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HARNESSING NEW TECHNOLOGIES FOR SUSTAINABLE OAT PRODUCTION AND UTILISATION

Background

- ❖ 65% of the oats grown in UK are IBERS varieties
- ❖ 140,000 ha grown in UK
 - ❖ (65% winter and 35% spring)
- ❖ 750,000t produced per year and increasing
- ❖ Husked oats for human consumption are increasing
- ❖ Programme: winter, spring, husked and naked
- ❖ Naked oats for poultry

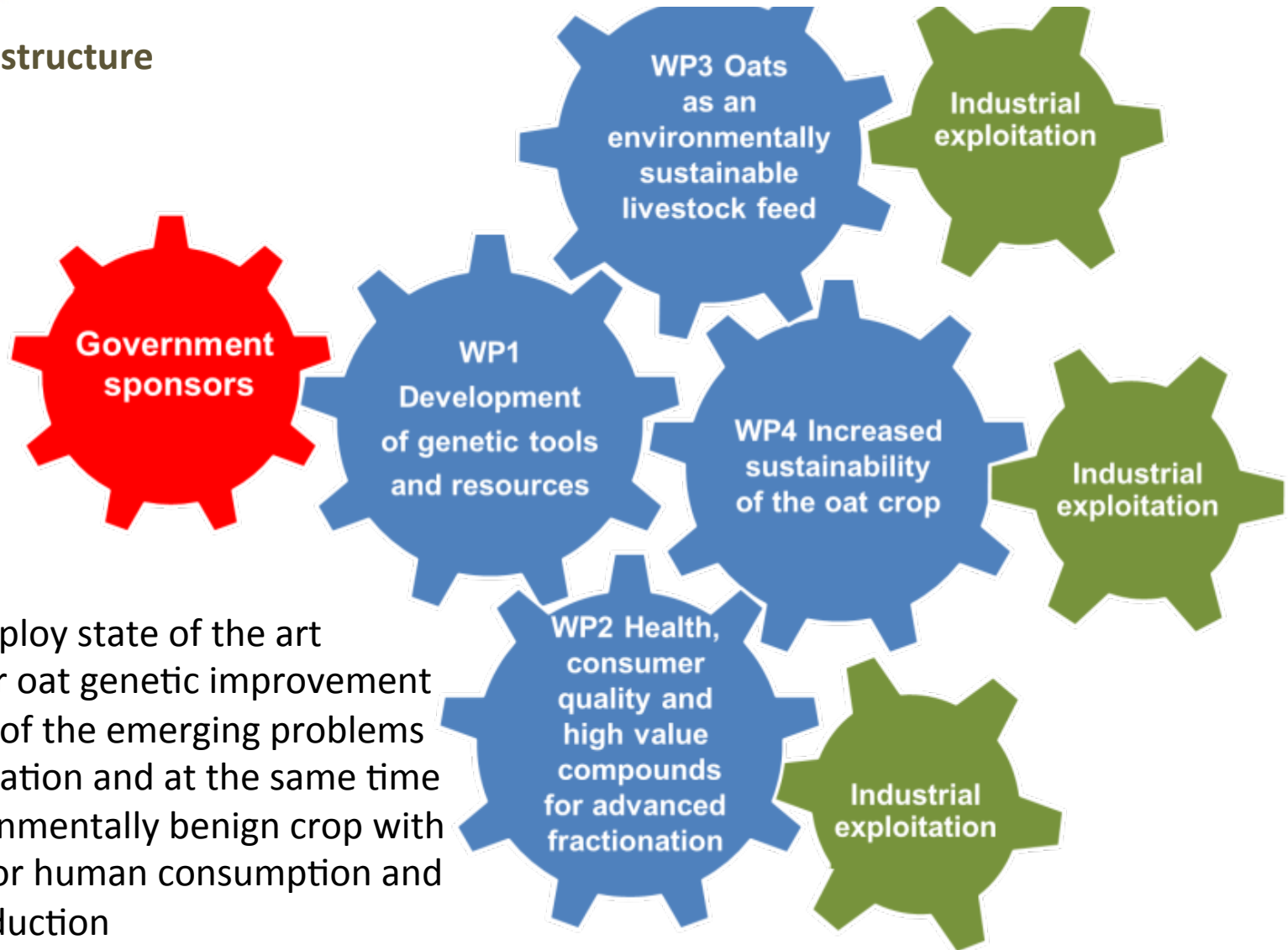




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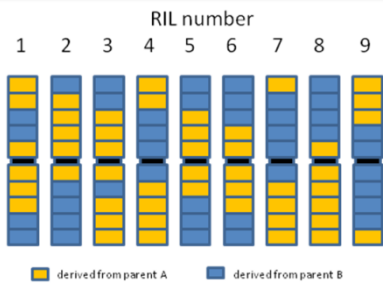
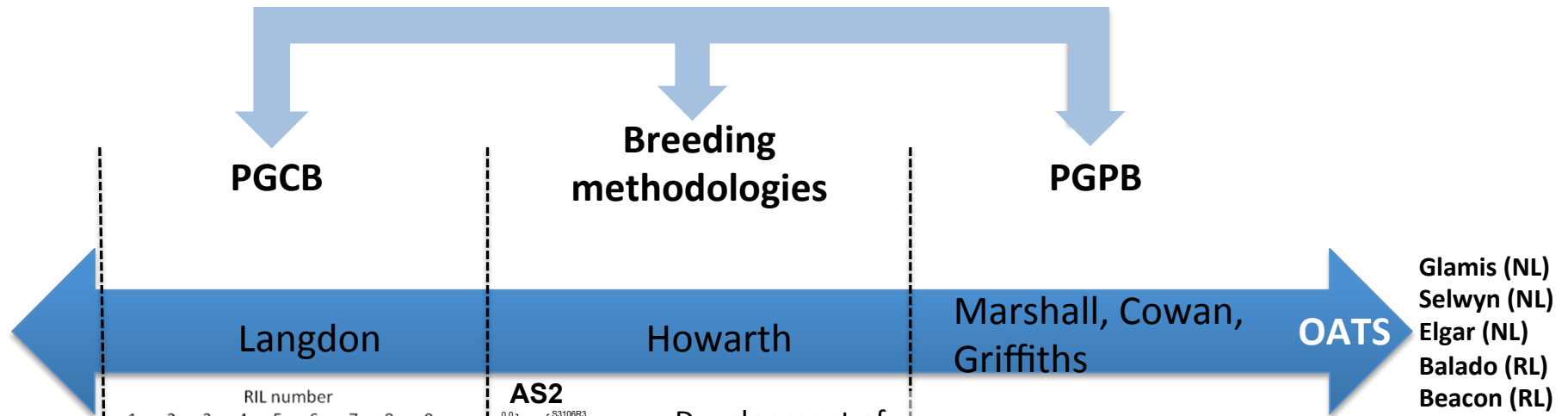
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Project structure

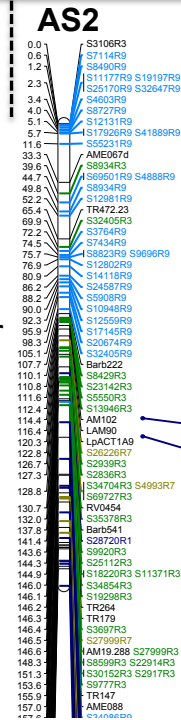


Overview: To employ state of the art genomic tools for oat genetic improvement to address some of the emerging problems with cereal cultivation and at the same time deliver an environmentally benign crop with health benefits for human consumption and for livestock production

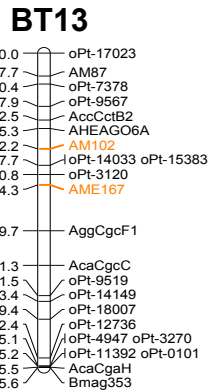
Plant Breeding Pipeline at IBERS



Genomic sequence and zipper techniques are underpinning gene discovery and marker development



Development of QTL-NIL lines for agronomically relevant traits e.g. flowering time



Buffalo **Tardis**

Tardis + Buffalo **Buffalo + Tardis** FT QTL on QTL on LG13 LG13



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Development and use of genetic resources

- ❖ Mapping populations
- ❖ Wild species
- ❖ Experimental populations
 - ❖ MAGIC (spring oats)
 - ❖ NAM



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Use of wild relatives as a source of novel variation

Oats have wild relatives at the hexaploid (6n) level with desirable traits

- ❖ Quality:
 - ❖ High oil
 - ❖ Seed size

- ❖ Resilience to environment:
 - ❖ Drought tolerance
 - ❖ Nitrogen use efficiency
 - ❖ Winter hardiness

- ❖ Disease resistance including durable resistance

- ❖ Diploid: 'A' genome map and QTL analysis
 - ❖ Grain quality
 - ❖ Domestication,
 - ❖ Disease resistance

Summary of validated markers currently in use in oat breeding programme

- Crown rust resistance (improve yield stability)
- Mildew resistance (improve yield stability)
- Height (improve lodging resistance)
- Flowering time (yield component)
- Components of grain compositional quality (grain quality)
- Waxy/ non-waxy leaves (DUS trait)
- Low-lignin husk (enhanced feed value)

How markers are being used:

- Assessment of genetic diversity of breeding programme
- Selection of appropriate parents to use in the crossing programme
- Characterising novel sources of traits
- Identifying/ verifying marker-trait associations
- Back-cross introgression of exotic alleles into a UK adapted background
- Fixing multiple disease resistance alleles at an early stage in the breeding programme
- Identification of individuals at an early stage in breeding programme containing desired allele combinations in conjunction with agronomic assessments.
- Checking uniformity of advanced breeding lines

High throughput phenotyping

Using Lab based NIR

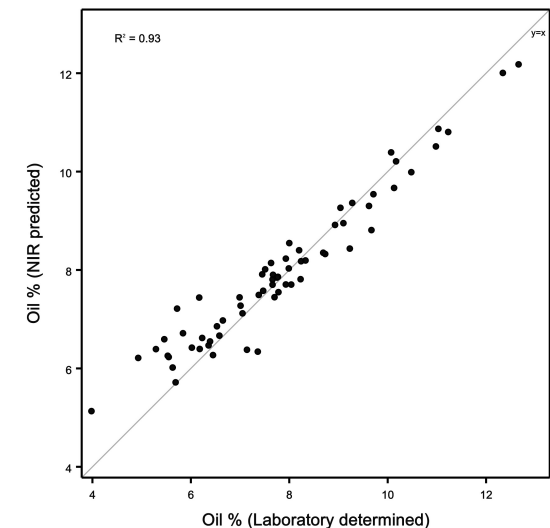


NIR calibrations on whole groats for Oil, Total N, beta glucan, also kernel content on whole grain basis, started whole grain screen for lignin

Wet Chemistry

Oil, protein, beta glucan , lignin

	type	N	Mean (%)	Range	R2	SECV
oil	Whole goroat	888	7.45	2.79-12.11	0.92	0.43
n	Whole goroat	869	1.84	0.8-2.87	0.94	0.09





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Poultry & livestock sectors

- ❖ Reduced environmental impact
- ❖ Alternative feedstock
 - ❖ High oil/low lignin/dwarf





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Oats have a good nutrient content as animal feed

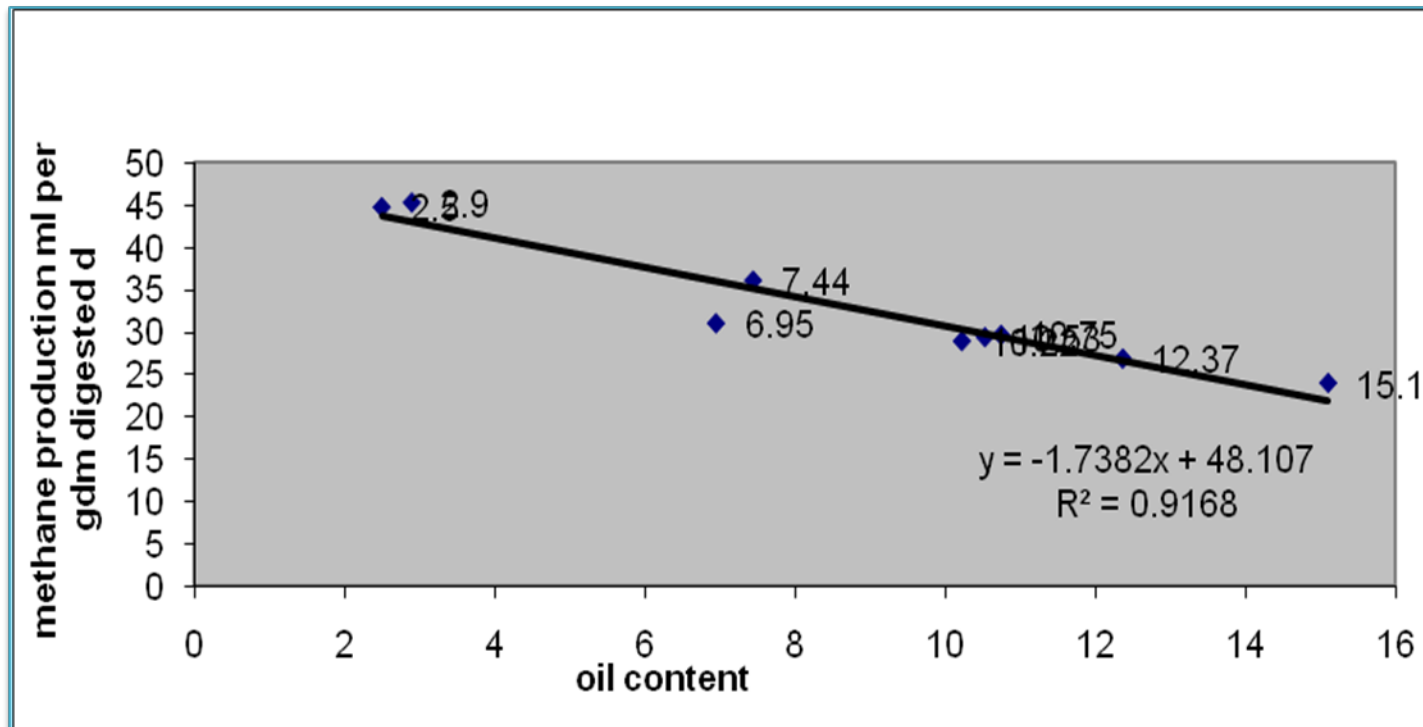
Selection	Crude Protein	Oil (B)	TME MJ/kg as fed
Gerald	11.6	8.1	11.5
Brochan	11.0	7.7	12.4
Hendon	11.3	10.2	15.3
Racoon	14.8	13.6	16.2
01-126Cn1	12.2	12.8	15.8
01-145Cn1	13.4	12.7	15.5
01-146Cn5	12.6	13.2	15.8
Zuton	14.0	9.0	15.4
Lennon	13.7	8.9	15.7
Frontier (wheat)	12.3	2.5	13.9



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High oil content reduces methane emissions

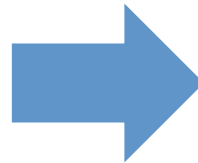
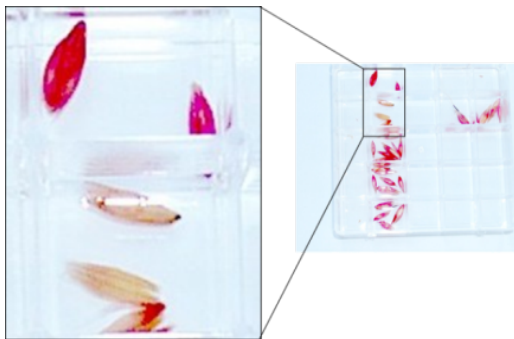




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Low lignin husk is being incorporated into new varieties to improve digestibility and enhance feed value



	1	2	3	4	5	6	7	8	9	10	11	12
A		■	■			■						■
B												
C	■	■	■					■		■		■
D					■							
E	■										■	
F	■		■	■				■	■			■
G	■					■						
H	■						■		S	S		

Low lignin can be detected by colorimetric methods

-time consuming and conducted post harvest

SNP assay
Rapid, accurate and uses leaf tissue

Low lignin and marker assisted selection

- Crosses completed in 2011 were selected for low lignin marker assisted selection (MAS)
 - 038-SO2011/F2
 - 96 progeny were phenotyped as F3 in field 2013, they were also scored using DNA markers of low lignin and crown rust resistance
 - 33 selected for agronomy
 - 19 selected for low lignin
 - 23 selected for crown rust resistance
 - 7 selections combined both agronomy and low lignin traits and are currently growing out in the field as F4s
 - 1 of these selections also has crown rust resistance

Marker assisted selection

Cross	Reason	Agronomy selection	Selection method 1	Selection method 2	Status 2014
011-SO2011	Yield	33	-	-	33 in field, all agronomy
038-SO2011	Crown rust	33	23 crown rust marker	19 low lignin marker	7 in field, all agronomy and low lignin, one with CR allele.
047-SO2011	Mildew	29	20 mildew marker	-	5 in field, all agronomy and mildew allele
050-SO2011	Low lignin	32	53 low lignin marker	67 crown rust marker	9 in field, all agronomy and low lignin, 7 with CR allele
058-SO2011	high oil	24	6 oil analysis	-	3 in polytunnel with agronomy and high oil 3 with high oil for parents
066-SO2011	Mildew	18	13 crown rust marker	-	5 in polytunnel with agronomy and mildew allele
072-SO2011	Beta glucan	29	14 crown rust marker	6 β -glucan analysis	3 in polytunnel with agronomy and high BG 3 in polytunnel with high BG for parents
074-SO2011	Beta glucan	29	6 β -glucan analysis		6 in polytunnel for agronomy and high BG

Marker assisted selection

- 2012 crosses
 - 9 were selected for MAS, progeny are currently being scored for agronomic performance in the field

Cross	Reason	Number rows
042-SO2012	Earliness	91
047-SO2012	Disease	96
049-SO2012	Disease	96
050-SO2012	Disease	93
055- SO2012	Disease	94
056- SO2012	Disease	96
069- SO2012	Low lignin	63
083- SO2012	Beta glucan	96
091- SO2012	Beta glucan	96

Disease pre-breeding

- F2 progeny from the pre-breeding crosses are currently being grown in the glasshouse in trays of 40. This includes the parents
- Leaf samples have been taken and samples are currently being analysed for disease resistance alleles
- Plants without resistance alleles will be discarded
- Single seeds will be grown from plants with disease resistance alleles for the production of disease resistance plants for crossing parents
- The remaining seed will be grown in the nursery for cultivar production

P1	P2	1	2	3	4	5	6
7	8	9	10	11	12	13	14
15	16	17	18	19	20	21	22
23	24	25	26	27	28	29	30
31	32	33	34	35	36	37	38

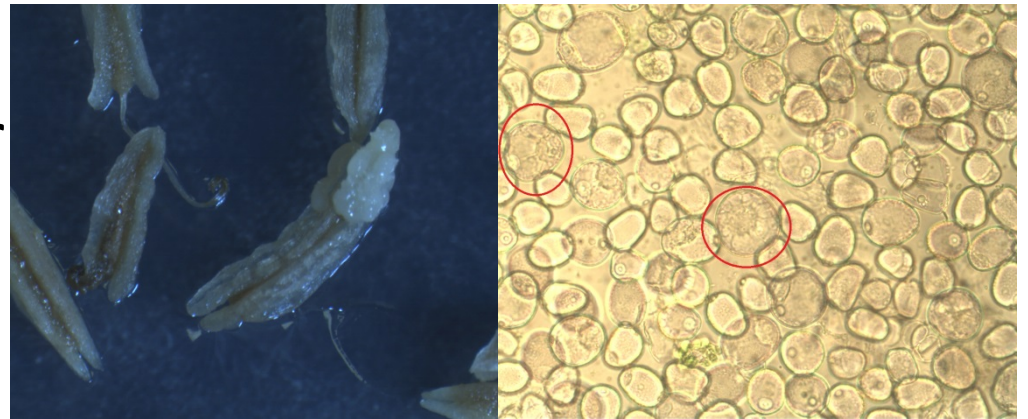
P1	P2		2	3			
7	8	9		11	12	13	14
	16			19		21	22
	24		26	27			
31	32	33				37	38

Single seed decent
for parent production

Remaining seed into
nursery for cultivar
production

Doubled Haploid Production

- Double Haploid production in oats (PhD started feb 2014)
- Joint industry and government funding
- Efficient method of anther culture protocol in oats
- Anther culture
- Microspore culture





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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.

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Thank you



Email syc@aber.ac.uk

Sandy Cowan

IBERS

Aberystwyth University

Gogerddan

Aberystwyth

Ceredigion

Wales UK

SY23 3EE

- Winter oats
- Spring oats
- Husked and naked
- MAS
- Image analysis
- Grain composition
- NIRS