CEREALS & OILSEEDS

Final Project Summary

Project title	Quantifying rooting at depth in a wheat doubled haploid population with introgression from wild emmer		
Project number	2180003	**Final Project Report**	SR41
Start date	01/09/2013	**End date**	30/09/2016
AHDB Cereals & Oilseeds funding	£37,500	**Total cost**	£75,000, plus an in-kind contribution of ~£100,000 in value

What was the challenge/demand for the work?

Wheat root systems may not be optimal to uptake water from the subsoil due to excessive root growth in surface soil layers and inadequate soil exploration at depth. The optimum root length density (RLD) to uptake soil water has been defined at 1 cm/cm^3 (van Noordwjick 1983) but past studies in UK field environments have shown evidence to support current wheat cultivars having RLDs less than this defined value below 40 cm depths (Hoad et al. 2004; White et al. 2015). This issue is of current importance due to the predicted decrease in summer rainfall in the UK and the sensitivity of anthesis and grain fill growth stages to water limited conditions.

Studying root systems, particularly at mature growth stages in the field, is time and labour intensive. Therefore, there is also a demand for more high throughput and repeatable root assessment methods which are relevant to deep rooting in the field.

How did the project address this?

This project studied the phenotypic and genetic diversity of rooting traits in the doubled haploid (DH) population of Shamrock x Shango. Shamrock has been shown to have significantly greater RLDs at depth compared to other UK grown cultivars below 40 cm depth in the field (Ford et al. 2006). Shamrock has recent introgression from wild emmer (*Triticum dicoccoides*) in which it has inherited a non-glaucous trait, reduction of the epicuticular wax on the leaves and stem. This trait maps to the short of chromosome 2B (2BS) and is associated with a characteristic green colour and delayed senescence. It is hypothesised that Shamrock's superior rooting at depth is associated with the wild emmer introgression, this project aimed to answer this question.

The DH population was grown in the field in two different growing seasons. Rooting profiles to a depth of 70 cm were measured for the DH parents Shamrock and Shango in the first season and rooting between 50-80 cm depth was measured in the DH population in the second season. Rooting traits were also studied in the DH population at the seedling stage and to tillering in root observation chambers.

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The population was genotyped with the help of Bristol University in order to identify quantitative trait loci (QTL) to identify areas of the genome which were contributing to differences in root phenotypes within the population.

The ability to predict genotypic differences in deep rooting in the field was assessed using high throughput canopy measurements of canopy temperature, normalised difference vegetation index (NDVI) and normalised water indices (NWI).

What outputs has the project delivered?

- Shamrock had significantly greater RLDs below 50 cm in the field compared to Shango in the first field season studied. This project identified significant genetic diversity for rooting traits at both early and mature growth stages in controlled and field environments in the Shamrock x Shango DH population. This allowed identification of important QTL which identified areas of the genome that explained the phenotypic variation in the population for multiple seedling root traits in addition to RLD, root dry weight and root diameter below 50 cm depth post-anthesis in the field (Fig 1.).
- QTL for seedling root length and surface area were identified on the long arm of chromosome 2B which has been confirmed in previous wheat seedling studies. QTL for RLD were identified on chromosomes 5D, 6B and 7B which explained between 8.4 and 14% of the phenotypic variation. This is the first study to our knowledge to identify QTL for rooting at depth in field conditions.
- Association of wild emmer introgression on 2BS in Shamrock showed contradictory evidence for its influence on deep rooting. Glaucous DH lines had greater seedling root length but selected non-glaucous DH lines grown to tillering in root observation chambers had significantly greater RLD between 40-80 cm depth (Fig. 2). In the field there was not an association between glaucousness and average RLD within 50-80 cm depth but glaucousness showed a significant interaction of RLD and soil depth because the mean ‘effect’ of glaucousness at 50-60 cm depth contrasted with that at 60-70 cm depth (Fig. 3). Consequently, a QTL was identified on 2BS, in close proximity to the glaucous QTL, explaining variation in RLD within the 50-60 cm soil layer.
- Canopy temperature measured at anthesis associated negatively with RLD at depth in the DH population with greater RLDs being associated with cooler canopy temperatures. However, hyperspectral indices (NDVI and NWI) measured at ear emergence showed contradictory relationships with rooting depending on glaucousness. Potentially, this was an effect of waxiness influencing light reflectance in the canopy and suggests characteristics such as wax and colour need to be considered when using these methods to associate with water uptake when comparing genotypes.

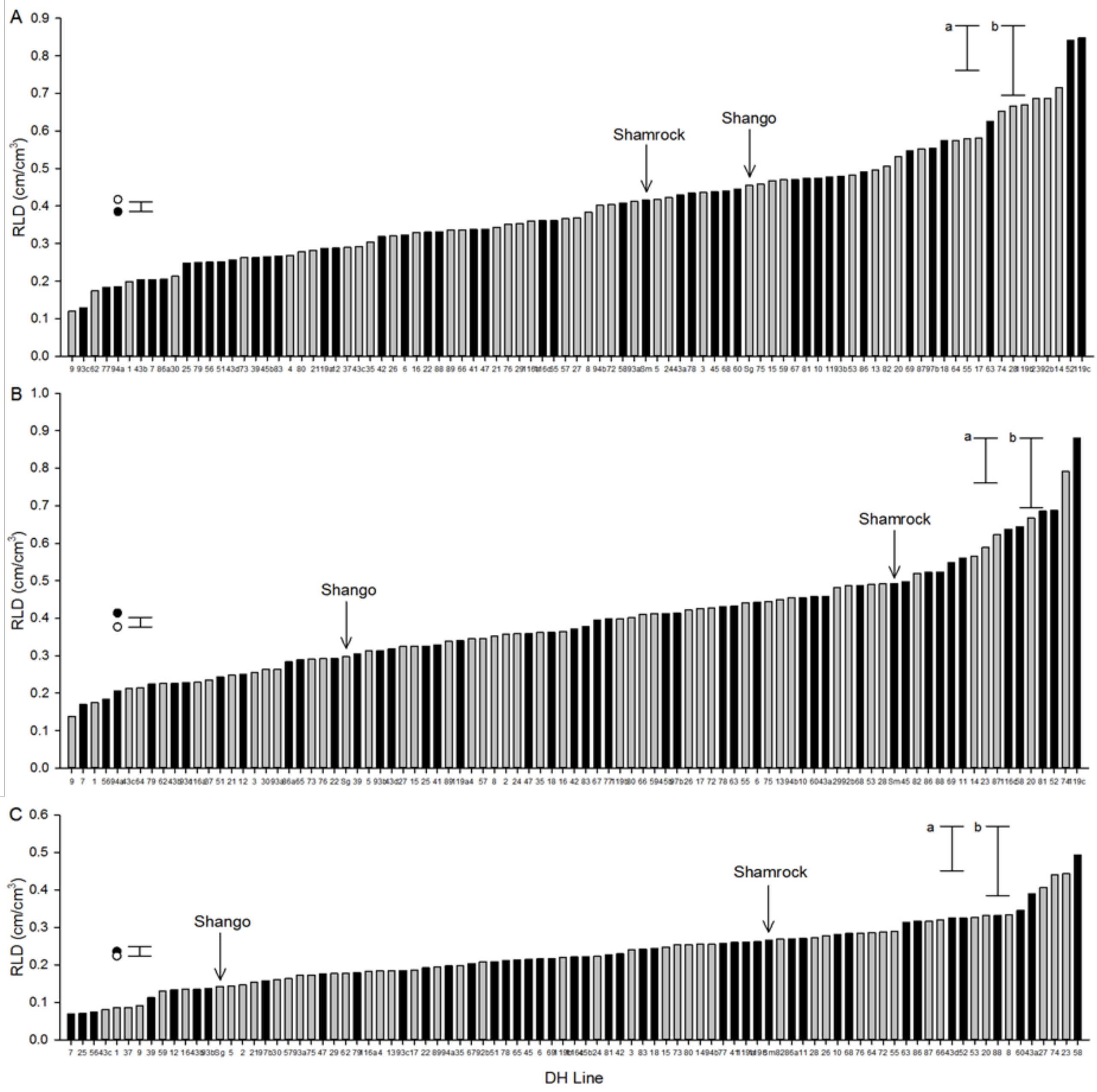

Figure 1. Root length densities (RLD) of a Shamrock x Shango doubled haploid (DH) population in field grown plots at anthesis. A) 50-60 cm depth B) 60-70 cm depth C) 70-80 cm depth. Black bars denote non-glaucous lines and grey bars glaucous lines. Shamrock and Shango means are labelled. Circle points represent means of glaucous (blank circles) and non-glaucous (filled circles) lines. Error bar is 1 SED for line means and glaucous and non-glaucous average; a) SED for Shamrock x Shango, n = 12 and b) SED for DH line, n = 6.

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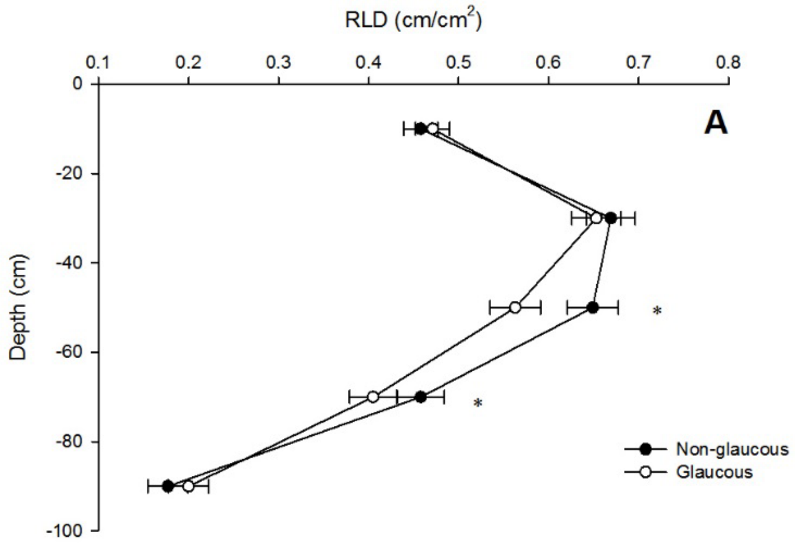

Figure 2. Root length (RLD) of A) Glaucous and non-glaucous selected DH lines, n = 27 and 30 respectively. Values derived from acetate tracings for the root profile of lines grown in rhizotrons. Error bar is 1 SED, * P<0.05.

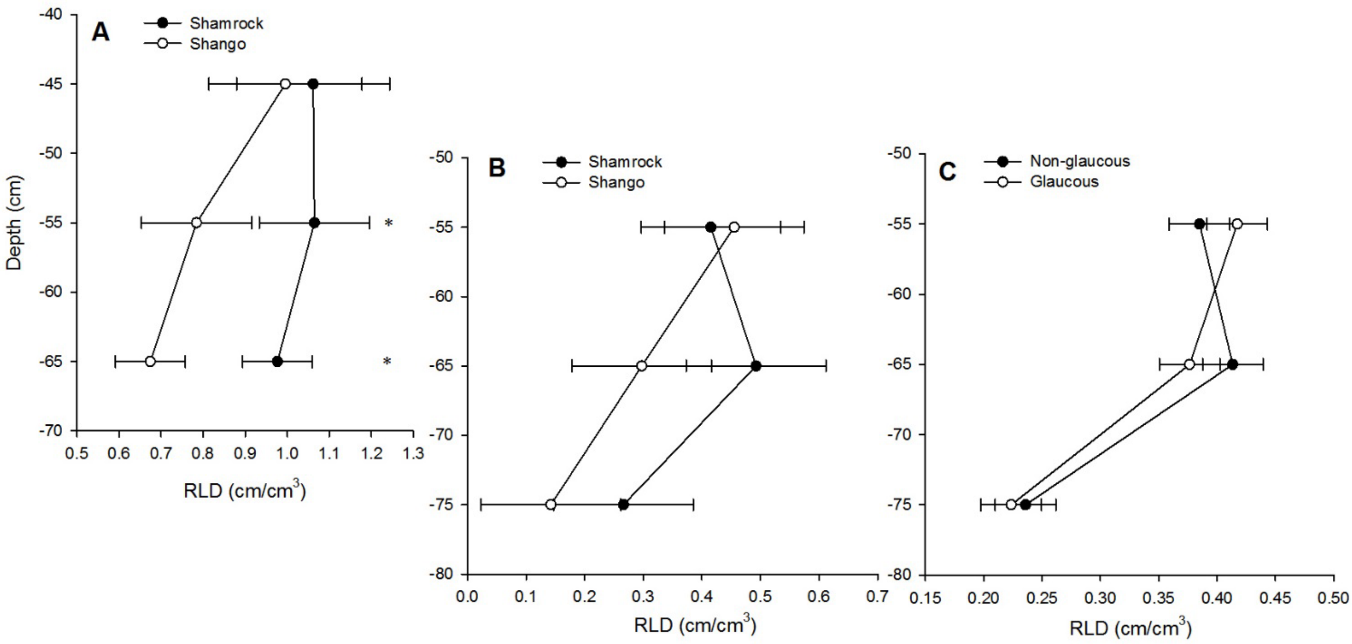

Figure 3. RLDs in field grown plots at anthesis for A) Shamrock and Shango in 2014, n = 32 B) Shamrock and Shango in 2015, n = 12 and C) Glaucous and Non-glaucous doubled haploid lines in 2015, n = 282 and 264 respectively. Error bars are 2 x SED and * P<0.05.

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Who will benefit from this project and why?
• Root researchers will benefit from this project in terms of evidence of QTL for deep rooting in the field, in addition to genetic material which shows transgressive segregation for root biomass allocation in deeper soil layers. This material can be further studied to identify important root architecture promoting rooting at depth or study further genetic influences of rooting. • Breeders will also benefit from this research with identification of important QTL for rooting at both early and mature growth stages which can be integrated into breeding programmes. • This project also draws attention to the importance of improving root allocation at depth in modern crop cultivars to sustainably increase or sustain yields in drier climates.

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

How have you benefited from this studentship?
During this three year project I have had the opportunity to interact with multiple respected scientists within the fields of wheat and root research and from this learn the best methodologies to assess rooting traits in terms of measurements in field and controlled environments as well as statistical techniques to critically analyse the collected data. Being part of Reading University's agricultural department taught me a lot about current issues in UK agriculture in addition to new progressions and knowledge gaps within the industry. From this experience I have obtained a job as a crop scientist within the crop physiology team at ADAS where I am now involved in multiple projects researching different aspects of crop performance and yield enhancement with multiple industry clients and partners.

Lead partner	AHDB and University of Reading
Scientific partners	University of Bristol, IBERS Aberystwyth University
Industry partners	JIC, ADAS
Government sponsor	