

Chasing wheat yields in challenging environments

Project deliverables:

This project aims to develop potential high yielding lines using marker-assisted selection for yield components integrated with modern high through-put phenotyping technologies, thereby increasing the yield potential of future South African wheat cultivars to the benefit of the entire wheat industry.

Introduction

Dryland wheat production in South Africa has been declining over the past few years due to various reasons. One of these is that it is simply not profitable anymore to produce wheat. Most of the wheat currently produced in South Africa is derived from spring wheat material. According to the SAGL 2014/2015 Wheat Report, 64% of the wheat planted during 2015 was in the Western Cape, followed by irrigation areas (24%) and dryland wheat production in the Free State (12%). Winter and facultative wheat is only produced in the Free State. As a result, spring wheat backgrounds are considered more important for germplasm and cultivar development and this study would therefore focus primarily on these backgrounds.

In the light of the recent droughts, due to climate change, that were experienced in South Africa, the available water for agriculture became significantly restricted. There is a need to increase wheat yields under these challenging environments, while ensuring better wheat stability for the wheat producer.

Yield is one of the most complex traits of wheat that is governed and controlled by multiple gene clusters that interact with one another and are significantly influenced by the environment. Several strategies have been proposed worldwide to increase wheat production (yield), namely increasing photosynthetic rate (Long et al., 2006; Parry et al., 2007), improvement of Rubisco activity (Prins et al., 2016), by improving wheat's ability to capture and process the sun's energy (Parry et al., 2011), through photosynthesis (Reynolds et al., 2012), and making sure that the captured carbon ends up in the wheat grain (Reynolds et al., 2009). However, these strategies all require modification of the photosynthetic components, which can only be achieved through genetic manipulation (Driever et al., 2014).

There is still much to be learned from the natural variation in photosynthetic capacity and performance that already exists between species and within cultivars, as well as their ability to survive or thrive under specific environmental stresses (Driever, 2014). The physiological or genetic mechanisms that underlie such natural variation in species or cultivars are largely untapped resources that may provide not only valuable information on the capacity, performance and yield stability of different cultivars under different environmental conditions but also an invaluable genetic resource that can be used to improve yield. A number of reports have identified significant QTL linked to various traits associated with yield components such as kernel size, tillers per plant, head size (spikelet number) (Gao et al., 2015; Mason et al., 2013; Su et al., 2016; Xue et al., 2010) and improved photosynthetic rate.

In recent years a number of genes responsible for various components of spike yield related to grain/kernel size and or overall thousand kernel mass (TKM) have been cloned and identified through reverse genetic approaches. Different diagnostic gene-specific molecular markers have been developed for these cloned genes that can be used for marker-assisted selection.

Some of the yield related genes to be targeted are:

- *TaGW2-6A* - controls/regulates endosperm cell number/cell division and late grain filling phase (Yang et al., 2012; Zhang et al., 2013; Qin et al., 2014)
- *TaTGW6-A1* - regulates IAA-glucose hydrolase activity (Hanif et al., 2016)
- *TaGS5-3A* - controls cell division (Ma et al., 2016)
- *TaGS-D1* - unknown function in wheat, but associated with kernel weight and kernel length (Zhang et al., 2014)
- *TaSus1* - regulates starch synthesis (Hou et al., 2014)
- *TaSUS2* - regulates conversion of sucrose to starch in the endosperm
- *TaCwi-A1* - cell-wall interface: sink tissue development and carbon partitioning (Jiang et al., 2014).

The favourable alleles regarding increasing kernel width and length, kernel weight and overall contribution to increase in TKM have been identified from literature. Each of the alleles of these genes mentioned contribute either positively or negatively in direct or indirect regulation of a spike yield component. The favourable alleles of the genes mentioned above singularly contribute between 5% and 16% of the observed phenotypic variation for kernel size, kernel weight and TKM. The stacking of these favourable alleles in developed germplasm through positive and negative MAS selection will allow for potential additive/pleiotropic gene effects to maximise yield potential. There is already reported evidence that selection for one or two of the genes results in the identification of higher yield potential germplasm. The selection for multiple spike yield component genes in this manner should be even more favourable for the development and identification of the highest yield potential germplasm. These yield component related genes and other QTL will be targeted for use in germplasm genotyping and employed in a marker-assisted backcross programme.

There are modern high-phenotyping technologies available that are able to generate plant physiological data that are required with a holistic view when chasing yields. These high-throughput phenotyping technologies are available and applied as public services offered by the Australian Plant Phenomics Facility (Plant Accelerator) located at the University of Adelaide's Waite Campus, Australia.

Materials and Methods

In the first year preliminary screening of seedlings from germplasm collections and international nurseries will be done with gene specific markers linked to targeted yield component traits (several cycles per year). The promising high potential germplasm will be sent to the Plant Accelerator high throughput system in Australia.

Based on MAS data of year 1 and 2 selected entries will be planted in a randomised block design with four replicates in the field with high- and low-yielding checks. Top performing

cultivars of each private company will be included as a threshold to assess improvement of yield. Phenotypic and physiological measurements including yield components (ears/plant, kernels/ear, TKM), kernel length and kernel width and photosynthesis readings will be done on field trials. We aim to correlate marker haplotypes and phenotypic data for overall high yield potential germplasm selection.

From the third year a crossing block will be established and top crosses/backcrosses with potential lines will be made to stack favorable yield component alleles. From year four the developed F₂'s will be screened with markers and selected material will be allowed to self for seed increase. The F₃ lines of developed material will be planted out in the field for phenotypic screening and yield potential analysis in year five.

The data from this study will be used to predict the yield potential of future cultivars.

Literature cited

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