Yan
Paul Murphy
Marty Carson
Mitch Wise
Fred Kolb
Brian Rossnagel
Aaron Beattie
Graham Scoles
Peter Ekstein

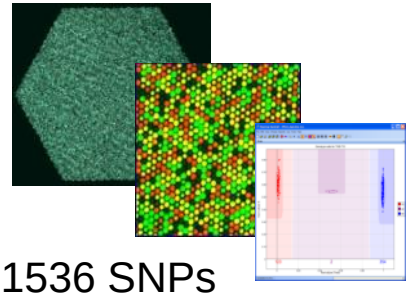
Strategic plan for oat marker-assisted breeding



Tools for Marker-assisted Breeding

Towards genome – wide selection





1536 SNPs simultaneously genotyped

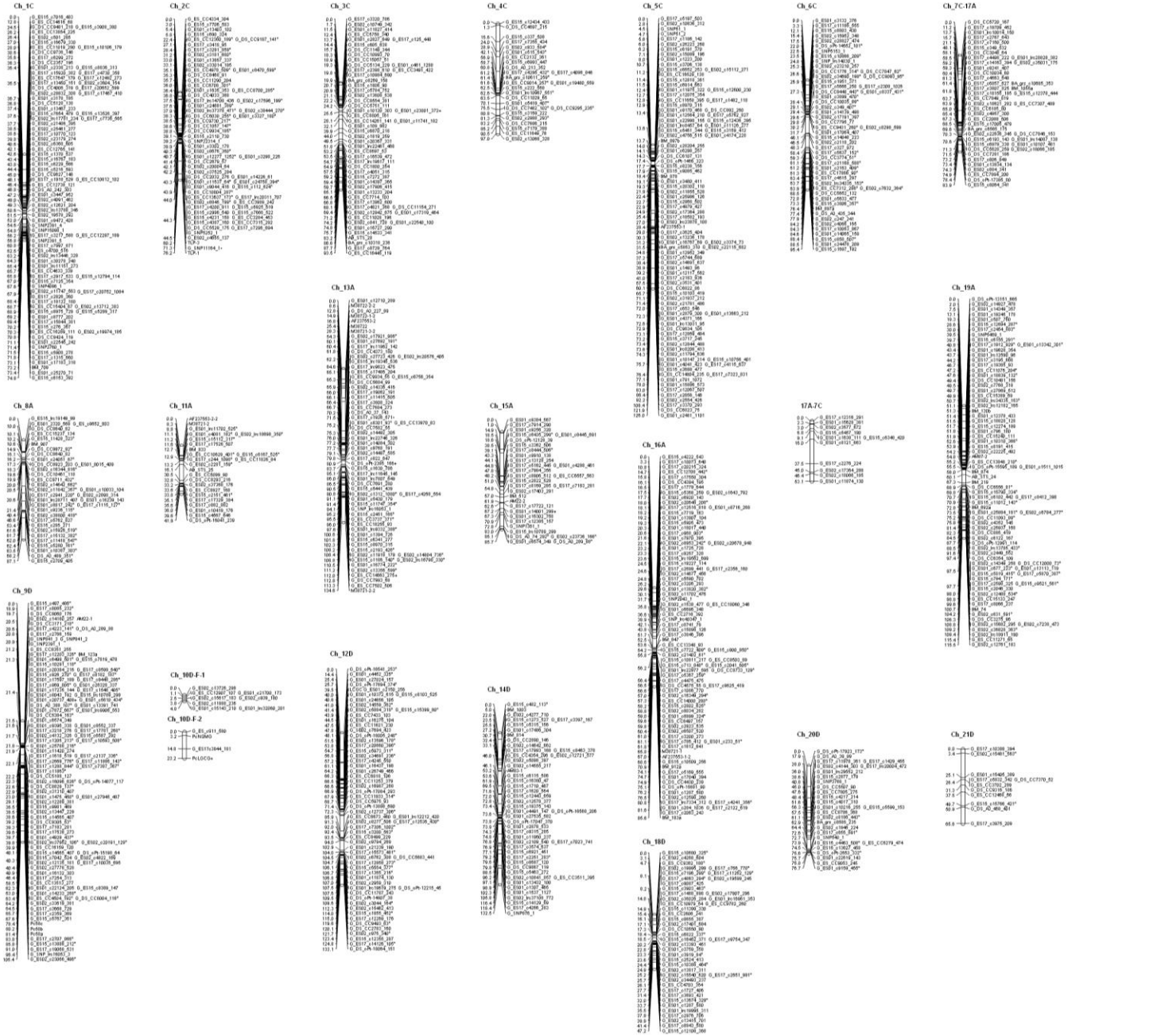
USDA

Prairie Oat Growers Association

North American Millers' Association NAMA

Agriculture and Agri-Food Canada | Agriculture et Agroalimentaire Canada

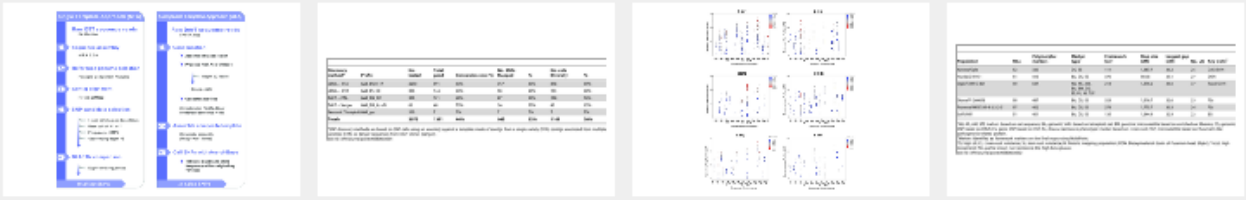
New Oat SNP Consensus Map



RESEARCH ARTICLE

SNP Discovery and Chromosome Anchoring Provide the First Physically-Anchored Hexaploid Oat Map and Reveal Synteny with Model Species

Rebekah E. Oliver, Nicholas A. Tinker, Gerard R. Lazo, Shiaoman Chao, Eric N. Jellen, Martin L. Carson, Howard W. Rines, Donald E. Obert, Joseph D. Lutz, Irene Shackelford, Abraham B. Korol, Charlene P. Wight, Kyle M. Gardner, Jiro Hattori, Aaron D. Beattie, Åsmund Bjørnstad, J. Michael Bonman, Jean-Luc Jannink, Mark E. Sorrells, Gina L. Brown-Guedira, Jennifer W. Mitchell Fetch, Stephen A. Harrison, Catherine J. Howarth, Amir Ibrahim, Frederic L. Kolb, Michael S. McMullen, J. Paul Murphy, Herbert W. Ohm, Brian G. Rossnagel, Weikai Yan, Kelci J. Miclaus, Jordan Hiller, Peter J. Maughan, Rachel R. Redman Hulse, Joseph M. Anderson, Emir Islamovic, Eric W. Jackson [view less]



Abstract

A physically anchored consensus map is foundational to modern genomics research; however, construction of such a map in oat (*Avena sativa* L., 2*n* = 6*x* = 42) has been hindered by the size and complexity of the genome, the scarcity of robust molecular markers, and the lack of aneuploid stocks. Resources developed in this study include a modified SNP discovery method

iSelect Oat 6K SNP Chip Development

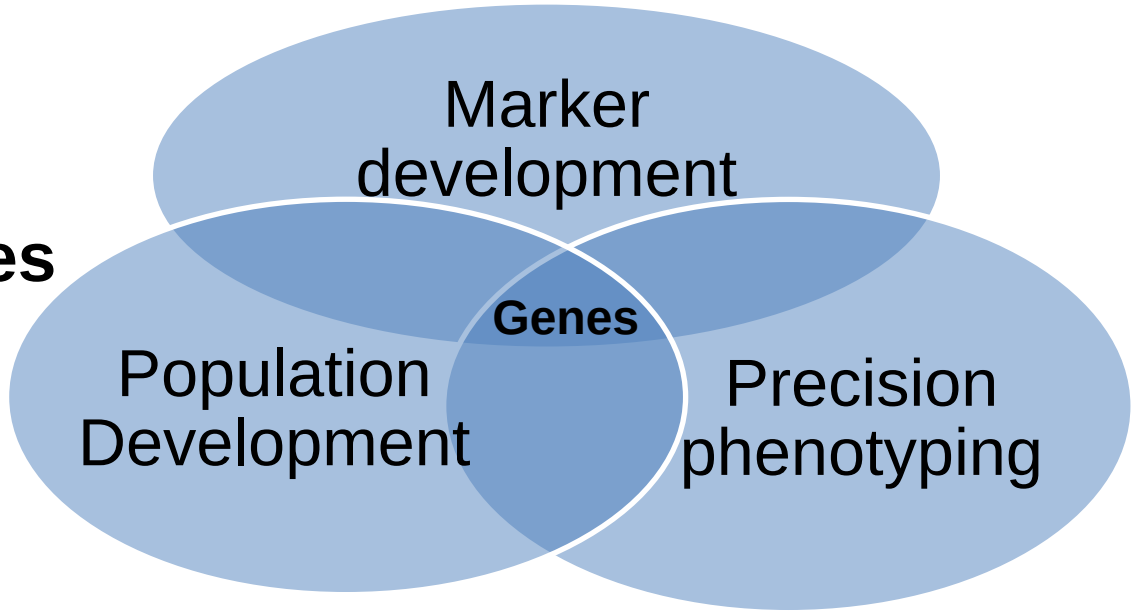
- **Infinium genotyping assay**
- **Contains 5743 SNPs**
  - cDNAs = 3847
  - DArT= 1162
  - GBS tags= 734
  - SNPs from pilot OPAs= 2018
- **6 partial mapping populations genotyped**
- **595 entry association mapping panel genotyped**
- **MAGIC population**

- **872 KASPar assays developed**

High throughput phenotyping

- **Chemical phenotyping**
  - **e.g. GC-MS, LC-MS, FTIR**
- **NIR**
- **Biochemical**
- **Image analysis of seed size/ shape**
- **Phenomics**

- **Field trials**
- **Disease nurseries**



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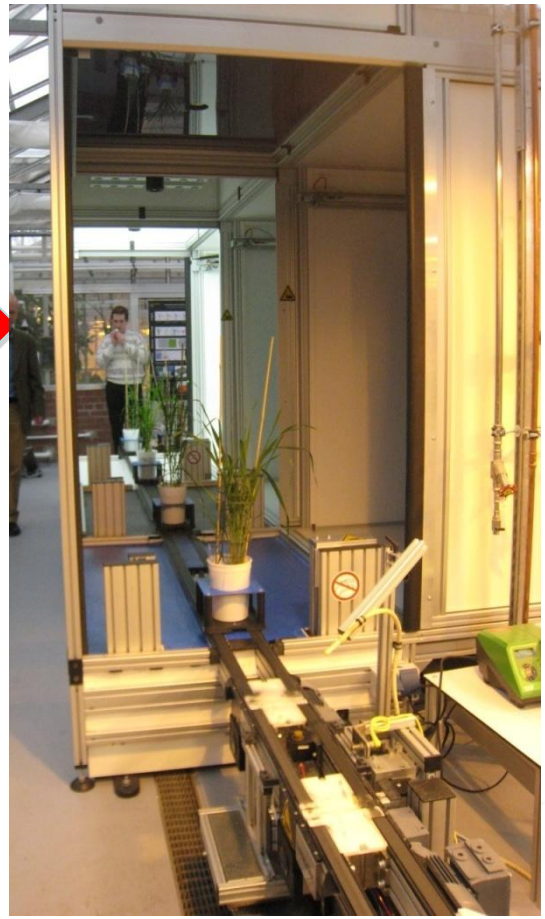
NPPC Capabilities:

A platform for non-destructive dynamic imaging of plant growth & development

- Conveyor based system
- c900 radio-tagged carriages
- Automated delivery to imaging stations



- Climate controlled glasshouses
- State-of-the art imaging stations
- High performance computational facilities to allow storage and retrieval of datasets
- Bio-informatics/ ontology framework
- Flexible layout:- randomisation in time and place

Buffalo x Tardis RIL population and MAGIC parents in phenomics centre

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Web site http://www.QUOATS.org

BBSRC bioscience for the future

defra Department for Environment Food and Rural Affairs

The Scottish Government

Llywodraeth Cymru Welsh Government

LINK collaborative research

ERDF

Llywodraeth Cymru Welsh Government

Ewrop & Chymru: Buddsoddi yn eich dyfodol
Cronfa Datblygu Rhanbarthol Ewrop
Europe & Wales: Investing in your future
European Regional Development Fund

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Technology Strategy Board
Driving Innovation