

FINAL REPORT

Optimised wheat root architecture for increased yield and yield stability in the face of a changing climate. Previously DAQ00143 **UQ00057**

Project Details

- **Project Code:** UQ00057
- **Project Title:** Optimised wheat root architecture for increased yield and yield stability in the face of a changing climate. Previously DAQ00143
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Summary

This project provided information, selection techniques and strategies to facilitate the development of high-yielding, stay-green wheat varieties for Australian growers through:

- Improved understanding of the relationships between seminal root traits and other root- and shoot-related traits in determining high-yielding, stay-green phenotypes.
- Molecular markers and rapid phenotypic screening methods that allow selection in breeding programs and identification of genetic regions controlling favourable traits.
- Identification of traits leading to high-yielding, stay-green phenotypes for particular target populations of environments using computer simulation studies.

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Conclusions

1. The stay-green trait QTL and the rapid stay-green phenotyping method may be used to select for high yield not only in water-limited situations but in well-watered environments as well.
2. The novel, rapid and robust method to characterise stay-green traits can provide more information about variation between stay-green phenotypes than previous methods.
3. Root trait QTL can be used to select for adaptation to water-limited environments.
4. A number of root, stay-green and yield QTL collocate and so may be used in the process of crop improvement.
5. Computer crop simulation studies reveal that the targeted root traits have substantial benefits not only in the northern region but in all major Australian cropping areas and are rarely predicted to limit yield in any region. In contrast, a number of other root traits were predicted to have little effect. The root-front growth rate confers an adaptive advantage in Western Australia. These results indicate that root architecture traits characterised in this and previous projects are important breeding targets with potential benefit for all Australian cropping regions.

Recommendations

1. Screen a wider range of germplasm for variation in stay-green and root traits.

The project has demonstrated that much value can be added for industry by characterising the specific root traits that lead to the advantage in particular cropping environments (Christopher et al 2008; Manschadi et al 2006, 2008, 2010). However, within the project team, studies have concentrated mainly on a population with known contrast in adaptation to Australian water-limited environments. The germplasm was chosen in part because it is closely related to germplasm used in major Australian commercial breeding programs, making the results highly relevant for commercial breeding. However, the studies have likely examined only a small part of the genetic diversity that exists for root and stay-green traits in wheat germplasm. It is recommended that the phenotyping and genotyping methods developed in UQ00057 now be used to screen a wider range of the genetic diversity in wheat in major production areas to identify and validate stay-green and root QTL and alleles of most relevance for Australian environments.

2. Examine the root architecture of a wider range of wheat genotypes through crop development.

Many crop root research programs have limited ability to examine crop root systems right through the crop life cycle to maturity. They likely fail to identify important root adaptations, particularly traits that are not fully expressed until late development. For example, the important seminal root angle and number traits were originally identified only after the mature root system of the adapted genotype was characterised (Manschadi et al. 2006). The seminal angle and number traits were later linked to surrogate traits detectable during earlier development that provided more efficient screening. In that project, important differences between genotypes in the degree and distribution of root growth post anthesis were also demonstrated. However, many root phenotyping programs only examine roots at early growth stages. Because root studies in later growth stages can be laborious and expensive, germplasm of particular interest, that has been characterised in the field and shows a particularly advantageous and potentially novel root genotype, should be targeted. Germplasm of particular interest with potentially novel root traits should be phenotyped in detail to increase understanding of root development and the genotypic variability that allows increased yield.

3. Use selection methods developed in UQ00057 to incorporate stay-green and root traits into lines for use in commercial breeding programs.

Results indicate that phenotyping methods and QTL for stay-green and root angle traits may be used to develop varieties with superior yield and yield stability under terminal moisture stress. It is recommended that a pre-breeding program should be established to introgress the identified stay-green and root traits into elite backgrounds from each major Australian cropping region.

Outcomes

Results from the project have important implications for wheat improvement in both water-limited and well-watered environments. They indicate that the stay-green phenotype under investigation does not negatively impact yield in high rainfall years. They demonstrate that identified stay-green traits are important for yield even in the absence of terminal moisture stress. Importantly, they can potentially be used to select for high yield in a wide range of well-watered and water-limited environments. Similarly for root traits, computer modelling indicates that the seminal root number and angle traits under study are predicted to have application in important areas in all major Australian cropping regions.

Economic outcomes

The outcomes of this project will lead to increased crop water productivity and reduced seasonal production variability. This will improve income security for producers. It will also increase the ability of the Australian cereals industry to reliably meet demand from export markets as well as domestic food, feed and energy markets making Australian producers more competitive.

Environmental outcomes

Improved crop production from existing land will reduce pressures to expand cropping to more marginal areas. Improved crop water extraction from deep soil layers will reduce deep water drainage which can lead to loss of nutrients as well as sub-soil salinity to aquifers and river systems.

Social outcomes

Increased producer income and income stability will have flow on effects for rural businesses and communities. Improved income security also reduces social stress and financial pressures that can lead to increased incidence of stress and mental illness.

Achievement/Benefit

The project team demonstrated in a previous project (UQ00037) that wheat genotype SeriM82, with greater root length density at depth and narrower seminal root angle, exhibited significantly higher yield than the standard variety Hartog. SeriM82 also retains green leaf area for longer during grain filling and so has a stay-green phenotype (Manschadi et al 2006, 2008, 2010; Christopher et al 2008). However, the relative contribution of root traits to the observed yield advantage and stay-green phenotype were not understood. A major aim of the current project was to confirm that root and stay-green traits were advantageous for yield and to determine whether the stay-green phenotype arises as a consequence of the identified root traits or is it determined independently. In this project a mapping population of 184 doubled haploids from a cross between SeriM82 and Hartog was characterised, firstly for root traits in the laboratory and secondly for stay-green parameters and yield in the field. The findings of the current project indicate that stay-green traits can be linked with yield even in well-watered conditions when root traits are expected to have reduced effect. This indicates that stay-green traits provide an additional selection tool for higher yielding genotypes.

The major achievements of the project relating to each major output are discussed below.

Output 1: Improved understanding of how yield interacts with root and shoot-related traits of wheat

- Stay-green traits correlate with yield even in well-watered environments when root traits are unlikely to have a major effect. This indicates that stay-green traits can affect yield independently of root traits. Therefore, stay-green traits could provide new tools in addition to root traits that would allow selection for high yield. Additionally, stay-green traits may allow selection for high yield in well-watered as well as water-limited environments.
- A powerful and objective method has been developed for detailed characterisation and analysis of stay-green traits by periodic monitoring of the normalised difference vegetative index (NDVI).
- A wheat senescence evaluation tool was developed in computer program R and used to analyse data for more than six parameters related to the timing and rate of leaf senescence (stay-green traits). These include maximum NDVI, maximum rate of senescence, as well as time from anthesis to senescence onset, to mid senescence and to senescence finishing.
- The method allows characterisation of hundreds of yield plots in a matter of hours. Therefore, it is possible to characterise the genotypes in molecular mapping populations.
- Stay-green traits have been characterised for 184 doubled haploid lines from a mapping population made by crossing the stay-green, narrow-rooted genotype SeriM82 with the senescent wider-rooted genotype Hartog. Traits were characterised in six well-watered field environments using the new techniques in 2010, 2011, and in three water-limited environments during 2012.
- Parameters relating to the timing of the onset of senescence and of 50% loss of the initial green leaf area were significantly correlated with yield in trials at a number of different sites and different years. These traits were correlated with yield not only in water-limited environments but also in environments not affected by severe terminal drought. In well-watered environments these parameters do not appear associated with root angle as measured in the laboratory and may be important independent targets for the improvement of wheat yield.

Output 2: Molecular markers and rapid phenotyping methods for root and shoot traits

- A molecular marker map has been constructed for a doubled haploid population of lines developed from crossing SeriM82 with Hartog using 606 diversity arrays technology (DART) markers plus additional simple sequence repeat (SSR) markers.
- Seminal root number and angle have been determined in the laboratory for the 179 doubled haploid lines.
- QTL for seminal root angle have been identified on chromosomes 2A, 3D, 6A and 6B. QTL for root number have been identified on chromosomes 4A and 6A. Root angle and root number QTL are not collocated.
- QTL for stay-green traits in well-watered and water-limited conditions have been identified. In a number of cases QTL for stay-green traits are correlated with yield QTL. In a sub-group of these QTL for stay-green, yield and root traits are collocated. Thus, there is potential to use marker assisted selection (MAS) for stay-green traits and root traits in wheat that lead to higher yield.
- MAS for root traits may be useful to select for yield in water-limited environments.
- MAS for stay-green traits may be useful to select for yield in both water-limited and well-watered environments.

Output 3: Computer simulation modelling

- Computer simulations on the effects of root traits using the Agricultural Production Simulator program (AP-SIM) have been significantly upgraded and extended to include not just the northern grains region, but all major Australian cropping regions.
- Simulations were extended to an increased range of root traits including a) root-front growth rate down the profile, b) water extraction rate in shallow and deep soil layers, and c) water extraction at depth.
- Increased water extraction in deep soil layers conferred advantage to varying degrees in each of the major cropping regions, indicating that the root traits under study in this project leading to increased water extraction are of benefit in all cropping regions. Importantly, they also indicated that genotypes with these traits are rarely predicted to perform worse than genotypes without.
- In contrast, an increased water extraction rate in both shallow and deep soil layers conferred little yield advantage in simulations for any Australian cropping region.
- Increased root-front growth rate down the profile conferred advantage in Western Australia but had a much smaller impact in other regions. This new finding will be useful for focussing wheat improvement for root traits in the west.
- These findings confirm that, of the root traits examined in simulation studies, the traits targeted in this project provide advantage in the widest range of environments. They also identify the root front growth rate as a new potential target for the west.

It is clear that results from this project have important implications for wheat breeding for Australian environments. They indicate that the targeted root traits can be used to select for high yield in water-limited environments for all major regions of Australia. They further demonstrate that selection for stay-green traits can select for higher yield in both well-watered as well as water-limited environments.

Christopher J.T., Manschadi A.M., Hammer G.L., and Borrell A.K. (2008). Developmental and physiological traits associated with high yield and stay-green phenotype in wheat. *Australian Journal of Agricultural Research* 59: 354-364

Manschadi A.M., Christopher J.T., Hammer G.L. and deVoil P. (2010). Experimental and modelling studies of drought-adaptive root architectural traits in wheat (*Triticum aestivum* L.). *Plant Biosystems*, Vol. 144, 458-462

Manschadi A.M., Hammer G.L., Christopher J.T. and deVoil P. (2006). The role of root architectural traits in adaptation of wheat to water-limited environments. *Functional Plant Biology* 33:823-837

Manschadi A.M., Hammer G.L., Christopher J.T., and DeVoil P. (2008) "Seedling root architectural traits and drought adaptation in wheat" *Plant and Soil* 303:115-129

Other Research

1. Screen a wider range of germplasm for root traits

The project has demonstrated that value to industry can be added by characterising specific root traits leading to advantage in target environments (Christopher et al 2008; Manschadi et al 2006, 2008, 2010). However, studies have sampled a limited part of the genetic diversity in wheat. Molecular methods have been used to select relatively small numbers of genotypes representing the majority of the molecular genetic diversity in large wheat germplasm collections such as the INRA core collection developed at the Centre for Genetic Resources. INRA Clermont-Ferrand, France, contains approximately 300 genotypes. This material together with elite lines identified worldwide should be characterised using the lab-based root and field-based stay-green phenotyping techniques to identify potentially superior sources of root and stay-green traits for Australian environments.

2. Examine root architecture of a wider range of wheat genotypes through crop development

It is important to examine root growth right through crop development to maturity to fully understand the effects of roots on water-uptake dynamics, and ultimately on yield. As examining roots in later stages is labour intensive and expensive, the phenotyping should be targeted at genotypes with superior adaptation to water-limitation. Extensive field screening of diverse collections of wheat genotypes for superior adaptation to water-limited environments by Australian and international researchers has identified wheat lines with differences in yield, canopy temperature, heat tolerance, soil moisture extraction and green leaf area retention. Differences in root systems are likely involved in many such lines. Extensive field root coring can be used to characterise tens of lines for root depth and density distribution in the soil. Such a method could detect differences in root architecture at maturity and identify candidates with variation of interest (Watt, et al 2013). Large root observation chambers should subsequently be used to characterise in detail the most promising germplasm, as described by Manschadi et al (2006). A better understanding of differences in root traits expressed at various stages of development will help the identification of new valuable traits and the setting up of new high-throughput phenotyping platforms adapted to screen for traits of most relevance.

Watt M, et al (2013): A rapid, controlled-environment seedling root screen for wheat correlates well with rooting depths at vegetative, but not reproductive, stages at two field sites. (*Annals of Botany* 112: 447-455)

3. Use selection methods developed in UQ00057 to incorporate trait combinations into lines suitable for incorporation in commercial breeding programs

Commercial breeding programs often lack the resources and or expertise to select for additional traits, particularly if the traits are under complex genetic control. The project has demonstrated that stay-green traits and root traits are each under the control of multiple genetic regions. An innovative approach such as using nested association populations with phenotyping and genotyping of progeny during the breeding cycle could be used to speed up trait introgression. Such a strategy has recently been successfully applied to sorghum improvement in Australia to select for improved yield stability under water-limitation and could be transferred to wheat.

Intellectual Property Summary

Lines, methods and markers arising from previous GRDC co-funded projects including UQ00057 are available for future research projects.

Collaboration Organisations

Dr. Ahmad M. Manschadi of the Department of Crop Sciences Division of Agronomy, University of Natural Resources and Life Sciences, Vienna, Austria has collaborated is both a collaborator and project participant. Dr Manschadi has provided vital information on root phenotyping techniques and is co-author of our publication.

Dr Mathew Reynolds, Leader of Physiological Breeding Program, at the International Centre for Maize and Wheat Improvement (CIMMYT), Mexico has provided methods of field evaluation of stay-green and recommendations about genetic variation for root and stay-green traits.

Additional Information

Christopher J.T, Christopher M.J., Jennings R., Jones S., Fletcher S., Borrell A.K., Manschadi A.M, Jordan D., Mace E., Hammer G.L. (2013). QTL for root angle and number in a population developed from bread wheats (*T. aestivum*) with contrasting adaptation to water-limited environments. *Theoretical and Applied Genetics* 126:1563-1574.

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- Wasson A, Richards R, Chatrath R, Misra S, Sai Prasad S, Rebetzke G, Kirkegaard J, Christopher J, Watt M. (2012). Traits and selection strategies to improve root systems and water uptake in water-limited wheat crops. *JxB* 63:3485-3498
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