Research Article

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Impact of different on-farm management practices on bread wheat quality: a case study in the Yaqui Valley

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Abstract

BACKGROUND: Continuous development of new wheat varieties is necessary to satisfy the demands of farmers, industry, and consumers. The evaluation of candidate genotypes for commercial release under different on-farm conditions is a strategy that has been strongly recommended to assess the performance and stability of new cultivars in heterogeneous environments and under different farming systems. The main objectives of this study were to evaluate the grain yield and quality performance of ten different genotypes across six contrasting farmers' field conditions with different irrigation and nitrogen fertilization levels, and to develop suggestions to aid breeding programs and farmers to use resources more efficiently. Genotype and genotype by environment (GGE) interaction biplot analyses were used to identify the genotypes with the strongest performance and greatest stability in the Yaqui Valley.

RESULTS: Analyses showed that some traits were mainly explained by the genotype effect, others by the field management conditions, and the rest by combined effects. The most representative and diverse field conditions in the Yaqui Valley were also identified, a useful strategy when breeders have limited resources. The independent effects of irrigation and nitrogen levels and their interaction were analyzed for each trait. The results showed that full irrigation was not always necessary to maximize grain yield in the Yaqui Valley. Other suggestions for more efficient use of resources are proposed.

CONCLUSIONS: The combination of on-farm trials with GGE interaction analyses is an effective strategy to include in breeding programs to improve processes and resources. Identifying the most outstanding and stable genotypes under real on-farm systems is key to the development of novel cultivars adapted to different management and environmental conditions.

Supporting information may be found in the online version of this article.

Keywords: wheat quality; on-farm; bread wheat; bread-making

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the most important staple crops worldwide. With 219 million hectares harvested and 760 Mmt produced in 2020, it provided approximately 20% of the calories and 20% of the proteins required for the human diet.[1] The first target of wheat breeding programs is grain yield combined with improved agronomic performance and disease resistance; grain quality is usually a second-level priority.[2] For example, over the last 50 years, while grain yield rates increased significantly grain protein content remained stable or suffered a reduction.[3,4] This can be explained partially by the negative association between grain yield and grain protein content and farmers' preferences for yield traits over quality.[5,6] In many breeding programs, quality traits are evaluated at the final stages because tests are expensive or because large amounts of grain samples are necessary.[2]

With wheat demand expected to increase by 60% by 2050,[7] an estimated 6% growth of the bakery industry globally, and the presence of more demanding consumers aware and concerned about the food nutritional value, there is a growing demand to produce higher quality and more nutritious food products.[8] Thus, additional efforts are necessary to ensure improvements in grain quality combined with high yields. However, the integration of quality traits in

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the breeding programs remains a challenge because, as well as yield, they interact with the environment, making the selection process more difficult.[9,10] For example, high water availability combined with N fertilization is associated with higher yield but diluted grain protein content whereas water stress combined with N fertilization is associated with a higher grain protein content and typically an improved breadmaking quality.[11,12] Because of this, the successful development of new wheat varieties that meet the demands of farmers, industry, and consumers, not only requires breeding programs that combine high yields and high quality but also selection processes under different agricultural management conditions to assess variability and performances under different environments conditioned by farmers.

Traditionally, breeders have used on-station trials to evaluate the performance of new cultivars. Consequently, outcomes of standardized conditions have tended to be different, reflecting the diversity of management practices applied by farmers.[4] To determine the performance of crops under real field conditions, gap analysis has been developed for different species (where the gap is defined as the differences between outcomes achievable under standardized experimental conditions and farmers' outcomes). However, most of the studies have been focused on grain yield,[13-15] the information on quality traits being limited.

The objectives of this study were: (i) to evaluate the grain yield and quality performance of ten different genotypes across six different farmers' fields; (ii) to identify the most outstanding and stable genotypes in the environments under analysis through genotype and genotype by environment (GGE) biplot analysis; (iii) to characterize the association between grain yield and quality traits in farmers' fields under investigation, and (iv) to develop suggestions to aid farmers for a more efficient use of resources for the environments under analysis.

MATERIALS AND METHODS

Field trials and experimental design

The trials were conducted in six different farmers' fields in two consecutive seasons, 2015–2016 and 2016–2017, at the Yaqui Valley, Sonora, Mexico. The panel of lines used included ten genotypes consisting of four commercial varieties and six candidate lines (full names of the genotypes and data are provided in Supplementary Table 1).

On each farmer's field, the experimental design was a randomized complete block with three replicates. Each experimental unit had an area of 10 m (length) by 3.2 m (width). Planting dates were between the end of November to the first week of December and harvest dates ranged from the last week of April to the first days of May. No preceding crops were cultivated for any of the seasons. Each farmer's field (considered as different environments hereafter) had different combinations of irrigation and nitrogen fertilization. The name of each environment was represented as a combination of the irrigation and total fertilization levels, where 'F' and 'R' refers to full or reduced irrigation, respectively, followed by the total N (kg ha^{-1}) applied as fertilizer (Table 1). The first and second furrow irrigations were performed 60 and 90 days after sowing. During grain filling, the third and fourth furrow irrigations were applied. Granular urea was used as N fertilizer; the first fertilization was applied prior to pre-plant irrigation, which occurred 18 days before sowing and the second fertilization at the end of tillering; 50 kg ha^{-1} of N was applied in some trials nearing heading (third fertilization). Pesticides and herbicides were applied in accordance with each farmer's practices, and weeds, diseases, and insects were controlled.

Meteorological conditions during the two crop seasons were obtained from the NASA Prediction of Worldwide Energy Resource (https://power.larc.nasa.gov/) and historical climate variables from Fischer et al.[16] (Supplementary Table 2).

Parameters quantified

Grain yield values (kg ha^{-1}) were adjusted to 12% moisture after harvesting and seed cleaning. Test weight (TW, kg hL^{-1}) and thousand kernel weight (TKW, g) were measured using the digital image system SeedCount SC5000 (Next Instruments, Canterbury-Bankstown, Australia). Grain protein content (GPC, %) was determined by near-infrared spectroscopy (NIR Systems 6500, Foss, Denmark) calibrated based on official American Association of Cereal Chemist (AACC) methods 39-10, 55-30, and 46-11A, respectively.[17] To calculate protein yield (PROTYLD, kg ha^{-1}), GPC data were multiplied by grain yield. For milling, grain samples were processed applying AACC method 26–95.[17] All samples were milled into flour using a Brabender Quadrumat Senior mill (CW Brabender, Duisburg, Germany) and flour yield (FYLD, %) was calculated. Sodium dodecyl sulfate sedimentation volume from flour samples (FSDS, mL) was measured as described by Peña et al.[18] and 35 g flour samples were tested in a Mixograph (National Mfg. Co., National Manufacturing Company, Lincoln, NE, USA) to obtain optimum dough peak time (MIXTIM, min) and %torque × min (TORQUE, Nm) according to AACC method 54-40A.[17] Dough strength (ALVW, $J \times 10^{-4}$) and tenacity/extensibility ratio (ALVPL) were determined using 60 g flour samples applying AACC method 54-30A.[17] The bread baking test was carried out using the direct dough method with 100 g of flour (AACC method 10-09) and loaf volume (LOFVOL, mL) was determined by rapeseed displacement using a volume meter.

Statistical analyses

Data were analyzed with R software version 4.0.1 (https://www.R-project.org/). The statistical model applied is described in supplementary file 1. Genotype and genotype by environment biplot procedures were carried out to define the stability of genotypes, rank environments, and genotypes using 'GGEBiplots' package for R.[19] For this analysis, data from both growing seasons were averaged.

RESULTS

Genotype, environment, year and interaction effects on grain yield and quality traits

Twelve traits related to grain yield and quality were analyzed in ten different genotypes in six different environments during the 2015–2016 and 2016–2017 crop seasons. Table 2 presents P-values from ANOVA including the significance of genotype (G), environment (E), year (Y), G × E, G × Y, E × Y, and G × E × Y effects. All the G × E × Y interactions were highly significant ($P < 0.001$), except for LOFVOL ($P < 0.05$), grain yield, and PROTYLD, which were not significant. Similar results were observed for G × E, G × Y, and E × Y interactions where high significances were obtained ($P < 0.001$) except for G × E LOFVOL interaction ($P < 0.01$) and G × Y interactions for grain yield, GPC, and PROTYLD, which were not significant. Main effects (G, E, and Y) also showed high significant P-values for all the traits ($P < 0.001$) except for ALVPL ($P < 0.05$). When the total sum of squares and the respective percentage of each effect were analyzed, the genotypic effect showed the greatest influence on TW, TKW, FSDS,

Table 1. Trial environments conditioned by management practices during the 2015–2016 and 2016–2017 seasons at the Yaqui Valley, Mexico

Environment	Irrigation (I)	1st I (mm)	2nd I (mm)	3rd I (mm)	4th I (mm)	1st N (kg ha^{-1})	2nd N (kg ha^{-1})	3rd N (kg ha^{-1})	Total N (kg ha^{-1})
F291	Full	120	80–100	80–100	80–100	241	50	0	291
F295	Full	120	80–100	80–100	80–100	149	96	50	295
F320	Full	120	80–100	80–100	80–100	195	75	50	320
F341	Full	120	80–100	80–100	80–100	241	50	50	341
R291	Reduced	120	80–100			241	50	0	291
R341	Reduced	120	80–100			241	50	50	341

(I) refers to irrigation (mm) and N to nitrogen fertilization (Kg ha^{-1})

MIXTIM, TORQUE, ALVW, and LOFVOL. The environmental effect, represented by the farmer fields showed the highest influence on variability for grain yield, GPC, and ALVPL. FLRYDL, and PROTYLD variability were controlled mainly by the year effect.

We then performed Tukey tests analyses for the double interactions (data not shown) and individual main effects. Similar trends among all analyses were found for top cultivars, environments and years. For this reason and to simplify the reporting of the results, Fig. 1 and Supplemental Fig. 1, show differences among genotypes, farmer's field conditions and years based on main effects (results were then compared and confirmed trough GGE biplot analyses). For yield, TW, TKW, and PROTYLD, genotype 7 had the highest means followed by genotype 8, which also had the best performance for GPC, FYLD, and LOFVOL. For gluten strength related parameters (FLRSD, MIXTIM, TORQUE, ALVW) and ALVPL, genotype 3 ranked in the top followed, mainly, by genotype 10. Other genotypes also had satisfactory performance in specific environments (Supplementary Table 3); for example, genotype 6 had high yield values in environments F291, F295, and R291; genotype 1 for GPC in environments F320 and R341; genotype 8 for ALVW at environments R291 and R341 and finally genotype 5 for LOFVOL in environments F295, F341, and R291.

Table 2. Sum of squares and percentage of the total SS (in parentheses) from ANOVA analysis in ten bread wheat genotypes across six different field conditions cultured in both 2015-2016 and 2016-2017

Source of variation	Yield		Test weight		Thousand kernel weight		Grain protein content		Protein yield		Flour yield	
Genotype (G)	1.90E+07	(3.4)***	140.9	(21)***	1801	(44.8)***	30.8	(14.6)***	5.70E+05	(7.7)***	293.7	(15.8)***
Environment (E)	1.50E+08	(27.2)***	48.1	(7.2)***	651.4	(16.2)***	83.2	(39.5)***	1.30E+06	(17.1)***	281.9	(15.1)***
Year (Y)	1.00E+08	(18.3)***	114.2	(17)***	26.9	(0.7)***	4.7	(2.3)***	2.00E+06	(26.6)***	508.3	(27.3)***
G × E	5.00E+07	(9)***	49.6	(7.4)***	324.1	(8.1)***	21.5	(10.2)***	5.90E+05	(7.8)***	165.2	(8.9)***
G × Y	5.70E+06	(1)ns	59.3	(8.8)***	82.2	(2)***	0.8	(0.4)ns	8.90E+04	(1.2)ns	55.6	(3)***
E × Y	1.10E+08	(20.2)***	80.4	(12)***	400.5	(10)***	23.4	(11.1)***	1.10E+06	(15)***	205.1	(11)***
G × E × Y	2.30E+07	(4)ns	52.5	(7.8)***	220.8	(5.5)***	12.3	(5.8)***	3.80E+05	(5.1)ns	103.3	(5.5)***

Source of variation	Flour SDS-sedimentation volume		Mixograph peak time		Mixograph torque		Alveograph W		Alveograph P/L[a]		Loaf volume	
Genotype (G)	962.9	(43.7)***	81.4	(41.6)***	1.00E+05	(41.5)***	7.30E+05	(38.2)***	15.2	(23.2)***	2.70E+05	(29.8)***
Environment (E)	431.3	(19.6)***	52.8	(27)***	6.10E+04	(25.5)***	2.30E+05	(12.2)***	19.1	(29.2)***	2.20E+05	(24.4)***
Year (Y)	289.8	(13.1)***	4.3	(2.2)***	1.30E+03	(0.6)***	1.90E+05	(10.1)***	0.2	(0.2)*	7.10E+04	(7.9)***
G × E	49.9	(2.3)***	10.8	(5.5)***	1.30E+04	(5.6)***	1.10E+05	(6)***	4.5	(6.9)***	4.50E+04	(5)**
G × Y	15.4	(0.7)***	13.6	(6.9)***	2.00E+04	(8.4)***	1.00E+05	(5.5)***	4.5	(6.9)***	3.50E+04	(3.9)***
E × Y	279.1	(12.7)***	13.7	(7)***	1.80E+04	(7.5)***	2.80E+05	(14.7)***	7.2	(11)***	8.70E+04	(9.6)***
G × E × Y	56.3	(2.6)***	7	(3.6)***	9.90E+03	(4.1)***	7.00E+04	(3.7)***	4.9	(7.4)***	4.20E+04	(4.6)*

[a] Alveograph P/L indicative of tenacity (P)/extensibility (L) ratio. Sum of squares (SS), Genotype (G), Environment (E), Year (Y), Flour Sodium dodecyl sulfate-sedimentation volume (Flour SDS-sedimentation volume).
*P < 0.05.
** P < 0.01.
*** (P < 0.001).

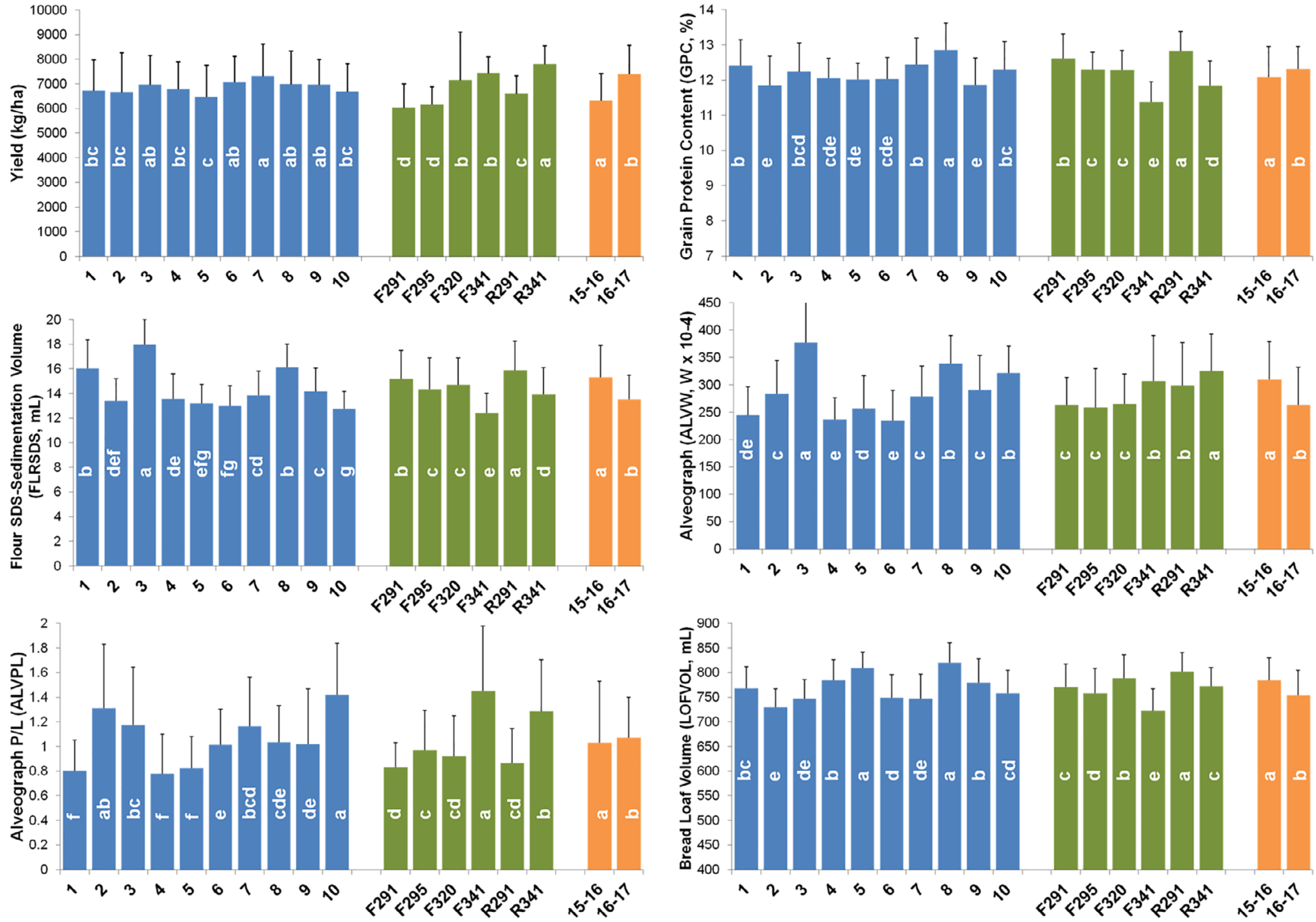

Figure 1. Mean values for genotypes (blue bars), environments (green bars), and years (orange bars). Values with the same letter are not significantly different at $P = 0.05$ according to the Tukey test. Black lines indicate standard deviation.

When the different field conditions were analyzed, environments F341 and R341 had the highest values for yield, TKW, PROTYLD, MIXTIM, TORQUE, ALVW, and ALVPL. For GPC, FSDS, and LOFVOL, environment R291 ranked in the top followed by F291 and F320. Environment F295 had the highest values for TW and FYLD. On the opposite side, environment F341 had the lowest values for TW, GPC, FSDS and LOFVOL. Environments with lowest levels of N (291–295 kg ha^{-1}) and full irrigation had the lowest mean values for yield, PROTYLD, FYLD, MIXTIM, TORQUE, ALVW, and ALVPL.

Differences among years were observed; the 2015–2016 season had higher significant mean values for TW, FYLD, FSDS, ALVW, and LOFVOL while the 2016–2017 season had the highest values for the rest of the traits.

Genotype and genotype × environment biplot analysis

Genotype and genotype × environment biplot procedures were carried out to analyze environmental and genotypic interaction effects in the Yaqui Valley in more detail. Three different analyses were performed: 'Mean against stability', 'ranking genotypes' and 'ranking environments'. To integrate the description of the results, plots were overlapped (Fig. 2 and Supplementary Fig. 2). While for the 'mean against stability' analysis the black single-arrowed line points to higher mean yield across environments, the distance to the abscissa indicates genotypes' stability; those closer to the abscissa were highly stable across environments.[20,21] For the 'ranking genotypes' analysis, those genotypes closer to the ideal genotype, represented by the green circle in Fig. 2 and Supplementary Fig. 2 showed the best performance and stability. The 'ranking environment' tool allows identifying an ideal environment (defined as the most discriminating and representative) and those environments closer to it were more representative of other environments.[20,21]

For 'mean against stability' and 'ranking genotypes', we ranked the genotypes, for each trait, according to mean values, stability values, and closeness to the ideal genotype. When the media values were evaluated across environments, genotypes 3, 7, and 8 were the most represented with the highest values. Genotypes 7 and 8 ranked in the top positions for yield. Test weight, TKW, GPC, PROTYLD, FYLD, FSDS, MIXTIM, TORQUE, ALVW, ALVPL, and LOFVOL, genotype 3 had the highest mean values for FSDS, MIXTIM, TORQUE, and ALVW. For ALVPL, genotype 10 ranked first, followed by genotypes 2 and 7. In the middle of the media values ranking, genotypes 1 and 9 were the most representative. Depending on the trait, the lowest media values were mainly represented by genotype 5, followed by genotypes 2, 4, 6 and, 10.

When stability was analyzed, genotypes 1, 3, 7, and 8 ranked in the top positions as the most stable cultivars. Genotype 7 ranked first for TKW, ALVW, and ALVPL, and genotype 8 ranked as the most stable cultivar for GPC, FYLD, and MIXTIM. While genotype 3 was the most stable for TESTW and LOFVOL, genotype 1 ranked first for FSDS and TORQUE. Genotype 10 showed the best values for yield and PROTYLD stability. In the middle of the stability

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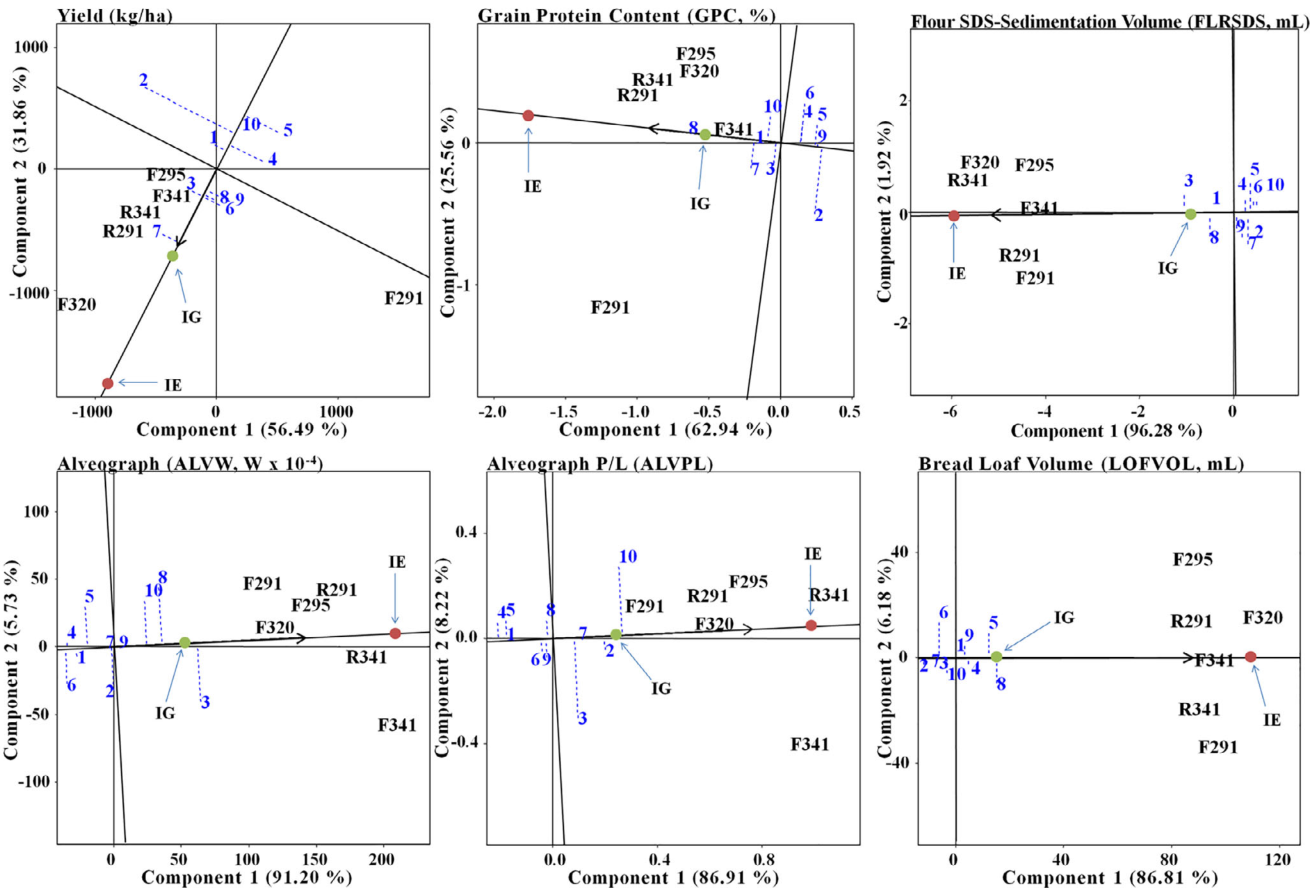

Figure 2. 'Mean against stability', 'ranking genotypes' and 'ranking environments' GGE biplot analysis for ten bread wheat genotypes across six different field conditions cultured in the 2015–2016 and 2016–2017 seasons. The arrowed line points to higher means across environments. Blue dotted lines indicate stability; genotypes closer to the abscissa were highly stable and vice-versa. Green and red points indicate ideal genotype (IG) and ideal environment (IE), respectively. Axes also indicate variation explained by components 1 and 2.

ranking, genotypes 4, 5, 7, and 9 were the most representative. The worst stability performance was for genotype 2; it was the most unstable cultivar for yield, TW, TKW, GPC, PROTYLD, FYLD, FSDS, MIXTIM, and TORQUE. Genotypes 5 and 6 also were represented as the most unstable for some traits.

In parallel with the previous results, the closest cultivars to the 'ideal genotype' for most of the traits were represented by genotypes 3, 7, and 8. Genotype 3 ranked first for FSDS, MIXTIM, TORQUE, and ALVW. Genotype 7 was closest to the ideal genotype for yield, TW, and TKW and genotype 8 ranked first for GPC, PROTYLD, FYLD, and LOFVOL. For ALVPL, genotype 2 had the closest proximity to the ideal genotype. In general terms, and depending on the trait, genotypes 4, 5, 6, and 10 represented the most outlying genotypes from the ideal genotype.

When environments in the Yaqui Valley were ranked, R341 was the closest to the ideal environment for TW, FYLD, FSDS, MIXTIM, TORQUE, ALVW, and ALVPL traits. F320 was the closest to the ideal environment for yield, PROTYLD, and LOFVOL (together with F341). Finally, R291 was the closest to the center point for GPC. F291 was the poorest environment for all traits except for TW and LOFVOL. The poorest environment for TW and LOFVOL was F295.

Correlation analysis

We performed correlation analysis for the 12 traits analyzed; the data were grouped in successive years and environments (Supplementary Table 4). Estimation of Pearson coefficients revealed significant correlations among traits. For example, yield displayed significant positive correlations with TKW, PROTYLD, MIXTIM, TORQUE, ALVW, and ALVPL, and was negatively correlated with FYLD, GPC, FSDS, and LOFVOL. Grain protein content was positively correlated with FSDS and LOFVOL and negatively correlated with TW, TKW, MIXTIM, TORQUE, ALVW, and ALVPL. In addition, MIXTIM and TORQUE displayed positive correlations with TKW, PROTYLD, ALVW, ALVPL, and negative correlations with FYLD, GPC, and LOFVOL. ALVW and ALVPL showed positive correlations with TW and TKW and displayed negative correlations with GPC. Finally, LOFVOL was positively correlated with FYLD, GPC, FSDS, and ALVW and negatively correlated with TKW, PROTYLD, and ALVPL.

Effects of irrigation and nitrogen levels

To determine the independent effects of nitrogen and irrigation levels applied by farmers and to develop potential proposals for more efficient use of resources in the Yaqui Valley, the main effects and interactions of fertilizer doses and irrigation levels were analyzed. For this analysis, data from environments F291, F341, R291, and F341, which allowed a full comparison of treatments across these environments, were used. Supplementary Table 5 shows the results for the main effects and their interactions for all traits. Half of the traits showed significant *p*-values for the interaction between irrigation and nitrogen levels (GPC, FYLD, FSDS, ALVW, ALVPL, and LOFVOL). For the other traits, irrigation and nitrogen main effects were highly significant except for TW where the irrigation level was not significant. For specific locations and conditions analyzed in this study, some suggestions to maximize yield or quality with lower use of resources could be developed. For example, while for higher yield production or TW it seemed unnecessary to apply full irrigation but elevated levels of nitrogen are recommended to maximize both; the highest values of TKW were obtained with full irrigation and high doses of nitrogen. On the other hand, high values of MIXTIM, TORQUE, and ALVW would be obtained with reduced irrigation combined with elevated levels of nitrogen. If the goal was to obtain high GPC or high LOFVOL, the best combination would be to apply reduced levels of irrigation with 291 kg ha^{-1} of nitrogen, avoiding excessive use of resources.

DISCUSSION

To develop high-yielding and high-quality cultivars for different environmental and agricultural management conditions, it is important to quantify what proportion of the phenotypic variation is explained by the genotype, the environment (field conditions/location/year), and their interaction, and identify which genotypes are more stable and adaptable across different environments.[22] Different studies quantify the wheat yield gap; however, information about how farmers' management practices impact on-farm wheat quality traits, is limited.

In our study, ten genotypes exposed to a range of farming conditions during two consecutive growing seasons were evaluated for yield and quality traits in the Yaqui Valley, Mexico. For most of the traits that were analyzed, both genotype and environment explained the variability in the data. Thousand kernel weight was the most sensitive variable to the genotype effect, followed by FSDS, MIXTIM, TORQUE, ALVW, LOFVOL, and TW, while yield, GPC, and ALVPL were more sensitive to the environment effect. Similar studies that analyzed different irrigation and fertilization regimes showed similar trends for yield. Guttieri *et al.*[23] observed that yield was mainly explained by fertilization and secondarily by the irrigation levels. For Saint Pierre *et al.*[24] the genotype had a low influence, and irrigation and fertilization explained most of the variation in this trait. For TW and TKW our results were in concordance with Bilgin *et al.*,[25] where these traits were mainly explained by the genotype. On the other hand, for Guzmán *et al.*[5] and Guttieri *et al.*,[23] climatic conditions and environments explained variation in TW and TKW while for Li *et al.*[26] the genotypic and environmental effects were predominant for TW and TKW, respectively. The differences observed in each study could be explained by the contrasting conditions and genotype diversity of each case. Grain protein content is also a trait that is highly influenced by the environment. In parallel with our results, other studies found that different environments explained most of the variability for this trait.[25,27] Similarly, to other studies, FSDS was mainly explained by the genotype effect. This trend was observed by Guzmán *et al.*[5] Li *et al.*[26] Magallanes-López *et al.*[28] and Massoudifar *et al.*[29]

When double and triple interactions were analyzed, most of them were highly significant for all traits. E × Y was the most representative among them. This could be explained, in part, by contrasting farming conditions and excessive rainfall in January/February in the second year. According to Guttieri *et al.*,[23] who analyzed similar traits using different genotypes, irrigation and nitrogen regimes, most of the double interactions were significant. Significant interactions also were observed in different multi-location trials[10,25,27] confirming the influence of the changing environments and management practices on yield and quality traits.

In this study, GGE biplot analyses were performed to identify the best and most stable genotypes across environments for each trait. Clearly, genotype 7 (Bourlag 100) had the best yield, TW, TKW, and PROTYL values combined with high stability; it also showed high values for GPC. For rheological parameters, it showed intermediate performance and one of the lowest values for LOFVOL. Genotype 8 (a candidate line to be released) also had a remarkable performance combining acceptable yield with the highest values for GPC, FYLD, and LOFVOL and intermediate performance for rheological parameters. It also showed high stability for most of the traits, except for TW and ALVW. For rheological traits, genotype 3 (Onavas F2009) showed the highest values for MIXTIM, TORQUE, ALVW, and FSDS with good stability (except for ALVW) and acceptable yield; however, its performance for other traits such as GPC, PROTYLD, FYLD, and ALVPL were similar to the general media and one of the lowest for TESTW and LOFVOL. In this sense, the Tukey test analysis allowed the identification of specific performances under specific management conditions, indicating different adaptive capacities of some genotypes. Although the physiological and/or phenological reasons for greater adaptation to certain conditions are beyond the scope of this study, it is possible to hypothesize that different allelic variants for phenology (flowering time, vernalization, photoperiod sensitivity), yield components (spikelet number per spike, flower fertility), resistance to biotic or abiotic factors (drought resistance, disease resistance), and quality traits (type of glutenins, starch synthesis), and their interactions with the different management practices and year under study may explain the performance that was observed.[30] The phenotypic characterization performed in this study could be used to prioritize the selection of genotypes to be sown in the Yaqui Valley, depending on the farmer or industry's goals. The GGE biplot analysis was also useful to identify those genotypes with the poorest performance and highest instability being candidates to be discarded (among them genotypes 4, 5 and 6). On the other hand, the ranking environment tool was a useful strategy to identify the most representative and discriminative locations and/or field conditions. When breeders have limited resources to develop multi-environment trials, they could use this tool to identify in which conditions the trials should be conducted. For example, for our specific conditions in the Yaqui Valley, R341 is a key environment to test most of the traits analyzed here, whereas F291 was the most expendable environment for testing genotypes.

Correlations analysis showed a strong association among traits; similar trends and significant values were also observed by Laidig *et al.*[4] Rathan *et al.*[31] and Thorwarth *et al.*[32] The typical negative correlation between yield and GPC was observed, confirming that simultaneous breeding for these traits has some limitations. This probably contributed to a small but significant correlation between yield and LOFVOL too. Yield also had a strong and direct correlation with ALVPL, which in practice means that the higher the productivity the more difficult it was to obtain balanced and extensible wheat doughs (ALVPL ≤1) and, therefore, the more difficult it was to achieve high bread-making quality.

Currently, sustainable agricultural practices are needed to reduce potential environmental risks. Poor nitrogen management practices not only produce losses from agricultural systems with a negative impact on the environment but also result in low profitability for farmers.[33,34] To identify the most efficient use of resources in these specific conditions, the irrigation and nitrogen effects were analyzed. For example, for similar field practices and weather conditions here described, it seems that full irrigation is not necessary to maximize yield or TW, so farmers could reduce the use of water; similar trends were observed by Yang *et al.*[34] and Walsh *et al.*[35] in trails under varied irrigation levels. Not many studies assess PROTYLD under different conditions of water and nitrogen regimes. Rathore *et al.*[33] observed increases for PROTYLD when rates of crop evapotranspiration and nitrogen levels increased. We observed that reduced irrigation plus 341 kg ha^{-1} of nitrogen maximized values under our conditions. The variation in GPC under different irrigation and nitrogen levels has been studied before. Rathore *et al.*[33] and Dai *et al.*[36] showed that GPC decreased when irrigation increased; on the other hand, GPC increased because of the increased N fertilization.[23,37,38,39] In our case, reduced irrigation combined with low doses of nitrogen (291 kg ha^{-1}) showed the highest values for GPC. For our study, the highest yield and lowest GPC values were obtained in environments with nitrogen doses of 341 kg ha^{-1}, indicating that high yield rates could dilute protein in the grain under these conditions. For gluten strength-related parameters, different trends could be observed. For FSDS, Magallanes-López *et al.*[28] and Massoudifar *et al.*[29] observed lower values for low irrigation at post-anthesis. For FSDS, Saint Pierre *et al.*[39] observed higher values with low irrigation levels and higher nitrogen levels. For MIXTIM, no differences between irrigation levels and higher values with low doses of nitrogen were observed. Guttieri *et al.*[23] observed that MIXTIM decreased with increases in water availability and increased with higher nitrogen rates. Lloveras *et al.*[40] and López-Bellido *et al.*[41] showed that higher doses of nitrogen increased W alveogram values and reduced ALVPL. For LOFVOL, Guttieri *et al.*[23] and Massoudifar *et al.*[29] observed increases with fertilization while Magallanes-López *et al.*[28] showed higher values when the water stress increased. In our case, the highest values for LOFVOL were obtained with low irrigation and 291 kg ha^{-1} of nitrogen followed by low irrigation and nitrogen doses of 341 kg ha^{-1}. Dilution of protein in the grain under increased doses of nitrogen combined with full irrigation and the high correlation among GPC and LOFVOL could explain, in part, the trends observed.

CONCLUSIONS

The present analysis allowed the identification of the best genotypes in terms of performance and stability across contrasting agricultural management conditions and among ten different genotypes grown in the Yaqui Valley in Mexico. Evaluating genotypes in different on-farm conditions is a valid strategy to assess the performance of new cultivars in heterogeneous environments and different farming systems to improve the breeding process and resources.

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DATA AVAILABILITY STATEMENT

The data that supports the findings of this study are available in the supplementary material of this article

SUPPORTING INFORMATION

Supporting information may be found in the online version of this article.

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