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Breeding wheat cultivars better adapted to conservation agriculture

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ABSTRACT

Conservation agriculture has improved the productivity and sustainability of cropping systems and reduced the costs of production. These more sustainable crop management strategies have changed the disease spectrum in some environments and plant breeders have responded by developing cultivars with a broader range of disease resistance. Nevertheless, the potential for yield improvement in the absence of diseases in farming systems where residues are retained and tillage is minimized is unclear. The genetic improvement of crops for specialized agronomic practices is dependent upon a genotype × practice interaction. Without such an interaction crops could be developed under full tillage and expected to adapt to zero-tillage systems where crop residues are retained.

A diverse set of cultivars were sown in two contrasting environments under two tillage regimes in Mexico between 2003 and 2005 and grain yield and grain quality estimated. Highly significant genotype × tillage practice interactions for grain yield and many grain quality attributes were noted, including protein content, SDS sedimentation and some mixographic properties. The results suggest that wheat cultivars with improved adaptation to conservation agriculture could be developed with more relevant market quality.

A mapping population of 150 entries derived from a cross between Berkut, one of the parents tested in Mexico and the Australian cultivar Krichauff, was then evaluated in Australia under contrasting tillage regimes. These parents were chosen for their contrasting response to tillage. A QTL analysis identified several QTL associated with specific adaptation to tillage regimes. Two regions were located on chromosome 2D (*wPt3728-cfd44 and gmw484-wmc27*) and one on 5B (*wmc99-wPt2373*) which explained 9, 9 and 12% of the variation for yield under zero-tillage, respectively. A major QTL on 5A (*cfa2155-wPt1370*), overlapping the Vrn1A locus, explained up to 25% of the variation for yield within this cross, but was not tillage regime specific.

Clearly it is possible to breed cultivars with specific adaption to conservation agriculture although the genetic control of adaptation appears highly complex and greatly influenced by environment, soil type, planting method and crop rotation.

1. Introduction

Conservation agriculture strives for sustainable productivity, quality and economic viability while leaving a minimal foot print on the environment. The preservation of soil and water are at the core of this approach (Jordan and Hutcheon, 1997; El Titi, 2003; SOWAP, 2006) and zero and minimum tillage are the key techniques used extensively in conservation agriculture. Of the 95 million ha of zero and reduced tillage globally, around 47% is found in South America, 39% in North America, 9% in Australia, and 3.9% in Europe, Asia and Africa combined (Dumanski et al., 2006).

Reduced tillage and the maintenance of crop residues alters the soil structure, shifts the host–pathogen and host–pest relationship, changes weed competition and improves the availability of moisture. The plant genotypes developed on conventional tillage may not necessarily adapt to the changed cropping environment and new specifically adapted genotypes may need to be developed (Duvick, 1990; Trethowan et al., 2005; Joshi et al., 2005). Most crop breeding programs are conducted on complete tillage regimes thus limiting the identification of crop genotypes responsive to conservation agriculture (Mahmood et al., 2009). Researchers studying genotype × tillage practice interaction (GT) have generally reported a lack of interaction in field crops including wheat (Cox, 1991), barley (Ullrich and Muir, 1986), sorghum (Francis et al., 1984), rice (Melo et al., 2005) and soybean (Elmore, 1990). Thus the probability of finding a significant GT interaction in improved crop germplasm

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Table 1
Genotypes tested under different tillage regimes in Mexico between 2003 and 2005.

Genotype	Cross identifier
1. Berkut	CMSS96M05638T-40Y-26M-010M-010SY-4M-0Y
2. Sokoll	CMSS97M00316S-0P20M-0P20Y-60M-010Y
3. Kambara 1	CGSS95B00016F-099Y-099B-099Y-099B-15Y-0B
4. Weebill 1	CGSS95B00014T-099Y-099B-099Y-099B-35Y-0B
5. Rebeca F2000	CM85295-0101TOPY-2M-0Y-0M-1Y-0M-(1-50)C-032R-0C
6. Romoga F96	CM62142-5Y-3M-1Y-2M-3Y-1M-0Y-0MEX
7. Nahuatl F2000	CMBW89Y00804-0TOPM-9R-0C-2R-3C-0R
8. Juchi F2000	TC920338-S-9C-04R-1C-0R-1C-0R
9. Temporalera M87	II47002-7R-101C-0R-0MEX
10. Tlaxcala F2000	TC920248-S-34C-06R-1C-0R-1C-0R

may be limited and the inclusion of greater genetic diversity may be necessary if better adapted cultivars are to be developed.

The agronomic aspects of conservation agriculture have been studied more methodically (Liebman and Davis, 2000; Cook, 2006) than the genetic control of crop adaptation (Mahmood et al., 2009). Much of the earlier work on genotype response was conducted by agronomists using relatively small numbers of genotypes which were developed under conventional tillage. It is vital that new materials be developed and tested under zero-tillage if traits useful for adaptation to conservation tillage are to be identified.

The present study investigates the occurrence of a GT interaction in a diverse set of wheat germplasm evaluated for yield and grain quality under contrasting tillage regimes at multiple sites on two continents. A mapping population based on a parental line identified in the GT study was then evaluated to identify chromosomal regions linked to superior performance under zero-tillage. The aim was to identify genetic variation that can be used to develop wheat cultivars better adapted to conservation agriculture.

2. Materials and methods

2.1. Trials in Mexico, 2003–2005

2.1.1. Genotypes and sites

Ten bread wheat genotypes were selected on the basis of their diversity, grain yield and grain quality performance in northern and southern Mexico (Table 1). Genotypes comprised released cultivars, designated by year of release following the genotype names, and advanced lines from the wheat breeding program of the International Maize and Wheat Improvement Center (CIMMYT). Experiments were conducted in 2003 and 2004 in the central Mexican highlands at El Batan (19°N, 2245 masl) and in 2003/2004 and 2004/2005 in the Sonoran desert near Ciudad Obregon (27°N, 38 masl). The El Batan site was sown on May 30th and June 10th in 2003 and 2004, respectively. In season rainfall was 612 mm in 2003 and slightly lower at 498 mm in 2004. The respective average maximum and minimum temperatures were 23.6 °C and 10.1 °C in 2003 and 24.0 °C and 10.0 °C in 2004. Nitrogen was applied to all treatments as a split application with 75 units applied before sowing and a further 75 units at jointing. The experiments were germinated with a single post sowing irrigation and were rainfed thereafter. The experiments at Ciudad Obregon were sown on December 15th and 18th in 2003 and 2004, respectively (hence forth the respective experiments are designated as 2004 and 2005 to indicate the primary growing season), and immediately irrigated to promote germination. In season rainfall was 180 mm in 2004 (with 140 mm falling in one event) and half this amount was recorded in 2005. The respective average maximum and minimum temperatures were 28.0 °C and 10.0 °C in 2004 and 27.1 °C and 10.1 °C in 2005. Nitrogen was split into two applications of 100 units each; one applied before sowing and the other at the first post-sowing irrigation.

The fully irrigated trials received four gravity fed irrigations of approximately 100 mm each at 4 week intervals between December and March each year. In comparison, the reduced irrigation treatment was irrigated twice; once in December and again in February (these coincided with the first and third irrigations of the fully irrigated trials). Long-term tillage treatments spanning 5-years at El Batan and 10-years at Ciudad Obregon were established by developing adjacent plots in which one half of the field was maintained without tillage and the other half tilled as per farmer practice in the respective regions. The alternating summer crop established at both locations was maize and wheat was sown directly into maize residue in the zero-till treatments. The maize residue was partially removed and the remainder incorporated using full tillage (designated as conventional tillage) in the tilled treatments. Plots were sown either on two adjacent beds of 2 m length with two rows on each bed or in five rows of 2 m on flat land. The entire plot area of 3 m^2 was harvested to assess yield and biomass. Rust diseases were controlled using fungicide.

2.1.2. Trial design and treatments

Trials were established as 2 × 2 × 2 × 2 × 10 factorials with two replications resulting in 320 plots of 3 m^2 at each location. Sowing rates were adjusted using thousand seed weight (TKW) to approximate 200 seed m^2. At El Batan the treatments consisted of (a) two sowing methods; raised beds and flat sowing, (b) two tillage treatments; zero-till (ZT) and conventional till (CT), (c) two sowing depths; 3 and 6 cm, (d) two seed sizes; average TKW and 20% higher than average TKW and (e) the 10 genotypes in Table 1. At Ciudad Obregon the treatments were (a) two irrigation regimes; full irrigation (FI) and reduced irrigation (RI), (b) two tillage treatments; ZT and CT, (c) two sowing depths; 3 cm and 10 cm, (d) two seed sizes; average thousand seed weight (TKW) and 20% higher than average and (e) the 10 genotypes in Table 1. Grain yield, biomass at anthesis, days to heading, plant height and TKW were assessed on all plots. Protein content and sedimentation (SDS) were assessed on all treatments except seed size (based on non-significant effects from the analysis of variance) and dough strength, dough mixing time and dough mixing stability estimated using a mixograph. The plots were sprayed with fungicide as required.

2.1.3. Data analysis

The analysis of variance was conducted using GENSTAT 11th edition and the significance of means estimated using the Tukey range test. In the multifactor model the dependent variables tested were grain yield, biomass and various grain quality parameters including grain protein %, sedimentation (SDS) and mixogram height, time and stability. The independent variables included genotype, seed size, sowing depth, tillage practice and sowing/irrigation method depending on the trial location. Interactions were calculated for all significant main effects, including genotype and tillage practice. The genotype × environment analysis for grain yield was conducted using the additive main effects and multiplicative interaction (AMMI) model with the result represented graphically using BIPLOT (Vargas and Crossa, 2000).

2.2. Trials in Australia 2007–2008

2.2.1. Genotypes and sites

Based on the performance of the genotype Berkut in the Mexican tillage contrast trials and other multi-environment trials, a mapping population of 148 doubled haploids from the cross Berkut × Krichauff was developed by Dr Hugh Wallwork from the South Australian Research and Development Institute. The population was genotyped and mapped and the details are described in Genc et al. (2010). Krichauff was chosen for its superior performance in dry environments in southern Australia. The population