Oat MAGIC

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Oat breeding at IBERs

- Winter and spring oats
- Husked and naked oats

65% of oats used in UK bred in Aberystwyth
The **Quality 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)
Stages in MAGIC population development

2009: 1\textsuperscript{st} generation of crosses successfully completed (28 x 2 way crosses)

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- **Female panicle selected and emasculated**
- **Set-up cross**
- **Male pollen donor**
2010: 2\textsuperscript{nd} generation of crossing successfully completed (28 crosses combining 4 genotypes)

2011: 3\textsuperscript{rd} generation of crossing successfully completed (42 crosses combining 8 genotypes)
1\textsuperscript{st} generation of single seed descent (SSD) harvested October 2011 (population size >500 individuals)

2012: 2\textsuperscript{nd} generation of SSD harvested June 2012
3\textsuperscript{rd} generation of SSD harvested December 2012

2013: 4\textsuperscript{th} generation of SSD sown February 2013 and population size increased
5\textsuperscript{th} 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

No. of individuals

Days to Heading

TAM-O 301  Hi-Fi,  AC  Pol,  CDC  Firth
Ogle  Assiniboia  Dancer  Sol-Fi

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 $\beta$-glucan, 2 low $\beta$-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)

Strategic plan for oat marker-assisted breeding

EST libraries from 24 genotypes

Complexity reduced fragments based on Methylation (DArT)

Illumina OOPA-1 and 2

Expanded DArT array

TaqMan® Assays For SNPs linked to traits of interest

Multilocation Association study

Trait specific markers

Beta Glucan

Crown Rust Rs

Groat %

BYDV Rs

Predictive Marker values

Tools for Marker-assisted Breeding

Towards genome – wide selection

1536 SNPs simultaneously genotyped
New Oat SNP Consensus Map
Abstract

A physically anchored consensus map is foundational to modern genomics research; however, construction of such a map in oat (Avena sativa L., 2n = 6x = 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
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
Thank you

Web site http://www.QUOATS.org
The QUOATS project, led by Aberystwyth University (IBERS), is jointly sponsored by BBSRC, by Defra through the Sustainable Arable LINK Programme, by European Regional Development Funding through the Welsh Government's Academic Expertise for Business (A4B) Programme, and through the Scottish Government Contract Research Fund with funding from AHDB and industry partners.


Work on disease resistance is an output from a Technology Strategy Board funded collaboration between IBERS, NIAB, TAG and Senova. Project no. 100895