Genotypic Variation in Grain Yield Response of Wheat to Rising CO₂: CO₂ Responsive Yield Related Traits for Future Climate Change

CL Thilakarathne^{1,2*}, S Tausz-Posch², M Tausz³ and S Seneweera²

¹Research Station, Department of Export Agriculture, Matale, Sri Lanka

²Department of Agriculture and Food Systems, Melbourne School of Land and Environment, The University of Melbourne, Horsham, Victoria Australia

Abstract

In order to investigate the intra-specific variation in grain yield response to rising CO_2 concentration [CO_2], seven genotypes of spring wheat (*Triticum aestivum* L.) were grown at either ambient [CO_2] (~38⁹4 µmol mol⁻¹) or elevated [CO_2] (700 µmol mol⁻¹) in temperature controlled glasshouses. The grain yield increased by 38% across all the genotype tested and this was associated with increases in both spike number (productive tillers) (r=0.868) and above ground biomass (r=0.942). Further investigation of leaf level traits revealed that leaf mass per unit area (LMA), carbon (C_{LA}) and N content on an area basis (N_{LA}) were also well associated with grain yield suggesting that inclusion of these traits to new plant breeding programs will be able to capture CO_2 responsiveness to increase crop yield.

Key words: Wheat, Rising CO₂, Genotypic variation, Yield related traits

Introduction

The CO_2 concentration $[CO_2]$ in the atmosphere is increasing and is predicted to double by the end of the 21^{st} century (IPCC, 2007). Elevated $[CO_2]$ is likely to have a profound effect on plant growth and yield, especially for C_3 plants because CO_2 is the primary substrate for plant photosynthesis (Bowes, 1991). However, these responses varied among the plant functional groups and species (Ainsworth et al., 2008). The results from enclosure studies suggest that yield increases by more than 30 % when $[CO_2]$ is doubled from 350 to 700 µmol mol⁻¹ for range of plant functional groups (Amthor, 2001). Understanding of fundamental mechanism of how plants response to elevated [CO₂] is immensely important to breed plants to capture extra CO₂ and thus improve the global crop productivity to feed the growing world population.

A number of experiments have been conducted to demonstrate the intra-specific variation in growth and yield in response to elevated $[CO_2]$ (De Costa et al., 2007, Shimono et al., 2009). Some potential mechanisms underlying such variability have been identified. Some of them are tillering capacity (Shimono et al., 2009, Ziska, 2008), differences in downward acclimation of photosynthesis (Ainsworth et al., 2004), differences in

reproductive sink strength such as grain size and spikelet density (Ziska, 2008), and subtle variation in plant development and/or growth rate (Van der Kooij et al., 2000). There is, however, a need to find better criteria for breeding new cultivars/genotypes adapted to predicted future CO_2 . In the present study, a range of wheat (*Triticum aestivum* L.) genotypes were exposed to elevated [CO_2] to investigate intra-specific variation in growth responses to elevated [CO_2] and to test whether leaf level traits such as LMA and leaf N . status are associated with growth and yield response to elevated [CO_2] aimed to understand the mechanisms governing intra-species variation in plant growth response to elevated [CO_2].

Methodology

Plant materials and growth conditions

Seven genotypes of spring wheat; H45, Drysdale, Hartog, Silverstar, Yitpi, Zebu and Gladius were selected based on important physiological traits and grown in environmentally controlled glasshouses at the Department of Primary Industries, Horsham, Victoria, Australia (36°45'07"S, 142°06'52"E, 127 m above sea level). Plants were exposed to sunlight and day/night temperature was maintained at 20/17°C. Two out of four glasshouses were kept as controls at 1

normal atmospheric $[CO_2]$ (~384 µmol $[CO_2]$ mol⁻¹) and two glasshouses were maintained at elevated $[CO_2]$ (~700 µmol $[CO_2]$ mol⁻¹).

Measurements on growth and yield

Plants were destructively sampled (one plant per pot) at post anthesis stage / three weeks after anthesis (DC70) and maturity (DC90) as described by Zadoks et al., (1974). Genotypes with asynchronous maturity were harvested separately. Plants were separated into leaf blades, stems (including sheaths) and spikes, and dried at 60°C for 48 hrs to estimate above ground biomass. Flag leaf area at post anthesis was measured using digital leaf area meter. Leaf mass per unit area (LMA = dry weight of the flag leaf blade / area of the flag leaf blade (gm⁻²) was calculated. Dried spikes were handthreshed using rubber threshing pads and aspirated using a vacuum Separator (KIMSEED, 97-068, Australia). Seeds were counted using a grain counter (PFEUFFERE-CONTADOR, 76-153, D-97318-Kitzingen). Grains were oven dried at 60°C for 48 hours for dry weight.

Cand Nanalysis

Flag leaf blades were sampled immediately after photosynthesis measurements. They were oven dried at 60°C for 48 hrs and ground using a ball mill grinder (QIAGEN TissueLyser II, Australia). Plant C and N were analysed by CNS analyser (Elementor, Germany, Vario isotope cube).

Experimental design and statistical analysis

The experiment was a completely randomised design with two factors (genotypes and CO_2 treatment) and four replicates. Treatment effects and interactions were assessed by two-way ANOVA followed by comparison of means with Student's unpaired t-test. MINITAB 16 and SAS 9.1 statistical software packages were used.

Results and Discussion

There was a significant interaction (p < 0.01) of growth $[CO_2]$ and genotype on the grain yield (Fig. 1c). Total grain yield increased on average by 38% across all genotypes at rising $[CO_2]$, and ranged from no stimulation in H45 to 98% stimulation in Gladius (Fig. 1c). Yield stimulation in this study is in firm agreement with results from previous experiments, where wheat



Fig. 1. Grain number per spike (a), spike number per plant (b) and grain yield per plant (c) of seven genotypes of wheat grown under either ambient $[CO_2]$ (384 µmol mol⁻¹; open bars)

Parameter	Correlation (r) for grain yield	coefficient	Significance	
Growth related parameters				
AGB at maturity	0.942		** *	
LMA	0.824		** *	
Yield related parameters		·		
Spikenumber per plant	0.868		** *	
Grain number per spike	0.304		n s	
Biochemical components Flag				σ
leaf NLA	0.771		** *	
Flag leaf CLA	0.609		* .	

Table 1: Correlation coefficients between grain yield and agronomic parameters

grain yield was stimulated with a 0-35% per 100 μ mol mol⁻¹ increase in [CO₂] (Seneweera et al., 2010, Tausz et al., 2011). Five of the seven genotypes showed significant increase of grain yield under high [CO₂], and the same five genotypes also showed significant increase in the number of grains per spike and spike number per plant (Fig. 1a, b and c). The highest grain yield was found for "Yitpi" at both ambient and high [CO₂] (Fig. 1c). Our findings were supported by the previous studies with different crop species, including wheat (Manderscheid and Weigel, 1997, Ziska et al., 2004, Ziska, 2008) and rice (Ziska et al., 1996, Shimono et al., 2009, De Costa et al., 2007).

The increase in grain yield was strongly correlated with increases in both spike number (productive tillers) (r=0.868, Table 1) and above ground biomass (r=0.942, Table 1). Across all the genotypes tested in our experiments, stimulation of spike number per plant (a surrogate for tiller number) and above ground biomass were associated with increased grain yield at elevated [CO₂] (r=0.942, Table 1). This result confirms earlier studies, some of them on wheat (Ziska et al., 2004) and rice (Shimono et al., 2009, De Costa et al., 2007), where the capacity to grow additional tillers (shoots) was suggested as a key determinant for yield response to elevated [CO2]. In addition, LMA was correlated with grain yield where r=0.824 (Table 1). Flag leaf C and N content on an area basis were also well associated with grain yield increase at rising [CO₂]. It is more likely that plasticity of genotypes to invest more leaf N and increase LMA and to produce more productive tillers is key plant trait for CO₂ response.

From this study, we conclude that whole plant level traits such as ability to form additional shoots/tillers are associated with yield responsiveness to elevated $[CO_2]$. Leaf level traits such as N_{LA} and LMA are also associated with grain yield response to elevated $[CO_2]$. Due to ease of their determination, N_{LA} and LMA traits could be used in large scale wheat genotype screening for CO_2 responsiveness.

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