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GENETIC ADVANCEMENT IN BREAD WHEAT VARIETIES RELEASED FOR THE BAJÍO REGION (MEXICO) UNDER NORMAL AND RESTRICTED IRRIGATION

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ABSTRACT

Wheat (*Triticum aestivum* L.) provides approximately 20 % of the proteins and calories consumed globally. Genetic advancement in yield is crucial to satisfy the demand of the growing world population. The aim of this study was to estimate genetic progress in agronomic traits of varieties released in El Bajío (Mexico) between 1975 and 2016 under normal and restricted irrigation. The hypothesis was: with the breeding of wheat varieties for over 40 years for the region of El Bajío, advances have been made in grain yield. The genotypes planted were Salamanca S75, Cortazar S94, Bárcenas S2002, Urbina S2007, Alondra F2014 and Cisne F2016 during the 2016-17 and 2020-21 agricultural cycles in three irrigation schedules, two at 0 and 55 days after planting, three at 0-45 and 75 and four at 0-45-75 and 100 days after planting. Phenology, yield and its components were measured, and the treatment design followed a randomized complete block design with arrangements in subdivided plots and three replications. Using the weighted phenotypic model and its graphical representation through the SREG biplot, it was determined that recently released varieties outperformed the grain yield of older varieties in all three irrigation schedules. The varieties released between 1975 and 2016 displayed no changes in days to heading and maturity, since only early genotypes were advanced in the selection process. For grain yield, a genetic progress was obtained of 26.3, 41.6 and 37.6 kg ha^{-1} year^{-1} for the two, three and four irrigation schedules, respectively, which was related to an increase ($p \leq 0.01$) in aerial biomass and a higher number of spikes and grains per unit area.

Keywords: water use efficiency, genetic gain, yield, irrigation schedules, earliness.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is a basic crop that provides approximately 20 % of the proteins and calories consumed globally (CGIAR, 2022). The average production of bread wheat in Mexico is at a shortfall (2.9 million t), forcing the import of 70.8 % of the national demand (CEDRSSA, 2019). In Mexico, the area of El Bajío, which comprises part of the states of Guanajuato, Michoacán, Jalisco and Querétaro, produces 23.3 % of the national wheat production (SIAP, 2022). The main problem in the region is the scarcity of water, since in the state of Guanajuato, the main wheat producer of the area, extraction levels are unsustainable for the currently exploited water sources. Around 4,000 hm^3 of water are extracted from aquifers in the state, which have an annual recharge of approximately 2,800 hm^3, hence the deficit of just over 1,000 hm^3 (Flores *et al.,* 2020). This deficit causes reductions of 2 to 3 meters per year, which have been, for some time now, a cause of direct negative economic effects on the agricultural production (Caldera *et al.,* 2020). Restricted irrigation, applying a lower amount than the required irrigation water, has been acknowledged as a feasible water-saving technique for future water scarcity scenarios (Zhao *et al.,* 2019).

The wheat breeding program in El Bajío has released 17 bread wheat varieties since 1975, with Salamanca S75 and Cortazar S94 being the most noteworthy and the ones which were planted for over 20 years in 80 % of the lands of this region. These varieties are known for their early growth cycle, which gives them advantages in this area in which two crops are planted every year: maize (*Zea mays* L.) or sorghum (*Sorghum bicolor* (L.) Moench) in the spring-summer cycle and wheat or barley (*Hordeum vulgare* L.) in the autumn-winter cycle (Solís *et al.,* 2014).

Estimating the progress of grain yield is important for breeding programs worldwide, and it must be carried out periodically to evaluate the effectiveness of breeding strategies. Ideally, such studies should include both experiments in optimum environments that help control the potential yield, in which lodging, and diseases are controlled, but also unprotected experiments. However, funding and logistics often restrict the dimensions of long-term trials (Mondal *et al.,* 2020). In order to feed the unevenly growing world population in different parts of the world, global average wheat productivity must increase by 1.3 % $year^{-1}$ (Yadav *et al.,* 2021). Under water stress, genetic progress in wheat has been made possible due to the additive genetic variance for yield found in the existing gene banks (Trethowan and Kazi, 2008). However, if genetic progress is to be kept under stress, it is necessary to incorporate new genetic variability via the formation of synthetic wheat lines, the introduction of the variability of local genotypes and the introgression of segments of exotic chromosomes (Ming *et al.,* 2020). Results from some studies show that, in low-yield environments, the genetic progress rate is lower than the ones obtained in high-yield environments (Manes *et al.,* 2012). These results are consistent with those obtained by Gerard *et al.* (2020), who evaluated among 30 and 50 wheat genotypes in 239 high- and low-rainfall environments. Their results showed that in high-rainfall environments, genetic gains of 3.8 % (160 kg ha^{-1} $year^{-1}$) were obtained, while in low-rainfall environments, there were gains of only 0.93 % (40 kg ha^{-1} $year^{-1}$). Crespo-Herrera *et al.* (2017) obtained opposite results: genetic gains of 1.63 % (102.7 kg ha^{-1} $year^{-1}$) in optimum environments and 2.7 % (88 kg ha^{-1} $year^{-1}$) in dry environments. Likewise, Paquini-Rodríguez *et al.* (2016) showed that the annual progress rate under restricted irrigation (1.35 %) was higher than the one obtained under normal irrigation (1.10 %). Studies on genetic advancement represent the evaluation of breeding programs and determine whether genetic gains are enough to meet the demands of a growing population or if the incorporation of new sources of genetic variability are needed to achieve greater progress. The wheat breeding program in El Bajío has been the source of varieties in this region for 47 years (1975), and the varieties released by this program cover more than 85 % of the region's planting area. Although the increases in yields can be found in the production statistics for the state of Guanajuato, no studies have been carried out on the genetic progress achieved by the program that include only the varieties released for this region. Therefore, the aim of this work was to evaluate the genetic gains in yield and agronomic traits of six bread wheat varieties released between 1975 and 2016 under both normal and restricted irrigation.

MATERIALS AND METHODS

This study was carried out in El Bajío Experimental Field, belonging to the National Forestry, Agricultural and Livestock Research Institute (INIFAP), located in Celaya, Guanajuato, Mexico, at 20° 32′ Latitude North, 100° 48′ Longitude West and an altitude of 1752 m; average annual rainfall and temperature are 578 mm and 19.8 °C, respectively.

Experimental management

The experiments were evaluated during the 2016-2017 and 2020-2021 autumn-winter cycles. For all cases, planting dates were December 1 of each year, and performed in double rows with a density of 120 kg ha^{-1}. Fertilization was carried out with a dose of 240-60-00, with all the P_2O_5 and half of the nitrogen applied in planting, followed by the remaining nitrogen in the first supplementary irrigation. The experiments were kept free of weeds and diseases by applying pesticides at the times recommended for the region (Solís Moya *et al.,* 2013). The experimental and useful plot consisted of two double rows, each one 3 m long with a separation of 75 cm.

Genetic material

The genotypes evaluated were Salamanca S75, Cortazar S94, Bárcenas S2002, Urbina S2007, Alondra F2014 and Cisne F2016, released in 1975, 1994, 2002, 2007, 2014 and 2016, respectively. The first four contain weak gluten and the last two, strong gluten. All varieties have been planted in over 20 thousand hectares, according to INIFAP's basic seed sale, with the most prominent being Salamanca S75 and Cortazar S94, planted in more than 500 thousand hectares.

Irrigation schedules

The six genotypes were evaluated under three irrigation schedules: two irrigations after 0 and 55 days, three after 0-45 and 75 days and four irrigations after 0-45-75 and

100 days after planting. The irrigation depths applied were 14 cm for the planting irrigation and depths of 10 cm for the supplementary irrigations, resulting in total irrigation depths of 24 cm, 34 cm, and 44 cm for the two, three and four irrigation schedules, respectively.

Experimental design

The experimental design was a randomized complete block with a split-plot arrangement and three replications per year. Factor A were the years, consisting of five levels (2016-2017 to 2020-2021). Factor B consisted of the irrigation schedules, which had three levels: 2, 3 and 4 irrigations. Factor C was the varieties, which included six levels (Salamanca S75, Cortazar S94, Bárcenas S2002, Urbina S2007, Alondra F2014 and Cisne F2016). The data obtained were subjected to a combined analysis of variance for the variables measured using the model proposed by McIntosh (1983).

Variables studied

The measured variables were: 1) plant height (PH), measured in cm from the base to the apex of the spike; 2) days to heading (HD), from the day of irrigation to the total emergence of spikes in at least 50 % of plants; 3) days to physiological maturity (MD) from the planting irrigation to when the plant peduncles turn yellowish; and 4) grain yield (GY), estimated in kg ha^{-1}. For the 2019-2020 and 2020-2021 cycles, the following variables were also estimated: 5) harvest index (HI), calculated as the ratio SGY/BSY, where SGY is the grain yield of 25 stalks from the plot, and BSY is the biological yield of 25 stalks from the plot; 6) biomass (BIO t ha^{-1}), calculated as GY t ha^{-1}/HI; 7) spikes per meter squared (SM2), equal to BIO g m^2/BSY in g; 8) grain weight (TKW, in g), obtained from the weight of 1000 grains; 9) grains per square meter (KNO), equal to GY g m^2/ grain weight in mg.

Analysis of the information

A principal components analysis was carried out using the package FactoMIneR (Lê *et al.*, 2008) with the PCA function, using the correlation matrix. To obtain the visualization based on ggplot2 (Wickham, 2016) the factoextra package was used (Kassambara and Mundt, 2020) with the function fviz_pca_biplot; both packages were executed in the free software R, version 4.1.1 (R Core Team, 2022). Combined analyses of variance were conducted across years of evaluation using the GLM procedure found in the software SAS, version 9.3. In order to analyze the genotype by environment interaction, the SREG biplot model was used for the yield trait using the metan-package function library version 1.12.0 (Olivoto and Lucio, 2020) under the program R, version 4.1.1 (R Core Team, 2022). The statistical model to estimate the genetic advancement was linear regression ($y=b_o + b_1X$), in which the response variables were PH, HD, MD and GY, and the explanatory was the year of release of each one of the varieties included in the study. The genetic progress regression figures were generated using the program Excel, version 16.7167.2062. To obtain the rate or percentage of genetic gain, the value of the coefficient of regression was divided by the value of the intercept, and the result was multiplied by one hundred (Molina, 1992).

$$ag = \frac{b_{y/x}}{y_0}\ 100$$

where:
ag = genetic advancement
$b_{y/x}$ = coefficient of regression
y_0 = intercept

RESULTS AND DISCUSSION

Principal components analysis

The eigenvalues of the correlation matrix showed that the first two principal components represent 72.3 % of the total variation (PC1 55.2 % and PC2 17.1 %). The results of the eigenvectors show that the first main component (PC1) had a positive association with original variables BIO, GY and MD. The second component (CP2) displayed a negative association with variables HI and TKW, and a positive one with PH (Figure 1).

A greater genotype variation was observed in CP1 than in CP2, since, as the number of irrigations increased, the differences in BIO, GY and MD were greater than the differences observed in HI, TKW and PH. Likewise, a greater variation was observed in HI, TKW and PH under restricted irrigation (2 and 3 irrigations) compared to normal irrigation (4 irrigations). In all three irrigation schedules, the genotypes which showed the highest values for BIO, GY and MD were Cisne F2016 and Alondra F2014, while the lowest values were registered for Urbina S2007 in the two-irrigation schedule, and Salamanca S75 in the three- and four-irrigation schedules. For all three irrigation schedules, the genotype that recorded the highest yield (Cisne F2016) had the lowest values for HI and TKW and the highest values for PH. In all three irrigation schedules, the variety Cortazar S94 obtained the highest values for HI and TKW and the lowest PH.

A high association rate was observed between GY and BIO, and a lower one with KNO, MD, PH, HI and TKW (Table 1). Diverse studies have shown a high association rate between yield and biomass in wheat, and they point out that a higher production of biomass could be the main cause of increases in yield in modern cultivars (Baye *et al.,* 2020). In this case, a higher yield and biomass may be related to a higher number of KNO and TKW, rather than with plant height. More increases in yield are expected because of the improvement of the biomass via the integration of modern genomic tools and a better understanding of physiological processes (Yadav *et al.,* 2017). The high positive association between yield and days to maturity was observed in the evaluation of the material under restricted irrigation; in these environments, the

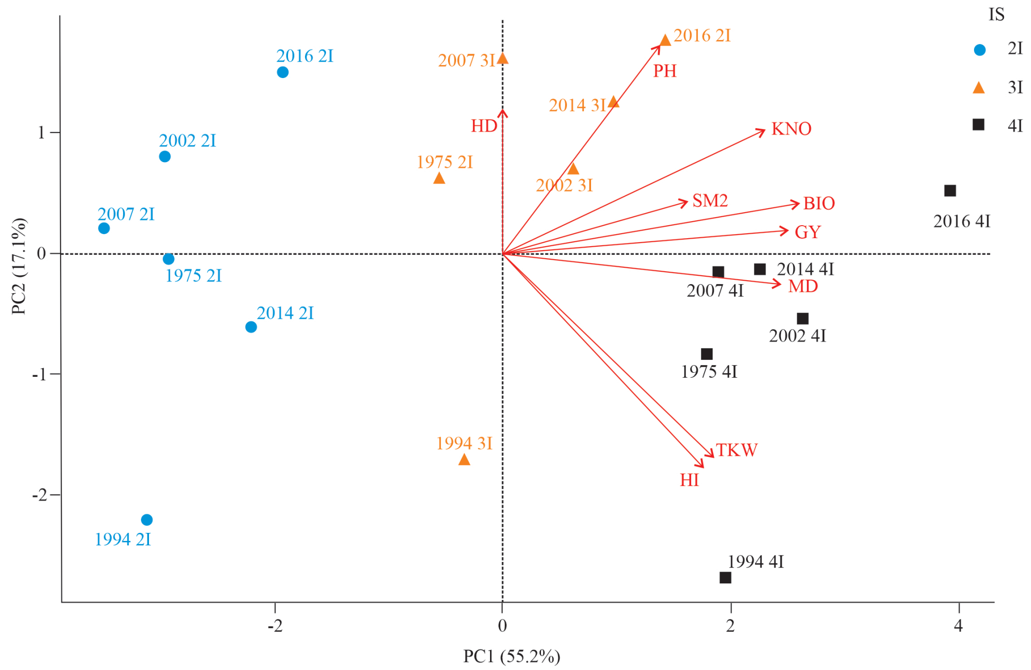

Figure 1. Biplot of the agronomic traits evaluated in six wheat (*Triticum aestivum* L.) varieties evaluated in three irrigation schedules during the autumn-winter 2019-2020 and 2020-2021 cycles. The codes 2I, 3I and 4I correspond to the performance of genotypes with 2, 3 and 4 irrigations. Thus, 1975 2I, 1975, 3I and 1975 4I represent the performance of Salamanca S75 with 2, 3 and 4 irrigations, and 1994, 2002, 2007, 2014, and 2016 with 2I, 3I and 4I, represent the performance of Cortazar S94, Bárcenas S2002, Urbina S2007, Alondra F2014 and Cisne F2016 in the three irrigation environments. HD = days to heading, PH = plant height, KNO = grains per square meter, SM2 = spikes per square meter, BIO = biomass, GY = grain yield, MD = days to maturity, TKW = weight of one thousand grains, HI = harvest index.

materials with a greater cycle registered a higher yield. The positive association between GY and KNO is due to the increase in the number of grains per spike and the number of grains per spikelet, though not to an increase in the number of spikelets per spike, which shows a negative association with yield (Philipp *et al.*, 2018). The association observed between GY and TKW was lower than the one observed with KNO. This low association between these factors was also reported by Rebetzke *et al.* (2016). A high positive association was also observed between HI and TKW, which may be due to the genotypes under restricted irrigation as a survival strategy reduce the production of vegetative organs and increase the amount of assimilates in the grain, increasing HI and TKW; this association was also documented by Rebetzke *et al.* (2016) indicating that increases in KNO are compensated by reductions in grain weight (Miralles and Slafer, 2007). The reduction in grain weight may possibly respond to a

Table 1. Correlation matrix across irrigation schedules among the variables measured in the study with six wheat (*Triticum aestivum* L.) varieties.

Variable	PH	HD	MD	GY	TKW	HI	BIO	KNO	SM2
PH	1	0.17	0.38	0.59**	0.06	-0.01	0.56*	0.58**	0.04
HD		1	0.25	-0.19	0	-0.16	-0.01	-0.08	0.04
MD			1	0.79**	0.75**	0.64**	0.86**	0.67**	0.58**
GY				1	0.58**	0.59**	0.94**	0.86**	0.41
TKW					1	0.85**	0.57**	0.24	0.23
HI						1	0.52*	0.35	0.19
BIO							1	0.92**	0.64**
KNO								1	0.64**
SM2									1

PH = plant height, HD = days to heading, MD = days to maturity, GY = grain yield, TKW = grain weight, HI = harvest index, BIO = biomass, KNO = grains per square meter, SM2 = spikes per square meter.

higher proportion of grains found in distal positions within the spikelets or within spikes in secondary tillers (Miralles and Slafer, 2007). These associations indicated by the angle of the vectors of the main component biplot was accurate among the highly correlated variables, although their precision was lower among low-association variables (Figure 1).

In the analysis of variance through cycles and irrigation schedules, highly significant differences ($p \leq 0.01$) were found among years (CYCLE) for all the variables evaluated, since years are a factor of random effects and indicate the variability between them. Highly significant differences ($p \leq 0.01$) were found between irrigation schedules (IS) in the variables PH, MD and GY, and differences ($p \leq 0.05$) in HD, which proves that the number of risks has a strong influence on the manifestation of differences between the variables. Likewise, highly significant differences ($p \leq 0.01$) were observed among varieties (VAR) for all variables, indicating the existence of genotypic variation for the variables evaluated (Table 2).

Highly significant differences ($p \leq 0.01$) were found in the cycle by irrigation schedule interaction (CYCLE*IS) in the variables of PH, MD and GY. These results show that the environment of the years was different, hence the variation in terms of irrigation calendars applied to the crop. As in the cycle by variety interaction (CYCLE*VAR), highly significant differences ($p \leq 0.01$) were found in all variables, indicating that the response of the varieties varied differentially among the evaluated cycles, i.e., they displayed a different response pattern when environmental conditions changed, and it may also be due to the genetic potential of the varieties. In the schedule by variety interaction (IS*VAR), highly significant effects were found ($p \leq 0.01$) for the variable GY, as well as differences ($p \leq 0.05$) in variable MD. This may be attributed to

Table 2. Mean squares of the analysis of variance of the evaluated variables of six bread wheat (*Triticum aestivum* L.) varieties evaluated during the 2016-2017 to 2020-2021 autumn-winter cycles in three irrigation schedules (2, 3 and 4 irrigations).

Attribute	Mean square				
SV	DF	PH	HD	MD	GY
CYCLE	4	2799.7 **	721.8 **	1200.9 **	31503207 **
BLOQUES	2	72.1	38.4	12.2	323459
Error A	8	53.7	13.7	2.6	227384
IS	2	729.6 **	58.8 *	1280.7 **	91498897 **
CYCLE*IS	8	87.4 *	17.7 ns	95.3 **	2744517 **
Error B	20	27.6	10.9	2.5	220754
VAR	5	1112.8 **	177.1 **	25.6 **	13891653 **
CYCLE*VAR	20	81.7 **	25.2 **	20.5 **	2042046 **
IS*VAR	10	27.7 ns	3.3 ns	5.6 *	513885 **
CYCLE*IS*VAR	40	25 ns	4 *	2.7 ns	307154 *
Residual error	150	23.2	2.5	2.9	188881
Total	269				
Mean		90.2	78.6	132.1	5901
CV_{cycle} (%)		8.1	4.7	1.2	8.1
CV_{IS} (%)		5.8	4.2	1.2	8
CV_{var} (%)		5.3	2	1.3	7.4

SV = source of variation; DF = degrees of freedom; HD = days to heading; MD = days to maturity; PH = plant height; GY = yield; IS = irrigation schedule; VAR = varieties; CV = coefficient of variation; **=highly significant differences ($p \leq 0.01$); *=significant differences ($p \leq 0.05$); ns = non-significant differences.

the fact that the potential yield of the varieties differs depending on the year of their release and on the responses of these varieties regarding the irrigation schedule. In the second-degree cycle by irrigation schedule by varieties (CYCLE*IS*VAR), significant differences ($p \leq 0.05$) were found in the GY variable.

The analysis of variance generated by three study factors and their interactions showed that the evaluation cycles contributed to a greater extent to the total variation found in the variables PH and HD, since the variability generated surpassed the one generated by the varieties and the irrigation calendars, probably due to the recorded temperatures. In addition, the irrigation schedules were observed to contribute to a greater extent to the total variation detected in the variables MD and GY, i.e., the variability of the yield potential and the maturity of the varieties change in response to the irrigation schedule. Among the interactions, the most important one was CYCLE*VAR, since it displayed highly significant values in all varieties. The coefficients of variation fluctuated from 1.1 to 8.3, which can be considered acceptable.

Analysis of the irrigation schedules by varieties interaction with the grain yield variable

The first two principal components obtained when adjusting the SREG biplot model explained 99 % of the variance of the yield of the six varieties evaluated in three irrigation calendars (Figure 2). In the biplot, the polygon "which won where" was integrated when joining genotypes 2016 (Cisne F2016), 2014 (Alondra F2014), 1975 (Salamanca S75) and 2002 (Bárcenas S2002), which are further away from the origin of the biplot. Thus, the varieties Cortazar S94 (1994) and Bárcenas S2002 are contained in the polygon, without standing out in any cycle (Figure 2A). The vertex genotypes have the longest vectors in their respective directions, which is a measure of their responsiveness in yield to the environments. The vertex genotypes are therefore found among the most sensitive genotypes; the two remaining genotypes respond less in their respective directions. Figure 2A shows that all environments (irrigation schedules) fell within the sector of the vertex genotype 2016 (Cisne F2016), indicating that Cisne F2016 obtained the highest yield across environments (Yan *et al.* 2007). This can be further confirmed in Figures 2B, C and D, where it is evident that Cisne F2016 was the variety with the highest yield in all three environments, with a better yield than Alondra F2014. In the three irrigation schedules, Alondra F2014 was second and Salamanca S75 had the lowest grain yield. In the two-irrigation schedule, Urbina S2007 outperformed Bárcenas S2002, although it was inferior in the three- and four-irrigation schedules. These results show that the strategy of evaluating the genetic material in restricted and normal irrigation environments helps select water use efficient genotypes that stand out for yield, both in normal or restricted irrigation environments. This breeding method has been successful in wheat (Griffiths, *et al.*, 2020) and barley (Rizza *et al.*, 2004).

Genetic advancement in yield and agronomic traits

The genetic advancement models for HD and MD resulted not significant in the three irrigation calendars, indicating that since 1975 these parameters have not changed in the recently released varieties, since within the range of earliness of the evaluated materials, the main objective of the selection was to increase yield, without widening the phenological stages, since the farmers of the El Bajío region plant two crops a year. The selection of early materials avoids the shift of optimum planting dates and the profitability of the crop pattern in the region (Table 3 and Figure 3).

For grain yield, the genetic progress obtained was 26.3, 41.6 y 37.6 kg ha^{-1} year^{-1} for the two, three and four irrigation schedules, respectively. Despite the genetic gains in yield vary, this variation is due mainly to varieties and its response to different environmental conditions, therefore the new genotypes must have the genes required for an appropriate yield, as well as being efficient in responding favorably to the environment. Some of the highest genetic gains include those reported by Matus *et al.* (2012) in Chile (246 kg ha^{-1} year^{-1}) and by Oury *et al.* (2012) in France (123 kg ha^{-1} year^{-1}) and among the lowest are those reported by Chairi *et al.* (2018) in Spain, with 24 kg ha^{-1}

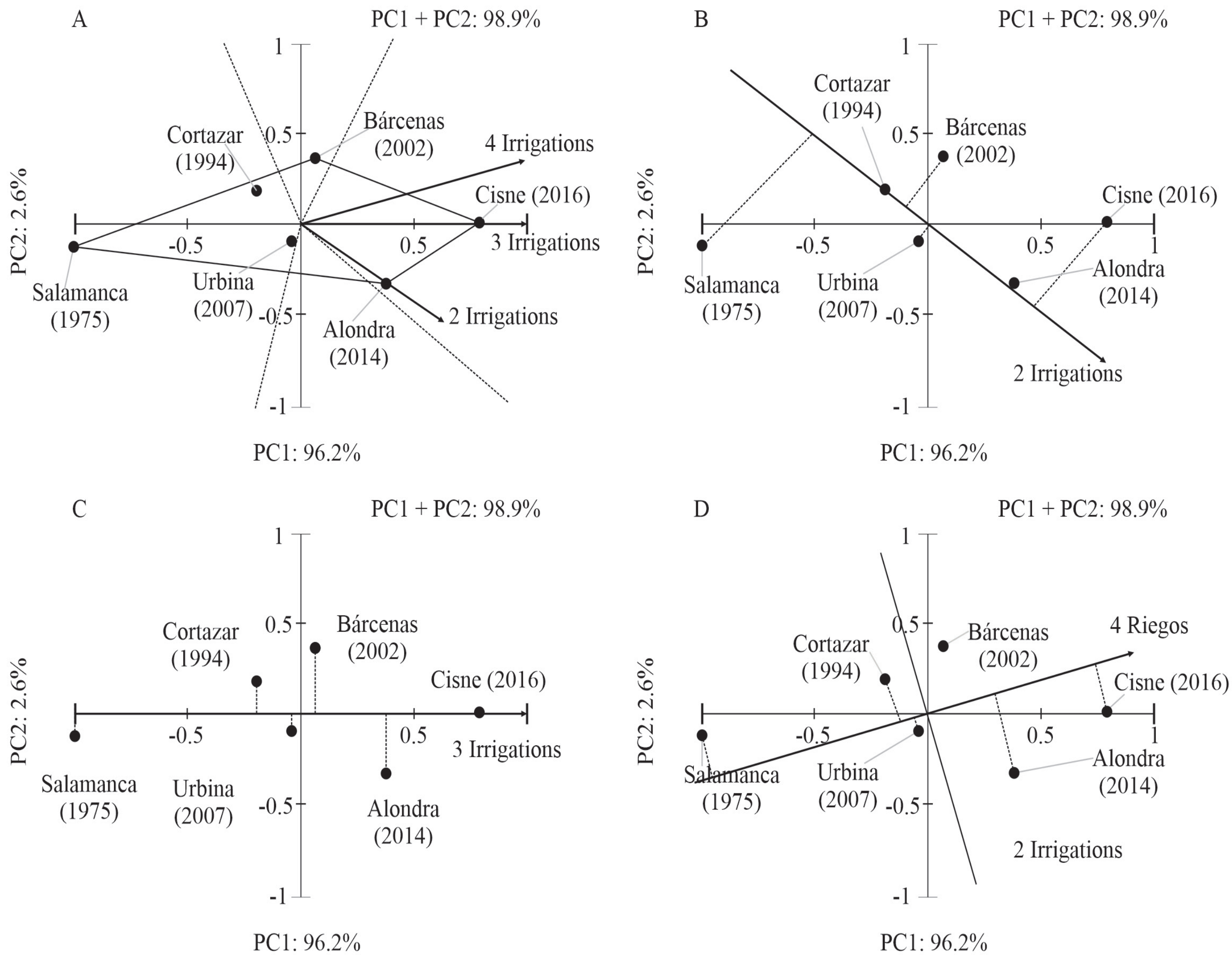

Figure 2. "Which won where" biplot (A) and by irrigation schedule (B) two irrigations, (C) three irrigations and (D) four irrigations, for six varieties of wheat (*Triticum aestivum* L.) evaluated for five agricultural cycles (2016-2017 to 2020-2021). In the figures, years correspond to varieties 1975 = Salamanca S75, 1994 = Cortazar S94, 2002 = Bárcenas S2002, 2007 = Urbina S2007, 2014 = Alondra F2014 y 2016 = Cisne F2016. Numbers 2, 3 and 4 represent the 2, 3 and 4 irrigation environments. In Figure A, all environments were located in the sector of genotype 2016 (Cisne F2016), indicating that this variety was the most prominent across the three environments. Figures B, C and D show the behavior of the varieties in each irrigation schedule (2, 3 and 4 irrigations); in all of these, the most prominent genotype (Cisne F2016) is found to the right.

Table 3. Genetic advancement (ga) in six wheat (*Triticum aestivum* L.) varieties regarding grain yield, plant height, days to heading and days to maturity.

Variable	Irrigation calendar	b	R^2	ga (%)
Yield (kg ha^{-1})				
	2I	26.34**	0.87	0.62
	3I	41.58**	0.96	0.85
	4I	37.57**	0.83	0.65
Plant height (cm)				
	2I	0.21**	0.48	0.24
	3I	0.23**	0.47	0.25
	4I	0.24**	0.42	0.27
Days to heading				
	2I	-0.04	0.10	-0.05
	3I	-0.05	0.15	-0.06
	4I	-0.07	0.23	-0.09
Days to maturity				
	2I	-0.02	0.07	-0.01
	3I	0.02	0.09	0.01
	4I	-0.02	0.20	-0.02

b = Estimated coefficient of regression; ga % = Genetic advancement; R^2 = Coefficient of determination; ** = Value *p* of the highly significant model; there is evidence indicating that the time of selection helps explain the increases in the variables.

year^{-1}. Genetic progress in yield has been reported as lower in low-yield environments (Manes *et al.*, 2012; Gerard *et al.*, 2020), which coincides with the results from this study, in which the two-irrigation schedule displayed an advancement 36.8 and 30.0 % lower than those obtained in the three- and four-irrigation calendars, although in this paper, the genetic advances obtained with three irrigations were 9.6 % higher than those obtained from the four-irrigation schedule, indicating that in intermediate environments, genetic progress has been greater than the one obtained in optimum environments, as reported by Crespo-Herrera *et al.* (2017) and Paquini *et al.* (2016).

In order to fulfill the demands of a growing population, average wheat yields must have a yearly growth of 1.3 % year^{-1} until 2050 (Rosegrant and Agcaoili, 2010). However, the results of our investigation and of most studies that have only included recently released varieties in their evaluations report growth rates lower than 1 %. These results suggest that the strategies used must help reach the genetic progresses imposed by the growing population. The use of selection assisted by molecular markers, based on physiological characteristics may contribute to overcoming this problem.

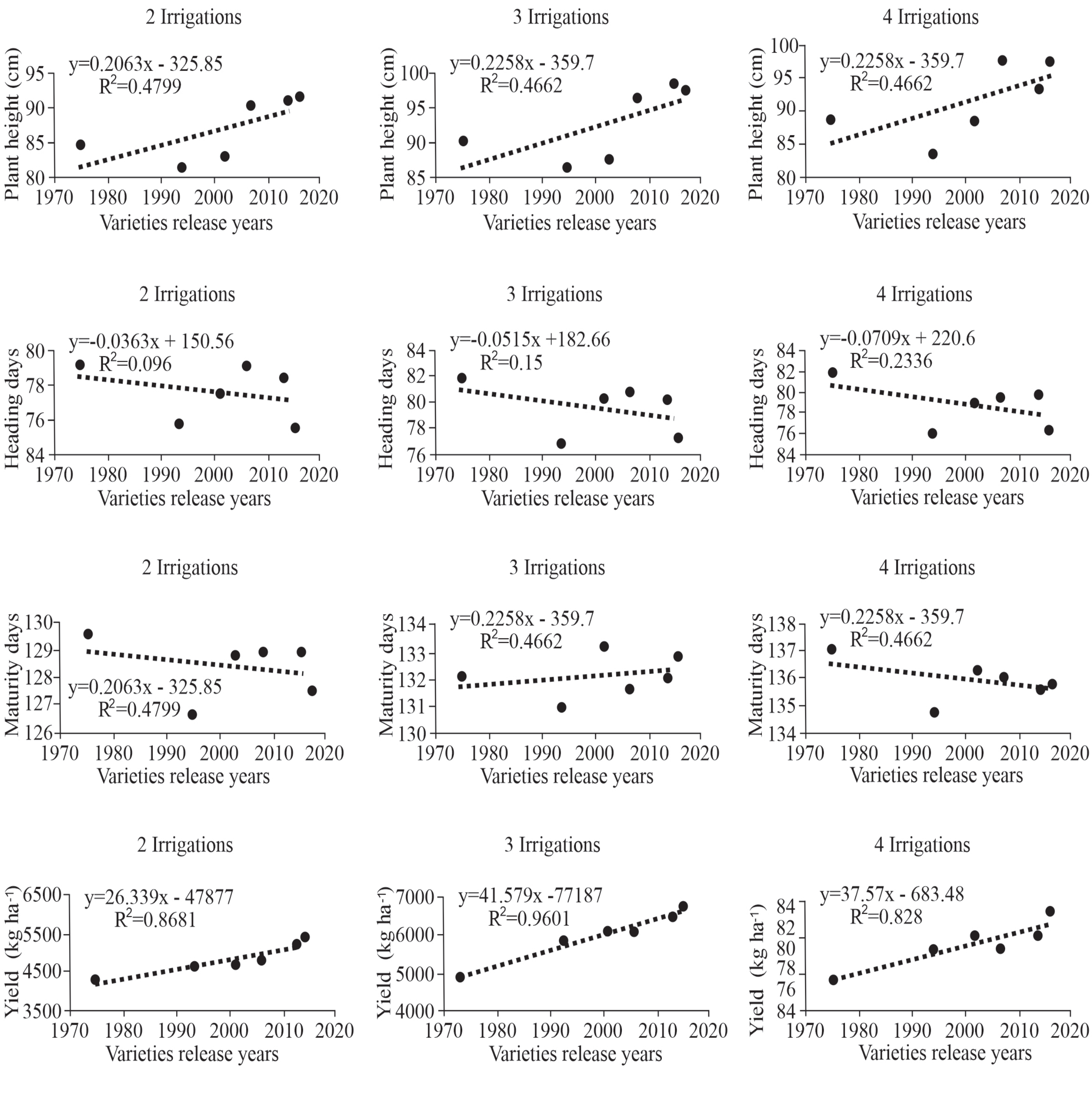

Figure 3. Genetic advancement (ag) in six wheat (*Triticum aestivum* L.) varieties regarding the variables plant height, days to heading, days to maturity and grain yield in bread wheat developed for El Bajío, under three humidity conditions: 2, 3 and 4 irrigations.

CONCLUSIONS

Gains in wheat yield for the two-, three- and four- irrigation schedules were 26.3, 41.6 and 37.6 kg ha^{-1} year^{-1}, which, as of the release of the variety Salamanca S75 in 1975, represented a cumulative increase of 1078, 1706 and 1542 kg ha^{-1}, respectively. This genetic progress was related to an increase in biomass, particularly with a higher number of spikes and grains per m^2.

The varieties Alondra F2014 and Cisne F2016 were higher than predicted under the three irrigation schedules, therefore gains can be obtained simultaneously in yield under normal and restricted irrigation.

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