

Final Project Summary

Project title	New wheat root ideotypes for Improved resource use efficiency and yield performance in reduced input agriculture		
Project number	RD-2008-3575	Final Project Report	PR567
Start date	1 March 2011	End date	31 March 2016 (including no-cost extension)
AHDB Cereals & Oilseeds funding	£100,005 (£15,900 in-kind)	Total cost	£1,050,275

What was the challenge/demand for the work?

Cereals account for 70% of the world's food production and in the UK wheat is the single largest crop. Significant challenges for wheat breeding are to stabilise yield in a changing and less predictable climate; reduce dependence on limited water and mineral resources, and to reduce CO₂ emissions. These considerations are tending to drive crop production towards reduced input regimes, particularly the use of NPK fertilisers. This project sought to look at the impact of wheat root growth and morphology on the efficiency of fertiliser uptake and hence crop yield. The overall ambition was to identify a suite of root phenotyping methods suitable for deployment by UK plant breeders and a suite of root phenotypes suitable for deployment in UK agriculture.

How did the project address this?

The level of genetic variation for root development was assessed in a range of wheat genotypes in controlled environments along with the performance of a sub-set of lines with contrasting root characters under field conditions. The project also explored how root growth interacts with environmental variation, differing agronomic practices and the diversity of soil micro fauna and flora; in particular, interactions with mycorrhizal fungi were assessed. Morphological variation for root development was also investigated by growing a range of approximately 100 wheat varieties and breeders' lines in controlled environments.

What outputs has the project delivered?

- Two bi-parental mapping populations have been created as a resource for plant breeders.
- A laboratory (DNA) based method capable of assessing root biomass in field grown crops has been devised and used to quantify root biomass in a series of agronomic and variety field trials.
- Results from the DNA based assay were comparable to those from soil washing experiments.
- The DNA-based assay can distinguish between genotypes (varieties) that differ in root phenotype.
- This technology is a potential tool for plant breeders and for exploring variation within agronomy trials.

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Table 1: Means for μg DNA /g roots in dry soil for varieties by depth from 2014 & 2015 variety trials

Variety	Year							
	Depth (mm)							
	2014				2015			
	0-250	250-500	500-750	750-1000	0-250	250-500	500-750	750-1000
Alchemy	155.8	39.2	37.0	14.5	32.9	16.3	8.4	0.0
Avalon	74.4	29.5	8.5	5.4	153.6	104.3	55.9	9.8
Beaver	42.1	11.7	6.8	5.1	31.5	12.8	0.3	0.0
SHW Xi19 / (Xi19 // SHW-218) >18	70.8	20.3	10.9	3.1	93.3	45.7	11.7	0.4
SHW Xi19 / (Xi19 // SHW-218) >19	98.6	45.1	9.5	14.7	199.6	90.0	55.8	24.2
Buster	50.5	16.9	32.8	4.2	37.8	17.9	0.1	0.0
Cadenza	80.8	46.9	49.8	28.4	22.5	11.8	7.2	6.4
Cappelle Deprez	54.8	14.7	10.0	2.6	81.5	30.2	12.6	0.1
Glasgow	27.5	14.1	4.3	3.5	31.4	14.7	0.7	0.1
Hereward	38.0	10.4	8.0	3.3	22.5	16.3	0.6	1.1
Mercia	38.8	10.4	6.3	4.1	25.2	13.3	5.1	0.1
Mercia Rht8	31.1	13.5	5.0	2.8	90.7	26.7	4.2	0.1
Mercia Rht8 D1b	38.6	20.3	9.9	5.6	60.7	33.8	2.4	0.1
Norman	93.8	34.5	28.3	16.7	124.7	55.8	8.5	2.3
Oakley	60.9	23.5	14.2	15.1	34.0	19.0	1.0	0.0
Paragon	104.8	48.2	14.1	7.3	113.5	54.3	32.0	1.8
Rialto	45.9	37.2	12.8	1.9	25.1	13.9	0.3	0.0
Robigus	34.4	11.6	10.8	3.4	44.6	12.7	0.1	0.0
Savannah	72.3	20.5	19.1	3.6	93.5	65.1	9.4	1.2
Soissons	19.0	25.9	8.7	2.2	57.6	40.9	34.5	0.6
Spark	176.4	62.4	12.3	11.3	13.5	29.0	9.7	3.0
Xi19	109.6	22.5	5.4	14.3	315.9	152.4	7.6	0.1
<i>Mean</i>	69.0	26.3	14.7	7.9	77.5	39.9	12.2	2.3

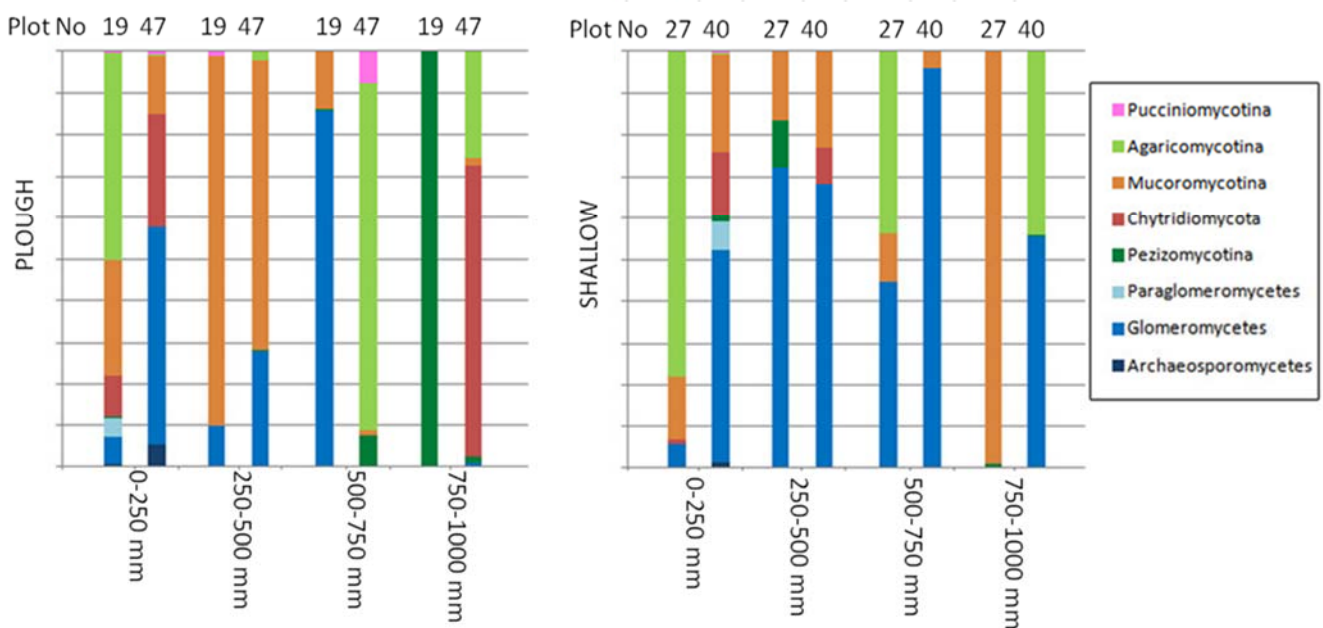
- Plant roots interact with a complex microbial community in the soil, including the arbuscular mycorrhizal fungi (AMF), which can provide demonstrated benefits for plant growth.
- A high resolution method has been devised to characterise the species diversity of arbuscular mycorrhizal fungal communities in plant roots and in surrounding soil.

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- The approach was to amplify a variable region of the 18S ribosomal RNA gene using AMF-specific primers, and then to pool samples and sequence using the Ion Torrent PGM™ platform.
- This tool was used in a number of different wheat trials, looking at contrasts in treatments and varieties. The method revealed high species diversity of AMF in both roots and soil, and high spatial variation in communities from one plot to another.
- Future studies will need to be carefully designed to take this variation into account in order to detect the effects of variables such as depth in the soil, agronomic treatments, or crop varieties.



Depth profile of fungal diversity associated with cultivar Santiago in the 2013 STAR project from replicate plots 19 and 47 (ploughed), 27 and 40 (shallow cultivation). AMF fungi (*Glomeromycota*) comprise the three orders Paraglomeromycetes, Glomeromycetes and Archaeosporomycetes shown in blue.

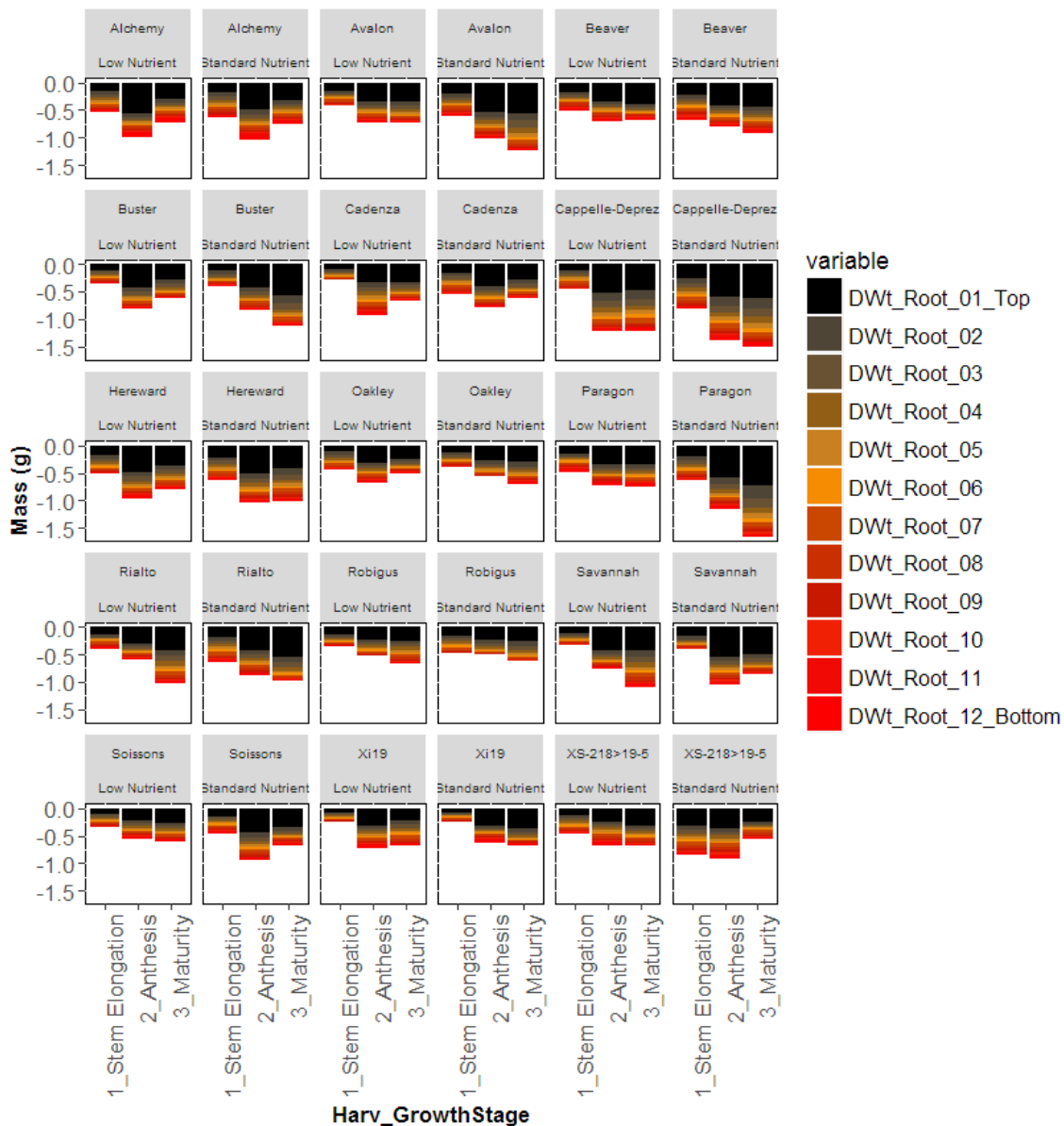
- Quantitative information on root phenotypes was collected in UK wheat varieties at four growth stages, using
 - a flat-bed filter paper based system to characterise roots at seedling stage; and
 - a metre-length rhizotube to characterise roots at stem elongation, anthesis and maturity.
- Root responses to nitrogen supply were also assessed using the rhizotube system.
- Significant differences were found between varieties in root size and in rooting depth and root shape.
- The overall increase in root size with development and depth depended on wheat variety but was significantly affected by the length of the growing season to anthesis.
- Large variations in root biomass distribution and shoot biomass were found between varieties and in response to reduced nutrient particularly in the 5-30cm zone.

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- There was evidence of differential responses of varieties to the reduced N supply. Changes in both root size and shape were found in response to nitrogen treatment, and in addition there was evidence of differences in the type of responses between varieties: some varieties reduced their root biomass under reduced N, others were able to maintain and or redistribute their root systems.



Root dry mass partitioning in 15 wheat varieties grown in rhizotubes with standard nitrogen or low nitrogen nutrient feed at the three different stages of growth when the plants were destructively harvested. Total root biomass is represented by the height of the bars. Individual colour sections represent the proportion of total root biomass contributed by each of the 12 root sections.

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Who will benefit from this project and why?

Taken together, the three strands of this research have created methods and datasets of value to root researchers, agronomists and plant breeders that will furnish a toolkit useful in development of new varieties for UK growers.

The difficulty of measuring root phenotypes has led to their neglect by researchers. Novel methods, including the DNA based assay will enable agronomists and plant breeders to measure and optimise crop root systems and thus improve crop performance.

Wheat roots in the field are colonised by a complex mixture of mycorrhizal fungal species that are present in the soil. While the methods to identify them are now available, more research is needed to understand which are most beneficial to the crop in terms of phosphorus nutrition, drought tolerance and protection against pathogens, and how to encourage these.

Parallel systems such as the rhizotube system enable plant breeders to have a more detailed assessment of root efficiency under different environmental conditions such as N supply (as demonstrated here), and this will assist in selection of varieties with different root properties for use by plant breeding.

If the challenge has not been specifically met, state why and how this could be overcome

The overall ambition was to identify a suite of root phenotyping methods suitable for deployment by UK plant breeders and a suite of root phenotypes suitable for deployment in UK agriculture. While success has been achieved in the first ambition, the second is a greater challenge.

To identify root phenotypes suitable for deployment in UK agriculture effort should be invested through comparative trials and through developing crop models to establish the link between specific phenotypes and economically important traits such as yield, nutrient use efficiency and drought tolerance. Considerable effort has been made in the last two decades to dissect the influence of flowering time and canopy management on yield; these efforts have paid dividends for UK agriculture. The same coordinated approach in root research could be equally rewarding.

Lead partner	The National Institute of Agricultural Botany (NIAB)
Scientific partners	ADAS, The James Hutton Institute, University of York
Industry partners	BASF plc, Frontier Agriculture Ltd, KWS UK Ltd, Limagrain UK Ltd, Monsanto UK Ltd, RAGT Seeds Ltd, and Syngenta Seeds Ltd
Government sponsor	Defra, BBSRC, The Scottish Government via RESAS

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