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INTERVARIETAL CROSSES, AN ALTERNATIVE FOR INCREASING YELLOW MAIZE (*Zea mays* L.) PRODUCTION IN VARIABLE ENVIRONMENTS

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ABSTRACT

In Mexico, maize (*Zea mays* L.) is grown under rainfed conditions within immensurable number of variable environments that limit production. To cope with these adversities, genotypes of different genetic constitution have been generated, such as intervarietal crosses; however, knowledge of the yield potential of those crosses in variable environments is limited. The objective of the study was to determine the yield potential of intervarietal crosses of yellow maize in environments of high-valley lands in central Mexico, as well as the components that influence yield under the hypothesis that intervarietal crosses are equal in yield to conventional hybrids. Crosses, open-pollinated parental varieties and commercial controls were evaluated in a randomized complete block design. Fifteen agronomic variables and yield components were measured. A combined analysis of variance and comparison of means (Tukey, $p \leq 0.05$) were applied, and Pearson's correlation coefficients were calculated. The analysis of variance detected statistical differences in all the factors of variation in most of the evaluated variables. The intervarietal crosses performed statistically equal to the controls but superior to the parents. The crosses excelled in ear diameter and ear length, total weight of grains in the ear, 100-grain weight, grain length, grain width, plant height, ear height, shelling corn coefficient and prolificacy index. In 23 crosses, the genotype × environment interaction effect was not significant. Intervarietal crosses have yield potential compared to conventional hybrids. Ear and grain traits had the greatest influence on yield. Intervarietal crosses represent an alternative to increase yield and production of yellow maize in the high-valley lands of central Mexico.

Keywords: *Zea mays* L., yield, yield components, agronomic traits, genotype × environment interaction.

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INTRODUCTION

In Mexico, yellow maize (*Zea mays* L.) is mainly used in the livestock and industrial sector, but the volume produced does not meet the national demand and about 70 % is imported (SIAP, 2021). Thus, it is necessary to increase production, either by extending the cultivated area or by increasing yield per area unit. Higher yields can be obtained with improvements in agronomic management or with the development of genotypes through plant breeding (Duvick, 2005). Genetic improvement programs have allowed the development of improved maize genotypes, such as local/traditional open-pollinated varieties (OPV) and hybrids. Regarding hybrids, conventional and non-conventional hybrids can be developed, such as top crosses lines and intervarietal crosses.

In Mexico, the use of conventional hybrids is not adopted on a large scale due to several factors, such as the high cost of acquiring the seed (García-Salazar and Guzmán-Soria, 2015). They are developed for flat areas and fertile agricultural lands (Freshley and Delgado-Serrano, 2020), lack of infrastructure, high demand for inputs and lack of adaptation to diverse environments (Pixley, 2006; García-Salazar y Guzmán-Soria, 2015). Furthermore, there are diverse conditions of climate, rugged orography and soil types that create a mega diversity of environments, micro-regions and ecological niches (Muñoz *et al*., 2009), conditions in which conventional hybrids do not thrive. One of these regions is the high-valley lands of central Mexico, which has variable environments with specific traits that limit crop growth and development, such as short growing season, scarce and poorly distributed rainfall, and low temperature, so it is necessary to adapt the biological cycles of crops to these environmental conditions (Barrales *et al*., 2002) and it is necessary to develop genotypes of wide adaptation and good yield to cope with these conditions.

Intervarietal crosses have been tested under conditions of small valleys, hillsides and not very steep slopes where yields are low and no improved varieties or conventional hybrids are planted; but they have similar or higher yields than in the study region (Palemón *et al*., 2011). In the high-valley lands of Mexico area, the yield potential of yellow maize genotypes has been little studied. Tadeo *et al*. (2012), Espinosa-Calderón *et al*. (2013) and Martínez-Yañez *et al*. (2017) have determined the productive capacity of varietal hybrids and varieties; Hernández-Vázquez *et al.* (2018) evaluated agronomic performance and identified populations as a germplasm source for the development of genotypes with high yield potential.

In the aforementioned studies, intervarietal crosses are highlighted that equal or exceed the yields of the genotypes planted in the area. In regard to the varieties and varietal hybrids, they show good yield, only that the parents (varieties and lines) used are from the same study area. The evaluation and identification of populations is important, but it is necessary to introduce and use, as immediately as possible, the present genetic diversity for the development of higher yielding genotypes for variable environments.

Currently, the demand for yellow maize is not met, conventional hybrids do not thrive in variable environments. There is genetic diversity for use in varieties development, and both the number and knowledge of genotypes adapted to diverse environments is limited. For this reason, more knowledge needs to be generated on responses of genotypes with a broad genetic base suitable for variable environments, precocious, resistant to biotic and abiotic factors, and with yield potential. One promising option is intervarietal crosses between improved varieties from different geographical areas, in order to take advantage of genetic diversity. Therefore, the objective of this research was to determine the yield potential of intervarietal crosses of yellow maize in environments of the high-valley lands in central Mexico, compared with conventional hybrids, open-pollinated varieties and their parental lines, adapted to the high-valley lands; as well as to determine the traits that influence yield. Under the hypothesis that intervarietal crosses are equal in yield to conventional hybrids.

MATERIALS AND METHODS

Experimental sites

The experiment was established in two locations; in Ayapango, State of Mexico (19° 08′ 11″ N and 98° 48′ 30″ O), at 2440 m with mean annual temperature of 14.2 °C and mean annual precipitation of 804.7 mm, and in the Experimental Fields of the Colegio de Postgraduados Campus Montecillo, Montecillo, Texcoco, State of Mexico (19° 27′ 38″ N and 98° 54′ 11″ O), at 2250 m with mean annual temperature of 15 °C and mean annual precipitation of 645 mm.

Plant material

A total of 71 genotypes were used; 56 yellow maize F_1 intervarietal crosses (C-1,.... C-56); the parental lines Reynoso 1 (Prog-1, Synthetic Yellow II from eight parents, temperate climate), Noel 2 (Prog-2, Yellow “Toro Vandeño” race, warm climate), Castillo 4 (Prog-3, a population of the “Chalqueño” race, temperate climate), Noel 3 (Prog-4, “Ocotito” Synthetic Yellow “Cristalinos del Caribe” race, warm climate), Carrera 2 (Prog-5, Chapingo hybrid 622: [4A × 6A] × CML-486), of transitional climate), Reynoso 3 (Prog-6, Sintético Amarillo I from eight parents, temperate climate), Arahón 1 (Prog-7, population HQ-15 25# Sel. Pob. Ama., temperate climate) and AGil 1 (Prog-8, population Tlax-CP-15 CPue-215 Am. Ts., temperate climate); as controls, four white grain F_2 hybrids of HS-2 (Tes-1, Mont-18 99#), H-155 (Tes-2, temperate climate hybrid, from INIFAP), Cherokee (Tes-3, temperate climate hybrid, from Aspros®) and HS-2 (Tes-4, temperate climate hybrid, from Colegio de Postgraduados); and three temperate climate yellow maize open-pollinated varieties (OPV) Castillo 11 (Tes-5), Castillo 12 (Tes-6) and Castillo 13 (Tes-7). White-grained hybrids were chosen because of the absence of yellow-coloured hybrids for comparison with the intervarietal crosses.

Design and experimental unit

The experimental design used was randomized complete blocks with three replicates. The experimental unit consisted of two furrows 5 m long and 0.8 m wide. The distance between plants was 0.5 m. Three seeds were sown per hole and after the thinning to two plants to obtain a density of 55 000 plants per ha.

Agronomic management

In Ayapango, sowing was done on April 28, 2020 under rainfed conditions. The fertilization dose used was 80-40-20 N-P-K with urea (46-00-00), diammonium phosphate (18-46-00) and potassium chloride (00-00-60) in a single application at 45 days after planting (das). At Montecillo, it was planted on May 14, 2020 under rainfed conditions with three relief irrigations during germination, emergence and flowering. The fertilization dose used was 160-80-00 N-P-K with urea (46-00-00) and diammonium phosphate (18-46-00), all the P and half of the N was applied at sowing and the rest of the N at 45 das. In both locations, wild plants control was carried out with an application of PRIMAGRAM® Gold herbicides in pre-emergence and MARVEL® in postemergence, at a rate of 3 L ha^{-1} for each.

Variables evaluated

The variables evaluated were grouped into yield components and agronomic traits, which were measured on five plants, five ears and 10 grains from each ear. Yield components were ear diameter (DM in mm), ear length (LM in cm), number of ear rows (NH), total ear grain weight (PGM in g), 100-grain weight (P100G in g), grain thickness (EG in mm), grain length (LG in cm), grain width (AG in mm), shelling corn coefficient (CD) and grain yield (REN in Mg ha^{-1}). The agronomic traits were days to female flowering (DFF), floral asynchrony (AF), plant height (AP in cm), ear height (AM in cm) and prolificacy index (IP).

Statistical analysis

A combined analysis of variance across environments, a comparison of means among genotypes (Tukey, $p \leq 0.05$) and Pearson correlation coefficients between variables were calculated. All analyses were performed with the statistical package SAS® version 9.4 (SAS Institute Inc., 2014).

RESULTS AND DISCUSSION

Analysis of variance

Across all sources of variation there were statistical differences in most variables in maize genotypes. In the factor Environments there were differences in 10 variables, in the factor Genotypes in all variables and in the interaction genotype × environment (Gen × Env) in 13 variables (Table 1). These results indicate that there is wide diversity in yield components and agronomic traits, due to the effect of the environment, genotypes, their interaction and the use of divergent varieties as parents of intervarietal crosses. The use of genetic diversity allows to identify favourable alleles for genetic improvement (Barrera-Guzmán *et al*., 2020; González-Martínez *et al*., 2020); get to know alternative heterotic patterns (Carena, 2005), which can be exploited for the

Table 1. Mean squares of the combined analysis of variance and significance for agronomic traits and yield components in yellow maize (*Zea mays* L.) crosses, their parents and controls evaluated in two environments.

Variation factor	GL	AP[†]	AM[¶]	AF[§]	DFF[Þ]	IP[¤]	DM[††]	LM[¶¶]
Environments (Env)	1	207523.7**	128725.3**	48.3*	56396**	0.18NS	97.6NS	34.6NS
Blo/Env	4	1545.6**	1111.1**	2.2NS	57.6**	0.04**	15.1**	11.9**
Genotypes (Gen)	70	3305.4**	3479.8**	3.8**	324.3**	0.09**	25.6**	3.5**
Gen × Env	70	505.4**	359.5**	3.2**	34.5**	0.03**	7.5**	1.4*
Error	280	222.1	176.1	1.1	8.5	0.01	3.6	1.1
CV (%)		6.4	11.1	60.4	3.0	10.28	4.2	6.8

Variation factor	NH[§§]	PGM[ÞÞ]	P100G[¤¤]	EG[†††]	LG[¶¶¶]	AG[§§§]	CD[ÞÞÞ]	REN[¤¤¤]
Environment (Env)	51.1 **	33989.5*	170.6NS	0.00095*	0.092**	0.0001NS	0.0388*	82.2**
Blo/Env	0.2 NS	3426.1**	30.6*	0.00006NS	0.004NS	0.0008NS	0.0043**	2.1*
Genotypes (Gen)	8.1 **	2280.6**	116.6**	0.00393**	0.088**	0.0103**	0.0062**	6.1**
Gen × Env	1.1 **	898.7**	27.6**	0.00045NS	0.009**	0.0023**	0.0005NS	3.7**
Error	0.6	367.0	9.9	0.00042	0.003	0.0012	0.0006	0.6
CV (%)	5.5	14.3	10.3	5.00485	4.824	4.0501	2.9812	14.9

GL: degrees of freedom, [†]AP: plant height, [¶]AM: ear height, [§]AF: floral asynchrony, [Þ]DFF: days to female flowering, [¤]IP: prolificacy index, [††]DM: ear diameter, [¶¶]LM: ear length, [§§]NH: number of ear rows, [ÞÞ]PGM: total grain weight of the ear, [¤¤]P100G: 100-grain weight, [†††]EG: grain thickness, [¶¶¶]LG: grain length, [§§§]AG: grain width, [ÞÞÞ]CD: shelling corn coefficient, [¤¤¤]REN: yield, Blo/Env: blocks nested in environments, Gen × Env: genotype × environment interaction, CV: coefficient of variation. NS: non- significant, *: $p \leq 0.05$, **: $p \leq 0.01$.

development of varieties with higher productive potential and wider adaptation (Eze *et al*., 2020; Velasco-García *et al*., 2019).

Yield and yield components

The yield of 73.2 % of the intervarietal crosses evaluated was statistically equal to the controls and superior to the parents, but only the five crosses with higher yield are shown (Table 2). The C-14 cross out-yielded Prog-5 by 187 %, Tes-5 by 53 % and MG by 31 %. The intervarietal crosses show yield potential, due to the similarity with the controls and the marked differences with the parents and with MG.

Conventional hybrids are generally superior in yield compared to other types of unimproved genotypes (Pixley, 2006; Duvick, 2005; Carena, 2005); however, the results of the present study do not agree with the theory. The yield of the intervarietal crosses was statistically equal to the controls, ranging from 5.15 to 7.09 Mg ha^{-1} and was equal to that of conventional hybrids, one OPV and it was superior to all parents. Different genotypes have been found to match or outperform hybrids, such as divergent population hybrids (Carena, 2005); improved OPV (Espinosa-Calderón *et al*., 2013); non-conventional hybrids and OPV (Martínez-Yañez *et al*., 2017); crosses between maize races (Velasco-García *et al*., 2019); population hybrids (Eze *et al*., 2020); experimental single hybrids (Cieza *et al*., 2020). Furthermore, the use of divergent parents tends to increase yield (Moll *et al*., 1965).

Table 2. Yield and yield components of outstanding yellow corn (*Zea mays* L.) crosses evaluated in two environments compared to their parents and controls.

Genotypes	DM[†] (mm)	LM[¶] (cm)	NH[§]	PGM[Þ] (g)	P100G[¤] (g)	EG[††] (mm)	LG[¶¶] (cm)	AG[§§] (mm)	CD[ÞÞ]	REN[¤¤] ($Mg\ ha^{-1}$)
C-14	46.9 a	16.0 a	13.1 c	157.5 a	37.4 a	0.40 b	1.41 a	0.91 a	0.85 a	7.09 a
C-51	46.8 b	15.3 a	13.4 c	151.3 a	35.8 a	0.39 b	1.40 a	0.90 a	0.88 a	7.07 a
C-28	45.7 b	15.8 a	13.9 b	149.5 a	34.3 b	0.41 b	1.32 b	0.89 a	0.86 a	7.06 a
C-35	47.2 a	15.5 a	16.3 a	157.8 a	32.9 b	0.41 b	1.33 b	0.83 b	0.87 a	7.05 a
C-8	46.8 a	15.9 a	14.0 b	144.2 a	30.1 b	0.4 b	1.25 b	0.89 a	0.83 b	6.88 a
Prog-1	44.4 b	15.5 a	14.8 b	121.9 b	28.6 b	0.42 b	1.15 c	0.83 b	0.80 b	4.75 b
Prog-2	43.9 b	13.8 b	13.1 c	78.4 c	22.8 c	0.40 b	1.13 c	0.87 b	0.79 b	2.92 c
Prog-3	38.4 c	13.9 b	12.4 c	97.5 b	26.3 c	0.36 c	1.30 b	0.76 c	0.89 a	3.72 b
Prog-4	41.3 c	14.1 b	13.4 c	84.2 b	22.6 c	0.41 b	1.03 d	0.85 b	0.77 c	3.00 c
Prog-5	43.3 b	12.1 b	16.7 a	70.4 c	18.9 d	0.42 b	0.95 d	0.76 c	0.77 c	2.47 c
Prog-6	42.6 b	15.3 a	14.8 b	108.0 b	27.8 b	0.45 a	1.10 c	0.83 b	0.82 b	3.69 b
Prog-7	46.1 b	15.6 a	13.8 b	130.1 a	32.8 b	0.42 b	1.24 b	0.91 a	0.83 b	4.89 b
Prog-8	45.4 b	13.8 b	13.9 b	130.2 a	34.2 b	0.40 b	1.45 a	0.83 b	0.88 a	4.19 b
Tes-1	46.0 b	14.6 a	16.3 a	148.1 a	31.3 b	0.41 b	1.37 a	0.80 b	0.87 a	6.04 a
Tes-2	46.1 b	14.6 a	16.4 a	124.1 b	24.4 c	0.38 b	1.21 b	0.82 b	0.84 a	6.74 a
Tes-3	45.9 b	15.6 a	14.8 b	144.2 a	34.5 b	0.45 a	1.31 b	0.86 b	0.83 b	6.13 a
Tes-4	46.9 a	15.0 a	16.2 a	157.5 a	33.0 b	0.41 b	1.40 a	0.82 b	0.88 a	7.01 a
Tes-5	48.4 a	15.3 a	14.2 b	156.9 a	41.1 a	0.45 a	1.47 a	0.90 a	0.85 a	4.62 b
Tes-6	51.3 a	16.4 a	16.6 a	174.6 a	36.6 a	0.43 a	1.43 a	0.87 b	0.83 b	5.75 a
Tes-7	48.7 a	15.3 a	13.9 b	148.3 a	42.4 a	0.47 a	1.48 a	0.91 a	0.85 a	4.75 b
MG	45.3	15.5	14.4	133.3	30.5	0.41	1.30	0.86	0.84	5.40

[†]DM: ear diameter, [¶]LM: ear length, [§]NH: number of ear rows, [Þ]PGM: total ear grain weight, [¤]P100G: 100-grain weight, [††]EG: grain thickness, [¶¶]LG: grain length, [§§]AG: grain width, [ÞÞ]CD: shelling corn coefficient, [¤¤]REN: yield, C: crosses, Prog: parents, Tes: controls, MG: overall mean. Means with different letters in the same column are statistically different (Tukey, $p \leq 0.05$).

The yield of the intervarietal crosses indicated that they have potential compared to conventional hybrids, due to the use of divergent parents, which favour the expression of traits that influence higher yield, such as agronomic traits and yield components.

Yield is a quantitative trait and is influenced by the joint expression of different yield components, although the expression of the components varies according to the constitution of the genotype. In the C-14 cross, 77.77 % of the components were expressed, 88.89 % in the controls and 33.33 % in the parents. The yield components with the highest expression in the genotypes evaluated were LM, PGM and CD, which positively and differentially influenced yield (Table 2). Different components are expressed, the most important of which are LM, DM, 200-grain weight, NH and the number of grains per row (Velasco-García *et al*., 2019); the number of grains, speed and duration of grain filling period (Zhang *et al*., 2019); DM, LM, NH (López-Morales *et al*., 2020); LM, DM, NH and number of grains per row (Santiago-López *et al*., 2020). In yellow maize they are LM, NH, grains per row and grains per ear (Espinosa-Calderón *et al*., 2013); CD, NH, ear weight, PGM, LG, AG and number of grains per row (Chura and Tejeda, 2014). Results in this study indicated that all the evaluated yield components had an influence on yield and coincided with those reported by different authors, but in the crosses the most important were DM, LM, PGM, P100G, LG, AG and CD, which translates into large ears and grains, higher proportion of grains per ear and, therefore, higher yield.

Agronomic performance

Agronomic traits, like yield components, positively and differentially influenced higher yield expression, although trait expression varied by genotype. In the C-14 and C-51 crosses, 80 % of the agronomic traits were expressed and 60 % in the controls and parents. The agronomic traits with the highest expression in the genotypes were AP, AF and IP (Table 3). Traits expressed vary, such as spike reduction, more erect leaves, fewer tillers and lower protein percentage (Duvick, 2005); tassel size and tassel branch number (Nardino *et al.*, 2016); days to male flowering and DFF (López-Morales *et al.*, 2020). In yellow maize, days to male flowering, DFF, leaf insertion angle and IP (Chura

Table 3. Agronomic performance of outstanding yellow maize (*Zea mays* L.) crosses evaluated in two environments compared to their parents and controls.

Genotypes	AP† (cm)	AM¶ (cm)	DFF§	AFþ	IP¤	REN†† (Mg ha^{-1})
C-14	253.2 a	150.6 a	93.8 d	3.3 a	1.22 a	7.09 a
C-51	258.1 a	148.7 a	93.3 d	1.8 a	1.16 a	7.07 a
C-28	246.3 a	140.8 b	97.8 c	1.1 b	1.30 a	7.06 a
C-35	230.4 b	126.9 b	93.3 d	1.0 b	1.06 b	7.05 a
C-8	243.9 b	137.0 b	99.6 c	2.0 a	1.25 a	6.88 a
Prog-1	219.0 b	99.8 c	90.6 d	1.5 a	1.10 b	4.75 b
Prog-2	230.1 b	136.9 b	110.0 b	1.8 a	0.99 b	2.92 c
Prog-3	267.2 a	158.4 a	99.3 c	3.0 a	0.90 b	3.72 b
Prog-4	188.4 c	95.9 c	114.0 a	1.6 a	1.14 b	3.00 c
Prog-5	180.3 c	91.0 c	118.0 a	2.1 a	0.94 b	2.47 c
Prog-6	186.3 c	74.1 d	88.8 e	1.5 a	0.97 b	3.69 b
Prog-7	215.3 b	100.5 c	91.5 d	2.5 a	1.04 b	4.89 b
Prog-8	239.8 b	135.7 b	90.6 d	3.6 a	0.81 c	4.19 b
Tes-1	240.5 b	125.7 b	93.1 d	2.0 a	1.20 a	6.04 a
Tes-2	221.7 b	120.1 b	107.0 b	0.1 b	1.42 a	6.74 a
Tes-3	206.7 c	90.7 c	87.0 e	0.0 b	1.19 a	6.13 a
Tes-4	254.9 a	134.1 b	96.0 d	1.6 a	1.36 a	7.01 a
Tes-5	282.2 a	178.5 a	100.0 c	3.8 a	0.77 c	4.62 b
Tes-6	266.1 a	141.8 b	103.0 c	3.3 a	0.88 c	5.75 a
Tes-7	279.5 a	173.2 a	98.1 c	4.0 a	0.75 c	4.75 b
MG	229.3	119.3	97.1	1.7	1.08	5.40

†AP: plant height, ¶AM: ear height, §DFF: days to female flowering, þAF: floral asynchrony, ¤IP: prolificacy index, ††REN: yield, C: crosses, Prog: parents, Tes: controls, MG: overall mean. Means with different letters in the same column are statistically different (Tukey, $p \leq 0.05$).

and Tejeda, 2014); days to male flowering, DFF, AP and AM (Espinosa-Calderón *et al.*, 2013). Results in this study indicated that all the agronomic traits evaluated influenced a greater expression of yield and agree with those reported by other authors, but in the evaluated crosses the most important traits were AP, AM, AF and IP, which translate into larger and more productive plants. Furthermore, they had low DFF values, indicating that they are precocious; this represents an advantage in the decrease of the biological cycle due to the presence of early frosts, late frosts and low temperatures in the study area.

Genotype × Environment interaction on yield

The yield of 23 crosses was statistically equal in both locations, in five parents and two controls, indicating there was no genotype × environment interaction. The yield of the five best crosses was consistent because it did not change from one environment to another (Table 4). Overall, the crosses and parents yielded more in Montecillo and the open-pollinated controls and the hybrid Tes-1 and Tes-4 in Ayapango, while Tes-2 and Tes-3 decreased their yield. Yield behaviour was different for each genotype and

Table 4. Yield performance of outstanding yellow maize (*Zea mays* L.) crosses evaluated in two environments compared to their parents and controls.

Genotypes	Yield (Mg ha^{-1})			
	Montecillo		Ayapango	
C-14	7.10	a	7.08	a
C-51	7.06	a	7.09	a
C-28	7.21	a	6.92	a
C-35	7.99	a	6.11	a
C-8	7.65	a	6.11	a
Prog-1	5.16	b	4.33	b
Prog-2	3.91	b	1.93	c
Prog-3	3.07	b	4.38	b
Prog-4	3.61	b	2.39	c
Prog-5	3.69	b	1.25	c
Prog-6	4.25	b	3.14	b
Prog-7	5.28	b	4.50	b
Prog-8	3.40	b	4.98	b
Tes-1	6.57	a	5.51	a
Tes-2	8.52	a	4.97	b
Tes-3	7.15	a	5.11	b
Tes-4	7.59	a	6.44	a
Tes-5	3.09	b	6.14	a
Tes-6	4.52	b	6.98	a
Tes-7	2.30	c	7.20	a

C: crosses, Prog: parents, Tes: controls. Means with different letters in the same row are statistically different (Tukey, $p \leq 0.05$).

environment individually, but it was not so for the crosses, which proves that they have wide adaptation and yield stability.

The genotype × environment interaction effect on yield stability of genotypes was different, due to the lack of adaptation to the environments evaluated. It varies by the diverse environmental conditions in which they develop; however, stable genotypes have been found as experimental single crosses (Sánchez-Ramírez *et al*., 216); hybrids (Alí *et al*., 2017) and population hybrids (Eze *et al*., 2020). Results in this study indicated that 23 crosses had consistent yields and can be grown in both evaluated locations, which may be attributed to a greater genetic variability that allowed them to ameliorate the effects of the environment, without causing drastic changes in yield, since their parents are divergent. For this reason, it may be assumed that they are widely adapted and have yield stability, that can be used immediately as a first approach to obtain improved genotypes, while genetic improvement is conducted towards obtaining hybrids with a higher level of inbreeding that exceed the yield potentials shown here by the intervarietal crosses.

Correlations

Statistical differences were found in most of the combinations of variables. Positive correlation was observed between REN and DM, LM, NH, PGM, P100G, LG, AG, CD and with all agronomic traits (Table 5). Positive correlations indicate a direct relationship and the higher the correlation, the stronger the association between the variables. The opposite happened with negative correlations, which are associated

Table 5. Pearson correlation coefficients between yield, yield components and agronomic traits in maize (*Zea mays* L.) genotypes.

	AP[†]	AM[¶]	DFF[§]	AF[þ]	CD[¤]	IP[††]	DM[¶¶]	LM[§§]	NH[þþ]	PGM[¤¤]	P100G[†††]	EG[¶¶¶]	LG[§§§]	AG[þþþ]
AM	0.94**													
DFF	-0.55**	-0.40**												
AF	0.03NS	0.09NS	0.25**											
CD	0.54**	0.51**	-0.40**	0.07NS										
IP	0.12NS	0.06NS	-0.10NS	-0.35**	0.07NS									
DM	0.15**	0.09NS	-0.23**	-0.10NS	-0.01NS	0.06NS								
LM	0.18**	0.08NS	-0.33**	-0.23**	0.11NS	0.15**	0.48**							
NH	-0.04NS	-0.12NS	-0.14**	-0.18**	-0.16**	0.10*	0.43**	0.12**						
PGM	0.42**	0.32**	-0.49**	-0.13**	0.46**	0.17**	0.74**	0.72**	0.25**					
P100G	0.36**	0.29**	-0.41**	0.07NS	0.42**	-0.06NS	0.61**	0.43**	-0.14**	0.76**				
EG	-0.26**	-0.31**	-0.07NS	-0.01NS	-0.34**	-0.19**	0.38**	0.22**	0.28**	0.15**	0.33**			
LG	0.56**	0.54**	-0.34**	0.14**	0.71**	-0.03NS	0.38**	0.22**	-0.14**	0.68**	0.75**	-0.17**		
AG	0.04NS	0.03NS	-0.07NS	-0.05NS	-0.07NS	0.03NS	0.46**	0.35**	-0.42**	0.32**	0.57**	0.24**	0.20**	
REN	0.44**	0.31**	-0.46**	-0.31**	0.39**	0.64**	0.43**	0.41**	0.16**	0.66**	0.47**	-0.05NS	0.43**	0.21**

[†]AP: plant height, [¶]AM: ear height, [§]DFF: days to female flowering, [þ]AF: floral asynchrony, [¤]CD: shelling corn coefficient, [††]IP: prolificacy index, [¶¶]DM: ear diameter, [§§]LM: ear length, [þþ]NH: number of rows, [¤¤]PGM: total grain weight of ear, [†††]P100G: weight of 100 grains, [¶¶¶]EG: grain thickness, [§§§]LG: grain length, [þþþ]AG: grain width, [¤¤¤]REN: yield. NS: not significant, *: $p \leq 0.05$, **: $p \leq 0.01$.

in the opposite direction. Variables positively associated with yield are grain weight and grains per ear (Milander *et al*., 2016); chlorophyll content, ears per plant, NH, total dry matter and DM (Ali *et al*., 2017); leaf area index, chlorophyll content and net photosynthesis (Zhang *et al*., 2018); IP, LM, DM and grains per ear row (Velasco-García *et al*., 2019); number of grains (Ruiz *et al*., 2019); ear weight and grain weight (Cieza *et al*., 2020). Similarly, negative associations have been found such as grain protein concentration (Butts-Wilmsmeyer *et al*., 2019). All the variables evaluated are associated with yield and coincide with that reported by those authors. The variables with the highest association with REN were PGM (r = 0.66), P100G (r = 0.47), LG (r = 0.43), IP (r = 0.64) and AP (r = 0.44), the higher the values of these in the genotypes, the higher the yield. The variables with negative correlations with REN were DFF (r = -0.46) and AF (r = -0.31), the higher their values, the lower the yield, because there shall be no synchronization with male flowering. Therefore, traits are differentially associated with yield and between traits.

This research highlights the yield potential of the intervarietal crosses, as they statistically yielded the same as the controls and outperformed their parents. Yield was due to the joint and differentiated expression of yield components and agronomic traits, resulting in large plants with good ear and grain characteristics, and precocious. Furthermore, in the crosses where there was no Gen × Env interaction, they may be assumed to be widely adapted and have stability in yield. For this reason, the development and use of intervarietal crosses as an improved variety to increase yield and production of yellow maize in variable environments is promising.

Another advantage is that seed production is easy and not expensive. The main limitation is that there is no certified seed production of this type of improved plant material. Therefore, it is necessary to join multidisciplinary efforts between institutions and public policies that support the development and promotion of this technology for unfavourable conditions. It is also advisable to evaluate in environments other than those studied, in order to corroborate the outstanding traits of the intervarietal crosses and to generate more knowledge of yield potential in wider sets of conditions.

CONCLUSIONS

The intervarietal crosses have yield potential compared to conventional hybrids (7.09 *vs*. 7.01 Mg ha^{-1}). The characteristics of ear, grain, plant height and prolificacy index had the greatest influence on yield expression. For this reason, intervarietal crosses represent a viable alternative to increase yield and production of yellow maize in variable environments.

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