INTERNATIONAL WHEAT YIELD PARTNERSHIP

Abstracts of Funded Projects for the IWYP 1st Competitive Call

IWYP61FP

Title

Realising Increased Photosynthetic Efficiency to Increase Wheat Yields

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Numerous studies of the effects of CO₂ enrichment in the field, including wheat, show that increased crop yields can be obtained through increased photosynthetic carbon assimilation. Furthermore, experiments conducted in the applicant’s laboratories on transgenic plants, in which activities of individual enzymes were altered, provided evidence that manipulation of the Calvin cycle has the potential to improve photosynthesis and increase plant productivity. These studies together with integrated systems modelling identified photosynthetic carbon assimilation as an untapped target to increase photosynthetic efficiency and yield by as much as 60%. The overall aim of this project is to exploit the extensive knowledge of photosynthesis and experience gained from its manipulation in model species to produce wheat plants with enhanced photosynthetic performance and increased yield. We will undertake growth, yield, physiological and molecular analysis of transgenic plants in high-light controlled environments, and test the most promising events these in replicated field trials in the UK and in Illinois. Given that our aim is to further increase yields we will be using two modern top yielding cultivars one adapted to W. European temperate conditions and the other to the US Midwest with high humidity and high temperature. Each will be tested in replicated trials in their “native” environments. Use of these two very
different growing environments and genetic backgrounds will test the broader efficacy of the transgenic modifications to provide a sound basis for the production of higher yielding varieties for the developing world. This project not only has the potential to produce a step change in yield of wheat to meet the predicted future needs to feed the growing population, but will also provide the means to achieve this within the timescale needed.

IWYP76FP

Title
Molecular Dissection of Spike Yield Components in Wheat

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Urgent action is needed to sustainably increase global wheat production. However, limited knowledge of the genes controlling wheat yield is hampering efforts to advance towards this goal using science-based solutions. The aim of this proposal is to define, characterize, and manipulate genes that regulate the early stages of spike and carpel/grain development and that govern spike yield components (grains per spike and grain weight). We will apply innovative sequencing-based approaches to exploit novel sources of induced genetic variation in these two traits to increase the genetic yield potential of wheat. We will test if this potential is realized in elite wheat varieties. Understanding the genes controlling different yield components will allow us to combine and exploit variation across all three homoeologous genomes, and to overcome the perennial problem of functional redundancy observed in polyploid wheat. The combination of novel allelic variants in genes affecting grain number and weight represents an opportunity to generate significant increases in wheat yield potential not previously exploited in wheat improvement programmes.

We propose an ambitious programme that will address the following specific objectives to increase wheat grain yield potential:

1. Define the changes in the wheat transcriptome associated with early spike and grain development
2. Identify key genes determining spike yield components through forward genetics
3. Implement reverse genetic tools to discover and characterise genes improving spike yield components
4. Engineer and deploy allelic combinations for increased wheat yield potential and characterise their pleiotropic effects and epistatic interactions

The main direct outcomes expected from this research are:

- Identification and characterisation (molecular, physiological and agronomic) of novel gene variants controlling wheat spike yield components
- Creation of double and triple mutants targeting all homoeologs for the selected genes to overcome functional redundancy
- Generation of adapted germplasm with new allelic combinations affecting complementary spike yield components

IWYP60FP

Title
Improving Yield by Optimising Energy Use Efficiency

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Greater than 85-90% of the energy captured by plants is used in ‘futile cycles’ and high-cost cellular processes, such as transport of nutrients and respiration, meaning about only 10-15% is allocated to yield. Thus, any small gain in energy redistribution and use for a costly process can have a marked positive impact on biomass accumulation and yield. Improvements in energy-use efficiency (EUE) can be achieved at the cell, tissue and whole-plant levels, with respiration being a prime target. Our initial screening of 138 Australian commercial cultivars has revealed a two-fold variation in rates of leaf respiration (Fig. 1), three-fold variation in the ratio of respiration to growth rate (Eqn 1) during early development, and significant heritability of 35%; this demonstrates there is untapped genetic variation in EUE amenable to fine-tuning and optimisation of biomass accumulation in the lead-up to anthesis, with concomitant positive knock-on effects on yield.
Wheat yield is limited by carbohydrate supply to the filling grain, which in turn depends on whole-canopy photosynthesis. Pre-breeding for photosynthetic traits typically focuses on traits of sun-exposed leaves in the upper canopy. However, potentially far greater gains could be made by focusing on the distribution of photosynthetic nitrogen, and photosynthetic capacity (PC), among different canopy layers. A vast body of literature, overlooked in crop pre-breeding, shows that whole-canopy photosynthesis is substantially reduced by inefficient vertical distribution of PC in relation to irradiance: specifically, upper-canopy leaves tend to have too little photosynthetic N, and lower-canopy leaves tend to have too much. Redistribution of this capacity could increase canopy carbon uptake and NUE by nearly 20% without affecting the total supply of N available for grain filling.

We propose to identify variation in the efficiency of canopy PC distribution, coupled to yield, by applying a novel and innovative rapid phenotyping screen for canopy PC distribution to a set of 310 diverse wheat genotypes, including lines in agronomically acceptable backgrounds developed from wild wheat, wheat relatives and ancestors, and all parental materials. We will then characterise canopy physiology and structure in detail for a subset of the most contrasting genotypes to identify key underlying traits and genetic markers, and deliver the resulting knowledge, germplasm and tools to our partners in the breeding industry in Australia and India, CIMMYT and to the IWYP.
Phenotyping photosynthetic characters from diverse lines of wheat will be combined with next generation genetic approaches to enable the identification of markers and genes associated with each trait. Such knowledge will enable combinations of these traits to be rapidly incorporated into elite wheat lines to increase yields based on improved photosynthetic efficiency. Moreover, identifying the genes and mutations responsible for the traits will provide an understanding of the biology underpinning the trait and the ability to use precision genome engineering tools in the future. The project will identify wheat material, develop markers and build bioinformatics tools. All of this will be made available to the international community via CIMMYT and iPlant. The project builds upon high throughput methods and knowledge developed by the wheat yield consortium and utilises exome capture technology to discover the relevant genetic information in a cost effective manner. The project combines the diverse expertise in photosynthesis, genetics, wheat physiology and breeding from Lancaster, Liverpool, ANU and CIMMYT and leverages off related existing research.
Aim: Enhancing wheat yield by exploiting and building synergy of three high value genes (AVP1, PSTOL1 and NAS) and enabling molecular breeding.

Project Objectives:

1. Develop two-gene and three-gene pyramiding combinations of AVP1, PSTOL1 and NAS using available transgenic wheat lines and quantify additive effects on yield in multi-location field and greenhouse trials (as a proof of concept).
2. Identify wheat orthologs and allelic variants of TaAVP1, TaPSTOL1 and TaNAS and design molecular markers to the best alleles for marker-assisted breeding.
3. Provide basic understanding of the physiological and molecular mechanisms behind improved yield and select wheat lines with the best allelic combination and field performance.
4. Assess the necessity for using genome editing technologies to optimize gene function and enhance positive effect on wheat yield by modifying expression of the wheat alleles.

The genes Vacuolar Proton Pyrophosphatase 1 (AVP1), Phosphorus Starvation Tolerance 1 (PSTOL1) and Nicotianamine Synthase (NAS) have been shown to improve plant biomass production and grain yield. Over-expression of these genes results in improved biomass production and grain yield in a range of plant species, including cereals (rice, barley, wheat), in optimal growing conditions. The enhanced yield of the plants is believed to be due to improved sugar transport from source to sinks (AVP1), enhanced root growth and nutrient uptake (AVP1, PSTOL1) and increase in shoot biomass and tiller number (AVP1, PSTOL1, NAS2). Identifying and pyramiding the wheat orthologs of these high-value genes provides a real opportunity to produce wheat with significantly improved field performance and higher grain yield.

Transgenic wheat plants with constitutive transgene expression of the above genes have been generated and are available for this project. Preliminary data for AVP1, PSTOL1 and NAS, derived from soil-based phenotyping experiments, already indicate that the genes are functional in wheat, improving nutrient uptake, biomass production and grain yield. Based on bioinformatics analyses of wheat genomes and evidence from other monocots, we have identified the evolutionarily conserved putative wheat orthologs of the three genes and allelic variation is likely to exist in wheat as has been observed in other species, e.g. the AVP1 homolog HVP10 in barley or the PSTOL1 homologs in sorghum (see below).

Within this project we will provide the opportunity to use available transgenic wheat lines as a proof of concept for the optimal combination of the three genes to improve wheat yield; while in parallel, screening of diverse germplasm will identify the best natural alleles of the wheat genes for introgression into elite wheat cultivars and breeding lines.

Within this project, we will also characterize the mechanisms underlying the observed positive gene effects on plant growth and yield, and will use the data derived from the transgenic lines to guide development of molecular markers to the best alleles of the wheat homologs of AVP1, PSTOL1 and NAS2, to facilitate the production of non-GM wheat line with enhanced grain yield.
IWYP25FP

Title

A Genetic Diversity Toolkit to Maximise Harvest Index by Controlling the Duration of Developmental Phases

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A comprehensive range of genetic and genomic resources have been brought together in this work having been specifically designed to maximise grain yields by optimizing plant and crop phenology to capitalise on enhanced carbon capture and biomass achieved elsewhere (IWYP Area C). The genetic architecture of adaptive traits for wheat will be defined with marker tagged variability available for the timing and duration of developmental phases, from the vegetative to reproductive transition (double ridge) until anthesis. The yield implications of variation in each of these steps will be validated using Near Isogenic Lines and modelling of adaptation will inform fine tuning of best phenology trait combinations as well as coarse tuning of heading date for stress avoidance and agronomic fit. New molecular targets, acting downstream of Ppd-1 and Vrn-1 in the phenology genetic network will be targeted to minimise pleiotropy and trade off. Novel molecular markers will be used to introgress new alleles into high biomass backgrounds to establish the use of these innovations in experimental breeding. A model of full community accessibility to knowledge and resources will ensure high agricultural impact and the long-term goal of harvest index consistently reaching 60% in high yield potential environments.
IWYP48FP

Title

Wider and Faster: High-Throughput Phenotypic Exploration of Novel Genetic Variation for Breeding High Biomass and Yield in Wheat

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The rate of genetic progress in biomass production per unit hectare of wheat must be improved if we are to meet global targets for grain production. However, selection for domestication traits has reduced the genetic variation in modern wheat cultivars, a fact that could severely limit the future rate of genetic gain. Wild relatives and landraces of wheat carry considerably more variation for target traits than modern day wheat varieties including substantial variation in photosynthesis; a direct factor in biomass production. The aims of this project are to (1) Generate, using wide crosses, landraces and existing cultivars, lines with substantial variation in their photosynthetic
properties. (2) Use novel high throughput screening techniques to identify progeny with enhanced photosynthetic capacity and efficiency, robustly expressed across environments, and which increase wheat biomass production and yield. (3) Investigate the genetic basis of the photosynthetic variation and with the IWYP HUB integrate these discoveries into a pre-breeding and breeding strategy. (4) Coordinate key centres of excellence to create a virtual crop photosynthesis hub for high throughput screening and analysis.

This strategy will enable our consortium to meet all of the requirements of the IWYP Research area A/B call, in particular uncovering new genetic variation in relatives and ancestors of wheat and novel optimized smart screens for photosynthesis.